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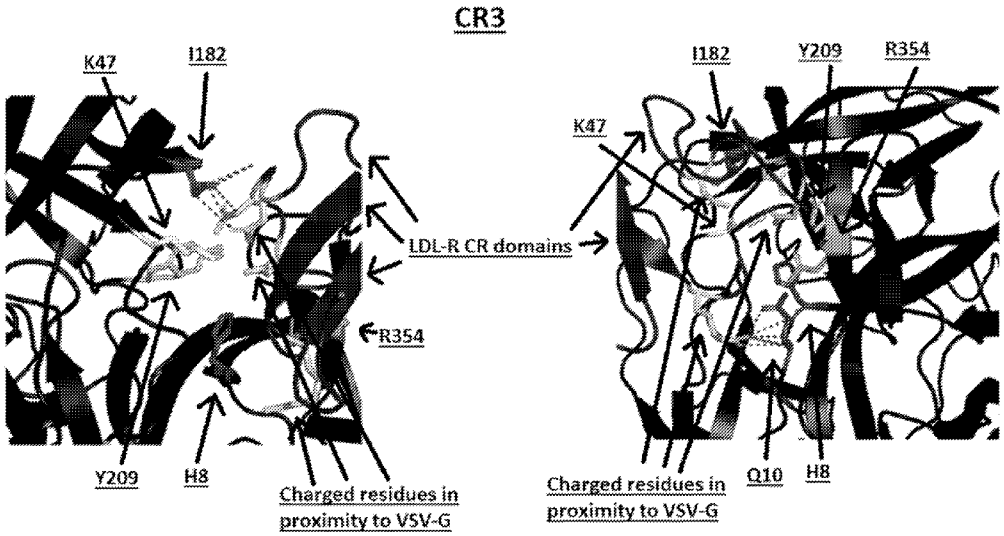


FIG. 1A

(57) **Abstract:** Provided for herein are viral particles comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide comprising a formula of T-S_1, wherein T is a target binding domain and $S_1$is a stalk portion. As provided for herein, the viral particles further comprise a nucleic acid molecule encoding for a heterologous molecule of interest. As provided for herein, the heterologous molecule of interest may be a CD19 CAR. Also provided for herein are compositions comprising the same, and methods of using the same.

WO 2024/258866 A1

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COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNOLOGICAL DISORDERS

RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application Ser. No. 63/507,531 filed June 12, 2023, and of U.S. Provisional Application Ser. No. 63/644,196 filed May 08, 2024, each of which is hereby incorporated by reference in its entirety.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0002] The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on June 6, 2024, is named "INH-029WO_SL" and is 180,160 bytes in size.

FIELD

[0003] Embodiments provided herein relate to viral particles comprising a heterologous viral glycoprotein and a targeting moiety having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. The stalk portion may comprise variant Fc domains. The stalk portion may comprise a flexible peptide domain. The viral particle may further comprise a nucleic acid molecule encoding for a heterologous molecule of interest. The heterologous molecule of interest may be useful in the treatment of a disease or disorder, such as but not limited to an immunological disorder. Embodiments provided herein further relate to compositions comprising the viral particles provided for herein and methods of using the same.

BACKGROUND

[0004] Vesicular stomatitis virus (VSV) is an enveloped, negative-strand RNA virus that belongs to the Vesiculovirus genus of the Rhabdovirus family. It is an arbovirus which can infect insects, cattle, horses and pigs. The VSV genome encodes five structural proteins, among which a single transmembrane glycoprotein (G). The glycoprotein is a classic type I membrane glycoprotein with an amino-terminal signal peptide, an ectodomain of about 450 amino acids, a single alpha helical transmembrane segment and a small intraviral carboxy-terminal domain. The signal peptide is cleaved in the lumen of the endoplasmic reticulum, and the native mature glycoprotein consists of the ectodomain, the transmembrane domain and the intraviral domain.

[0005] G plays a critical role during the initial steps of virus infection (Albertini, A. A. V., Baquero, E., Ferlin, A., and Gaudin, Y. (2012). Molecular and Cellular Aspects of Rhabdovirus Entry. Viruses 4, 117-139.), which is hereby incorporated by reference in its entirety. First, it is responsible for virus attachment to specific receptors. After binding, virions enter the cell by

a clathrin-mediated endocytic pathway. In the acidic environment of the endocytic vesicle, G triggers the fusion between the viral and endosomal membranes, which releases the genome in the cytosol for the subsequent steps of infection. Fusion is catalyzed by a low-pH-induced large structural transition from a pre-toward a post-fusion conformation which are both trimeric (Roche, S., Bressanelli, S., Rey, F. A., and Gaudin, Y. (2006). Crystal structure of the low-pH form of the vesicular stomatitis virus glycoprotein G. Science 313, 187-191. Roche, S., Rey, F. A., Gaudin, Y., and Bressanelli, S. (2007). Structure of the prefusion form of the vesicular stomatitis virus glycoprotein g. Science 315, 843-848), each of which is hereby incorporated by reference in its entirety).

[0006] The polypeptide chain of G ectodomain folds into three distinct domains which are the fusion domain (FD), the pleckstrin homology domain (PHD), and the trimerization domain (TrD). During the structural transition, the FD, the PHD and the TrD retain their tertiary structure. Nevertheless, they undergo large rearrangements in their relative orientation due to secondary changes in hinge segments (S1 to S5) which refold during the low-pH induced conformational change (Roche et al., 2006; Roche et al., 2007).

[0007] It has been shown that low-density lipoprotein receptor (LDL-R) and other members of this receptor family serve as VSV receptors (Finkelshtein, D., Werman, A., Novick, D., Barak, S., and Rubinstein, M. (2013). LDL receptor and its family members serve as the cellular receptors for vesicular stomatitis virus. Proceedings of the National Academy of Sciences of the United States of America 110, 7306-7311, which is hereby incorporated by reference in its entirety). VSV-G can be used for pseudotyping other viruses and VSV-G-pseudotyped lentiviruses (VSV-G-LVs) exhibit the same broad tropism as VSV. However, this broad tropism can inhibit the selective targeting of specific cell types. Therefore, there is a need, for modified (mutated or mutant) VSV-G proteins that can be used to pseudotype viruses that abrogate its binding to the LDL receptor. The present embodiments, fulfill these needs as well as others.

BRIEF SUMMARY

[0008] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety wherein the targeting moiety comprises a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion.

[0009] In some embodiments, the stalk portion S_1 comprises variant Fc protein. In some embodiments, the variant Fc protein comprises a transmembrane domain, such as, but not

limited to, a CD8 or CD28 transmembrane domain. In some embodiments, the variant Fc protein comprises an effector mutation, wherein the effector mutation inhibits the interaction between the Fc protein and a Fc interacting protein, such as FcγR, C1q, FcRβ, or FcRn.

[0010] In some embodiments, the variant Fc protein is a variant IgG1 Fc protein comprising one or more mutations selected from the group consisting of : L234A, L235A, N297A, P329G, I253A, H310A, and H435A.

[0011] In some embodiments, the variant IgG1 Fc protein comprises an amino acid sequence having at least 80% identity to SEQ ID NO: 104, at least 85% identity to SEQ ID NO: 104, at least 90% identity to SEQ ID NO: 104, at least 95% identity to SEQ ID NO: 104, at least 98% identity to SEQ ID NO: 104, or at least 100% identity to SEQ ID NO: 104.

[0012] In some embodiments, the variant Fc protein is a variant IgG2 Fc protein comprising one or more mutations selected from the group consisting of: N297A, P329G, I253A, H310A, and H435A.

[0013] In some embodiments, the variant Fc protein is a variant IgG4 Fc protein comprising one or more mutations selected from the group consisting of: S228P, L235E, N297A, P329G, I253A, H310A, and H435A.

[0014] In some embodiments, the targeting moiety having the formula T-S_1 comprises a stalk portion S_1 having a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker or absent, Fc is a variant Fc protein, L_2 is a linker or absent, and X_1 is a polypeptide comprising the transmembrane domain, wherein the targeting moiety having the formula T-S_1 has a formula of T-L_1-Fc-L_2-X_1.

[0015] In some embodiments, the polypeptide comprising the transmembrane domain (X_1) comprises a polypeptide having a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or is absent; T_M is a transmembrane domain of a transmembrane protein; and ICD is an intracellular domain or a protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or is absent; wherein the targeting moiety having the formula of T-L_1-Fc-L_2-X_1 has a formula of T-L_1-Fc-L_2-ECD-T_M-ICD.

[0016] In some embodiments, the stalk portion S_1 comprises a formula of L_3-X_1, wherein L_3 is a flexible peptide linker, and X_1 is a polypeptide comprising a transmembrane domain; wherein the targeting moiety having the formula T-S_1 has a formula of T-L_3-X_1.

[0017] In some embodiments, the polypeptide comprising the transmembrane domain (X_1) comprises a polypeptide having a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or is absent; T_M is a transmembrane domain of a transmembrane protein; and ICD is an intracellular domain or a protein that

facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or is absent; wherein the targeting moiety having the formula of T-L_3-X_1 has a formula of T-L_3-ECD-T_M-ICD.

[0018] In some embodiments, the targeting moiety binds to CD7. In some embodiments, the targeting moiety comprises a polypeptide having a heavy chain variable region comprising a HCDR1 of SEQ ID NO: 30, a HCDR2 of SEQ ID NO: 31, and an HCDR3 of SEQ ID NO: 32, or variants of any of the forging. In some embodiments, the targeting moiety comprises a polypeptide having a light chain variable region comprising a LCDR1 of SEQ ID NO: 33, a LCDR2 of SEQ ID NO: 34, and an LCDR3 of SEQ ID NO: 35, or variants of any of the forging. In some embodiments, the heavy chain comprises a heavy chain variable region having at least 90% sequence identity to SEQ ID NO: 36. In some embodiments, the light chain comprises a light chain variable region having at least 90% sequence identity to SEQ ID NO: 37. In some embodiments, the targeting moiety that binds to CD7 comprises a polypeptide having a sequence having at least 90% sequence identity to SEQ ID NO: 38. In some embodiments, the targeting moiety that binds to CD7 comprises a polypeptide having a sequence having at least 90% sequence identity to SEQ ID NO: 39.

[0019] In some embodiments, the targeting moiety binds to CD8. In some embodiments, the targeting moiety comprises a polypeptide having a heavy chain variable region comprising a HCDR1 of SEQ ID NO: 42, a HCDR2 of SEQ ID NO: 43, and an HCDR3 of SEQ ID NO: 44, or variants of any of the forging. In some embodiments, the targeting moiety comprises a polypeptide having a light chain variable region comprising a LCDR1 of SEQ ID NO: 45, a LCDR2 of SEQ ID NO: 46, and an LCDR3 of SEQ ID NO: 47, or variants of any of the forging. In some embodiments, the heavy chain comprises a heavy chain variable region having at least 90% sequence identity to SEQ ID NO: 48. In some embodiments, the light chain comprises a light chain variable region having at least 90% sequence identity to SEQ ID NO: 49. In some embodiments, the targeting moiety that binds to CD8 comprises a polypeptide having a sequence having at least 90% sequence identity to SEQ ID NO: 50. In some embodiments, the targeting moiety that binds to CD8 comprises a polypeptide having a sequence having at least 90% sequence identity to SEQ ID NO: 51.

[0020] In some embodiments, the heterologous viral glycoprotein is a SVCV-G polypeptide as provided for herein.

[0021] In some embodiments, the heterologous viral glycoprotein is a VSV-G polypeptide. In some embodiments, the VSV-G polypeptide comprises substitutions at positions I182, T214, and T352 of SEQ ID NO: 2. In some embodiments, the substitution at position 182 is I182D

or I182E. In some embodiments, the substitution at position 214 is T214N. In some embodiments, the substitution at position 352 is T352A.

[0022] In some embodiments, the viral particle provided for herein further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR. In some embodiments, the CAR comprises an antigen binding domain having a heavy chain variable region having at least 95% identity to SEQ ID NO: 89 and a light chain variable region having at least 95% identity to SEQ ID NO: 90. In some embodiments, the CAR comprises an antigen binding domain having a heavy chain variable region having at least 95% identity to SEQ ID NO: 94 and a light chain variable region having at least 95% identity to SEQ ID NO: 95.

[0023] In some embodiments, the CAR comprises an antigen binding domain having an amino acid sequence having at least 95% identity to SEQ ID NO: 92. In some embodiments, the CAR comprises an antigen binding domain having an amino acid sequence having at least 95% identity to SEQ ID NO: 93. In some embodiments, the CAR comprises an antigen binding domain having an amino acid sequence having at least 95% identity to SEQ ID NO: 96. In some embodiments, CAR comprises an antigen binding domain having an amino acid sequence having at least 95% identity to SEQ ID NO: 97.

[0024] In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99, at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99.

[0025] In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105, at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105.

[0026] In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106, at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106.

[0027] In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107, at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[0028] In some embodiments, a method of infecting a cell is provided. In some embodiments the method comprises contacting the cell with a viral particle as provided for herein.

[0029] In some embodiments, a method of infecting a cell in a subject is provided. In some embodiments, the method comprises administering to the subject a pharmaceutical composition comprising a viral particle as provided for herein.

[0030] In some embodiments, a method of delivering a heterologous molecule of interest to a cell is provided. In some embodiments, the method comprises contacting the cell with a viral particle as provided for herein, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest.

[0031] In some embodiments, a method of delivering a heterologous molecule of interest to a cell in a subject is provided. In some embodiments, the method comprises administering to the subject a viral particle as provided for herein, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest.

[0032] In some embodiments, a method of treating a disease or disorder in a subject is provided. In some embodiments, the method comprises administering to the subject a viral particle as provided for herein, wherein the viral particle comprises a nucleic acid molecule encoding a heterologous molecule of interest to treat the disease or disorder.

[0033] In some embodiments, a method of treating an immune disorder is provided. In some embodiments, the method comprises administering to the subject a viral particle as provided for herein, wherein the viral particle comprises a nucleic acid molecule encoding a heterologous molecule of interest to treat the disease or disorder. In some embodiments, the immune disorder is multiple sclerosis (MS), systemic lupus erythematosus (SLE), systemic sclerosis (SSc), lupus nephritis (LN), warm autoimmune hemolytic anemia (WAHA), primary sclerosing cholangitis (PSC), or IgG4-related disease (IGG4-RD).

[0034] In some embodiments, a method of delivering a heterologous molecule to a target cell is provided. In some embodiments, the method comprises contacting the cell with a viral particle as provided for herein, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule.

[0035] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. . In some embodiments, the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the targeting binding domain comprises a

sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51. In some embodiments, the stalk portion S_1 comprises a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28. In some embodiments, the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A and H435A. In some embodiments, the variant Fc protein further comprises a transmembrane domain comprising a sequence selected from SEQ ID NO: 61 or SEQ ID NO: 62.

[0036] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51. In some embodiments, the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker comprising a sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, or SEQ ID NO: 76, or is absent; Fc is a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28, L_2 is a linker comprising a sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, or SEQ ID NO: 76, or is absent; and X_1 is a polypeptide comprising a transmembrane domain. In some embodiments, the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A and H435A. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain having a sequence selected from SEQ ID NO: 59 or SEQ ID NO: 60, or

is a fragment thereof, or is absent; T_M is a transmembrane domain having a sequence of SEQ ID NO: 61 or SEQ ID NO: 62 or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64, or the ICD is absent.

[0037] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51. In some embodiments, the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker comprising a sequence of SEQ ID NO: 55 or is absent; Fc is a variant Fc protein comprises a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28, L_2 is a linker comprising a sequence of SEQ ID NO: 55 or is absent; and X_1 is a polypeptide comprising a transmembrane domain. In some embodiments, the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A and H435A. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain having a sequence of SEQ ID NO: 60, or a fragment thereof, or is absent; T_M is a transmembrane domain having a sequence of SEQ ID NO: 62 or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64, or the ICD is absent.

[0038] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 23 or SEQ ID NO: 25. In some embodiments, the target binding domain

comprises a of SEQ ID NO: 39. In some embodiments, the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker comprising a sequence of SEQ ID NO: 55; Fc is a variant Fc protein comprising a sequence of SEQ ID NO: 104, L_2 is a linker and is absent; and X_1 is a polypeptide comprising a transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain having a sequence of SEQ ID NO: 60; T_M is a transmembrane domain having a sequence of SEQ ID NO: 62; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63.

[0039] In some embodiments, a viral particle is provided, wherein the viral particle comprises a heterologous viral glycoprotein and a targeting moiety. In some embodiments, the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 23 or SEQ ID NO: 25, having at least 95% identity to SEQ ID NO: 23 or SEQ ID NO: 25, having at least 99% identity to SEQ ID NO: 23 or SEQ ID NO: 25, or having at least 100% identity to SEQ ID NO: 23 or SEQ ID NO: 25. In some embodiments, the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98.

[0040] In some embodiments, a viral particle is provided, wherein the viral particle comprises a heterologous viral glycoprotein and a targeting moiety. In some embodiments, the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 52 or SEQ ID NO: 53, having at least 95% identity to SEQ ID NO: 52 or SEQ ID NO: 53, having at least 99% identity to SEQ ID NO: 52 or SEQ ID NO: 53, or having at least 100% identity to SEQ ID NO: 52 or SEQ ID NO: 53. In some embodiments, the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98.

[0041] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the target binding domain comprises an amino acid sequence of SEQ ID NO: 38 or SEQ ID NO: 39. In some embodiments, the stalk portion S_1 comprises a formula L_3-X_1, wherein L_3 is a flexible peptide linker comprising an amino acid sequence of

SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58 and X_1 is a polypeptide linker comprising a transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent, T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64, or the ICD is absent.

[0042] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the target binding domain comprises an amino acid sequence of SEQ ID NO: 50 or SEQ ID NO: 51. In some embodiments, the stalk portion S_1 comprises a formula L_3-X_1, wherein L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58 and X_1 is a polypeptide linker comprising a transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent, T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64, or the ICD is absent.

[0043] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the target binding domain comprises an amino acid sequence of SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51. In some embodiments, the stalk portion S_1 comprises a formula L_3-X_1, wherein L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58 and X_1 is a polypeptide linker comprising a

transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent, T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64, or the ICD is absent.

[0044] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the target binding domain comprises an amino acid sequence of SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51. In some embodiments, the stalk portion S_1 comprises a formula L_3-X_1, wherein L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 55, and X_1 is a polypeptide linker comprising a transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent, T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64, or the ICD is absent.

[0045] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 23 or SEQ ID NO: 25. In some embodiments, the target binding domain comprises an amino acid sequence of SEQ ID NO: 39. In some embodiments, the stalk portion S_1 comprises a formula L_3-X_1, wherein L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 55, and X_1 is a polypeptide linker comprising a transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has

a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59, T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

[0046] In some embodiments, a viral particle is provided. In some embodiments, the viral particle comprises a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 52 or SEQ ID NO: 53. In some embodiments, the target binding domain comprises an amino acid sequence of SEQ ID NO: 39. In some embodiments, the stalk portion S_1 comprises a formula L_3-X_1, wherein L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 55, and X_1 is a polypeptide linker comprising a transmembrane domain. In some embodiments, the polypeptide comprising a transmembrane domain (X_1) has a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59, T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

[0047] In some embodiments, the viral particle as provided for herein further comprises a nucleic acid molecule encoding for a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99, at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105, at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106, at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some

embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107, at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

BRIEF DESCRIPTION OF FIGURES

[0048] FIG. 1A and FIG. 1B illustrate crystal structures of VSV-G bound to LDL-R. FIG. 1A illustrates the crystal structure of VSV-G bound to CR3 of the LDL-R. FIG. 1B illustrates the crystal structure of VSV-G bound to CR2 of the LDL-R.

[0049] FIG. 2A and FIG. 2B illustrate the effect of adding negatively charged amino acids to the VSV-G:LDL-R binding interface on native tropism and fusogenicity. FIG.2A illustrates the titration of VSV-G constructs on SupT1 cells. FIG. 2B illustrates functional titer of each construct calculated from the titration in FIG. 2A.

[0050] FIG. 3 illustrates an alignment of the ectodomains of different VSV-G proteins from different strains.

[0051] FIG. 4 illustrates the effect of various VSV-G mutations on the serum stability of viral constructs in combination with a CD7 binder.

[0052] FIG. 5 illustrates the effect of various VSV-G mutations on the serum stability of viral constructs in combination with a CD7 binder.

[0053] FIG. 6 illustrates the ability of various rhabdovirus G proteins to transduce SupT1 and PBMC cells alone or in combination with a CD7 binder.

[0054] FIG. 7A-L show flow cytometry data of human PBMCs transduced with exemplary vectors comprising CD7 binders as disclosed herein.

[0055] FIG. 7M shows flow cytometry data of human PBMCs transduced with exemplary vectors comprising CD7 binders as disclosed herein.

[0056] FIG. 8A-L shows flow cytometry data of non-human primate PBMCs transduced with exemplary vectors comprising CD7 binders as disclosed herein.

[0057] FIG. 8M shows flow cytometry data of non-human primate PBMCs transduced with exemplary vectors comprising CD7 binders as disclosed herein.

[0058] FIG. 9A shows flow cytometry data of human PBMCs transduced with exemplary vectors comprising CD8 binders as disclosed herein.

[0059] FIG. 9B shows flow cytometry data of non-human primate PBMCs transduced with exemplary vectors comprising CD8 binders as disclosed herein.

[0060] FIG. 10A illustrates the ability of VSV-G* pseudotyped lentiviral particles harboring a CD7 binder with a variant Fc stalk to transduce SupT1 cells as well as human and non-human primate PBMCs. FIG 10B illustrates the transduction of cells in the absence of the CD7 binder. FIG. 10C illustrates the transduction of human and non-human primate PBMCs in terms of MOI calculated from SupT1 titration. VSV-G* denotes VSV-G (I182E, T214N, T352A).

[0061] FIG. 11A illustrates the ability of VSV-G* pseudotyped lentiviral particles harboring a CD7 binder with a flexible stalk to transduce SupT1 cells as well as human and non-human primate PBMCs. FIG. 11B illustrates the transduction of cells in the absence of the CD7 binder. FIG 11C illustrates the transduction of human and non-human primate PBMCs in terms of MOI calculated from SupT1 titration. VSV-G* denotes VSV-G (I182E, T214N, T352A).

[0062] FIG. 12A illustrates the ability of viral particles harboring a CD7 binder with flexible stalks of varying length to transduce SupT1 cells in comparison to other IgG based binders. FIG. 12B illustrates the ability of viral particles harboring a CD7 binder with flexible stalks of varying length to transduce activated PBMC cells in comparison to other IgG based binders.

[0063] FIG. 13A illustrates the ability of SVCV-G pseudotyped lentiviral particles harboring a CD7 binder with a variant Fc stalk to transduce SupT1 cells as well as human and non-human primate PBMCs. FIG 13B illustrates the transduction of cells in the absence of the CD7 binder. FIG. 13C illustrates the transduction of human and non-human primate PBMCs in terms of MOI calculated from SupT1 titration.

[0064] FIG. 14A illustrates the ability of SVCV-G pseudotyped lentiviral particles harboring a CD7 binder with a flexible stalk to transduce SupT1 cells as well as human and non-human primate PBMCs. FIG. 14B illustrates the transduction of cells in the absence of the CD7 binder. FIG 14C illustrates the transduction of human and non-human primate PBMCs in terms of MOI calculated from SupT1 titration.

[0065] FIG. 15A-D is a comparison of the ability of VSV-G* pseudotyped lentiviral particles (panels A and B) and SVCV-G pseudotyped lentiviral particles (panels C and D) to transduce SupT1 cells as well as human and non-human primate PBMCs. VSV-G* denotes VSV-G (I182E, T214N, T352A).

[0066] FIG. 16A-D is a comparison of the ability of VSV-G* pseudotyped lentiviral particles (panels A and B) and SVCV-G pseudotyped lentiviral particles (panels C and D) to transduce SupT1 cells as well as human and non-human primate PBMCs. VSV-G* denotes VSV-G (I182E, T214N, T352A).

[0067] FIG. 17A-H illustrate the assessment of off target transduction by VSV-G* pseudotyped lentiviral particles harboring a CD7 binder with a variant Fc stalk delivering a

CD20 CAR (CAR20), CD19 CAR (SEQ ID NO: 107, SEQ ID NO: 105, or SEQ ID NO: 132), or control CAR. FIG. 17A illustrates that the pseudotyped lentiviral particles were able to successfully transduce T cells (SupT1) with all CAR constructs. FIG. 17B illustrates the transduction of the various CAR constructs in Raji B-cells. FIG. 17C illustrates the transduction of the various CAR constructs in DB B-cells. FIG. 17D illustrates the transduction of the various CAR constructs in HT B-cells. FIG. 17E illustrates the transduction of the various CAR constructs in Rec1 B-cells. FIG. 17F illustrates the transduction of the various CAR constructs in Nalm6 B-cells. FIG. 17G illustrates the transduction of the various CAR constructs in JVM13 B-cells. FIG. 17H illustrates the transduction of the various CAR constructs in VL51 B-cells.

[0068] FIG. 18A-B illustrate the ability of CAR19+ PBMCs transduced with a VSV-G* pseudotyped lentiviral particles delivering a CD19 CAR transgene as provided for herein to kill CD19+ B cells. FIG. 18A illustrates the results for Daudi cells. FIG. 18B illustrates the results for Raji cells.

[0069] FIG. 19A-C illustrate that B-cell killing induced by CAR19 expressing T-cells is CD19 dependent. FIG. 19A illustrate the % B-cell killing of Raji-GFP cells, CD19 KO Raji cells, and CD20 KO Raji cells by PBMCs transduced with a CD19 CAR corresponding to SEQ ID NO: 105. FIG. 19B illustrate the % B-cell killing of Raji-GFP cells, CD19 KO Raji cells, and CD20 KO Raji cells by PBMCs transduced with a CD19 CAR corresponding to SEQ ID NO: 107. FIG. 19C illustrate the % B-cell killing of Raji-GFP cells, CD19 KO Raji cells, and CD20 KO Raji cells by PBMCs transduced with a control CD20 targeted CAR.

[0070] FIG. 20A and B illustrate the results of an experiment to assess risk of generating CAR-resistant B cells. FIG. 20A illustrates the ability of CAR19 positive PBMCs to kill Rec-1 cells either expressing the CAR19 or GFP. FIG. 20B illustrates the results of CAR19 assessment of remaining cells.

[0071] FIG. 21A illustrates the experimental design of a mouse model utilized herein.

[0072] FIG. 21B illustrates the level of CAR19 (either SEQ ID NO: 105 or SEQ ID NO: 107) detectable in the blood of mice administered a VSV-G* pseudotyped lentiviral particles harboring a CD7 binder with a variant Fc stalk and the respective CAR19 transgene.

[0073] FIG. 22A and B illustrate B-cell depletion in mice administered a VSV-G* pseudotyped lentiviral particles harboring a CD7 binder with a variant Fc stalk and the respective CAR19 transgene. FIG. 22A illustrates B-cell depletion as measured by percentage of CD19 positive cells in the population of CD45 positive cells. FIG. 22B illustrates B-cell

depletion as measured by percentage of CD20 positive cells in the population of CD45 positive cells.

[0074] FIG. 23A and B illustrate B-cell depletion in select organs of mice administered a VSV-G* pseudotyped lentiviral particles harboring a CD7 binder with a variant Fc stalk and the respective CAR19 transgene. FIG. 23A illustrates B-cell depletion in the spleen of mice as measured by CD19 and CD20 levels. FIG. 23B illustrates B-cell depletion in bone marrow as measured by CD19 and CD20 levels.

DETAILED DESCRIPTION

[0075] Provided for herein are viral particles comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having the formula of T-S_1, wherein T is a target binding domain, and S_1 is a stalk portion. In some embodiments, S_1 comprises a mutant Fc polypeptide that can be, for example, linked to a transmembrane domain as provided for herein. In some embodiments, S_1 comprises flexible polypeptides as provided for herein. The mutant Fc polypeptides or the flexible polypeptides can be incorporated into a viral particle to help facilitate the targeting of the viral particle to a specific cell type.

[0076] Additionally, the viral particle can comprise VSV-G proteins that can be used, for example, to pseudotype a virus, such as a lentivirus. In some embodiments, the pseudotyped viral-like particles are pseudotyped using viral glycoproteins of a vesicular stomatitis New Jersey virus strain, a vesicular stomatitis Indiana virus strain, a vesicular stomatitis Alagoas virus strain, a vesicular stomatitis Maraba virus strain, or a vesicular stomatitis Carajas virus strain. Examples of such proteins are provided for herein.

[0077] The pseudotyped viruses comprising the mutant VSV-G proteins, such as those provided for herein, can be used in conjunction with a targeting moiety to facilitate the fusion of the pseudotyped virus with a specific cell or tissue based on the expression of the target on the cell or the tissue. As provided for herein, the targeting moiety can be linked to a Fc protein, which can be referred to a stalk protein that comprises a transmembrane domain to facilitate the attachment of the targeting moiety to the surface of the virus. In some embodiments, the Fc protein comprises a Fc effector mutation, such as those provided for herein.

[0078] Unless defined otherwise, all technical and scientific terms have the same meaning as is commonly understood by one of ordinary skill in the art to which the embodiments disclosed belongs.

[0079] As used herein, the terms "a" or "an" means that "at least one" or "one or more" unless the context clearly indicates otherwise.

[0080] As used herein, the term "about" means that the numerical value is approximate and small variations would not significantly affect the practice of the disclosed embodiments. Where a numerical limitation is used, unless indicated otherwise by the context, "about" means the numerical value can vary by ±10% and remain within the scope of the disclosed embodiments. Additionally, where a phrase recites "about x to y," the term "about" modifies both x and y and can be used interchangeably with the phrase "about x to about y" unless context dictates differently.

[0081] As used herein, the term "individual" or "subject," or "patient" used interchangeably, means any animal, including mammals, such as mice, rats, other rodents, rabbits, dogs, cats, swine, cattle, sheep, horses, or primates, such as humans.

[0082] As used herein, the terms "comprising" (and any form of comprising, such as "comprise", "comprises", and "comprised"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including, such as "includes" and "include"), or "containing" (and any form of containing, such as "contains" and "contain"), are inclusive or open-ended and do not exclude additional, unrecited elements or method steps. Any step or composition that uses the transitional phrase of "comprise" or "comprising" can also be said to describe the same with the transitional phase of "consisting of" or "consists."

[0083] As used herein, the term "contacting" means bringing together of two elements in an in vitro system or an in vivo system. For example, "contacting" virus or vector described herein with an individual or patient or cell includes the administration of the virus to an individual or patient, such as a human, as well as, for example, introducing a compound into a sample containing a cellular or purified preparation containing the cell.

[0084] As used herein, the term "fused" or "linked" when used in reference to a protein having different domains or heterologous sequences means that the protein domains are part of the same peptide chain that are connected to one another with either peptide bonds or other covalent bonding. The domains or section can be linked or fused directly to one another or another domain or peptide sequence can be between the two domains or sequences and such sequences would still be considered to be fused or linked to one another. In some embodiments, the various domains or proteins provided for herein are linked or fused directly to one another or a linker sequences, such as the glycine/serine sequences described herein link the two domains together.

[0085] A "disease" is a state of health of an animal wherein the animal cannot maintain homeostasis, and wherein if the disease is not ameliorated then the animal's health continues to deteriorate. In contrast, a "disorder" in an animal is a state of health in which the animal is able to maintain homeostasis, but in which the animal's state of health is less favorable than it would be in the absence of the disorder. Left untreated, a disorder does not necessarily cause a further decrease in the animal's state of health.

[0086] "Effective amount" or "therapeutically effective amount" are used interchangeably herein, and refer to an amount of a compound, formulation, material, or composition, as described herein effective to achieve a particular biological result or provides a therapeutic or prophylactic benefit. Such results may include, but are not limited to an amount that when administered to a mammal, causes a detectable level of immune cell activation compared to the immune cell activation detected in the absence of the composition. The immune response can be readily assessed by a plethora of art-recognized methods. The skilled artisan would understand that the amount of the composition administered herein varies and can be readily determined based on a number of factors such as the disease or condition being treated, the age and health and physical condition of the mammal being treated, the severity of the disease, the particular compound being administered, and the like.

[0087] "Encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (i.e., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

[0088] "Expression vector" refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression can be supplied by the host cell or in an in vitro expression system. Expression vectors include all those known in the art, such as cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., Sendai viruses, lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

[0089] As used herein, the phrase "ex vivo" in reference to a cell being transduced, transfected or transformed ex vivo, refers to a cell being transduced, transfected or transformed outside of the subject, that is with the cells being removed from the subject before such cells are transduced, transfected or transformed.

[0090] "Identity" as used herein refers to the subunit sequence identity between two polymeric molecules such as between two nucleic acid or amino acid molecules, such as, between two polynucleotide or polypeptide molecules. When two amino acid sequences have the same residues at the same positions; e.g., if a position in each of two polypeptide molecules is occupied by an Arginine, then they are identical at that position. The identity or extent to which two amino acid or two nucleic acid sequences have the same residues at the same positions in an alignment is often expressed as a percentage. The identity between two amino acid or two nucleic acid sequences is a direct function of the number of matching or identical positions; e.g., if half of the positions in two sequences are identical, the two sequences are 50% identical; if 90% of the positions (e.g., 9 of 10), are matched or identical, the two amino acids sequences are 90% identical.

[0091] By "substantially identical" is meant a polypeptide or nucleic acid molecule exhibiting at least 50% identity to a reference amino acid sequence (for example, any one of the amino acid sequences described herein) or nucleic acid sequence (for example, any one of the nucleic acid sequences described herein). In some embodiments, such a sequence is at least 60%, 80% or 85%, or 90%, 95% or even 99% identical at the amino acid level or nucleic acid to the sequence used for comparison. Other percentages of identity in reference to specific sequences are described herein.

[0092] Sequence identity can be measured/determined using sequence analysis software (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wis. 53705, BLAST, BESTFIT, GAP, or PILEUP/PRETTYBOX programs). Such software matches identical or similar sequences by assigning degrees of homology to various substitutions, deletions, and/or other modifications. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. In an exemplary approach to determining the degree of identity, a BLAST program may be used, with a probability score between e3 and e100 indicating a closely related sequence. In some embodiments, sequence identity is determined by using BLAST with the default settings.

[0093] To the extent embodiments provided for herein, includes composition comprising various proteins, these proteins may, in some instances, comprise amino acid sequences that have sequence identity to the amino acid sequences disclosed herein. Therefore, in certain embodiments, depending on the particular sequence, the degree of sequence identity is preferably greater than 50% (e.g. 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more) to the SEQ ID NOs disclosed herein. In addition to these percentages, other percentages of identity are provided for herein. Identity between polypeptides can be determined by the Smith-Waterman homology search algorithm as implemented in the MPSRCH program (Oxford Molecular), using an affine gap search with parameters gap open penalty – 12 and gap extension penalty = 1.

[0094] These proteins may, compared to the disclosed proteins, include one or more (e.g. 1, 2, 3,4, 5, 6, 7, 8, 9, 10, etc.) conservative amino acid replacements i.e. replacements of one amino acid with another which has a related side chain. Genetically-encoded amino acids are generally divided into four families: (1) acidic i.e. aspartate, glutamate; (2) basic i.e. lysine, arginine, histidine; (3) non polar i.e. alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar i.e. glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In general, Substitution of single amino acids within these families does not have a major effect on the biological activity. The proteins may have one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) single amino acid deletions relative to the disclosed protein sequences. The proteins may also include one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) insertions (e.g. each of 1, 2, 3, 4 or 5 amino acids) relative to the disclosed protein sequences.

[0095] As used herein, the phrase "in vivo" in reference to a cell being transduced, transfected or transformed in vivo, refers to a cell being transduced, transfected or transformed in the subject without the cells being removed from the subject before such cells are transduced, transfected or transformed.

[0096] "Isolated" means altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not "isolated," but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is "isolated." An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

[0097] A "lentivirus" as used herein refers to a genus of the Retroviridae family that is able to infect non-dividing cells. Non-limiting examples of lentiviruses are HIV, SIV, and FIV.

Vectors or viral-like particles derived from lentiviruses can be used to transduce cells and deliver genes or other molecules and have them expressed in a cell either in vitro (ex-vivo) or in vivo.

[0098] By the term "modified" as used herein, is meant a changed state or structure of a molecule or cell as provided herein. Molecules may be modified in many ways, including chemically, structurally, and functionally, such as mutations, substitutions, insertions, or deletions (e.g. internal deletions truncations). Cells may be modified through the introduction of nucleic acids or the expression of heterologous proteins.

[0099] By the term "modulating," as used herein, is meant mediating an increase or decrease in the level of a response in a subject compared with the level of a response in the subject in the absence of a treatment or compound, and/or compared with the level of a response in an otherwise identical but untreated subject. The term encompasses perturbing and/or affecting a native signal or response thereby mediating a beneficial therapeutic response in a subject, such as, a human.

[00100] Unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. The phrase nucleotide sequence that encodes a protein or an RNA may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s).

[00101] The term "oligonucleotide" typically refers to short polynucleotides. It will be understood that when a nucleotide sequence is represented by a DNA sequence (i.e., A, T, C, G), this also provides the corresponding RNA sequence (i.e., A, U, C, G) in which "U" replaces "T."

[00102] "Parenteral" administration of a composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), or intrasternal injection, or infusion techniques.

[00103] The term "polynucleotide" as used herein is defined as a chain of nucleotides. Furthermore, nucleic acids are polymers of nucleotides. Thus, the terms "nucleic acids" and "polynucleotides" as used herein are interchangeable. As used herein polynucleotides include, but are not limited to, all nucleic acid sequences which are obtained by any methods available in the art, including, without limitation, recombinant methods, i.e., the cloning of nucleic acid sequences from a recombinant library or a cell genome, using cloning technology and PCR, and the like, and by synthetic means.

[00104] As used herein, the terms "peptide," "polypeptide," and "protein" are used interchangeably, and refer to a compound comprised of a plurality of amino acid residues

covalently linked by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. "Polypeptides" include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. The polypeptides include natural peptides, recombinant peptides, synthetic peptides, or a combination thereof.

[00105] Unless explicitly stated otherwise, the terms "heterologous viral structural protein" and "heterologous viral glycoprotein" as used herein are used synonymously and interchangeably. Accordingly, unless explicitly stated otherwise, an embodiment referring to a "heterologous viral structural protein" is understood to be referring to a "heterologous viral glycoprotein" and vice versa.

[00106] The term "pseudotyped" or "pseudotyped viral particle", as used herein, refers to a viral particle bearing glycoproteins derived from other viruses having envelopes or a viral vector encoding envelope glycoproteins from a virus that is different from the parental virus. The host range of the vector particles can thus be expanded or altered depending on the type of cell surface receptor used by the glycoprotein. For example, a virus can be pseudotyped with a VSV-G mutant protein as provided for herein.

[00107] By the term "specifically binds," as used herein with respect to an antibody, is meant an antibody which recognizes a specific antigen, but does not substantially recognize or bind other molecules in a sample. For example, an antibody that specifically binds to an antigen from one species may also bind to that antigen from one or more species. But, such cross-species reactivity does not itself alter the classification of an antibody as specific. In another example, an antibody that specifically binds to an antigen may also bind to different allelic forms of the antigen. However, such cross reactivity does not itself alter the classification of an antibody as specific. In some instances, the terms "specific binding" or "specifically binding," can be used in reference to the interaction of an antibody, a protein, or a peptide with a second chemical species, to mean that the interaction is dependent upon the presence of a particular structure (e.g., an antigenic determinant or epitope) on the chemical species; for example, an antibody recognizes and binds to a specific protein structure rather than to proteins generally. If an antibody is specific for epitope "A", the presence of a molecule containing epitope A (or free, unlabeled A), in a reaction containing labeled "A" and the antibody, will reduce the amount of labeled A bound to the antibody. In some embodiments, the targeting moieties described herein that can be used to target the viral particles comprising the mutant

VSV-G protein, or other viral structural proteins used to pseudotype a virus, can specifically bind to their target.

[00108] The term "subject" includes living organisms, including those in which an immune response can be elicited (e.g., mammals). A "subject" or "patient," as used therein, may be a human or non-human mammal. Non-human mammals include, for example, livestock and pets, such as ovine, bovine, porcine, canine, non-human primates, feline and murine mammals. In some embodiments, the subject is human.

[00109] The term "therapeutic" as used herein means a treatment and/or prophylaxis. A therapeutic effect is obtained by suppression, remission, or eradication of a disease state.

[00110] The term "transfected" or "transformed" or "transduced" as used herein refers to a process by which exogenous nucleic acid is transferred or introduced into a cell. A "transfected" or "transformed" or "transduced" cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject cell and its progeny. In some embodiments, the transfection, transformation, or transduction is performed or occurs in vivo.

[00111] To "treat" a disease as the term is used herein, means to reduce the frequency or severity of at least one sign or symptom of a disease or disorder experienced by a subject.

[00112] A "vector" is a composition of matter which comprises an isolated nucleic acid encoding a protein or a peptide. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, plasmids, DNA, and RNA. Examples of viral vectors include, but are not limited to, Sendai viral vectors, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, lentiviral vectors, and the like.

[00113] A "carrier" or "delivery vehicle" includes viral particles, viruses, polylysine compounds, and liposomes, which facilitate transfer of nucleic acid into cells. A carrier or delivery vehicle can also be used to deliver a protein or peptide to a cell.

[00114] Ranges: throughout this disclosure, various aspects of the embodiments can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6.

This applies regardless of the breadth of the range. Unless otherwise explicitly stated to the contrary, a range that is disclosed also includes the endpoints of the range.

Viral Particles Comprising Heterologous Viral Glycoprotein and Targeting Moiety

[00115] In some embodiments, viral particles are provided comprising a heterologous viral glycoprotein and a targeting moiety. In some embodiments, the targeting moiety comprises a polypeptide having the formula T-S_1, wherein T is a target binding domain, and S_1 is a stalk portion. In some embodiments, S_1 comprises a variant Fc protein, wherein the variant Fc protein comprises a transmembrane domain, such as, but not limited to a CD8 or CD28 transmembrane domain. Accordingly, in some embodiments, the stalk portion S_1 comprises an N-terminus to C-terminus orientation of variant Fc – transmembrane domain. In some embodiments, the variant Fc protein comprises an effector mutation, wherein the effector mutation inhibits the interaction between the Fc protein and a Fc interacting protein, such as FcγR, C1q, FcRβ, or FcRn.

[00116] In some embodiments, the S_1 stalk portion is attached to the surface of the viral particle through the transmembrane domain. In some embodiments, the variant Fc protein is a variant of an IgG1 Fc, IgG2 Fc or IgG4 Fc protein. In some embodiments, the variant Fc protein comprises a variant of a sequence of SEQ ID NO: 26 (IgG1 Fc), SEQ ID NO: 27 (IgG2 Fc), or SEQ ID NO: 28 (IgG4 Fc).

[00117] In some embodiments, the variant Fc protein is a variant IgG1 Fc protein (SEQ ID NO: 26). In some embodiments, the variant IgG1 Fc protein comprises one or more of the mutations that corresponds to those selected from the group consisting of: L234A, L235A, N297A, P329G, I253A, H310A, and H435A of SEQ ID NO: 26, numbered according to the EU numbering index of Kabat as described in Edelman, G M et al. "The covalent structure of an entire gammaG immunoglobulin molecule." *Proceedings of the National Academy of Sciences of the United States of America* vol. 63,1 (1969): 78-85. doi:10.1073/pnas.63.1.78, hereby incorporated by reference in its entirety. Any of the mutations L234A, L235A, N297A, P329G, I253A, H310A, and H435A of SEQ ID NO: 26 may be present or absent and the mutations may be combined in any combination. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to L234A and L235A of SEQ ID NO: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to N297A of SEQ ID NO: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to P329G of SEQ ID NO: 26. In some embodiments, the variant

IgG1 Fc protein comprises a mutation that corresponds to L234A, L235A, N297A, and P329G of SEQ ID N: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to I253A of SEQ ID NO: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to H310A of SEQ ID NO: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to H435A of SEQ ID NO: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to I253A, H310A, and H435A of SEQ ID NO: 26. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to L234A, L235A, N297A, P329G, I253A, H310A, and H435A of SEQ ID NO: 26.

[00118] In some embodiments, the variant Fc protein comprising a variant IgG1 Fc protein comprises a truncation of the IgG1 Fc sequence. The truncation can comprise the deletion of any number of amino acids from the N-terminus, the C-terminus, or both of the IgG1 Fc sequence. In some embodiments, the variant Fc protein comprising a variant IgG1 Fc protein comprises a truncation of SEQ ID NO: 26. The truncation can comprises the deletion of any number of amino acids from the N-terminus, the C-terminus, or both of SEQ ID NO: 26. In some embodiments, the truncation comprises the deletion of amino acids from the N-terminus of SEQ ID NO: 26. In some embodiments, the truncation comprises the deletion of amino acids from the C-terminus of SEQ ID NO: 26. In some embodiments, the truncation comprises the deletion of amino acids from both the N-terminus and the C-terminus of SEQ ID NO: 26. In some embodiments, the truncation of SEQ ID NO: 26 comprises an amino acid sequence of SEQ ID NO: 103:

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 103)

[00119] In some embodiments, the variant IgG1 Fc protein comprises one or more mutations relative to SEQ ID NO: 103 selected from the group consisting of: L19A, L20A, N82A, P114G, I38A, H95A, and H220A. It is to be understood that the positions L19, L20, N82, P114, I38, H95, and H220 are in reference to SEQ ID NO: 103 only. The skilled artisan would readily recognize that positions L234, L235, N297, P329, I253, H310, and H435 numbered according to the EU numbering system of Kabat correspond to positions L19, L20, N82, P114, I38, H95, and H220, respectively, of SEQ ID NO: 103. Any of the mutations L19A, L20A, N82A, P114G, I38A, H95A, and H220A of SEQ ID NO: 103 may be present of absent and the mutations may be combined in any combination. In some embodiments, the variant IgG1 Fc

protein comprises a mutation that corresponds to L19A and L20A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to N82A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc comprises a mutation that corresponds to P114G of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc comprises a mutation that corresponds to L19A, L20A, N82A, and P114G of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to I38A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to H95A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to H220A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to I38A, H95A, and H220A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to L19A, L20A N82A, P114G, I38A, H95A, and H220A of SEQ ID NO: 103. In some embodiments, the variant IgG1 Fc protein comprises a mutation that corresponds to each of L18A, L19A N82A, P114G, I38A, H95A, and H220A of SEQ ID NO: 103. An exemplary variant IgG1 protein that comprises each of L18A, L19A N82A, P114G, I38A, H95A, and H220A is shown below in the amino acid sequence of SEQ ID NO: 104:

EPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMASRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLAQDWLNGKEY
KCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNAYTQKSLSLSPGK (SEQ ID NO: 104)

[00120] In some embodiments, the variant Fc protein is a variant IgG2 Fc protein (SEQ ID NO: 27). In some embodiments, the variant IgG2 Fc protein comprises one or more mutations selected from the group consisting of: N297A, P329G, I253A, H310A, and H435A as those position correspond to SEQ ID NO: 27, numbered according to the EU numbering index of Kabat. Any of the mutations N297A, P329G, I253A, H310A, and H435A of SEQ ID NO: 27 may be present or absent and the mutations may be combined in any combination. In some embodiments, the variant IgG2 Fc protein comprises a mutation that corresponds to N297A of SEQ ID NO: 27. In some embodiments, the variant IgG2 Fc protein comprises a mutation that corresponds to P329G of SEQ ID NO: 27. In some embodiments, the variant IgG2 Fc protein comprises a mutation that corresponds to N297A and P329G of SEQ ID NO: 27. In some embodiments, the variant IgG2 Fc protein comprises a mutation that corresponds to I253A of SEQ ID NO: 27. In some embodiments, the variant IgG2 Fc protein comprises a mutation that

corresponds to H310A of SEQ ID NO: 27. In some embodiments, the variant IgG2 Fc protein comprises a mutation that corresponds to H435A of SEQ ID NO: 27. In some embodiments, the variant IgG2 Fc protein comprises a mutation that corresponds to I253A, H310A, and H435A of SEQ ID NO: 27.

[00121] In some embodiments, the variant Fc protein comprising a variant IgG2 Fc protein comprises a truncation of the IgG2 Fc sequence. The truncation can comprise the deletion of any number of amino acids from the N-terminus, the C-terminus, or both of the IgG2 Fc sequence. In some embodiments, the variant Fc protein comprising a variant IgG2 Fc protein comprises a truncation of SEQ ID NO: 27. The truncation can comprises the deletion of any number of amino acids from the N-terminus, the C-terminus, or both of SEQ ID NO: 27. In some embodiments, the truncation comprises the deletion of amino acids from the N-terminus of SEQ ID NO: 27. In some embodiments, the truncation comprises the deletion of amino acids from the C-terminus of SEQ ID NO: 27. In some embodiments, the truncation comprises the deletion of amino acids from both the N-terminus and the C-terminus of SEQ ID NO: 27.

[00122] In some embodiments, the variant Fc protein is a variant IgG4 Fc protein (SEQ ID NO: 28). In some embodiments, the variant IgG4 Fc protein comprises one or more mutations selected from the group consisting of: S228P, L235E, N297A, P329G, I253A, H310A, and H435A as those positions correspond to SEQ ID NO: 28, numbered according to the EU numbering index of Kabat. Any of the mutations S228P, L235E, N297A, P329G, I253A, H310A, and H435A of SEQ ID NO: 28 may be present or absent and the mutations may be combined in any combination. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to S228P of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to L235E of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to N297A of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to P329G of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to S228P, L235E, N297A, and P329G of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to I253A of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to H310A of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to H435A of SEQ ID NO: 28. In some embodiments, the variant IgG4 Fc protein comprises a mutation that corresponds to I253A, H310A, and H435A of SEQ ID NO: 28.

[00123] In some embodiments, the variant Fc protein comprising a variant IgG4 Fc protein comprises a truncation of the IgG4 Fc sequence. The truncation can comprise the deletion of any number of amino acids from the N-terminus, the C-terminus, or both of the IgG4 Fc sequence. In some embodiments, the variant Fc protein comprising a variant IgG4 Fc protein comprises a truncation of SEQ ID NO: 28. The truncation can comprises the deletion of any number of amino acids from the N-terminus, the C-terminus, or both of SEQ ID NO: 28. In some embodiments, the truncation comprises the deletion of amino acids from the N-terminus of SEQ ID NO: 28. In some embodiments, the truncation comprises the deletion of amino acids from the C-terminus of SEQ ID NO: 28. In some embodiments, the truncation comprises the deletion of amino acids from both the N-terminus and the C-terminus of SEQ ID NO: 28.

[00124] In some embodiments, the stalk portion S_1 comprising a variant Fc protein is given by the formula L_1-Fc-L_2-X_1, wherein L_1 is a linker or absent; Fc is the variant Fc protein; L_2 is a linker or absent; and X_1 is a polypeptide comprising the transmembrane domain. Accordingly, the targeting moiety comprising the formula T-S_1 may also be given by the formula T-L_1-Fc-L_2-X_1, wherein: T is a target binding domain; L_1 is a linker or absent; Fc is the variant Fc protein; L_2 is a linker or absent; and X_1 is a polypeptide comprising the transmembrane domain. Therefore, it is to be understood that, in some embodiments, the stalk portion S_1 may be given by the formula L_1-Fc-L_2- X_1. In some embodiments, the target binding domain T is as provided for herein. In some embodiments, the variant Fc protein is as provided for herein.

[00125] In some embodiments, L_1 and L_2 are each, independently, a polypeptide linker. In some embodiments, the polypeptide linker comprises $(GGGGA)_n$ (SEQ ID NO: 54), $(GGGGS)_n$ (SEQ ID NO: 55), $(EAAAK)_n$ (SEQ ID NO: 73), $A(EAAAK)_nA$ (SEQ ID NO: 74), $(XP)_n$ (SEQ ID NO: 75), wherein X is Ala, Lys, or Glu, GSAGSAAGSGEF (SEQ ID NO: 56), KESGSVSSEQLAQFRSLD (SEQ ID NO: 57), EGKSSGSGSESKST (SEQ ID NO: 58), AEAAAKEAAAKA (SEQ ID NO: 76), or a combination thereof, wherein each n is, independently, 1-5. In some embodiments, each n is, independently, 1. In some embodiments, each n is, independently, 2. In some embodiments, each n is, independently, 3. In some embodiments, each n is, independently, 4. In some embodiments, each n is, independently, 5. In some embodiments, each n is, independently, greater than 5. In some embodiments, L_1 is absent. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 1-5. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 1. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein

each n is, independently, 2. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 3. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 4. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 5. In some embodiments, L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, greater than 5. In some embodiments, L_2 is absent. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 1-5. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 1. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 2. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 3. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 4. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, 5. In some embodiments, L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is, independently, greater than 5.

[00126] In some embodiments, X_1 comprises a polypeptide having a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or is absent; T_M is a transmembrane domain of a transmembrane protein; and ICD is an intracellular domain of a protein or a protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or is absent. Accordingly, in some embodiments, the targeting moiety comprising the formula T-S_1 that may also be given by the formula T-L_1-Fc-L_2-X_1 may also be given by the formula T-L_1-Fc-L_2-ECD-T_M-ICD, wherein T is a target binding domain; L_1 is a linker or absent; Fc is the variant Fc protein; L_2 is a linker or absent; ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or is absent; T_M is a transmembrane domain of a transmembrane protein; and ICD is an intracellular domain of a protein or a protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or is absent. Therefore, it is to be understood that, in some embodiments, the stalk portion S_1 may be given by the formula L_1-Fc-L_2- ECD-T_M-ICD.

[00127] In some embodiments, the stalk portion S_1 does not comprise a variant Fc region. In some embodiments, the stalk portion S_1 is given by the formula L_3-X_1, wherein L_3 is a flexible peptide linker and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. Accordingly, in some embodiments, the targeting moiety comprising the formula T-S_1

may also be given by the formula T-L_3-X_1, wherein T is a target binding domain, L_3 is a flexible peptide linker, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. Therefore, it is to be understood that, in some embodiments, the stalk portion S_1 may be given by the formula L_3-X_1. In some embodiments, the S_1 stalk portion is attached to the surface of the viral particle through the transmembrane domain.

[00128] In some embodiments, the flexible peptide linker L_3 may be any flexible peptide linker. In some embodiments, L_3 is selected from the group of flexible linkers including, but not limited to, $(GGGGA)_n$ (SEQ ID NO: 54), $(GGGGS)_n$ (SEQ ID NO: 55), GSAGSAAGSGEF (SEQ ID NO: 56), KESGSVSSEQLAQFRSLD (SEQ ID NO: 57), EGKSSGSGSESKST (SEQ ID NO: 58), or any combination thereof, wherein each n is, independently, an integer selected from 1-4. In some embodiments, each n is, independently, an integer selected from 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, or 1-10. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. In some embodiments, n is 6. In some embodiments, n is 7. In some embodiments, n is 8. In some embodiments, n is 9. In some embodiments, n is 10. In some embodiments, each n is, independently, greater than 10. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 1. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 2. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 3. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 4. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 5. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 6. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 7. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 8. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 9. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 10. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is greater than 10. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 1. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 2. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 3. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 4. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 5. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 6. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 7. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 8. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 9. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 10. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is greater than 10. In some embodiments, L_3 is GSAGSAAGSGEF (SEQ ID NO: 56). In some embodiments, L_3 is

KESGSVSSEQLAQFRSLD (SEQ ID NO: 57). In some embodiments, L_3 is EGKSSGSGSESKST (SEQ ID NO: 58).

[00129] In some embodiments, the flexible peptide linker L_3 may be any flexible peptide linker. In some embodiments, L_3 is selected from the group of flexible linkers including, but not limited to, $(GGGGA)_n$ (SEQ ID NO: 54), $(GGGGS)_n$ (SEQ ID NO: 55), GSAGSAAGSGEF (SEQ ID NO: 56), KESGSVSSEQLAQFRSLD (SEQ ID NO: 57), EGKSSGSGSESKST (SEQ ID NO: 58), or any combination thereof, wherein each n is, independently, an integer selected from 1-4. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 1. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 2. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 3. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 4. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 1. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 2. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 3. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 4. In some embodiments, L_3 is GSAGSAAGSGEF (SEQ ID NO: 56). In some embodiments, L_3 is KESGSVSSEQLAQFRSLD (SEQ ID NO: 57). In some embodiments, L_3 is EGKSSGSGSESKST (SEQ ID NO: 58).

[00130] In some embodiments, L_3 is selected from the group of flexible linkers including, but not limited to, $(GGGGA)_n$ (SEQ ID NO: 54), $(GGGGS)_n$ (SEQ ID NO: 55), GSAGSAAGSGEF (SEQ ID NO: 56), KESGSVSSEQLAQFRSLD (SEQ ID NO: 57), EGKSSGSGSESKST (SEQ ID NO: 58), or any combination thereof, wherein each n is, independently, an integer selected from 1, 2, or 4. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 4. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 1. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 2. In some embodiments, L_3 is $(GGGGA)_n$ (SEQ ID NO: 54) and n is 4. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 1. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 2. In some embodiments, L_3 is $(GGGGS)_n$ (SEQ ID NO: 55) and n is 4. In some embodiments, L_3 is GSAGSAAGSGEF (SEQ ID NO: 56). In some embodiments, L_3 is KESGSVSSEQLAQFRSLD (SEQ ID NO: 57). In some embodiments, L_3 is EGKSSGSGSESKST (SEQ ID NO: 58).

[00131] In some embodiments, X_1 comprises a polypeptide having a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or is absent; T_M is a transmembrane domain of a transmembrane protein; and ICD is an

intracellular domain of a protein or a protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or is absent. Accordingly, in some embodiments, the targeting moiety comprising the formula T-S_1 that may also be given by the formula T-L_3-X_1, may also be given by the formula T-L_3- ECD-T_M-ICD, wherein T is a target binding domain, L_3 is a flexible peptide linker ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or is absent; T_M is a transmembrane domain of a transmembrane protein; and ICD is an intracellular domain of a protein or a protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or is absent. Therefore, it is to be understood that, in some embodiments, the stalk portion S_1 may be given by the formula L_3- ECD-T_M-ICD.

[00132] In some embodiments, the ECD is absent. In some embodiments, the ECD can be any appropriate extracellular domain or fragment thereof. In some embodiments, the ECD is from a different protein as compared to the transmembrane domain. The ECD domain can be the entire ECD domain or a fragment thereof. In some embodiments, the ECD domain is a CD8 or CD28 ECD domain, or a fragment thereof. In some embodiments, the ECD domain is a CD8 ECD domain or fragment thereof. In some embodiments, the CD8 ECD domain comprises the polypeptide of FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 59). In some embodiments, the CD8 ECD domain consists or consists essentially of the polypeptide of FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 59). In some embodiments, the ECD domain comprises a polypeptide that is 25-45 amino acids in length. In some embodiments, the ECD comprises a polypeptide that is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 59). In some embodiments, the ECD domain is a CD28 ECD domain or fragment thereof. In some embodiments, the CD28 ECD domain comprises the polypeptide of KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP (SEQ ID NO: 60). In some embodiments, the CD28 ECD domain consists or consists essentially of the polypeptide of KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP (SEQ ID NO: 60). In some embodiments, the ECD domain comprises a polypeptide that is 25-45 amino acids in length. In some embodiments, the ECD comprises a polypeptide that is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP (SEQ ID NO: 60).

[00133] In some embodiments, the T_M can be any appropriate transmembrane domain or fragment thereof. In some embodiments, the T_M domain is a CD8 or CD28 T_M domain or a fragment thereof. In some embodiments, the T_M domain is a CD8 T_M domain or fragment thereof. In some embodiments, the CD8 T_M domain comprises the polypeptide of IYIWAPLAGTCGVLLLSLVITLYCNHRN (SEQ ID NO: 61). In some embodiments, the CD8 T_M domain consists or consists essentially of the polypeptide of IYIWAPLAGTCGVLLLSLVITLYCNHRN (SEQ ID NO: 61). In some embodiments, the T_M comprises a polypeptide that is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of IYIWAPLAGTCGVLLLSLVITLYCNHRN (SEQ ID NO: 61). In some embodiments, the T_M domain is a CD28 T_M domain or fragment thereof. In some embodiments, the CD28 T_M domain comprises the polypeptide of FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 62). In some embodiments, the CD28 T_M domain consists or consists essentially of the polypeptide of FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 62). In some embodiments, the T_M comprises a polypeptide that is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 62).

[00134] In some embodiments, the T_M domain is from the same protein as the ECD. In some embodiments, the T_M domain is from a different protein as the ECD. In some embodiments, the T_M domain is a CD8, or CD28 T_M domain or a fragment thereof and the ECD domain is a CD8, or CD28 ECD domain or fragment thereof. In some embodiments, the T_M domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of IYIWAPLAGTCGVLLLSLVITLYCNHRN (SEQ ID NO: 61) and the ECD domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 59). In some embodiments, the T_M domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of IYIWAPLAGTCGVLLLSLVITLYCNHRN (SEQ ID NO: 61) and the ECD domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP (SEQ ID NO: 60). In some embodiments, the T_M domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 62) and the ECD domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of

FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 59). In some embodiments, the T_M domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 62) and the ECD domain is at least, or is about, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to a peptide of KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP (SEQ ID NO: 60).

[00135] In some embodiments, the transmembrane domain is linked to an intracellular domain (ICD) of a cellular transmembrane protein, or a fragment thereof. In some embodiments, the ICD is absent. In some embodiments, the ICD is from the same or different protein as the TM domain. In some embodiments, the ICD comprises an Env incorporation motif. An Env incorporation motif is a molecule, e.g., polypeptide, that can help to facilitate the incorporation of a protein into the envelope of the virus. A non-limiting example of an Env incorporation motif is a polypeptide comprising the amino acid sequence of NRVRQGYS (SEQ ID NO: 63). This is a non-limiting example and other peptide sequences can be used, such as, but not limited to, GGTETSQVAPA (SEQ ID NO: 64). In some embodiments, the Env incorporation motif comprises an amino acid sequence of SEQ ID NO: 63, SEQ ID NO: 64, or a combination thereof. In some embodiments, the Env incorporation motif comprises an amino acid sequence of SEQ ID NO: 63. In some embodiments, the Env incorporation motif comprises an amino acid sequence of SEQ ID NO: 64.

[00136] In some embodiments, the target binding domain "T" is any polypeptide or polynucleotide that may be used to bind to a desired target. In some embodiments, T is any polypeptide, polynucleotide, or fragment thereof that binds to CD7, CD8, cKit (CD117), CD4, CD3, CD5, CD6, CD2, TCR alpha, TCR beta, TCR gamma, TCR delta, CD10, CD34, CD110, CD33, CD14, CD68, CCR7, CD62L, CD25, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, or CXCR3, A glycosylated CD43 epitope expressed on acute leukemia or lymphoma but not on hematopoietic progenitors; A glycosylated CD43 epitope expressed on non-hematopoietic cancers; A kinase anchor protein 4 (AKAP-4); Adrenoceptor beta 3 (ADRB3); AFP; Anaplastic lymphoma kinase (ALK); Androgen receptor; Angiopoietin-binding cell surface receptor 2 (Tie 2); Auto antibody to desmoglein 1 (Dsgl); Auto antibody to desmoglein 3 (Dsg3); B7H3 (CD276); Biotin; Bone marrow stromal cell antigen 2 (BST2); BST1/CD157; Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-la); Carbonic anhydrase IX (CA1X); Carcinoembryonic antigen (CEA); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS or Brother of the Regulator of Imprinted Sites); CCR4; CD5; CD19; CD20; CD22; CD24; CD30; CD32 (FCGR2A); CD33; CD34; CD38; CD44v6; CD72; CD79a;

CD79b; CD97; CD99; CD123; CD171; CD179a; CD179b-IGLl1; CD200R; CD276/B7H3; CD300 molecule-like family member f (CD300LF); CDH1-CD324; CDH6; CDH17; CDH19; Chromosome X open reading frame 61 (CXORF61); Claudin 6 (CLDN6); Claudinl8.2 (CLD18A2 or CLDN18A.2); CMV pp65; C-MYC epitope Tag; Cripto; CS1 (also referred to as CD2 subset 1 or CRACC or SLAMF7 or CD319 or 19A24); CSF2RA (GM-CSFR-alpha); C-type lectin domain family 12 member A (CLEC12A); C-type lectin-like molecule-1 (CLL-1 or CLECL1); Cyclin Bl; Cytochrome P450 IB 1 (CYP1B 1); DLL3; EBV-EBNA3c; EGF-bke module- containing mucin-like hormone receptor-like 2 (EMR2); Elongation factor 2 mutated (ELF2M); Ephrin B2; Ephrin type-A receptor 2 (EphA2); Epidermal growth factor receptor (EGFR); Epidermal growth factor receptor variant III (EGFRviii); Epithelial cell adhesion molecule (EPCAM); ERG; ETS translocation-variant gene 6 located on chromosome 12p (ETV6-AML); Fc fragment of IgA receptor (FCAR or CD89); Fc receptor-like 5 (FCRL5); Fibroblast activation protein alpha (FAP); FITC; Fms Like Tyrosine Kinase 3 (FLT3); Folate receptor alpha (FRa or FR1); Folate receptor beta (FRb); Follicle stimulating hormone receptor (FSHR); Fos-related antigen 1; Fucosyl-GMl; G protein coupled receptor class C group 5 member D (GPRC5D); G protein-coupled receptor 20 (GPR20); GAD; Ganglioside G2 (GD2) ; Ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); Ganglioside GM3 (aNeu5Ac(2-3)bDClalp(l- 4)bDGlcp(l-l)Cer); GD3; GFRalpha4; Glycoprotein 100 (gplOO); Glypican-3 (GPC3); Gonadotropin Hormone receptor (CGHR or GR); GpA33; GpNMB; GPRC5D; Guanylyl cyclase C (GCC); Heat shock protein 70-2 mutated (mut hsp70-2); Hepatitis A virus cellular receptor 1 (HAVCR1); Hexasaccharide portion of globoH glycoceramide (GloboH); High molecular weight-melanoma associated antigen (HMWMAA); HIV1 envelope glycoprotein; HLA; HLA-DOA; HLA-A; HLA-A2; HLA-B; HLA-C; HLA-DM; HLA-DOB; HLA-DP; HLA-DQ; HLA-DR; HLA-G; HTLVl-Tax; Human papilloma virus E6 (HPV E6); Human papilloma virus E7 (HPV E7); Human Telomerase reverse transcriptase (hTERT); IgE; IL13Ra2; ILl lRa; Immunoglobulin lambda-like polypeptide 1 (IGLL1); Influenza A hemagglutinin (HA); Insulin-like growth factor 1 receptor (IGF-I receptor); Interleukin 11 receptor alpha (IL-llRa); Interleukin- 13 receptor subunit alpha-2 (IL-13Ra2 or CD213A2); Intestinal carboxyl esterase; KIT (CD117); KSHV K8.1; KSHV-gH; LAMP1 ; Legumain; Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Leutenizing hormone receptor (LHR); Lewis(Y) antigen; Lews Ag; Livl; Locus K 9 (LY6K); Low conductance chloride channel; Lymphocyte antigen 6 complex; Lymphocyte antigen 75 (LY75); Lymphocyte-specific protein tyrosine kinase (LCK); Mammary gland differentiation

antigen (NY-BR-1); Melanoma antigen recognized by T cells 1 (MelanA or MARTI); Melanoma- associated antigen 1 (MAGE-A1); Melanoma cancer testis antigen-1 (MAD-CT-1); Melanoma cancer testis antigen-2 (MAD-CT-2); Melanoma inhibitor of apoptosis (ML-IAP); Mesothelin; MPL; Mucin 1 cell surface associated (MUC1); N-Acetyl glucosaminyl-transferase V (NA17); Nectin-4; Neural cell adhesion molecule (NCAM); NKG2D; NYBR1; O-acetyl-GD2 ganglioside (OAcGD2); Olfactory receptor 51E2 (OR51E2); Oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); P53 mutant; Paired box protein Pax-3 (PAX3); Paired box protein Pax-5 (PAX5); Pannexin 3 (PANX3); PDL1; P-glycoprotein; Placenta-specific 1 (PLAC1); Platelet-derived growth factor receptor beta (PDGFR-beta); Polysialic acid; Proacrosin binding protein sp32 (OY-TES1); Prostase; Prostate carcinoma tumor antigen-1 (PCT A-l or Galectin 8); Prostate stem cell antigen (PSCA); Prostate-specific membrane antigen (PSMA); Prostatic acid phosphatase (PAP); Prostein; Protease Serine 21 (Testisin or PRSS21); Proteasome (Prosome Macropain) Subunit Beta Type 9 (LMP2); PTK7; Ras G12V; Ras Homolog Family Member C (RhoC); Rat sarcoma (Ras) mutant; Receptor for Advanced Gly cation Endproducts (RAGE-1); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Receptor tyrosine-protein kinase ERBB2 or Her-22/neu; Renal ubiquitous 1 (RU1); Renal ubiquitous 2 (RU2); Sarcoma translocation breakpoints; Serine 2 (TMPRSS2) ETS fusion gene; Sialyl Lewis adhesion molecule (sLe); SLAMF4; SLAMF6; Slea (CA19.9 or Sialyl Lewis Antigen); Sperm protein 17 (SPA17); Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Stage-specific embryonic antigen-4 (SSEA-4); STEAP1; Survivin; Synovial sarcoma X breakpoint 2 (SSX2); TCR Gamma Alternate Reading Frame Protein (TARP); TCR-beta1 chain; TCR-beta2 chain; TCR-delta chain; TCR-gamma chain; TCRgamma-delta; Telomerase; TGFbetaR2; The antigen recognized by TNT antibody; Thyroid stimulating hormone receptor (TSHR); Timl-/HVCR1; Tissue Factor 1 (TF1); Tn ag; Tn antigen ((Tn Ag) or (GalNAca-Ser/Thr)); TNF receptor family member B cell maturation (BCMA); Transglutaminase 5 (TGS5); Transmembrane protease; TROP2; Tumor endothelial marker 1 (TEM1/CD248); Tumor endothelial marker 7-related (TEM7R); Tumor protein p53 (p53); Tumor-associated glycoprotein 72 (TAG72); Tyrosinase; Tyrosinase-related protein 2 (TRP-2); Uroplakin 2 (UPK2); Vascular endothelial growth factor receptor 2 (VEGFR2); V-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Wilms tumor protein (WT1); or X Antigen Family Member 1A (XAGE1). In some embodiments, the targeting moiety "T" binds to CD7. In some embodiments, the target binding domain "T" binds to CD8. In some embodiments, the target binding domain "T" is an antibody. It is to be

understood that in the context of the present disclosure "antibody" not only refers to a "complete" antibody comprising two identical heavy chains, two identical light chains, and two antigen binding fragments, but also refers to antibodies of any isotype, fragments of antibodies including, but not limited to, Fab, Fv, scFv, and Fd fragments, chimeric antibodies, humanized antibodies, single chain antibodies (scAb), single domain antibodies (dAb), single domain heavy chain antibodies, single domain light chain antibodies, bi-specific antibodies, multi-specific antibodies, and fusion proteins comprising an antigen-binding portion of an antibody and a non-antibody protein. In some embodiments, the antibody is selected from the group comprising a scFv, Fab, VHH, single domain antibody, and the like. In some embodiments, the antibody is a scFv. In some embodiments the antibody is a Fab. In some embodiments, the antibody is a VHH. In some embodiments, the antibody is a single domain antibody.

[00137] In some embodiments, the viral particles provided for herein are pseudotyped viral particles. In some embodiments, the viral particles are pseudotyped using viral glycoproteins of viruses of the Paramyxoviridae family. In some embodiments, the pseudotyped viral-like particles are pseudotyped using viral glycoproteins of morbillivirus, such as Measles virus. In some embodiments, the pseudotyped viral-like particles are pseudotyped using viral glycoproteins of the Measles virus. In some embodiments, the pseudotyped viral-like particles are pseudotyped using viral glycoproteins of henipavirus, such as Nipah virus, Cedar virus, or Hendra virus. In some embodiments, the pseudotyped viral-like particles are pseudotyped using viral glycoproteins of the Nipah virus. In some embodiments, a polypeptide or an antibody as provided herein is linked via a linker to an envelope glycoprotein G or H of a virus of the Paramyxoviridae family. In some embodiments, the virus of the Paramyxoviridae family is a morbillivirus, such as Measles virus. In some embodiments, the virus of the Paramyxoviridae family is a henipavirus, such as Nipah virus, Cedar virus, or Hendra virus.

[00138] As provided for herein, the viruses can be pseudotyped with a VSV-G protein, either wild-type or mutant of the same. Without being bound to any particular theory, the mutant VSV-G protein that can be used to pseudotype a virus (*e.g.* lentivirus) comprising a mutation at position 182 can be used to pseudotype a virus and transduce a cell when the virus comprises a targeting moiety. This mutation inhibits or reduces the VSV-G affinity to its natural co-receptor, the LDL-R. The mutant VSV-G proteins as provided can be used, in some embodiments, to transduce a target cell and deliver a heterologous molecule to the targeted cells.

[00139] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 198 as compared to SEQ ID NO: 1 or at position 182 as compared to SEQ ID NO: 2. SEQ ID NO: 1 is the full length protein and SEQ ID NO: 2 is the ectodomain of the VSV-G protein. The 16-mer signal peptide of MKCLLYLAFLFIGVNC (SEQ ID NO: 65) as shown at the N-terminus of SEQ ID NO: 1 is cleaved leaving a protein of SEQ ID NO: 2. Thus, although a mutation may be referred to in the context of SEQ ID NO: 2, it should be understood to also be made in the context of SEQ ID NO: 1, which contains the leader sequence, and thus would be a position number that is 16 more than the position recited for SEQ ID NO: 2. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a I182D mutation as compared to SEQ ID NO: 2. In some embodiments, the mutation is a I182E mutation as compared to SEQ ID NO: 2.

[00140] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 198 as compared to SEQ ID NO: 10 or at position 182 as compared to SEQ ID NO: 11. SEQ ID NO: 10 is the full length protein and SEQ ID NO: 11 is the ectodomain of the VSV-G protein. The 16-mer signal peptide of MLSYLIFALVVSPILG (SEQ ID NO: 66) as shown at the N-terminus of SEQ ID NO: 10 is cleaved leaving a protein of SEQ ID NO: 11. Thus, although a mutation may be referred to in the context of SEQ ID NO: 11, it should be understood to also be made in the context of SEQ ID NO: 10, which contains the leader sequence, and thus would be a position number that is 16 more than the position recited for SEQ ID NO: 11. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a T182D mutation as compared to SEQ ID NO: 11. In some embodiments, the mutation is a T182E mutation as compared to SEQ ID NO: 11.

[00141] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 198 as compared to SEQ ID NO: 12 or at position 182 as compared to SEQ ID NO: 13. SEQ ID NO: 12 is the full length protein and SEQ ID NO: 13 is the ectodomain of the VSV-G protein. The 16-mer signal peptide of MLRLFLFCFLALGAHS (SEQ ID NO: 67) as shown at the N-terminus of SEQ ID NO: 12 is cleaved leaving a protein of SEQ ID NO: 13. Thus, although a mutation may be referred to in the context of SEQ ID NO: 13, it should be understood to also be made in the context of SEQ ID NO: 12, which contains the leader sequence, and thus would be a position number that is 16 more than the position recited for SEQ ID NO: 13. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a A182D

mutation as compared to SEQ ID NO: 13. In some embodiments, the mutation is a A182E mutation as compared to SEQ ID NO: 13.

[00142] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 203 as compared to SEQ ID NO: 14 or at position 182 as compared to SEQ ID NO: 15. SEQ ID NO: 14 is the full length protein and SEQ ID NO: 15 is the ectodomain of the VSV-G protein. The 21-mer signal peptide of MKMKMVIAGLILCIGILPAIG (SEQ ID NO: 68) as shown at the N-terminus of SEQ ID NO: 14 is cleaved leaving a protein of SEQ ID NO: 15. Thus, although a mutation may be referred to in the context of SEQ ID NO: 15, it should be understood to also be made in the context of SEQ ID NO: 14, which contains the leader sequence, and thus would be a position number that is 21 more than the position recited for SEQ ID NO: 15. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a V182D mutation as compared to SEQ ID NO: 15. In some embodiments, the mutation is a V182E mutation as compared to SEQ ID NO: 15.

[00143] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 199 as compared to SEQ ID NO: 16 or at position 182 as compared to SEQ ID NO: 17. SEQ ID NO: 16 is the full length protein and SEQ ID NO: 17 is the ectodomain of the VSV-G protein. The 17-mer signal peptide of MTPAFILCMLLAGSSWA (SEQ ID NO: 69) as shown at the N-terminus of SEQ ID NO: 16 is cleaved leaving a protein of SEQ ID NO: 17. Thus, although a mutation may be referred to in the context of SEQ ID NO: 17, it should be understood to also be made in the context of SEQ ID NO: 16, which contains the leader sequence, and thus would be a position number that is 17 more than the position recited for SEQ ID NO: 17. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a V182D mutation as compared to SEQ ID NO: 17. In some embodiments, the mutation is a V182E mutation as compared to SEQ ID NO: 17.

[00144] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 199 as compared to SEQ ID NO: 18 or at position 182 as compared to SEQ ID NO: 19. SEQ ID NO: 18 is the full length protein and SEQ ID NO: 19 is the ectodomain of the VSV-G protein. The 17-mer signal peptide of MNFLLLTFIVLPLCSHA (SEQ ID NO: 70) as shown at the N-terminus of SEQ ID NO: 18 is cleaved leaving a protein of SEQ ID NO: 19. Thus, although a mutation may be referred to in the context of SEQ ID NO: 19, it should be understood to also be made in the context of SEQ ID NO: 18, which contains the leader sequence, and thus would be a position number that is 17 more than the position recited for

SEQ ID NO: 19. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a V182D mutation as compared to SEQ ID NO: 19. In some embodiments, the mutation is a V182E mutation as compared to SEQ ID NO: 19.

[00145] In some embodiments, a VSV-G protein is provided that comprises a mutation at position 199 as compared to SEQ ID NO: 20 or at position 182 as compared to SEQ ID NO: 21. SEQ ID NO: 20 is the full length protein and SEQ ID NO: 21 is the ectodomain of the VSV-G protein. The 17-mer signal peptide of MLVLYLLLSLLALGAQC (SEQ ID NO: 71) as shown at the N-terminus of SEQ ID NO: 20 is cleaved leaving a protein of SEQ ID NO: 21. Thus, although a mutation may be referred to in the context of SEQ ID NO: 21, it should be understood to also be made in the context of SEQ ID NO: 20, which contains the leader sequence, and thus would be a position number that is 17 more than the position recited for SEQ ID NO: 21. In some embodiments, the mutation inhibits or decreases the binding of the VSV-G protein to the LDL receptor (LDL-R). In some embodiments, the mutation is a I182D mutation as compared to SEQ ID NO: 21. In some embodiments, the mutation is a I182E mutation as compared to SEQ ID NO: 21.

[00146] As used herein, when a polypeptide is said to have a mutation as compared to a reference sequence, such comparison is based on an alignment such as using BlastP or ClustalW or ClutalOmega alignment software using default parameters. For example, position 182 can be found in SEQ ID NO: 2 and also as compared to the other strains as illustrated in FIG. 3. FIG. 3 illustrates a clustal alignment of the wild-type sequences of the ectodomains of the various strains of the VSV-G protein. The residue that is bolded and underlined are the residues that align to position 182 of SEQ ID NO: 2 of the various strains. SEQ ID NO: 2 refers to ectodomain of the VSV-G protein of the Indiana strain. SEQ ID NO: 11 refers to ectodomain of the VSV-G protein of the New Jersey strain. SEQ ID NO: 13 refers to ectodomain of the VSV-G protein of the Marraba strain. SEQ ID NO: 15 refers to ectodomain of the VSV-G protein of the Carajas strain. SEQ ID NO: 17 refers to ectodomain of the VSV-G protein of the Alagoa strain. SEQ ID NO: 19 refers to ectodomain of the VSV-G protein of the Cocal strain. SEQ ID NO: 21 refers to ectodomain of the VSV-G protein of the Morreton strain. Accordingly, the residue that aligns to residues 182 as compared to SEQ ID NO: 2 can also be mutated as provided for herein.

[00147] In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 2 is not an alanine. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 2 is not a valine.

[00148] In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 2 is I182S, I182H, I182T, I182Q, or I182N. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 11 is T182S, T182H, T182Q, or T182N. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 13 is A182S, A182H, A182T, A182Q, or A182N. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 15 is V182S, V182H, V182T, V182Q, or V182N. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 17 is V182S, V182H, V182T, V182Q, or V182N. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 19 is V182S, V182H, V182T, V182Q, or V182N. In some embodiments, the mutation at position 182 as compared to SEQ ID NO: 21 is I182S, I182H, I182T, I182Q, or I182N. In some embodiments, the mutation at position 182 is not a hydrophobic residue. In some embodiments, the mutation at position 182 is a charged residue. In some embodiments, the mutation at position 182 is a negatively charged residue.

[00149] Although, the mutations may be described in reference to SEQ ID NO: 1 or SEQ ID NO: 2, which is the VSV-G protein from the Indiana strain, the mutation can also be used in other strains of the VSV-G protein. For example, the mutation can be made in the New Jersey Strain of VSV-G, the Marraba strain of VSV-G, the Carajas strain of VSV-G, the Alagoa strain of VSV-G, the Cocal strain of VSV-G, or the Morreton strain of VSV-G. In some embodiments, the sequences of each are as provided herein. Examples of these can be found, for example in U.S. Patent Application Publication No. 20200216502, which is hereby incorporated by reference. For example, the wild-type full length or ectodomain of the New Jersey Strain of VSV-G are SEQ ID NO: 10 and SEQ ID NO: 11, respectively, the wild-type full length or ectodomain of Marraba strain of VSV-G are SEQ ID NO: 12 and SEQ ID NO: 13, respectively, the wild-type full length or ectodomain of Carajas strain of VSV-G are SEQ ID NO: 14 and SEQ ID NO: 15, respectively, the wild-type full length or ectodomain of Alagoa strain of VSV-G are SEQ ID NO: 16 and SEQ ID NO: 17, respectively, the wild-type full length or ectodomain of Cocal strain of VSV-G are SEQ ID NO: 18 and SEQ ID NO: 19, respectively, or the wild-type full length or ectodomain of Morreton strain of VSV-G are SEQ ID NO: 20 and SEQ ID NO: 21, respectively.

[00150] A VSV-G protein comprising a mutation at position 182 as compared to SEQ ID NO: 2 can also comprise other mutations, such as those described in U.S. Patent Application Publication No. 20200216502, which is hereby incorporated by reference in its entirety. For example, the VSV-G protein can comprise a mutation at a position that corresponds to positions of 8, 47, 209 and/or 354 of SEQ ID NO: 2.

[00151] In some embodiments, the substitution at position 8 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except Y. In some embodiments, the substitution at position 209 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except H. In some embodiments, the substitution at position 47 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except K or R. In some embodiments, the substitution at position 354 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except K or R.

[00152] In some embodiments, the substitution is at position 47 or at position 354, or at both positions 47 and 354 are substituted by A, G, F or Q. In some embodiments, the substitution is A or Q.

[00153] In some embodiments, the substitution at position 8 is an alanine, i.e., H8A.

[00154] In some embodiments, the substitution at position 47 is Q or N, i.e., K47Q or K47N.

[00155] In some embodiments, the protein comprises a mutation (substitution) at position 10. In some embodiments, the substitution/mutation is Q10A, Q10R, or Q10K.

[00156] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 2 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 2 (or SEQ ID NO: 1 if using the full length protein). In some embodiments, the polypeptide comprises a I182D or I182E mutation. In some embodiments, the VSV-G protein comprises a I182S, I182H, I182T, I182Q, or I182N mutation.

[00157] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 11 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 11 (or SEQ ID NO: 10 if using the full length protein). In some embodiments, the polypeptide comprises a T182D or T182E mutation. In some embodiments, the VSV-G protein comprises a T182S, T182H, T182Q, or T182N mutation.

[00158] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 13 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 13 (or SEQ ID NO: 12 if using the full length protein). In some embodiments,

the polypeptide comprises a A182D or A182E mutation. In some embodiments, the VSV-G protein comprises a A182S, A182H, A182T, A182Q, or A182N mutation.

[00159] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 15 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 15 (or SEQ ID NO: 14 if using the full length protein). In some embodiments, the polypeptide comprises a V182D or V182E mutation. In some embodiments, the VSV-G protein comprises a V182S, V182H, V182T, V182Q, or V182N mutation.

[00160] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 17 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 17 (or SEQ ID NO: 16 if using the full length protein). In some embodiments, the polypeptide comprises a V182D or V182E mutation. In some embodiments, the VSV-G protein comprises a V182S, V182H, V182T, V182Q, or V182N mutation.

[00161] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 19 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 19 (or SEQ ID NO: 18 if using the full length protein). In some embodiments, the polypeptide comprises a V182D or V182E mutation. In some embodiments, the VSV-G protein comprises a V182S, V182H, V182T, V182Q, or V182N mutation.

[00162] In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 21 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 21 (or SEQ ID NO: 20 if using the full length protein). In some embodiments, the polypeptide comprises a I182D or I182E mutation. In some embodiments, the VSV-G protein comprises a I182S, I182H, I182T, I182Q, or I182N mutation.

Viral Glycoproteins

[00163] The mutant VSV-G proteins can be used, for example, to pseudotype a virus, such as, but not limited to a lentivirus. Accordingly, in some embodiments, a viral particle comprising

a mutant VSV-G protein as provided herein are provided. In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 198 as compared to SEQ ID NO: 1. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 2 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 2 (or SEQ ID NO: 1 if using the full length protein). In some embodiments, the polypeptide comprises a I182D or I182E mutation as compared to SEQ ID NO: 2. In some embodiments, the VSV-G protein comprises a I182S, I182H, I182T, I182Q, or I182N mutation.

[00164] In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 198 as compared to SEQ ID NO: 10. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 11 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 11 (or SEQ ID NO: 10 if using the full length protein). In some embodiments, the polypeptide comprises a T182D or T182E mutation as compared to SEQ ID NO: 11. In some embodiments, the VSV-G protein comprises a T182S, T182H, T182Q, or T182N mutation.

[00165] In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 198 as compared to SEQ ID NO: 12. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 13 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 13 (or SEQ ID NO: 12 if using the full length protein). In some embodiments, the polypeptide comprises a A182D or A182E mutation as compared to SEQ ID NO: 13. In some embodiments, the VSV-G protein comprises a A182S, A182H, A182T, A182Q, or A182N mutation.

[00166] In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 203 as compared to SEQ ID NO: 14. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 15 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 15 (or SEQ ID NO: 14

if using the full length protein). In some embodiments, the polypeptide comprises a V182D or V182E mutation as compared to SEQ ID NO: 15. In some embodiments, the VSV-G protein comprises a V182S, V182H, V182T, V182Q, or V182N mutation.

[00167] In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 199 as compared to SEQ ID NO: 16. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 17 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 17 (or SEQ ID NO: 16 if using the full length protein). In some embodiments, the polypeptide comprises a V182D or V182E mutation as compared to SEQ ID NO: 17. In some embodiments, the VSV-G protein comprises a V182S, V182H, V182T, V182Q, or V182N mutation.

[00168] In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 199 as compared to SEQ ID NO: 18. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 19 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 19 (or SEQ ID NO: 18 if using the full length protein). In some embodiments, the polypeptide comprises a V182D or V182E mutation as compared to SEQ ID NO: 19. In some embodiments, the VSV-G protein comprises a V182S, V182H, V182T, V182Q, or V182N mutation.

[00169] In some embodiments, the viral particle comprises a VSV-G protein comprising a mutation at position 199 as compared to SEQ ID NO: 20. In some embodiments, a protein comprising a mutation at position 182 as compared to SEQ ID NO: 21 comprises a mutation at position 182 and at least, or about, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical as compared to SEQ ID NO: 21 (or SEQ ID NO: 20 if using the full length protein). In some embodiments, the polypeptide comprises a I182D or I182E mutation as compared to SEQ ID NO: 21. In some embodiments, the VSV-G protein comprises a I182S, I182H, I182T, I182Q, or I182N mutation.

[00170] In some embodiments, the VSV-G protein further comprises a mutation at position that corresponds to positions 214 and/or 352 of SEQ ID NO: 2. In some embodiments, the residue that corresponds to position 214 of SEQ ID NO: 2 is T214. In some embodiments, the residue that corresponds to position 352 of SEQ ID NO: is T352. In some embodiments, the

VSV-G protein comprises mutation that corresponds to T214N mutation as compared to SEQ ID NO: 2. In some embodiments, the VSV-G protein comprises mutation that corresponds to T352A mutation as compared to SEQ ID NO: 2. In some embodiments, the VSV-G protein comprises a T214N and T352A mutations as compared to SEQ ID NO: 2. These mutations can be combined with any other mutations as provided for herein. In some embodiments, the T214N and/or T352A mutations are combined with the I182E or I182D mutations. In some embodiments, a VSV-G protein comprises an amino acid sequence of SEQ ID NO: 22 and SEQ ID NO: 23, which combines the I182D or I182E, respectively, with the T214N and T352A mutations. The sequences are also illustrated below with the leader sequences, which are removed during protein processing.

VSV-G Protein_ I196D, T230N and T368A mutations (with leader sequence and adjusted numbering)

MKCLLYLAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSSDLN
WHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGPK
YITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVI
VQVTPHHVLVDEYTGEWVDSQFINGKCSNYICPTVHNSTTWHSDYKV
KGLCDSNLDSMDITFFSEDGELSSLGKEGTGFRSNYFAYENGGKACK
MQYCKHWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSV
DVSLIQDVERILDYSLCQETWSKIRAGLPISPVDLSYLAPKNPGTGPAFT
IINGTLKYFETRYIRVDIAAPILSRMVGMISGTTAERELWDDWAPYEDV
EIGPNGVLRTSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAA
SQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIASFFFIIGLIIGLFLVL
RVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 24)

VSV-G Protein_I182D, T214N and T352A mutations (without leader sequence)

KFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPK
SHKAIQADGWMCHASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCKE
SIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGE
WVDSQFINGKCSNYICPTVHNSTTWHSDYKVKGLCDSNLDSMDITFFS
EDGELSSLGKEGTGFRSNYFAYENGGKACKMQYCKHWGVRLPSGVW
FEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQ
ETWSKIRAGLPISPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDI
AAPILSRMVGMISGTTAERELWDDWAPYEDVEIGPNGVLRTSSGYKFP
LYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLS

KNPIELVEGWFSSWKSSIASFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKR
QIYTDIEMNRLGK (SEQ ID NO: 22)

VSV-G Protein with I196E, T230N and T368A mutations (with leader sequence and adjusted numbering)

MKCLLYLAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSSDLN
WHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGPK
YITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVI
VQVTPHHVLVDEYTGEWVDSQFINGKCSNYICPTVHNSTTWHSDYKV
KGLCDSNLESMDITFFSEDGELSSLGKEGTGFRSNYFAYENGGKACKM
QYCKHWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVD
VSLIQDVERILDYSLCQETWSKIRAGLPISPVDLSYLAPKNPGTGPAFTII
NGTLKYFETRYIRVDIAAPILSRMVGMISGTTAERELWDDWAPYEDVE
IGPNGVLRTSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAAS
QLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIASFFFIIGLIIGLFLVL
RVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 25)

VSV-G Protein with I182E, T214N and T352A mutations (without leader sequences)

KFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPK
SHKAIQADGWMCHASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCKE
SIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGE
WVDSQFINGKCSNYICPTVHNSTTWHSDYKVKGLCDSNLESMDITFFS
EDGELSSLGKEGTGFRSNYFAYENGGKACKMQYCKHWGVRLPSGVW
FEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQ
ETWSKIRAGLPISPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDI
AAPILSRMVGMISGTTAERELWDDWAPYEDVEIGPNGVLRTSSGYKFP
LYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLS
KNPIELVEGWFSSWKSSIASFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKR
QIYTDIEMNRLGK (SEQ ID NO: 23)

[00171] The other strains of the VSV-G protein as described herein can also comprises the mutations that correspond to T214N and/or T352A in SEQ ID NO: 2 and as illustrated in SEQ ID NO: 22 and SEQ ID NO: 23.

[00172] In some embodiments, the composition comprises a mutation as described in Hwang et al., Gene Ther 2013 Aug;20(8):807-15. (Epub 2013 Jan 31), which is hereby incorporated by reference in its entirety. For example, the mutations can be. at positions 230, 368, 66, and/or

162 that corresponds to SEQ ID NO: 1. The positions will be 16 positions less as compared to SEQ ID NO: 2, when the leader sequence is removed. In some embodiments, the mutations at those positions are, for example, T230N, T368A, K66T, S162T, or any combination thereof. In some embodiments, the VSV-G protein comprises a T230N and a T368A mutation. In some embodiments, the VSV-G polypeptide comprises a K66T, S162T, T230N, and a T368A. These positions are those that correspond to the positions in the full length protein (SEQ ID NO: 1). In some embodiments, the VSV-G protein comprises T230N mutation, a T368A mutation, a K66T mutation, a S162T mutation, or any combination thereof. In some embodiments, the VSV-G protein further comprises one or more mutations in addition to the mutation that corresponds to position 182 of SEQ ID NO: 2, such as those described in U.S. Patent Application Publication No. 20200216502, which is hereby incorporated by reference in its entirety. For example, the VSV-G protein can further comprise a mutation at a position that corresponds to positions of 8, 47, 209 and/or 354 of SEQ ID NO: 2.

[00173] In some embodiments, the substitution at position 8 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except Y. In some embodiments, the substitution at position 209 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except H. In some embodiments, the substitution at position 47 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except K or R. In some embodiments, the substitution at position 354 is by any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except K or R. In some embodiments, the substitution is at position 47 or at position 354, or at both positions 47 and 354 are substituted by A, G, F or Q. In some embodiments, the substitution is A or Q. In some embodiments, the substitution at position 8 is an alanine, i.e., H8A. In some embodiments, the substitution at position 47 is Q or N, i.e., K47Q or K47N. In some embodiments, the protein comprises a mutation (substitution) at position 10. In some embodiments, the substitution/mutation is Q10A, Q10R, or Q10K.

[00174] Additionally, in some embodiments, instead of the VSV-G protein or mutant thereof, the viruses can be pseudotyped with other viral structural proteins.

[00175] For example, the viral particle can be pseudotyped with a Spring viremia of carp virus G (SVCV-G) protein and transduce a cell when the virus comprises a targeting moiety. The Spring viremia of carp virus G protein as provided can be used, in some embodiments, to transduce a target cell and deliver a heterologous molecule to the targeted cells. In some embodiments, a Spring viremia of carp virus G protein is provided that comprises SEQ ID NO:

52. SEQ ID NO: 52 is the full length protein and SEQ ID NO: 53 is the ectodomain of the Spring viremia of carp virus G protein that has the N-terminal signal peptide removed. Accordingly, in some embodiments, the protein comprises an amino acid sequence of SEQ ID NO: 53. The Spring viremia of carp virus G protein can be used, for example, to pseudotype a virus, such as, but not limited to a lentivirus. Accordingly, in some embodiments, a viral particle comprising a Spring viremia of carp virus G protein as provided herein are provided. In some embodiments, the viral particle comprises a Spring viremia of carp virus G protein comprising SEQ ID NO: 52 or SEQ ID NO: 53 or sequence that is at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 52 or SEQ ID NO: 53.

[00176] The sequence of Spring Viremia of Carp Virus – G (SEQ ID NO: 52-with leader sequence)

MSIISYIAFLLLIDSNLGIPIFVPSGRNISWQPVIQPFDYQCPIHGNLPNTMGLSATKLTIK
SPSVFSTDKVSGWICHAAEWKTTCDYRWYGPQYITHSIHPISPTIDECRRIIQRIASGTDED
LGFPPQSCGWASVTTVSNTNYRVVPHSVHLEPYGGHWIDHEFNGGECREKVCEMKGNHSIWI
TEETVQHECAKHIEEVEGIMYGNVPRGDVMYANNFIIDRHHRVYRFGGSCQMKFCNKDGIKF
ARGDWVEKTAGTLTTIHDNVPKCVDGTLVSGHRPGLDLIDTVFNLENVVEYTLCEGTKRKIN
KQEKLTSVDLSYLAPRIGGFGSVFRVRNGTLERGSTTYIRIEVEGPIVDSLNGTDPRTNASR
VFWDDWELDGNIYQGFNGVYKGKDGKIHIPLNMIESGIIDDELQHAFQADIIPHPHYDDDEI
REDDIFFDNTGENGNPVDAVVEWVSGWGTSLKFFGMTLVALILIFLLIRCCVACTYLMKRSK
RPATESHEMRSLV

[00177] The sequence of Spring Viremia of Carp Virus – G (SEQ ID NO: 53-without leader sequence):

IPIFVPSGRNISWQPVIQPFDYQCPIHGNLPNTMGLSATKLTIKSPSVFSTDKVSGWICHAA
EWKTTCDYRWYGPQYITHSIHPISPTIDECRRIIQRIASGTDEDLGFPPQSCGWASVTTVSN
TNYRVVPHSVHLEPYGGHWIDHEFNGGECREKVCEMKGNHSIWITEETVQHECAKHIEEVEG
IMYGNVPRGDVMYANNFIIDRHHRVYRFGGSCQMKFCNKDGIKFARGDWVEKTAGTLTTIHD
NVPKCVDGTLVSGHRPGLDLIDTVFNLENVVEYTLCEGTKRKINKQEKLTSVDLSYLAPRIG
GFGSVFRVRNGTLERGSTTYIRIEVEGPIVDSLNGTDPRTNASRVFWDDWELDGNIYQGFNG
VYKGKDGKIHIPLNMIESGIIDDELQHAFQADIIPHPHYDDDEIREDDIFFDNTGENGNPVD
AVVEWVSGWGTSLKFFGMTLVALILIFLLIRCCVACTYLMKRSKRPATESHEMRSLV

Targeting Moieties

[00178] In some embodiments, the viral particle comprises a targeting moiety having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion. The targeting moiety can be used to target the viral particle comprising the mutant VSV-G protein or the SVCV-G protein to a cell that expresses the target to which the targeting moiety binds to. In some embodiments, the target binding domain is an antibody, a scFv antibody, an antigen

binding domain, an ankyrin repeat (e.g., DARPIN), a VHH domain antibody, a nanobody, single domain antibody, a FN3 domain, or any combination thereof. The target binding domain can be attached to the viral surface through a variant Fc protein (e.g. L_1-Fc-L_2-X_1) as provided for herein or through a flexible polypeptide (e.g., L_3-X_1) as provided for herein. In some embodiments, the targeting moiety is attached (fused or linked) an envelope glycoprotein G or H of a virus of the Paramyxoviridae family, such as a morbillivirus, such as Measles virus, or a henipavirus, such as Nipah virus, Cedar virus, or Hendra virus. In some embodiments, the targeting moiety can be attached (fused or linked) to a glycoprotein of a virus of the Rhabdoviridae family, such as a vesicular stomatitis New Jersey virus, a vesicular stomatitis Indiana virus, a vesicular stomatitis Alagoas virus, a vesicular stromatitis Maraba virus, a vesicular stomatitis Carajas virus, Parainfluenza virus, Spodoptera frugiperda rhabdovirus isolate Sf G, Drosophila obscura sigmavirus 10A, Wuhan insect virus 7, Perch virus, or Spring viremia of carp virus. In some embodiments, the VSV protein is the mutated proteins, such as those provided for herein. In some embodiments, the targeting moiety is attached to a glycoprotein of a virus of the Filoviridae family, such as Ebola virus or a glycoprotein of a virus of the Arenaviridae family, such as Machupo virus.

[00179] In some embodiments, the target binding domain is a scFv. In some embodiments, the target binding domain is a single domain antibody. In some embodiments, the target binding domain is a VHH.

[00180] In some embodiments, the targeting moiety binds to CD7, CD8, cKit (CD117), CD4, CD3, CD5, CD6, CD2, TCR alpha, TCR beta, TCR gamma, TCR delta, CD10, CD34, CD110, CD33, CD14, CD68, CCR7, CD62L, CD25, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, or CXCR3, A glycosylated CD43 epitope expressed on acute leukemia or lymphoma but not on hematopoietic progenitors; A glycosylated CD43 epitope expressed on non-hematopoietic cancers; A kinase anchor protein 4 (AKAP-4); Adrenoceptor beta 3 (ADRB3); AFP; Anaplastic lymphoma kinase (ALK); Androgen receptor; Angiopoietin-binding cell surface receptor 2 (Tie 2); Auto antibody to desmoglein 1 (Dsgl); Auto antibody to desmoglein 3 (Dsg3); B7H3 (CD276); Biotin; Bone marrow stromal cell antigen 2 (BST2); BST1/CD157; Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-la); Carbonic anhydrase IX (CA1X); Carcinoembryonic antigen (CEA); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS or Brother of the Regulator of Imprinted Sites); CCR4; CD5; CD19; CD20; CD22; CD24; CD30; CD32 (FCGR2A); CD33; CD34; CD38; CD44v6; CD72; CD79a; CD79b; CD97; CD99; CD123; CD171; CD179a; CD179b-IGLll; CD200R; CD276/B7H3; CD300 molecule-like family member f (CD300LF); CDH1-CD324; CDH6; CDH17; CDH19;

Chromosome X open reading frame 61 (CXORF61); Claudin 6 (CLDN6); Claudinl8.2 (CLD18A2 or CLDN18A.2); CMV pp65; C-MYC epitope Tag; Cripto; CS1 (also referred to as CD2 subset 1 or CRACC or SLAMF7 or CD319 or 19A24); CSF2RA (GM-CSFR-alpha); C-type lectin domain family 12 member A (CLEC12A); C-type lectin-like molecule-1 (CLL-1 or CLECL1); Cyclin Bl; Cytochrome P450 IB 1 (CYP1B 1); DLL3; EBV-EBNA3c; EGF-bke module- containing mucin-like hormone receptor-like 2 (EMR2); Elongation factor 2 mutated (ELF2M); Ephrin B2; Ephrin type-A receptor 2 (EphA2); Epidermal growth factor receptor (EGFR); Epidermal growth factor receptor variant III (EGFRviii); Epithelial cell adhesion molecule (EPCAM); ERG; ETS translocation-variant gene 6 located on chromosome 12p (ETV6-AML); Fc fragment of IgA receptor (FCAR or CD89); Fc receptor-like 5 (FCRL5); Fibroblast activation protein alpha (FAP); FITC; Fms Like Tyrosine Kinase 3 (FLT3); Folate receptor alpha (FRa or FR1); Folate receptor beta (FRb); Follicle stimulating hormone receptor (FSHR); Fos-related antigen 1; Fucosyl-GMl; G protein coupled receptor class C group 5 member D (GPRC5D); G protein-coupled receptor 20 (GPR20); GAD; Ganglioside G2 (GD2) ; Ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); Ganglioside GM3 (aNeu5Ac(2-3)bDClalp(l- 4)bDGlcp(l-l)Cer); GD3; GFRalpha4; Glycoprotein 100 (gplOO); Glypican-3 (GPC3); Gonadotropin Hormone receptor (CGHR or GR); GpA33; GpNMB; GPRC5D; Guanylyl cyclase C (GCC); Heat shock protein 70-2 mutated (mut hsp70-2); Hepatitis A virus cellular receptor 1 (HAVCR1); Hexasaccharide portion of globoH glycoceramide (GloboH); High molecular weight-melanoma associated antigen (HMWMAA); HIV1 envelope glycoprotein; HLA; HLA-DOA; HLA-A; HLA-A2; HLA-B; HLA-C; HLA-DM; HLA-DOB; HLA-DP; HLA-DQ; HLA-DR; HLA-G; HTLVl-Tax; Human papilloma virus E6 (HPV E6); Human papilloma virus E7 (HPV E7); Human Telomerase reverse transcriptase (hTERT); IgE; IL13Ra2; ILl lRa; Immunoglobulin lambda-like polypeptide 1 (IGLL1); Influenza A hemagglutinin (HA); Insulin-like growth factor 1 receptor (IGF-I receptor); Interleukin 11 receptor alpha (IL-llRa); Interleukin- 13 receptor subunit alpha-2 (IL-13Ra2 or CD213A2); Intestinal carboxyl esterase; KIT (CD117); KSHV K8.1; KSHV-gH; LAMP1 ; Legumain; Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Leutenizing hormone receptor (LHR); Lewis(Y) antigen; Lews Ag; Livl; Locus K 9 (LY6K); Low conductance chloride channel; Lymphocyte antigen 6 complex; Lymphocyte antigen 75 (LY75); Lymphocyte-specific protein tyrosine kinase (LCK); Mammary gland differentiation antigen (NY-BR-1); Melanoma antigen recognized by T cells 1 (MelanA or MARTI); Melanoma- associated antigen 1 (MAGE-A1); Melanoma cancer testis antigen-1 (MAD-CT-

1); Melanoma cancer testis antigen-2 (MAD-CT-2); Melanoma inhibitor of apoptosis (ML-IAP); Mesothelin; MPL; Mucin 1 cell surface associated (MUC1); N-Acetyl glucosaminyl-transferase V (NA17); Nectin-4; Neural cell adhesion molecule (NCAM); NKG2D; NYBR1; O-acetyl-GD2 ganglioside (OAcGD2); Olfactory receptor 51E2 (OR51E2); Oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); P53 mutant; Paired box protein Pax-3 (PAX3); Paired box protein Pax-5 (PAX5); Pannexin 3 (PANX3); PDL1; P-glycoprotein; Placenta-specific 1 (PLAC1); Platelet-derived growth factor receptor beta (PDGFR-beta); Polysialic acid; Proacrosin binding protein sp32 (OY-TES1); Prostase; Prostate carcinoma tumor antigen-1 (PCT A-1 or Galectin 8); Prostate stem cell antigen (PSCA); Prostate-specific membrane antigen (PSMA); Prostatic acid phosphatase (PAP); Prostein; Protease Serine 21 (Testisin or PRSS21); Proteasome (Prosome Macropain) Subunit Beta Type 9 (LMP2); PTK7; Ras G12V; Ras Homolog Family Member C (RhoC); Rat sarcoma (Ras) mutant; Receptor for Advanced Gly cation Endproducts (RAGE-1); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Receptor tyrosine-protein kinase ERBB2 or Her-22/neu; Renal ubiquitous 1 (RU1); Renal ubiquitous 2 (RU2); Sarcoma translocation breakpoints; Serine 2 (TMPRSS2) ETS fusion gene; Sialyl Lewis adhesion molecule (sLe); SLAMF4; SLAMF6; Slea (CA19.9 or Sialyl Lewis Antigen); Sperm protein 17 (SPA17); Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Stage-specific embryonic antigen-4 (SSEA-4); STEAP1; Survivin; Synovial sarcoma X breakpoint 2 (SSX2); TCR Gamma Alternate Reading Frame Protein (TARP); TCR-beta1 chain; TCR-beta2 chain; TCR-delta chain; TCR-gamma chain; TCRgamma-delta; Telomerase; TGFbetaR2; The antigen recognized by TNT antibody; Thyroid stimulating hormone receptor (TSHR); Timl-/HVCR1; Tissue Factor 1 (TF1); Tn ag; Tn antigen ((Tn Ag) or (GalNAca-Ser/Thr)); TNF receptor family member B cell maturation (BCMA); Transglutaminase 5 (TGS5); Transmembrane protease; TROP2; Tumor endothelial marker 1 (TEM1/CD248); Tumor endothelial marker 7-related (TEM7R); Tumor protein p53 (p53); Tumor-associated glycoprotein 72 (TAG72); Tyrosinase; Tyrosinase-related protein 2 (TRP-2); Uroplakin 2 (UPK2); Vascular endothelial growth factor receptor 2 (VEGFR2); V-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Wilms tumor protein (WT1); or X Antigen Family Member 1A (XAGE1). In some embodiments, the targeting moiety binds to CD7. In some embodiments, the targeting moiety binds to CD8.

[00181] In some embodiments, the targeting moiety binds to a target that is present on a cell, such as an immune cell. In some embodiments, the cell is an immune cell, such as, but not limited to, T cell, B cell; NK cell, dendritic cell, neutrophils, macrophages, a cancer cell; or,

for example, CD3+ T cell; CD4+ T cell; CD7+ T cell, CD8+ T cell; CD19+ B cell; CD19+ cancer cell; CD20+ B cell; CD20+ cancer cell; CD30+ lung epithelial cell; CD34+ haematopoietic stem cell; CD105+ endothelial cell; CD105+ haematopoietic stem cell; CD117+ haematopoietic stem cell; CD133+ cancer cell; EpCAM+ cancer cell; GluA2+ neuron; GluA4+ neuron; Haematopoietic stem cell; Hepatocyte; Her2/Neu+ cancer cell; NKG2D+ natural killer cell; SLC1A3+ astrocyte; SLC7A10+ adipocyte. In some embodiments, the cell is a T cell. In some embodiments, the cell is a B cell. In some embodiments, the cell is a CD7+ T cell and/or CD8+ T cell.

CD7 binding polypeptides

[00182] In some embodiments, the targeting moiety (e.g. polypeptide) binds to CD7.

[00183] In some embodiments, the polypeptide that binds to CD7 is an antibody which binds to non-human primate CD7. In some embodiments, the polypeptide that binds to CD7 is an antibody which binds to human CD7. The sequence of human CD7 (UniProtKB P09564) is as follows (SEQ ID NO: 29):

MAGPPRLLLLPLLLALARGLPGALAAQEVQQSPHCTTVPVGASVNITCSTSGG
LRGIYLRQLGPQPQDIIYYEDGVVPTTDRRFRGRIDFSGSQDNLTITMHRLQLS
DTGTYTCQAITEVNVYGSGTLVLVTEEQSQGWHRCSDAPPRASALPAPPTGS
ALPDPQTASALPDPPAASALPAALAVISFLLGLGLGVACVLARTQIKKLCSWR
DKNSAACVVYEDMSHSRCNTLSSPNQYQ (SEQ ID NO: 29).

[00184] In some embodiments, the CD7 that the polypeptide binds to is expressed on the surface of a cell. In some embodiments, the cell is an immune cell. In some embodiments, the immune cell is a CD7+ T cell, CD4+ T cell, CD8+ T cell, NK cell, alpha-beta T cell, gamma-delta T cell, lymphoid progenitor cell, hematopoietic stem cell, myeloid cell, monocyte, macrophage, central memory T cell, effector memory T cell, stem-cell like memory T cells, naïve T cell, activated T cell, regulatory T cell (TReg), terminally differentiated effector memory T cell (TEMRA), resident memory T cell (TRM) or a T-cellCD8+CCR7+.

[00185] In some embodiments, the antibody comprises a Fc region. The Fc region can be linked to the heavy or light chain of the antibody. In some embodiments, the Fc region is an IgG Fc. In some embodiments, the IgG is selected from IgG1, IgG2, IgG3, or IgG4. In some embodiments, the IgG fc is IgG1 Fc. In some embodiments, the antibody comprises an Fc constant region as set forth herein, such as SEQ ID NO: 26, 27, or 28 or a mutant thereof as provided for herein.

[00186] In some embodiments, polypeptides (e.g. CD7-binding polypeptide) are provided herein. In some embodiments, antibodies (*e.g.* an anti-CD7 antibody) are provided herein. In some embodiments, the antibody is a recombinant antibody that binds to CD7. In some embodiments, the CD7 protein is a human CD7 protein. In some embodiments, the CD7 protein is a non-human CD7 protein (e.g., mouse, rat, pig, dog, non-human primate). As used herein, the term "recombinant antibody" refers to an antibody that is not naturally occurring. In some embodiments, the term "recombinant antibody" refers to an antibody that is not isolated from a human subject.

[00187] In some embodiments, an antibody, or antigen binding fragment thereof is provided, wherein the antibody or antibody fragment comprises a peptide selected from the following table, which illustrate the CDRs based on Chothia numbering.

Chothia CDRs						
Ab ID No	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
CD7AB1	GYPFTSY (*SEQ ID NO: 30*)	DPNSGD (*SEQ ID NO: 31*)	SPYYSNDNSMDY (*SEQ ID NO: 32*)	RASQSIGTSIH (*SEQ ID NO: 33*)	YASESIS (*SEQ ID NO: 34*)	QQSNSWPTT (*SEQ ID NO: 35*)

[00188] In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy or light chain CDR as provided in the tables above. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy or light chain CDR as provided in the tables above and binds to non-human primate CD7. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy or light chain CDR as provided in the tables above and binds to human CD7. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence selected from SEQ ID NO: 33-35. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence of SEQ ID NO: 33. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence of SEQ ID NO: 34. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence of SEQ ID NO: 35. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence selected from SEQ ID NO: 30-32. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence of SEQ ID NO: 30. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a

sequence of SEQ ID NO: 31. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence of SEQ ID NO: 32. The CDRs referenced in the embodiments throughout the present specification can be interchanged with the CDRs that are characterized by different formats, such as Kabat and IMGT.

[00189] In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain variable region having a LCDR1, a LCDR2, and a LCDR3, wherein the LCDR1 has a sequence of SEQ ID NO: 33, the LCDR2 has a sequence of SEQ ID NO: 34, and the LCDR3 has a sequence of SEQ ID NO: 35.

[00190] In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain variable region having a HCDR1, a HCDR2, and a HCDR3, wherein the HCDR1 has a sequence of SEQ ID NO: 30, the HCDR2 has a sequence of SEQ ID NO: 31, and the HCDR3 has a sequence of SEQ ID NO: 32.

[00191] In some embodiments, a polypeptide, an antibody or antibody binding fragment thereof, comprises: (i) a light chain having any one of the foregoing recited combinations of LCDR1, LCDR2, and LCDR3 sequences; and (ii) a heavy chain having any one of the foregoing recited combinations of HCDR1, HCDR2, and HCDR3 sequences.

[00192] The different CDR motifs can be combined in any combination including those not depicted in the table above. For example, the following embodiments are provided as non-limiting examples of such combinations.

[00193] In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises: (i) a light chain variable region comprising light chain CDRl, CDR2, and CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 33; the light chain CDR2 has the amino acid sequence of SEQ ID NO: 34; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 35; and (ii) a heavy chain variable region comprising heavy chain CDR1, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 30; the heavy chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 31; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 32; or variants of any of the foregoing.

[00194] Although the preceding paragraphs may make reference to CDRs under the Chothia system the equivalent CDR sequences can be used from the IMGT and Kabat designations.

[00195] In some embodiments, the light chain variable region CDR1 is replaced with any of the other light chain CDR1 sequences. In some embodiments, the light chain variable region CDR2 is replaced with any of the other light chain CDR2 sequences. In some embodiments,

the light chain variable region CDR3 is replaced with any of the other light chain CDR3 sequences. In some embodiments, the heavy chain variable region CDR1 is replaced with any of the other heavy chain CDR1 sequences. In some embodiments, the heavy chain variable region CDR2 is replaced with any of the other heavy chain CDR2 sequences. In some embodiments, the heavy chain variable region CDR3 is replaced with any of the other heavy chain CDR3 sequences.

[00196] In some embodiments, the polypeptide comprises a heavy chain variable region peptide having one of the following sequences, or a variant thereof:

SEQ ID NO:	AB ID NO.	Sequence
36	CD7AB1	QVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGL EWLGRIDPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSED SAVYYCARSPYYSNDNSMDYWGQGTSVTVSS

[00197] In some embodiments, the polypeptide comprises a light chain variable region peptide having one of the following sequences, or a variant thereof:

SEQ ID NO:	AB ID NO.	Sequence
37	CD7AB1	DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNDSPR LLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQ SNSWPTTFGGGTKLEIKR

[00198] In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide of SEQ ID NO: 36. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_L peptide of SEQ ID NO: 37. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide and a V_L peptide, wherein the wherein the V_H peptide comprises a sequence of SEQ ID NO: 36, or a variant thereof; and the V_L peptide comprises a sequence of SEQ ID NO: 37, or a variant thereof. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide and a V_L peptide, wherein the wherein the V_H peptide comprises a sequence of SEQ ID NO: 36, or a variant thereof; and the V_L peptide comprises a sequence of SEQ ID NO: 37, or a variant thereof, and the polypeptide, the antibody, or antigen binding fragment thereof, binds to non-human primate CD7. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide and a V_L peptide, wherein the wherein the V_H peptide comprises a sequence of SEQ ID NO: 36, or a variant thereof; and the V_L peptide comprises a sequence of SEQ ID NO: 37, or a variant thereof, and the polypeptide, the antibody, or antigen binding fragment thereof, binds to human

CD7. In some embodiments, the V_H peptide comprises a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence of SEQ ID NO: 37.

[00199] The V_H and the V_L sequences can be in any format, including, but not limited to an scFv format where the V_H and V_L regions are linked with a peptide linker. Examples of peptide linkers that can be used to link various peptides provided for herein include, but are not limited to: $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. In some embodiments, the variable regions are not linked with a peptide linker. In some embodiments, the polypeptide comprises SEQ ID NO: 36 and SEQ ID NO: 37.

[00200] As provided for herein, the polypeptide, antibodies, or antigen binding fragments thereof can be variants of the sequences.

[00201] The sequences of the polypeptides or antibodies can be modified to yield human IgG antibodies. The conversion of the sequences provided herein can be modified to yield other types of antibodies. The CDRs can also be linked to other antibodies, proteins, or molecules to create antibody fragments that bind CD7.

[00202] In some embodiments, a polypeptide or an antibody as provided herein is a targeting moiety on the surface of an engineered viral particle. In some embodiments, the targeting moiety allows for binding to a target cell. In some embodiments, the targeting moiety is a CD7 binding moiety, such as a polypeptide or an antibody as provided herein. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38:

DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYAS
ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKL
EIKRGGGGSGGGGSGGGGSGGGGSQVQLQQPGAELVKPGASVKLSCKASGYP
FTSYWIHWVKQRPGRGLEWLGRIDPNSGDTKYNEKFKNKATLTVDKSSTTAY
MQLSSLTSEDSAVYYCARSPYYSNDNSMDYWGQGTSVTVSS (SEQ ID NO:
38)

or is substantially similar to SEQ ID NO: 38, or is an active fragment of SEQ ID NO: 38. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 38. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 38. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 38. In some embodiments, the target binding domain

("T") comprises a sequence as set forth in SEQ ID NO: 38. In some embodiments, the target binding domain ("T") as set forth in SEQ ID NO: 38 is an antibody, or an antigen binding fragment thereof. In some embodiments, the target binding domain ("T") is an anti-CD7 antibody.

[00203] In some embodiments, a polypeptide or an antibody as provided for herein is a targeting moiety on the surface of an engineered viral particle. In some embodiments, the engineered viral particle is a pseudotyped viral-like particle. In some embodiments, the targeting moiety allows for binding to a target cell. In some embodiments, the targeting moiety is a CD7 binding moiety, such as a polypeptide or an antibody as provided herein. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 39.

QVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGLEWLGRID
PNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARSPYYSN
DNSMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSDILLTQSPAILSVSP
GERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESISGIPSRFSGSGS
GTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKR (SEQ ID NO:
39)

or is substantially similar to SEQ ID NO: 39, or is an active fragment of SEQ ID NO: 39. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 39. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 39. In some embodiments, the target binding domain ("T") comprises a sequence as set forth in SEQ ID NO: 39. In some embodiments, the target binding domain ("T") as set forth in SEQ ID NO: 39 is an antibody, or an antigen binding fragment thereof. In some embodiments, the target binding domain ("T") is an anti-CD7 antibody. In some embodiments, the anti-CD7 antibody binds to non-human primate CD7. In some embodiments, the anti-CD7 antibody binds to human CD7.

CD8 binding polypeptides

[00204] In some embodiments, the targeting moiety (*e.g.* a polypeptide) can bind to CD8.

[00205] In some embodiments, the polypeptide binds to CD8. In some embodiments, the polypeptide binds to CD8-alpha. In some embodiments, the polypeptide binds to CD8-beta. In some embodiments, the polypeptide binds to CD8 heterodimer. In some embodiments, the CD8

heterodimer comprises CD8-alpha and CD8-beta subunits. In some embodiments, the polypeptide binds to CD8-alpha homodimer. In some embodiments, the polypeptide that binds to CD8 is an antibody which binds to non-human primate CD8. In some embodiments, the antibody that binds to non-human primate CD8 is an antibody which binds to non-human primate CD8-alpha. In some embodiments, the antibody that binds to non-human primate CD8 is an antibody which binds to non-human primate CD8-beta. In some embodiments, the antibody that binds to non-human primate CD8 is an antibody which binds to non-human primate CD8-alpha homodimer. In some embodiments, the antibody that binds to non-human primate CD8 is an antibody which binds to non-human primate CD8 heterodimer. In some embodiments, the polypeptide that binds to CD8 is an antibody which binds to human CD8. In some embodiments, the antibody that binds to human CD8 is an antibody which binds to human CD8-alpha. In some embodiments, the antibody that binds to human CD8 is an antibody which binds to human CD8-beta. In some embodiments, the antibody that binds to human CD8 is an antibody which binds to human CD8-alpha homodimer. In some embodiments, the antibody that binds to human CD8 is an antibody which binds to human CD8 heterodimer. The sequence of human CD8-alpha (UniProtKB Q8TAW8) is as follows (SEQ ID NO: 40):

MALPVTALLLPLALLLHAARPSQFRVSPLDRTWNLGETVELKCQVLLSNPTS
GCSWLFQPRGAAASPTFLLYLSQNKPKAAEGLDTQRFSGKRLGDTFVLTLSD
FRRENEGCYFCSALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSL
RPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRNR
RRVCKCPRPVVKSGDKPSLSARYV (SEQ ID NO: 40).

[00206] The sequence of human CD8-beta (UniProtKB Q8TD28) is as follows (SEQ ID NO: 41):

MRPRLWLLLAAQLTVLHGNSVLQQTPAYIKVQTNKMVMLSCEAKISLSNMR
IYWLRQRQAPSSDSHHEFLALWDSAKGTIHGEEVEQEKIAVFRDASRFILNLT
SVKPEDSGIYFCMIVGSPELTFGKGTQLSVVDFLPTTAQPTKKSTLKKRVCRLP
RPETQKGPLCSPITLGLLVAGVLVLLVSLGVAIHLCCRRRRARLRFMKQLYK
(SEQ ID NO: 41).

[00207] In some embodiments, the CD8 that the polypeptide binds to is expressed on the surface of a cell. In some embodiments, the cell is an immune cell. In some embodiments, the immune cell is a CD7+ T cell, CD4+ T cell, CD8+ T cell, NK cell, alpha-beta T cell, gamma-delta T cell, lymphoid progenitor cell, hematopoietic stem cell, myeloid cell, monocyte,

macrophage, central memory T cell, effector memory T cell, stem-cell like memory T cells, naïve T cell, activated T cell, regulatory T cell (TReg), terminally differentiated effector memory T cell (TEMRA), resident memory T cell (TRM) or a T-cell CD8+CCR7+. In some embodiments, the cell is a CD8+ T cell. In some embodiments, the cell is a CD8+ cell.

[00208] In some embodiments, the antibody comprises a Fc region. The Fc region can be linked to the heavy or light chain of the antibody. In some embodiments, the Fc region is an IgG Fc. In some embodiments, the IgG is selected from IgG1, IgG2, IgG3, or IgG4. In some embodiments, the IgG Fc is IgG1 Fc. In some embodiments, the antibody comprises an Fc constant region as set forth herein, such as SEQ ID NO: 26, 27, or 28 or a variant thereof.

[00209] In some embodiments, polypeptides (e.g. CD8-binding polypeptide) are provided herein. In some embodiments, antibodies (*e.g.* an anti-CD8 antibody) are provided herein. In some embodiments, the antibody is a recombinant antibody that binds to CD8. In some embodiments, the CD8 protein is a human CD8 protein. In some embodiments, the CD8 protein is a non-human CD8 protein (e.g., mouse, rat, pig, dog, non-human primate). As used herein, the term "recombinant antibody" refers to an antibody that is not naturally occurring. In some embodiments, the term "recombinant antibody" refers to an antibody that is not isolated from a human subject.

[00210] In some embodiments, an antibody, or antigen binding fragment thereof is provided, wherein the antibody or antibody fragment comprises a peptide selected from the following table, which illustrate the CDRs based on Chothia numbering.

Chothia CDRs						
Ab ID No	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
CD8AB1	RYTFTDY (SEQ ID NO: *42*)	YPYNGG (SEQ ID NO: *43*)	DHRYNEGVSFDY (SEQ ID NO: *44*)	RASESVDGFGNSFMN (SEQ ID NO: *45*)	LASNLES (SEQ ID NO: *46*)	QQNNEDPYT (SEQ ID NO: *47*)

[00211] In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy or light chain CDR as provided in the tables above. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy or light chain CDR as provided in the tables above and binds to non-human primate CD8. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy or light chain CDR as provided in the tables above and binds to human CD8.

In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence selected from SEQ ID NO: 45-47. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence of SEQ ID NO: 45. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence of SEQ ID NO: 46. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain CDR having a sequence of SEQ ID NO: 47. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence selected from SEQ ID NO: 42-44. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence of SEQ ID NO: 42. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence of SEQ ID NO: 43. In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain CDR having a sequence of SEQ ID NO: 44. The CDRs referenced in the embodiments throughout the present specification can be interchanged with the CDRs that are characterized by different formats, such as Kabat and IMGT.

[00212] In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a light chain variable region having a LCDR1, a LCDR2, and a LCDR3, wherein the LCDR1 has a sequence of SEQ ID NO: 45, the LCDR2 has a sequence of SEQ ID NO: 46, and the LCDR3 has a sequence of SEQ ID NO: 47.

[00213] In some embodiments, a polypeptide, an antibody, or antibody binding fragment thereof, comprises a heavy chain variable region having a HCDR1, a HCDR2, and a HCDR3, wherein the HCDR1 has a sequence of SEQ ID NO: 42, the HCDR2 has a sequence of SEQ ID NO: 43, and the HCDR3 has a sequence of SEQ ID NO: 44.

[00214] In some embodiments, a polypeptide, an antibody or antibody binding fragment thereof, comprises: (i) a light chain having any one of the foregoing recited combinations of LCDR1, LCDR2, and LCDR3 sequences; and (ii) a heavy chain having any one of the foregoing recited combinations of HCDR1, HCDR2, and HCDR3 sequences.

[00215] The different CDR motifs can be combined in any combination including those not depicted in the table above. For example, the following embodiments are provided as non-limiting examples of such combinations.

[00216] In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises: (i) a light chain variable region comprising light chain CDR1, CDR2, and

CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 45; the light chain CDR2 has the amino acid sequence of SEQ ID NO: 46; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 47; and (ii) a heavy chain variable region comprising heavy chain CDR1, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 42; the heavy chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 43; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 44; or variants of any of the foregoing.

[00217] Although the preceding paragraphs may make reference to CDRs under the Chothia system the equivalent CDR sequences can be used from the IMGT and Kabat designations.

[00218] In some embodiments, the light chain variable region CDR1 is replaced with any of the other light chain CDR1 sequences. In some embodiments, the light chain variable region CDR2 is replaced with any of the other light chain CDR2 sequences. In some embodiments, the light chain variable region CDR3 is replaced with any of the other light chain CDR3 sequences. In some embodiments, the heavy chain variable region CDR1 is replaced with any of the other heavy chain CDR1 sequences. In some embodiments, the heavy chain variable region CDR2 is replaced with any of the other heavy chain CDR2 sequences. In some embodiments, the heavy chain variable region CDR3 is replaced with any of the other heavy chain CDR3 sequences.

[00219] In some embodiments, the polypeptide comprises a heavy chain variable region peptide having one of the following sequences, or a variant thereof:

SEQ ID NO:	AB ID NO.	Sequence
48	CD8AB1	EVQLQQSGPELVKPGASVKISCKASRYTFTDYNLHWVKLSHEKSL EWIGFIYPYNGGTGYNQKFKNKAKLTVDYSSSTAYMELRSLTSVD AAVYYCARDHRYNEGVSFDYWGQGTTLTVSS

[00220] In some embodiments, the polypeptide comprises a light chain variable region peptide having one of the following sequences, or a variant thereof:

SEQ ID NO:	AB ID NO.	Sequence
49	CD8AB1	NIVLTQSPASLAVSLGQRATISCRASESVDGFGNSFMNWYQQKPG QSPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATY YCQQNNEDPYTFGGGTKLEIKR

[00221] In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide of SEQ ID NO: 48. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_L peptide of SEQ ID NO: 49. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises

a V_H peptide and a V_L peptide, wherein the wherein the V_H peptide comprises a sequence of SEQ ID NO: 48, or a variant thereof; and the V_L peptide comprises a sequence of SEQ ID NO: 49, or a variant thereof. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide and a V_L peptide, wherein the wherein the V_H peptide comprises a sequence of SEQ ID NO: 48, or a variant thereof; and the V_L peptide comprises a sequence of SEQ ID NO: 49, or a variant thereof, and the polypeptide, the antibody, or antigen binding fragment thereof, binds to non-human primate CD8. In some embodiments, a polypeptide, an antibody, or antigen binding fragment thereof, comprises a V_H peptide and a V_L peptide, wherein the wherein the V_H peptide comprises a sequence of SEQ ID NO: 48, or a variant thereof; and the V_L peptide comprises a sequence of SEQ ID NO: 49, or a variant thereof, and the polypeptide, the antibody, or antigen binding fragment thereof, binds to human CD8. In some embodiments, the V_H peptide comprises a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence of SEQ ID NO: 49.

[00222] The V_H and the V_L sequences can be in any format, including, but not limited to an scFv format where the V_H and V_L regions are linked with a peptide linker. Examples of peptide linkers that can be used to link various peptides provided for herein include, but are not limited to: (GGGGS)n (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. In some embodiments, the variable regions are not linked with a peptide linker. In some embodiments, the polypeptide comprises SEQ ID NO: 48 and SEQ ID NO: 49.

[00223] As provided for herein, the polypeptide, antibodies, or antigen binding fragments thereof can be variants of the sequences.

[00224] The sequences of the polypeptides or antibodies can be modified to yield human IgG antibodies. The conversion of the sequences provided herein can be modified to yield other types of antibodies. The CDRs can also be linked to other antibodies, proteins, or molecules to create antibody fragments that bind CD8.

[00225] In some embodiments, a polypeptide or an antibody as provided herein is a targeting moiety on the surface of an engineered viral particle. In some embodiments, the targeting moiety allows for binding to a target cell. In some embodiments, the target binding domain ("T") is a CD8 binding moiety, such as a polypeptide or an antibody as provided herein. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50:

NIVLTQSPASLAVSLGQRATISCRASESVDGFGNSFMNWYQQKPGQSPKLLI
YLASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGG
GTKLEIKRGGGGSGGGGSGGGGSGGGGSEVQLQQSGPELVKPGASVKISCKA
SRYTFTDYNLHWVKLSHEKSLEWIGFIYPYNGGTGYNQKFKNKAKLTVDYSS
STAYMELRSLTSVDAAVYYCARDHRYNEGVSFDYWGQGTTLTVSS (SEQ ID
NO: 50)

or is substantially similar to SEQ ID NO: 50, or is an active fragment of SEQ ID NO: 50. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 50. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 50. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 50. In some embodiments, the target binding domain ("T") comprises a sequence as set forth in SEQ ID NO: 50. In some embodiments, the target binding domain ("T") as set forth in SEQ ID NO: 50 is an antibody, or an antigen binding fragment thereof. In some embodiments, the targeting moiety is an anti-CD8 antibody.

[00226] In some embodiments, a polypeptide or an antibody as provided for herein is a targeting moiety on the surface of an engineered viral particle. In some embodiments, the engineered viral particle is a pseudotyped viral-like particle. In some embodiments, the targeting moiety allows for binding to a target cell. In some embodiments, the target binding domain ("T") is a CD8 binding moiety, such as a polypeptide or an antibody as provided herein. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51:

EVQLQQSGPELVKPGASVKISCKASRYTFTDYNLHWVKLSHEKSLEWIGFIY
PYNGGTGYNQKFKNKAKLTVDYSSSTAYMELRSLTSVDAAVYYCARDHRYNE
GVSFDYWGQGTTLTVSSGGGGSGGGGSGGGGSGGGGSNIVLTQSPASLAVSL
GQRATISCRASESVDGFGNSFMNWYQQKPGQSPKLLIYLASNLESGVPARFS
GSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGTKLEIKR (SEQ ID
NO: 51)

or is substantially similar to SEQ ID NO: 51, or is an active fragment of SEQ ID NO: 51. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 51. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 51. In some embodiments, the target binding domain ("T") comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 51. In some embodiments, the target binding domain ("T") comprises a sequence as set forth in SEQ ID NO: 51. In some embodiments, the target

binding domain ("T") as set forth in SEQ ID NO: 51 is an antibody, or an antigen binding fragment thereof. In some embodiments, the targeting moiety is an anti-CD8 antibody. In some embodiments, the anti-CD8 antibody binds to non-human primate CD8. In some embodiments, the anti-CD8 antibody binds to human CD8.

Targeting moieties comprising an Fc domain

[00227] In some embodiments, the V_H and V_L polypeptides are linked to a stalk portion S_1 comprising an Fc region. In some embodiments, the Fc region is as provided for herein. In some embodiments, the Fc region is a variant Fc region as provided for herein. Non-limiting mutations in the Fc region are provided for herein. In some embodiments, the variant Fc region comprises a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28 as provided for herein. In some embodiments, the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A as provided for herein. In some embodiments, the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A as provided for herein. In some embodiments, the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A as provided for herein. As provided for herein, the heavy chain can be linked to a Fc region. In some embodiments, the Fc region further comprises (*e.*g.linked to) a transmembrane domain. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. Examples of ECD include, but are not limited to, a CD8 and/or CD28 extracellular domain as provided for herein. Examples of T_M include, but are not limited to, a CD8 and/or CD28 transmembrane domain as provided for herein. In some embodiments, X_1 comprises a T_M and the ECD and ICD are absent. In some embodiments, X_1 comprises an ECD, a T_M, and the ICD is absent. In some embodiments, X_1 comprises a T_M and an ICD and the ECD is absent. In some embodiments, X_1 comprises an ECD, a T_M, and an ICD. In any of the following embodiments, it is to be understood that the ECD, the

ICD, or both may be optionally absent. Accordingly, an embodiment wherein X_1 comprises a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD comprising an Env incorporation motif is understood to encompass the following X_1 members: i) a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD comprising an Env incorporation motif; ii) a CD8 and/or CD28 T_M, and an ICD comprising an Env incorporation motif wherein the ECD is absent; iii) a CD8 and/or CD28 ECD, and a CD8 and/or CD28 T_M, wherein the ICD is absent; and iv) a CD8 and/or CD28 T_M wherein both the ECD and the ICD are absent. Similarly, an embodiment wherein X_1 comprises a CD8 and/or CD28 T_M and an ICD comprising an Env incorporation motif is understood to encompass the following X_1 members: i) a CD8 and/or CD28 T_M and an ICD comprising an Env incorporation motif; and ii) a CD8 and/or CD28 T_M wherein the ICD is absent. Similarly, an embodiment wherein X_1 comprises a CD8 and/or CD28 ECD and a CD8 and/or CD28 T_M is understood to encompass the following X_1 members: i) a CD8 and/or CD28 ECD and a CD8 and/or CD28 T_M; and ii) a CD8 and/or CD28 T_M wherein the ECD is absent. It is to be further understood that the preceding explanation is also true in embodiments where a specific ECD, T_M, or ICD are not recited. For example, an embodiment wherein X_1 comprises an ECD, a CD8 and/or CD28 T_M, and an ICD would be understood to encompass the following X_1 members: i) an ECD, a CD8 and/or CD28 T_M, and an ICD; ii) an ECD, and a CD8 and/or CD28 T_M wherein the ICD is absent; iii) a CD8 and/or CD28 T_M, and an ICD wherein the ECD is absent; and iv) a CD8 and/or CD28 T_M wherein the ECD and the ICD are absent. Similarly, an embodiment wherein X_1 comprises a CD8 and/or CD28 T_M and an ICD is understood to encompass the following X_1 members: i) a CD8 and/or CD28 T_M and an ICD; and ii) a CD8 and/or CD28 T_M wherein the ICD is absent. Similarly, an embodiment wherein X_1 comprises an ECD and a CD8 and/or CD28 T_M is understood to encompass the following X_1 members: i) an ECD and a CD8 and/or CD28 T_M; and ii) a CD8 and/or CD28 T_M wherein the ECD is absent. Unless explicitly stated, the preceding examples and explanations are applicable to any embodiments that follow.

[00228] In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, X_1 comprises an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, X_1 comprises an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, X_1 comprises an ECD, a CD8 and/or CD28 T_M,

and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein.

[00229] In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region comprising a transmembrane domain as provided for herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or absent. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1)

comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L polypeptides bind to an immune cell, such as those provided herein.

[00230] In some embodiments, a V_H peptide having a sequence as set forth in SEQ ID NO: 36 and a V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to an a stalk portion (S_1) comprising Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/ or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 linked to a stalk portion (S_1) comprising an

Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L polypeptides bind to an immune cell, such as those provided herein.

[00231] In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region comprising a transmembrane domain as provided for herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or absent. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1)

comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L polypeptides bind to an immune cell, such as those provided herein.

[00232] In some embodiments, a polypeptide is provided comprising a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37.

[00233] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_H peptide and a V_L peptide comprises a light chain CDR having a sequence of SEQ ID NO: 33-35; and/or a heavy chain CDR having a sequence of SEQ ID NO: 30-32. In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_H peptide and a V_L peptide comprise a light chain CDR1 having a sequence of SEQ ID NO: 33; a light chain CDR2 having a sequence of SEQ ID NO: 34; a light chain CDR3 having a sequence of SEQ ID NO: 35; and/or a heavy chain CDR1 having a sequence of SEQ ID NO: 30; a heavy chain CDR2 having a sequence of SEQ ID NO: 31; and

a heavy chain CDR3 having a sequence of SEQ ID NO: 32. In some embodiments, the CDRs in the V_H or V_L chain are as set forth in the combinations provided for herein.

[00234] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 33; a LCDR2 having a sequence of SEQ ID NO: 34; and a LCDR3 having a sequence of SEQ ID NO: 35; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 30; a HCDR2 having a sequence of SEQ ID NO: 31; and a HCDR3 having a sequence of SEQ ID NO: 32.

[00235] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 33, wherein the LCDR1 comprises at most 1 conservative amino acid substitution, a LCDR2 having a sequence of SEQ ID NO: 34, wherein the LCDR2 comprises at most 1 conservative amino acid substitution, and a LCDR3 having a sequence of SEQ ID NO: 35, wherein the LCDR3 comprises at most 1 conservative amino acid substitution; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 30, wherein the HCDR1 comprises at most 1 conservative amino acid substitution, a HCDR2 having a sequence of SEQ ID NO: 31, wherein the HCDR2 comprises at most 1 conservative amino acid substitution, and a HCDR3 having a sequence of SEQ ID NO: 32, wherein the HCDR3 comprises at most 1 conservative amino acid substitution.

[00236] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence of SEQ ID NO: 36 and the V_L peptide comprises a sequence of SEQ ID NO: 37.

[00237] In some embodiments, the polypeptide as provided herein binds to non-human primate CD7. In some embodiments, the polypeptide as provided herein binds to human CD7.

[00238] As provided for herein, the different polypeptides (V_H or V_L) described herein can be linked with a peptide linker or not linked with a peptide linker and instead for a continuous

sequence. In some embodiments, the peptide linker comprises a sequence of $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. The linked peptide format can be represented by a formula of V_H-Z-V_L or V_L-Z-V_H, wherein Z is the peptide linker. In some embodiments, Z is $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5.

[00239] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_L-Z-V_H comprises a heavy chain variable region as set forth in SEQ ID NO: 36 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a light chain variable region as set forth in SEQ ID NO: 37. In some embodiments, the polypeptide comprising a V_L linked via a peptide linker to a V_H has the sequence as set forth below,

DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESIS
GIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKRGG
GGSGGGGSGGGGSGGGGSQVQLQQPGAELVKPGASVKLSCKASGYPFTSYW
IHWVKQRPGRGLEWLGRIDPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLS
SLTSEDSAVYYCARSPYYSNDNSMDYWGQGTSVTVSS (SEQ ID NO: 38).

[00240] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 38. In some embodiments, the polypeptide as set forth in SEQ ID NO: 38 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD7 antibody. In some embodiments, the anti-CD7 antibody binds to non-human primate CD7. In some embodiments, the anti-CD7 antibody binds to human CD7.

[00241] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_H-Z-V_L comprises a light chain variable region as set forth in SEQ ID NO: 37 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a heavy chain variable region as set forth in SEQ ID NO: 36. In some embodiments, the polypeptide comprising a V_H linked via a peptide linker to a V_L has the sequence as set forth below,

QVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGLEWLGRI
DPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARSPYYS
NDNSMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSDILLTQSPAILSVS
PGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESISGIPSRFSGSGSGT
DFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKR (SEQ ID NO: 39).

[00242] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 39. In some embodiments, the polypeptide as set forth in SEQ ID NO: 39 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD7 antibody. In some embodiments, the anti-CD7 antibody binds to non-human primate CD7. In some embodiments, the anti-CD7 antibody binds to human CD7.

[00243] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some

embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for

herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00244] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a

T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00245] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain, such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence having a

sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 38 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00246] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain, such as those provided

herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 39 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is

anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00247] In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1, wherein T is a target binding domain and S_1 is a stalk portion, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98:

METDTLLLWVLLLWVPGSTGDSAQVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGLEWLGRI
DPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARSPYYSNDNSMDYWGQGTSVTVSSGGGGS
GGGGSGGGGSGGGGSDILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESISGIPSRFSG
SGSGTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKRASGGGGSGGGGSGGGGSEPKSCDKTHTCPPCP
APEAAGGPSVFLFPPKPKDTLMASRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV
LTVLAQDWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNAYTQKSLSLSPGKKIEVMYPPPYL
DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNRVRQGYS
(SEQ ID NO: 98)

or is substantially similar to SEQ ID NO: 98, or is an active fragment of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence of SEQ ID NO: 98.

[00248] In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 167:

SAQVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGLEWLGR
IDPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARSPYY
SNDNSMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSDILLTQSPAILSV
SPGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESISGIPSRFSGS
GSGTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKRASGGGGSGG
GGSGGGGSEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMASRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLAQ
DWLNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNAYTQKSLSLSPGKKIEVMYPPPYLDNEKSNGTI

IHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRS
RLLHSDYMNRVRQGYS (SEQ ID NO: 167)

[00249] In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having 90% identity to SEQ ID NO: 167. In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having 95% identity to SEQ ID NO: 167. In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having 98% identity to SEQ ID NO: 167. In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence of SEQ ID NO: 167.

[00250] In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 168:

QVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGLEWLGRID
PNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARSPYYSN
DNSMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSDILLTQSPAILSVSP
GERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESISGIPSRFSGSGS
GTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKRASGGGGSGGGG
SGGGGSEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMASRTPEVTC
VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLAQDW
LNGKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNAYTQKSLSLSPGKKIEVMYPPPYLDNEKSNGTIIH
VKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRL
LHSDYMNRVRQGYS (SEQ ID NO: 168)

[00251] In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having 90% identity to SEQ ID NO: 168. In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having 95% identity to SEQ ID NO: 168. In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence having 98% identity to SEQ ID NO: 168. In some embodiments, the targeting moiety comprising a formula of T-S1 comprises an amino acid sequence of SEQ ID NO: 168.

[00252] In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1, wherein T is a target binding domain and S_1 is a stalk portion, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, and

wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98.

[00253] In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1, wherein T is a target binding domain comprising a V_H and a V_L, and S_1 is a stalk portion, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding

domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-S_1 comprises an amino acid sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, and wherein the stalk portion "S_1" of the polypeptide corresponds to amino acids 284-634 of SEQ ID NO: 98.

[00254] In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1, wherein T is a target binding domain, L_1 is a polypeptide linker or is absent, Fc is a variant Fc domain as provided for herein, L_2 is a polypeptide linker or is absent, and X_1 is a polypeptide comprising a transmembrane domain, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid

sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98.

[00255] In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1, wherein T is a target binding domain comprising a V_H and a V_L, L_1 is a polypeptide linker or is absent, Fc is a variant Fc domain as provided for herein, L_2 is a polypeptide linker or is absent, and X_1 is a polypeptide comprising a transmembrane domain, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the

target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-X_1 comprises an amino acid sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, and X_1 corresponds to amino acids 543-634 of SEQ ID NO: 98.

[00256] In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD, wherein T is a target binding domain, L_1 is a polypeptide linker or is absent, Fc is a variant Fc domain as provided for herein, L_2 is a polypeptide linker or is absent, ECD is an extracellular domain, T_M is a transmembrane domain, and ICD is an intracellular domain comprising a env incorporation motif, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of

SEQ ID NO: 98, L_2 is absent, ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98.

[00257] In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD, wherein T is a target binding domain comprising a V_H and a V_L, L_1 is a polypeptide linker or is absent, Fc is a variant Fc domain as provided for herein, L_2 is a polypeptide linker or is absent, ECD is an extracellular domain, T_M is a transmembrane domain, and ICD is an intracellular domain comprising a env incorporation motif, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 90% identical to a sequence

of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid of SEQ ID NO: 98, wherein the V_H of the target binding domain corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises amino acids 284-301 of SEQ ID NO: 98, Fc comprises amino acids 302-542 of SEQ ID NO: 98, L_2 is absent ECD comprises amino acids 543-584 of SEQ ID NO: 98, T_M comprises amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises amino acids 627-634 of SEQ ID NO: 98.

[00258] In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD, wherein T is a target binding domain, L_1 is a polypeptide linker or

is absent, Fc is a variant Fc domain as provided for herein, L_2 is a polypeptide linker or is absent, ECD is an extracellular domain, T_M is a transmembrane domain, and ICD is an intracellular domain comprising a env incorporation motif, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide comprises an amino acid sequence SEQ ID NO: 39 and corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide comprises an amino acid sequence SEQ ID NO: 39 and corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide comprises an amino acid sequence SEQ ID NO: 39 and corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence

of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide comprises an amino acid sequence SEQ ID NO: 39 and corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence of SEQ ID NO: 98, wherein the target binding domain "T" of the polypeptide comprises an amino acid sequence SEQ ID NO: 39 and corresponds to amino acids 25-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98.

[00259] In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD, wherein T is a target binding domain comprising a V_H and a V_L, L_1 is a polypeptide linker or is absent, Fc is a variant Fc domain as provided for herein, L_2 is a polypeptide linker or is absent, ECD is an extracellular domain, T_M is a transmembrane domain, and ICD is an intracellular domain comprising a env incorporation motif, comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 98, wherein the V_H of

the target binding domain comprises an amino acid sequence of SEQ ID NO: 36 and corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain comprises an amino acid sequence of SEQ ID NO: 37 and corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain comprises an amino acid sequence of SEQ ID NO: 36 and corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain comprises an amino acid sequence of SEQ ID NO: 37 and corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain comprises an amino acid sequence of SEQ ID NO: 36 and corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain comprises an amino acid sequence of SEQ ID NO: 37 and corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence

of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain comprises an amino acid sequence of SEQ ID NO: 36 and corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain comprises an amino acid sequence of SEQ ID NO: 37 and corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98. In some embodiments, the polypeptide provided for herein comprising the formula of T-L_1-Fc-L_2-ECD-T_M-ICD comprises an amino acid sequence of SEQ ID NO: 98, wherein the V_H of the target binding domain comprises an amino acid sequence of SEQ ID NO: 36 and corresponds to amino acids 25-150 of SEQ ID NO: 98, the V_L of the target binding domain comprises an amino acid sequence of SEQ ID NO: 37 and corresponds to amino acids 172-283 of SEQ ID NO: 98, L_1 comprises an amino acid sequence of SEQ ID NO: 72 and corresponds to amino acids 284-301 of SEQ ID NO: 98, Fc comprises an amino acid sequence of SEQ ID NO: 104 and corresponds to amino acids 302-542 of SEQ ID NO: 98, L_2 is absent, ECD comprises an amino acid sequence of SEQ ID NO: 60 and corresponds to amino acids 543-584 of SEQ ID NO: 98, T_M comprises an amino acid sequence of SEQ ID NO: 62 and corresponds to amino acids 585-612 of SEQ ID NO: 98, and ICD comprises amino acids 613-634 of SEQ ID NO: 98, wherein the env incorporation motif comprises an amino acids sequence of SEQ ID NO: 63 and corresponds to amino acids 627-634 of SEQ ID NO: 98.

[00260] In some embodiments, a V_H peptide having a sequence as set forth in SEQ ID NO: 48 and a V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L

peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L peptides bind to an immune cell, such as those provided herein.

[00261] In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to

a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region further comprising a transmembrane domain. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, TM is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to an a stalk portion (S_1) comprising Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%

identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 linked to a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle,

such as those provided for herein. In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, V_H and V_L peptides bind to an immune cell, such as those provided herein.

[00262] In some embodiments, a polypeptide is provided comprising a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49.

[00263] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_H peptide and a V_L peptide comprises a light chain CDR having a sequence of SEQ ID NO: 45-47; and/or a heavy chain CDR having a sequence of SEQ ID NO: 42-44. In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_H peptide and a V_L peptide comprise a light chain CDR1 having a sequence of SEQ ID NO: 45; a light chain CDR2 having a sequence of SEQ ID NO: 46; a light chain CDR3 having a sequence of SEQ ID NO: 47; and/or a heavy chain CDR1 having a sequence of SEQ ID NO: 42; a heavy chain CDR2 having a sequence of SEQ ID NO: 43; and a heavy chain CDR3 having a sequence of SEQ ID NO: 44. In some embodiments, the CDRs in the V_H or V_L chain are as set forth in the combinations provided for herein.

[00264] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 45; a LCDR2 having a sequence of SEQ ID NO: 46; and a LCDR3 having a sequence of SEQ ID

NO: 47; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 42; a HCDR2 having a sequence of SEQ ID NO: 43; and a HCDR3 having a sequence of SEQ ID NO: 44.

[00265] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 45, wherein the LCDR1 comprises at most 1 conservative amino acid substitution, a LCDR2 having a sequence of SEQ ID NO: 46, wherein the LCDR2 comprises at most 1 conservative amino acid substitution, and a LCDR3 having a sequence of SEQ ID NO: 47, wherein the LCDR3 comprises at most 1 conservative amino acid substitution; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 42, wherein the HCDR1 comprises at most 1 conservative amino acid substitution, a HCDR2 having a sequence of SEQ ID NO: 43, wherein the HCDR2 comprises at most 1 conservative amino acid substitution, and a HCDR3 having a sequence of SEQ ID NO: 44, wherein the HCDR3 comprises at most 1 conservative amino acid substitution.

[00266] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence of SEQ ID NO: 48 and the V_L peptide comprises a sequence of SEQ ID NO: 49.

[00267] In some embodiments, the polypeptide as provided herein binds to non-human primate CD8. In some embodiments, the polypeptide as provided herein binds to human CD8.

[00268] As provided for herein, the different polypeptides (V_H or V_L) described herein can be linked with a peptide linker or not linked with a peptide linker and instead for a continuous sequence. In some embodiments, the peptide linker comprises a sequence of $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. The linked peptide format can be represented by a formula of V_H-Z-V_L or V_L-Z-V_H, wherein Z is the peptide linker. In some embodiments, Z is $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5.

[00269] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_L-Z-V_H comprises a heavy chain variable region as set forth in SEQ ID NO: 48 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a light chain variable region as set forth in SEQ ID NO: 49. In some embodiments, the polypeptide comprising a V_L linked via a peptide linker to a V_H has the sequence as set forth below,

NIVLTQSPASLAVSLGQRATISCRASESVDGFGNSFMNWYQQKPGQSPKLLIY LASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGT KLEIKRGGGGSGGGGSGGGGSGGGGSEVQLQQSGPELVKPGASVKISCKASR YTFTDYNLHWVKLSHEKSLEWIGFIYPYNGGTGYNQKFKNKAKLTVDYSSST AYMELRSLTSVDAAVYYCARDHRYNEGVSFDYWGQGTTLTVSS (SEQ ID NO: 50).

[00270] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 50. In some embodiments, the polypeptide as set forth in SEQ ID NO: 50 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD8 antibody. In some embodiments, the anti-CD8 antibody binds to non-human primate CD8. In some embodiments, the anti-CD8 antibody binds to human CD8.

[00271] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_H-Z-V_L comprises a light chain variable region as set forth in SEQ ID NO: 49 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a heavy chain variable region as set forth in SEQ ID NO: 48. In some embodiments, the polypeptide comprising a V_H linked via a peptide linker to a V_L has the sequence as set forth below,

EVQLQQSGPELVKPGASVKISCKASRYTFTDYNLHWVKLSHEKSLEWIGFIYP YNGGTGYNQKFKNKAKLTVDYSSSTAYMELRSLTSVDAAVYYCARDHRYN EGVSFDYWGQGTTLTVSSGGGGSGGGGSGGGGSGGGGSNIVLTQSPASLAVS LGQRATISCRASESVDGFGNSFMNWYQQKPGQSPKLLIYLASNLESGVPARFS GSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGTKLEIKR (SEQ ID NO: 51).

[00272] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 51. In some embodiments, the polypeptide as set forth in SEQ ID NO: 51 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD8 antibody. In some embodiments, the anti-CD8 antibody binds to non-human primate CD8. In some embodiments, the anti-CD8 antibody binds to human CD8.

[00273] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain, such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00274] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region, such

as those provided herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain, such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a TM, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises

an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00275] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain, such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or

CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 50 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00276] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region, such as those provided herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region, said Fc region further comprising a transmembrane domain, such as those provided herein. In some embodiments, the Fc region further comprising a transmembrane domain has a formula of L_1-Fc-L_2-X_1, wherein L_1 is a linker as provided for herein or is absent, Fc is a variant Fc region as provided for herein, L_2 is a linker as provided for herein or is absent, and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided

for herein, X_1 may comprises a polypeptide having the formula ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 51 and comprising a stalk portion (S_1) comprising an Fc region (L_1-Fc-L_2-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_1, Fc, L_2, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

Targeting moieties comprising flexible polypeptides

[00277] In some embodiments, the V_H and V_L polypeptides are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the V_H and V_L polypeptides are linked to a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein or is absent, T_M is a transmembrane domain as provided for herein, and ICD is an intracellular domain as provided for herein or is absent. Examples of ECD include, but are not limited to, a CD8 and/or CD28 ECD as provided for herein. Examples of T_M include, but are not limited to, a CD8 and/or CD28 transmembrane domain as provided for herein. In any of the following embodiments, it is to be understood that the ECD, the ICD, or both may be optionally absent. Accordingly, an embodiment wherein X_1 comprises a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD comprising an Env incorporation motif is understood to encompass the following X_1 members: i) a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD comprising an Env incorporation motif; ii) a CD8 and/or CD28 T_M, and an ICD comprising an Env incorporation motif wherein the ECD is absent; iii) a CD8 and/or CD28 ECD, and a CD8 and/or CD28 T_M, wherein the ICD is absent; and iv) a CD8 and/or CD28 T_M wherein both the ECD and the ICD are absent. Similarly, an embodiment wherein X_1 comprises a CD8 and/or CD28 T_M and an ICD comprising an Env incorporation motif is understood to encompass the following X_1 members: i) a CD8 and/or CD28 T_M and an ICD comprising an Env incorporation motif; and ii) a CD8 and/or CD28 T_M wherein the ICD is absent. Similarly, an embodiment wherein X_1 comprises a CD8 and/or CD28 ECD and a CD8 and/or CD28 T_M is understood to encompass the following X_1 members: i) a CD8 and/or CD28 ECD and a CD8 and/or CD28 T_M; and ii) a CD8 and/or CD28 T_M wherein the ECD is absent. It is to be further understood that the preceding explanation is also true in embodiments where a specific ECD, T_M, or ICD are not recited. For example, an embodiment wherein X_1 comprises an ECD, a CD8 and/or CD28 T_M, and an ICD would be understood to encompass the following X_1 members: i) an ECD, a CD8 and/or CD28 T_M, and an ICD; ii) an ECD, and a CD8 and/or CD28 T_M wherein the ICD is absent; iii) a CD8 and/or CD28 T_M, and an ICD wherein the ECD is absent; and iv) a CD8 and/or CD28 T_M wherein the ECD and the ICD are absent. Similarly, an embodiment wherein

X_1 comprises a CD8 and/or CD28 T_M and an ICD is understood to encompass the following X_1 members: i) a CD8 and/or CD28 T_M and an ICD; and ii) a CD8 and/or CD28 T_M wherein the ICD is absent. Similarly, an embodiment wherein X_1 comprises an ECD and a CD8 and/or CD28 T_M is understood to encompass the following X_1 members: i) an ECD and a CD8 and/or CD28 T_M; and ii) a CD8 and/or CD28 T_M wherein the ECD is absent. Unless explicitly stated, the preceding examples and explanations are applicable to any embodiments that follow.

[00278] In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, X_1 comprises an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, X_1 comprises an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, X_1 comprises an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, X_1 comprises a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein.

[00279] In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments the flexible polypeptide (L_3) further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or a fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some

embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H and V_L polypeptides provided herein linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_3, X_1, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L polypeptides bind to an immune cell, such as those provided herein.

[00280] In some embodiments, a V_H peptide having a sequence as set forth in SEQ ID NO: 36 and a V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID

NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 36 and V_L peptide having a sequence as set forth in SEQ ID NO: 37 linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_3, X_1, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L peptides bind to an immune cell, such as those provided herein.

[00281] In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a

transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein, or is absent. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising

a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37 linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_3, X_1, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L peptides bind to an immune cell, such as those provided herein.

[00282] In some embodiments, a polypeptide is provided comprising a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37.

[00283] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_H peptide and a V_L peptide comprises a light chain CDR having a sequence of SEQ ID NO: 33-35; and/or a heavy chain CDR having a sequence of SEQ ID NO: 30-32. In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide,

wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_H peptide and a V_L peptide comprise a light chain CDR1 having a sequence of SEQ ID NO: 33; a light chain CDR2 having a sequence of SEQ ID NO: 34; a light chain CDR3 having a sequence of SEQ ID NO: 35; and/or a heavy chain CDR1 having a sequence of SEQ ID NO: 30; a heavy chain CDR2 having a sequence of SEQ ID NO: 31; and a heavy chain CDR3 having a sequence of SEQ ID NO: 32. In some embodiments, the CDRs in the V_H or V_L chain are as set forth in the combinations provided for herein.

[00284] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 33; a LCDR2 having a sequence of SEQ ID NO: 34; and a LCDR3 having a sequence of SEQ ID NO: 35; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 30; a HCDR2 having a sequence of SEQ ID NO: 31; and a HCDR3 having a sequence of SEQ ID NO: 32.

[00285] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 36; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 37; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 33, wherein the LCDR1 comprises at most 1 conservative amino acid substitution, a LCDR2 having a sequence of SEQ ID NO: 34, wherein the LCDR2 comprises at most 1 conservative amino acid substitution, and a LCDR3 having a sequence of SEQ ID NO: 35, wherein the LCDR3 comprises at most 1 conservative amino acid substitution; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 30, wherein the HCDR1 comprises at most 1 conservative amino acid substitution, a HCDR2 having a sequence of SEQ ID NO: 31, wherein the HCDR2 comprises at most 1 conservative amino acid substitution, and a HCDR3

having a sequence of SEQ ID NO: 32, wherein the HCDR3 comprises at most 1 conservative amino acid substitution.

[00286] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence of SEQ ID NO: 36 and the V_L peptide comprises a sequence of SEQ ID NO: 37.

[00287] In some embodiments, the polypeptide as provided herein binds to non-human primate CD7. In some embodiments, the polypeptide as provided herein binds to human CD7.

[00288] As provided for herein, the different polypeptides (V_H or V_L) described herein can be linked with a peptide linker or not linked with a peptide linker and instead for a continuous sequence. In some embodiments, the peptide linker comprises a sequence of $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. The linked peptide format can be represented by a formula of V_H-Z-V_L or V_L-Z-V_H, wherein Z is the peptide linker. In some embodiments, Z is $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5.

[00289] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_L-Z-V_H comprises a heavy chain variable region as set forth in SEQ ID NO: 36 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a light chain variable region as set forth in SEQ ID NO: 37. In some embodiments, the polypeptide comprising a V_L linked via a peptide linker to a V_H has the sequence as set forth below,

DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESIS
GIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKRGG
GGSGGGGSGGGGSGGGGSQVQLQQPGAELVKPGASVKLSCKASGYPFTSYW
IHWVKQRPGRGLEWLGRIDPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLS
SLTSEDSAVYYCARSPYYSNDNSMDYWGQGTSVTVSS (SEQ ID NO: 38).

[00290] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 38. In some embodiments, the polypeptide comprises a sequence

as set forth in SEQ ID NO: 38. In some embodiments, the polypeptide as set forth in SEQ ID NO: 38 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD7 antibody. In some embodiments, the anti-CD7 antibody binds to non-human primate CD7. In some embodiments, the anti-CD7 antibody binds to human CD7.

[00291] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_H-Z-V_L comprises a light chain variable region as set forth in SEQ ID NO: 37 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a heavy chain variable region as set forth in SEQ ID NO: 36. In some embodiments, a polypeptide comprising a V_H linked via a peptide linker to a V_L has the sequence as set forth below,

QVQLQQPGAELVKPGASVKLSCKASGYPFTSYWIHWVKQRPGRGLEWLGRI
DPNSGDTKYNEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARSPYYS
NDNSMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSDILLTQSPAILSVS
PGERVSFSCRASQSIGTSIHWYQQRTNDSPRLLIKYASESISGIPSRFSGSGSGT
DFTLSINSVESEDIADYYCQQSNSWPTTFGGGTKLEIKR (SEQ ID NO: 39).

[00292] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 39. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 39. In some embodiments, the polypeptide as set forth in SEQ ID NO: 39 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD7 antibody. In some embodiments, the anti-CD7 antibody binds to non-human primate CD7. In some embodiments, the anti-CD7 antibody binds to human CD7.

[00293] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, a polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the

formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M,

and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 38 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00294] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein, or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the

polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 39 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00295] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a

polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 38 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 38 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00296] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, a polypeptide comprises a sequence having

a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein, or is absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 39 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 39 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a

viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00297] In some embodiments, a V_H peptide having a sequence as set forth in SEQ ID NO: 48 and a V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and the V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein, or is absent. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and the V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide

having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide having a sequence as set forth in SEQ ID NO: 48 and V_L peptide having a sequence as set forth in SEQ ID NO: 49 linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_3, X_1, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L peptides bind to an immune cell, such as those provided herein.

[00298] In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%

identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and

an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 are linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the V_H peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49 linked to a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD are anchored to the surface of a viral particle, such as those provided for herein. In some embodiments, the identities of L_3, X_1, ECD, T_M, and ICD are as provided for herein. In some embodiments, the V_H and V_L peptides bind to an immune cell, such as those provided herein.

[00299] In some embodiments, a polypeptide is provided comprising a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49.

[00300] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_H peptide and a V_L peptide comprise a light chain CDR having a sequence of SEQ ID NO: 45-47; and/or a heavy chain CDR having a sequence of SEQ ID NO: 42-44. In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%,

91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_H peptide and a V_L peptide comprise a light chain CDR1 having a sequence of SEQ ID NO: 45; a light chain CDR2 having a sequence of SEQ ID NO: 46; a light chain CDR3 having a sequence of SEQ ID NO: 47; and/or a heavy chain CDR1 having a sequence of SEQ ID NO: 42; a heavy chain CDR2 having a sequence of SEQ ID NO: 43; and a heavy chain CDR3 having a sequence of SEQ ID NO: 44. In some embodiments, the CDRs in the V_H or V_L chain are as set forth in the combinations provided for herein.

[00301] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 45; a LCDR2 having a sequence of SEQ ID NO: 46; and a LCDR3 having a sequence of SEQ ID NO: 47; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 42; a HCDR2 having a sequence of SEQ ID NO: 43; and a HCDR3 having a sequence of SEQ ID NO: 44.

[00302] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 48; and the V_L peptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 49; provided that the V_L peptide comprises a LCDR1 having a sequence of SEQ ID NO: 45, wherein the LCDR1 comprises at most 1 conservative amino acid substitution, a LCDR2 having a sequence of SEQ ID NO: 46, wherein the LCDR2 comprises at most 1 conservative amino acid substitution, and a LCDR3 having a sequence of SEQ ID NO: 47, wherein the LCDR3 comprises at most 1 conservative amino acid substitution; and the V_H peptide comprises a HCDR1 having a sequence of SEQ ID NO: 42, wherein the HCDR1 comprises at most 1 conservative amino acid substitution, a HCDR2 having a sequence of SEQ ID NO: 43, wherein the HCDR2 comprises at most 1 conservative amino acid substitution, and a HCDR3 having a sequence of SEQ ID NO: 44, wherein the HCDR3 comprises at most 1 conservative amino acid substitution.

[00303] In some embodiments, the polypeptide comprises a V_H peptide and a V_L peptide, wherein the V_H peptide comprises a sequence of SEQ ID NO: 48 and the V_L peptide comprises a sequence of SEQ ID NO: 49.

[00304] In some embodiments, the polypeptide as provided herein binds to non-human primate CD8. In some embodiments, a polypeptide as provided herein binds to human CD8.

[00305] As provided for herein, the different polypeptides (V_H or V_L) described herein can be linked with a peptide linker or not linked with a peptide linker and instead for a continuous sequence. In some embodiments, the peptide linker comprises a sequence of $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. The linked peptide format can be represented by a formula of V_H-Z-V_L or V_L-Z-V_H, wherein Z is the peptide linker. In some embodiments, Z is $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiments, n is 1. In some embodiments, n is 2. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5.

[00306] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_L-Z-V_H comprises a heavy chain variable region as set forth in SEQ ID NO: 48 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a light chain variable region as set forth in SEQ ID NO: 49. In some embodiments, the polypeptide comprising a V_L linked via a peptide linker to a V_H has the sequence as set forth below,

NIVLTQSPASLAVSLGQRATISCRASESVDGFGNSFMNWYQQKPGQSPKLLIY LASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGT KLEIKRGGGGSGGGGSGGGGSGGGGSEVQLQQSGPELVKPGASVKISCKASR YTFTDYNLHWVKLSHEKSLEWIGFIYPYNGGTGYNQKFKNKAKLTVDYSSST AYMELRSLTSVDAAVYYCARDHRYNEGVSFDYWGQGTTLTVSS (SEQ ID NO: 50).

[00307] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 50. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 50. In some embodiments, the polypeptide as set forth in SEQ ID

NO: 50 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD8 antibody. In some embodiments, the anti-CD8 antibody binds to non-human primate CD8. In some embodiments, the anti-CD8 antibody binds to human CD8.

[00308] In some embodiments, the polypeptide comprising the linked peptide represented by a formula of V_H-Z-V_L comprises a light chain variable region as set forth in SEQ ID NO: 49 linked via a linker sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 72) to a heavy chain variable region as set forth in SEQ ID NO: 48. In some embodiments, the polypeptide comprising a V_H linked via a peptide linker to a V_L has the sequence as set forth below,

EVQLQQSGPELVKPGASVKISCKASRYTFTDYNLHWVKLSHEKSLEWIGFIYP YNGGTGYNQKFKNKAKLTVDYSSSTAYMELRSLTSVDAAVYYCARDHRYN EGVSFDYWGQGTTLTVSSGGGGSGGGGSGGGGSGGGGSNIVLTQSPASLAVS LGQRATISCRASESVDGFGNSFMNWYQQKPGQSPKLLIYLASNLESGVPARFS GSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGTKLEIKR (SEQ ID NO: 51).

[00309] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence that is at least 90% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence that is at least 95% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence that is at least 99% identical to a sequence of SEQ ID NO: 51. In some embodiments, the polypeptide comprises a sequence as set forth in SEQ ID NO: 51. In some embodiments, the polypeptide as set forth in SEQ ID NO: 51 is an antibody, or an antigen binding fragment thereof. In some embodiments, the antibody is an anti-CD8 antibody. In some embodiments, the anti-CD8 antibody binds to non-human primate CD8. In some embodiments, the anti-CD8 antibody binds to human CD8.

[00310] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the

formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M,

and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 50 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00311] In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the

polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a sequence of SEQ ID NO: 51 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00312] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a

polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein or is absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 50 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 50 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

[00313] In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3) as provided for herein. In some embodiments, the polypeptide comprises a sequence

having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide further comprising a polypeptide comprising a transmembrane domain as provided for herein. In some embodiments, the flexible polypeptide further comprising a polypeptide comprising a transmembrane domain is represented by the formula L_3-X_1, wherein L_3 is a flexible polypeptide as provided for herein and X_1 is a polypeptide comprising a transmembrane domain as provided for herein. As provided for herein, X_1 may comprise a polypeptide having the formula of ECD-T_M-ICD, wherein ECD is an extracellular domain, or fragment thereof as provided for herein, or is absent; T_M is a transmembrane domain as provided for herein; and ICD is an intracellular domain as provided for herein, or is absent. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprises a sequence having a sequence as set forth in SEQ ID NO: 51 and comprises a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising a CD8 and/or CD28 ECD, a CD8 and/or CD28 T_M, and an ICD, wherein the ICD comprises an Env incorporation motif as provided for herein. In some embodiments, the polypeptide comprising a sequence having a sequence as set forth in SEQ ID NO: 51 and comprising a stalk portion (S_1) comprising a flexible polypeptide (L_3-X_1) comprising an ECD, a T_M, and an ICD, is anchored to the surface of a

viral particle, such as those provided for herein . In some embodiments, the identities of L_3, ECD, T_M, and ICD are as provided for herein. In some embodiments, the polypeptide bind to an immune cell, such as those provided herein.

Expressed polypeptides of interest

[00314] In some embodiments, the viral particle comprising a heterologous viral glycoprotein and a targeting moiety further comprises a nucleic acid molecule encoding for a heterologous molecule of interest or "cargo." In some embodiments, the heterologous viral glycoprotein is as provided for herein. In some embodiments, the targeting moiety is as provided for herein. As used herein, heterologous molecule of interest is meant to refer to any product that may be encoded by a nucleic acid molecule. As non-limiting examples, "cargo" or "heterologous molecule of interest" may refer to an siRNA, an shRNA, a peptide, a polypeptide, a protein, a viral payload, a viral genome, or a combination thereof. In some embodiments, the heterologous molecule of interest is an siRNA, an shRNA, a non-coding RNA (e.g. a guide RNA for a CRISPR system), a peptide, a polypeptide, a protein, a viral payload, a viral genome, a chimeric antigen receptor ("CAR"), or a combination thereof. In some embodiments, the polypeptide is a CAR.

[00315] A "chimeric antigen receptor" or "CAR" as used herein refers to an antigen-binding domain that is fused, directly, or indirectly (e.g. via a hinge or transmembrane domain to an intracellular signaling domain capable of activating or stimulating an immune cell. Most commonly, the CAR's extracellular binding domain is composed of a single chain variable fragment (scFv) derived from fusing the variable heavy and light regions of a murine or humanized monoclonal antibody. Alternatively, scFvs may be used that are derived from Fab's (instead of from an antibody, e.g., obtained from Fab libraries). In various embodiments, this scFv is fused to a transmembrane domain and then to an intracellular signaling domain. However, the antigen binding domain can be any molecule that can bind to the target on the cell. For example, the antigen binding domain of a CAR can be an antibody, a scFv antibody, an antigen binding domain, an ankyrin repeat (e.g. DARPIN), a VHH domain antibody, a nanobody, single domain antibody, a FN3 domain, an affibody, an affilin, an affimer, an affitin, an alphabody, an anticalin, an avimer, a fynomer, a gastrobody, a Kunitz domain peptide, a monobody, a nanoCLAMP, an optimer, a repebody, a pronectin, a centyrin, an obody, or any combination thereof. In some embodiments, a CAR includes those that solely provide CD3ζ signals upon antigen binding. In some embodiments, the CAR includes those that provide both

costimulation (e.g. CD28 or CD137) and activation (CD3 ζ). In some embodiments, the CARs include those that provide multiple costimulation (e.g. CD28 and CD137) and activation (CD3ζ). In various embodiments, the CAR is selected to have high affinity or avidity for the antigen. In some embodiments, the antigen-binding domain binds to CD19. In some embodiments, the antigen-binding domain comprises a CD19 antibody, or fragment thereof. In some embodiments, antibody fragments are as provided for herein, such as but not limited to a scFv antibody, an antigen binding domain, an ankyrin repeat (e.g. DARPIN), a VHH domain antibody, a nanobody, single domain antibody, a FN3 domain, or any combination thereof.

[00316] In some embodiments, the antigen-binding domain of the CAR comprises an antibody, or antigen binding fragment thereof, wherein the antibody or antigen binding fragment comprises a peptide selected from the following table, which illustrates the CDRs based on Chothia numbering.

Chothia CDRs						
Ab ID No	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
CD19AB1	GYSFSSS (SEQ ID NO: 108)	YPDDSD (SEQ ID NO: 109)	HVTMIWGVII DF (SEQ ID NO: 110)	RASQGISSALA (SEQ ID NO: 111)	DASSLES (SEQ ID NO: 112)	QQFNSYPYT (SEQ ID NO: 113)

[00317] In some embodiments, the antigen-binding domain of the CAR comprises a heavy or light chain CDR as provided in the tables above. In some embodiments, the antigen-binding domain of the CAR comprises a heavy or light chain CDR as provided in the tables above and binds to non-human primate CD19. In some embodiments, the antigen-binding domain of the CAR comprises a heavy or light chain CDR as provided in the tables above and binds to human CD19. In some embodiments, a polypeptide, the antigen-binding domain of the CAR comprises a light chain CDR having a sequence selected from SEQ ID NO: 111-113. In some embodiments, the antigen-binding domain of the CAR, comprises a light chain CDR having a sequence of SEQ ID NO: 111. In some embodiments, the antigen-binding domain of the CAR comprises a light chain CDR having a sequence of SEQ ID NO: 112. In some embodiments, the antigen-binding domain of the CAR comprises a light chain CDR having a sequence of SEQ ID NO: 113. In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain CDR having a sequence selected from SEQ ID NO: 108-110. In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain CDR having a sequence of SEQ ID NO: 108. In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain CDR having a sequence of SEQ ID NO: 109. In some embodiments,

the antigen-binding domain of the CAR, comprises a heavy chain CDR having a sequence of SEQ ID NO: 110. The CDRs referenced in the embodiments throughout the present specification can be interchanged with the CDRs that are characterized by different formats, such as Kabat and IMGT.

[00318] In some embodiments, the antigen-binding domain of the CAR comprises a light chain variable region having a LCDR1, a LCDR2, and a LCDR3, wherein the LCDR1 has a sequence of SEQ ID NO: 111, the LCDR2 has a sequence of SEQ ID NO: 112, and the LCDR3 has a sequence of SEQ ID NO: 113.

[00319] In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain variable region having a HCDR1, a HCDR2, and a HCDR3, wherein the HCDR1 has a sequence of SEQ ID NO: 108, the HCDR2 has a sequence of SEQ ID NO: 109, and the HCDR3 has a sequence of SEQ ID NO: 110.

[00320] In some embodiments, the antigen-binding domain of the CAR comprises: (i) a light chain having any one of the foregoing recited combinations of LCDR1, LCDR2, and LCDR3 sequences; and (ii) a heavy chain having any one of the foregoing recited combinations of HCDR1, HCDR2, and HCDR3 sequences.

[00321] The different CDR motifs can be combined in any combination including those not depicted in the table above. For example, the following embodiments are provided as non-limiting examples of such combinations.

[00322] In some embodiments, the antigen-binding domain of the CAR comprises: (i) a light chain variable region comprising light chain CDR1, CDR2, and CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 111; the light chain CDR2 has the amino acid sequence of SEQ ID NO: 112; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 113; and (ii) a heavy chain variable region comprising heavy chain CDR1, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 108; the heavy chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 109; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 110; or variants of any of the foregoing.

[00323] Although the preceding paragraphs may make reference to CDRs under the Chothia system the equivalent CDR sequences can be used from the IMGT and Kabat designations.

[00324] In some embodiments, the light chain variable region CDR1 is replaced with any of the other light chain CDR1 sequences. In some embodiments, the light chain variable region CDR2 is replaced with any of the other light chain CDR2 sequences. In some embodiments,

the light chain variable region CDR3 is replaced with any of the other light chain CDR3 sequences. In some embodiments, the heavy chain variable region CDR1 is replaced with any of the other heavy chain CDR1 sequences. In some embodiments, the heavy chain variable region CDR2 is replaced with any of the other heavy chain CDR2 sequences. In some embodiments, the heavy chain variable region CDR3 is replaced with any of the other heavy chain CDR3 sequences.

[00325] In some embodiments, the antigen-binding domain of the CAR comprises a V_H domain, a V_L domain, or a V_H and a V_L domain. In some embodiments, the V_H domain comprises an amino acid sequence having at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, or any value or range in-between.

EVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIGWVRQMPGKGLEWMGIIY
PDDSDTRYSPSFQGQVTISADKSIRTAYLQWSSLKASDTAMYYCARHVTMIW
GVIIDFWGQGTLVTVSS (SEQ ID NO: 89)

[00326] In some embodiments, the V_H domain comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 89. In some embodiments, the V_H domain comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 89. In some embodiments, the V_H domain comprises an amino acid sequence having at least 98% identity to SEQ ID NO: 89. In some embodiments, the V_H domain comprises an amino acid sequence having at least 99% identity to SEQ ID NO: 89. In some embodiments, the V_H domain comprises an amino acid sequence having the sequence of SEQ ID NO: 89.

[00327] In some embodiments, the V_L domain comprises an amino acid sequence having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90, or any value or range in-between.

AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDAS
SLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPYTFGQGTKL
EIK (SEQ ID NO: 90)

[00328] In some embodiments, the V_L domain comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 90. In some embodiments, the V_L domain comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 90. In some embodiments, the V_L domain comprises an amino acid sequence having at least 98% identity to SEQ ID NO: 90. In some embodiments, the V_L domain comprises an amino acid sequence having at least 99% identity to SEQ ID NO: 90. In some embodiments, the V_L domain comprises an amino acid sequence having the sequence of SEQ ID NO: 90.

[00329] In some embodiments, the antigen-binding domain of the CAR comprises a V_H domain and a V_L domain. In some embodiments, the V_H and V_L domain are not linked by a linker peptide. In some embodiments, the V_H and V_L domain are linked by a linker peptide, such as those as provided for herein, including but not limited to: $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5. In some embodiment n is 1. In some embodiment n is 2. In some embodiment n is 3. In some embodiment n is 4. In some embodiment n is 5.

[00330] In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, and comprises a V_L having at least 90% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, and comprises a V_L having at least 95% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, and comprises a V_L having at least 98% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, and comprises a V_L having at least 99% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 89, and comprises a V_L having the sequence of SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 90% identity to SEQ ID NO: 89, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR

comprising a V_H domain and a V_L domain comprises a V_H domain having at least 95% identity to SEQ ID NO: 89, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 98% identity to SEQ ID NO: 89, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 99% identity to SEQ ID NO: 89, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having an amino acid sequence of SEQ ID NO: 89, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 90% identity to SEQ ID NO: 89, and comprises a V_L having at least 90% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 95% identity to SEQ ID NO: 89, and comprises a V_L having at least 90% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 90% identity to SEQ ID NO: 89, and comprises a V_L having at least 95% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 95% identity to SEQ ID NO: 89, and comprises a V_L having at least 95% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 98% identity to SEQ ID NO: 89, and comprises a V_L having at least 98% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 99% identity to SEQ ID NO: 89, and comprises a V_L having at least 99% identity to SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having an amino acid sequence of SEQ ID NO: 89, and comprises a V_L having an amino acid sequence of SEQ ID NO: 90.

[00331] In some embodiments, the antigen-binding domain of the CAR comprises a formula of V_H-Z-V_L, wherein V_H is a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 89, Z is a linker comprising the amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 91), and V_L is a light chain variable region comprising the amino acid sequence of SEQ ID NO: 90. In some embodiments, the antigen-binding domain of the CAR comprising a formula of V_H-Z-V_L has an amino acid sequence as set forth below:

EVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIGWVRQMPGKGLEWMGIIY
PDDSDTRYSPSFQGQVTISADKSIRTAYLQWSSLKASDTAMYYCARHVTMIW
GVIIDFWGQGTLVTVSSGGGGSGGGGSGGGGSAIQLTQSPSSLSASVGDRVT
ITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFT
LTISSLQPEDFATYYCQQFNSYPYTFGQGTKLEIK (SEQ ID NO: 92)

[00332] In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence of SEQ ID NO: 92. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 90% identity to a sequence of SEQ ID NO: 92. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 95% identity to a sequence of SEQ ID NO: 92. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 98% identity to a sequence of SEQ ID NO: 92. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 99% identity to a sequence of SEQ ID NO: 92. In some embodiments, the antigen-binding domain of the CAR comprises the amino acid sequence of SEQ ID NO: 92.

[00333] In some embodiments, the antigen-binding domain of the CAR comprises a formula of V_L-Z-V_H, wherein V_L is a light chain variable region comprising the amino acid sequence of SEQ ID NO: 90, Z is a linker comprising the amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 91), and V_H is a light chain variable region comprising the amino acid sequence of SEQ ID NO: 89. In some embodiments, the antigen-binding domain of the CAR comprising a formula of V_L-Z-V_H has an amino acid sequence as set forth below:

AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDAS
SLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPYTFGQGTKL
EIKGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWI
GWVRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADKSIRTAYLQWSSL
KASDTAMYYCARHVTMIWGVIIDFWGQGTLVTVSS (SEQ ID NO: 93)

[00334] In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence of SEQ ID NO: 93. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 90% identity to a sequence of SEQ ID NO: 93. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 95% identity to a sequence of SEQ ID NO: 93. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 98% identity to a sequence of SEQ ID NO: 93. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 99% identity to a sequence of SEQ ID NO: 93. In some embodiments, the antigen-binding domain of the CAR comprises the amino acid sequence of SEQ ID NO: 93.

[00335] In some embodiments, the antigen-binding domain of the CAR comprises an antibody, or antigen binding fragment thereof, wherein the antibody or antigen binding fragment comprises a peptide selected from the following table, which illustrates the CDRs based on Chothia numbering.

Chothia CDRs						
Ab ID No	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
CD19AB2	GGTFSSY (SEQ ID NO: 114)	IPIFGT (SEQ ID NO: 115)	EAVAADWLDP (SEQ ID NO: 116)	RASQSVSSSYL A (SEQ ID NO: 117)	GASSRAT (SEQ ID NO: 118)	QQYGSSRFT (SEQ ID NO: 119)

[00336] In some embodiments, the antigen-binding domain of the CAR comprises a heavy or light chain CDR as provided in the tables above. In some embodiments, the antigen-binding domain of the CAR comprises a heavy or light chain CDR as provided in the tables above and binds to non-human primate CD19. In some embodiments, the antigen-binding domain of the CAR comprises a heavy or light chain CDR as provided in the tables above and binds to human CD19. In some embodiments, a polypeptide, the antigen-binding domain of the CAR comprises a light chain CDR having a sequence selected from SEQ ID NO: 117-119. In some embodiments, the antigen-binding domain of the CAR, comprises a light chain CDR having a sequence of SEQ ID NO: 117. In some embodiments, the antigen-binding domain of the CAR comprises a light chain CDR having a sequence of SEQ ID NO: 118. In some embodiments, the antigen-binding domain of the CAR comprises a light chain CDR having a sequence of SEQ ID NO: 119. In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain CDR having a sequence selected from SEQ ID NO: 114-116. In some

embodiments, the antigen-binding domain of the CAR comprises a heavy chain CDR having a sequence of SEQ ID NO: 114. In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain CDR having a sequence of SEQ ID NO: 115. In some embodiments, the antigen-binding domain of the CAR, comprises a heavy chain CDR having a sequence of SEQ ID NO: 116. The CDRs referenced in the embodiments throughout the present specification can be interchanged with the CDRs that are characterized by different formats, such as Kabat and IMGT.

[00337] In some embodiments, the antigen-binding domain of the CAR comprises a light chain variable region having a LCDR1, a LCDR2, and a LCDR3, wherein the LCDR1 has a sequence of SEQ ID NO: 117, the LCDR2 has a sequence of SEQ ID NO: 118, and the LCDR3 has a sequence of SEQ ID NO: 119.

[00338] In some embodiments, the antigen-binding domain of the CAR comprises a heavy chain variable region having a HCDR1, a HCDR2, and a HCDR3, wherein the HCDR1 has a sequence of SEQ ID NO: 114, the HCDR2 has a sequence of SEQ ID NO: 115, and the HCDR3 has a sequence of SEQ ID NO: 116.

[00339] In some embodiments, the antigen-binding domain of the CAR comprises: (i) a light chain having any one of the foregoing recited combinations of LCDR1, LCDR2, and LCDR3 sequences; and (ii) a heavy chain having any one of the foregoing recited combinations of HCDR1, HCDR2, and HCDR3 sequences.

[00340] The different CDR motifs can be combined in any combination including those not depicted in the table above. For example, the following embodiments are provided as non-limiting examples of such combinations.

[00341] In some embodiments, the antigen-binding domain of the CAR comprises: (i) a light chain variable region comprising light chain CDR1, CDR2, and CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 117; the light chain CDR2 has the amino acid sequence of SEQ ID NO: 118; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 119; and (ii) a heavy chain variable region comprising heavy chain CDR1, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 114; the heavy chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 115; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 116; or variants of any of the foregoing.

[00342] Although the preceding paragraphs may make reference to CDRs under the Chothia system the equivalent CDR sequences can be used from the IMGT and Kabat designations.

[00343] In some embodiments, the light chain variable region CDR1 is replaced with any of the other light chain CDR1 sequences. In some embodiments, the light chain variable region CDR2 is replaced with any of the other light chain CDR2 sequences. In some embodiments, the light chain variable region CDR3 is replaced with any of the other light chain CDR3 sequences. In some embodiments, the heavy chain variable region CDR1 is replaced with any of the other heavy chain CDR1 sequences. In some embodiments, the heavy chain variable region CDR2 is replaced with any of the other heavy chain CDR2 sequences. In some embodiments, the heavy chain variable region CDR3 is replaced with any of the other heavy chain CDR3 sequences.

[00344] In some embodiments, the antigen-binding domain of the CAR comprises a V_H domain, a V_L domain, or a V_H and a V_L domain. In some embodiments, the V_H domain comprises an amino acid sequence having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, or any value or range in-between.

QVQLVQSGAEVKKPGSSVKVSCKDSGGTFSSYAISWVRQAPGQGLEWMGGII
PIFGTTNYAQQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAVAAD
WLDPWGQGTLVTVSS (SEQ ID NO: 94)

[00345] In some embodiments, the V_H domain comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 94. In some embodiments, the V_H domain comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 94. In some embodiments, the V_H domain comprises an amino acid sequence having at least 98% identity to SEQ ID NO: 94. In some embodiments, the V_H domain comprises an amino acid sequence having at least 99% identity to SEQ ID NO: 94. In some embodiments, the V_H domain comprises an amino acid sequence having the sequence of SEQ ID NO: 94.

[00346] In some embodiments, the V_L domain comprises an amino acid sequence having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95, or any value or range in-between.

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA
SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGTK
VDIK (SEQ ID NO: 95)

[00347] In some embodiments, the V_L domain comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 95. In some embodiments, the V_L domain comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 95. In some embodiments, the V_L domain comprises an amino acid sequence having at least 98% identity to SEQ ID NO:

95. In some embodiments, the V_L domain comprises an amino acid sequence having at least 99% identity to SEQ ID NO: 95. In some embodiments, the V_L domain comprises an amino acid sequence having the sequence of SEQ ID NO: 95.

[00348] In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, and comprises a V_L having at least 90% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, and comprises a V_L having at least 95% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, and comprises a V_L having at least 98% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, and comprises a V_L having at least 99% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 94, and comprises a V_L having the sequence of SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 90% identity to SEQ ID NO: 94, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 95% identity to SEQ ID NO: 94, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95.

In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 98% identity to SEQ ID NO: 94, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 99% identity to SEQ ID NO: 94, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having an amino acid sequence of SEQ ID NO: 94, and comprises a V_L having at least 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 90% identity to SEQ ID NO: 94, and comprises a V_L having at least 90% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 95% identity to SEQ ID NO: 94, and comprises a V_L having at least 90% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 90% identity to SEQ ID NO: 94, and comprises a V_L having at least 95% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 95% identity to SEQ ID NO: 94, and comprises a V_L having at least 95% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 98% identity to SEQ ID NO: 94, and comprises a V_L having at least 98% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having at least 99% identity to SEQ ID NO: 94, and comprises a V_L having at least 99% identity to SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a V_H domain and a V_L domain comprises a V_H domain having an amino acid sequence of SEQ ID NO: 94, and comprises a V_L having an amino acid sequence of SEQ ID NO: 95.

[00349] In some embodiments, the antigen-binding domain of the CAR comprises a formula of V_H-Z-V_L, wherein V_H is a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 94, Z is a linker comprising the amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 91), and V_L is a light chain variable region comprising the amino acid sequence

of SEQ ID NO: 95. In some embodiments, the antigen-binding domain of the CAR comprising a formula of V_H-Z-V_L has an amino acid sequence as set forth below:

QVQLVQSGAEVKKPGSSVKVSCKDSGGTFSSYAISWVRQAPGQGLEWMGGII
PIFGTTNYAQQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAVAAD
WLDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLS
CRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTL
TISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIK (SEQ ID NO: 96)

[00350] In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence of SEQ ID NO: 96. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 90% identity to a sequence of SEQ ID NO: 96. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 95% identity to a sequence of SEQ ID NO: 96. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 98% identity to a sequence of SEQ ID NO: 96. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 99% identity to a sequence of SEQ ID NO: 96. In some embodiments, the antigen-binding domain of the CAR comprises the amino acid sequence of SEQ ID NO: 96.

[00351] In some embodiments, the antigen-binding domain of the CAR comprises a formula of V_L-Z-V_H, wherein V_L is a light chain variable region comprising the amino acid sequence of SEQ ID NO: 95, Z is a linker comprising the amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 91), and V_H is a light chain variable region comprising the amino acid sequence of SEQ ID NO: 94. In some embodiments, the antigen-binding domain of the CAR comprising a formula of V_L-Z-V_H has an amino acid sequence as set forth below:

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA
SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGTK
VDIKGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKDSGGTFSSYA
ISWVRQAPGQGLEWMGGIIPIFGTTNYAQQFQGRVTITADESTSTAYMELSS
LRSEDTAVYYCAREAVAADWLDPWGQGTLVTVSS (SEQ ID NO: 97)

[00352] In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence of SEQ ID NO: 97. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 90% identity to a sequence of SEQ ID NO: 97. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 95%

identity to a sequence of SEQ ID NO: 97. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 98% identity to a sequence of SEQ ID NO: 97. In some embodiments, the antigen-binding domain of the CAR comprises an amino acid sequence having at least 99% identity to a sequence of SEQ ID NO: 97. In some embodiments, the antigen-binding domain of the CAR comprises the amino acid sequence of SEQ ID NO: 97.

[00353] In some embodiments, the antigen-binding domain of the CAR comprises any anti-CD19 antibody, or an scFv thereof, or an active fragment thereof. In some embodiments, the antigen-binding domain of the CAR comprises axicabtagene ciloleucel (KTEX19, Yescarta), brexucabtagene autoleucel (Tecartus), lisocabtagene maraleucel (JCAR017, Breyanzi), tisagenlecleucel (CTL019, Kymriah), tafasitamab (MOR208, XmAb5574, Monjuvi), loncastuximab tesirine (ADCT-402), anti-CD19 antibody clone 21D4, 21D4a, 47G4, FMC63, SJ25C1, inebilizumab, blinatumomab (MT103, AMG103, Blincyto), coltuximab ravtansine (SAR3419), MEDI-551, Denintuzumab mafodotin (SGN-CD19A), taplitumomabpaptox, XmAb 5871, MDX-1342, IKS03, AMG562, CLN-978, TNB-486 CD19/CD3, 41BB-CD3ζ LV20.19, CD19/CD20 biscpecific CAR-T cell therapy (Johnson Comprehensive Cancer Center), ALLO-501/ALLO-501A, Kyverna KYV-101, PBCAR0191, LY3541860, Merck modified B4 mAb anti-CD19 (Merck), or AFM11. In some embodiments, the antigen binding domain of the CAR is an antibody, or an scFv thereof, or an active fragment thereof, as provided in U.S. Patent Serial No. 8,097,703B2, U.S. Patent Serial No. 10,287,350B2, U.S. Patent Serial No. 11,236,161B2, U.S. Patent Publication No. 2022/0153838A1, and U.S. Patent Publication No. 2022/0204619A1; each of which are hereby incorporated by reference in their entirety. In some embodiments, the CAR comprises the 4-1BB domain as well.

[00354] In some embodiments, the antigen binding domain of the CAR comprises a VH and a VL as provided for herein. In some embodiments, the antigen binding domain of the CAR comprises a VH and/or a VL as provided in the table below.

Exemplary CD19 scFv VH and VL sequences		
Generic Name	SEQ ID NO	Sequence
Axicabtagene ciloleucel (KTEX19)	135 (VH)	EVKLQESGPGLVAPSQSLSVTTCTVSGVSLPDYGVSWIRQPP PRKGLEWLGVIWGSETTYYNSSALKSRLTIIKDNSKSQVFLK KMNSLQTDDTAIYYCAKHYYYYGGSYAMDYWGQGTSVTVSS
	136 (VL)	DIQMTQQTTSSLSASLGDRVTISCRASSQDISKYLNWYQQKP DGTVKLLLIYHTSRLHSGVPSRFSGSGGSGTDYSLTISNLEQ EDIATYYFCQQGNTLPYTFGGGTKLEI

Exemplary CD19 scFv VH and VL sequences		
Brexucabtagene autoleucel	137 (VH)	EVKLQESGPGLVAPSQSLSVTTCTVSGVSLPDYGVSWIRQPP PRKGLEWLGVIWGSETTYYNSSALKSRLTIIKDNSKSQVFLK KMNSLQTDDTAIYYCAKHYYYYGGSYAMDYWGQGTSVTVSS
	138 (VL)	DIQMTQQTTSSLSASLGDRVTISCRASSQDISKYLNWYQQKP DGTVKLLLIYHTSRLHSGVPSRFSGSGGSGTDYSLTISNLEQ EDIATYYFCQQGNTLPYTFGGGTKLEI
Lisocabtagene maraleucel (JCAR017)	139 (VH)	EVKLQESGPGLVAPSQSLSVTTCTVSGVSLPDYGVSWIRQPP PRKGLEWLGVIWGSETTYYNSSALKSRLTIIKDNSKSQVFLK KMNSLQTDDTAIYYCAKHYYYYGGSYAMDYWGQGTSVTVSS
	140 (VL)	DIQMTQQTTSSLSASLGDRVTISCRASSQDISKYLNWYQQKP DGTVKLLLIYHTSRLHSGVPSRFSGSGGSGTDYSLTISNLEQ EDIATYYFCQQGNTLPYTFGGGTKLEI
Tisagenlecleucel (CTL019)	141 (VH)	EVKLQESGPGLVAPSQSLSVTTCTVSGVSLPDYGVSWIRQPP PRKGLEWLGVIWGSETTYYNSSALKSRLTIIKDNSKSQVFLK KMNSLQTDDTAIYYCAKHYYYYGGSYAMDYWGQGTSVTVSS
	142 (VL)	DIQMTQQTTSSLSASLGDRVTISCRASSQDISKYLNWYQQKP DGTVKLLLIYHTSRLHSGVPSRFSGSGGSGTDYSLTISNLEQ EDIATYYFCQQGNTLPYTFGGGTKLEI
Tafasitamab (MOR208, XmAb5574)	143 (VH)	EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPG KGLEWIGYINPYNDGTKYNEKFQGRVTISSDKSISTAYMELS SLRSEDTAMYYCARGTYYYGTRVFDYWGQGTLVTVSS
	144 (VL)	DIVMTQSPATLSLSPGERATLSCRSSKSLQNVNGNTYLYWFQ QKPGQSPQLLIYRMSNLNSGVPDRFSGSGSGTEFTLTISSLE PEDFAVYYCMQHLEYPITFGAGTKLEIK
Inebilizumab (MEDI-551)	145 (VH)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSWMNWVRQAPG KGLEWVGRIYPGDGDTNYNVKFKGRFTISRDDSKNSLYLQMN SLKTEDTAVYYCARSGFITTVRDFDYWGQGTLVTVSS
	146 (VL)	EIVLTQSPDFQSVTPKEKVTITCRASESVDTFGISFMNWFQQ KPDQSPKLLIHEASNQGSGVPSRFSGSGSGTDFTLTINSLEA EDAATYYCQQSKEVPFTFGGGTKVEIK
Denintuzumab mafodotin (SGN-CD19A)	147 (VH)	QVQLQESGPGLVKPSQTLSLTCTVSGGSISTSGMGVGWIRQH PGKGLEWIGHIWWDDDKRYNPALKSRVTISVDTSKNQFSLKL SSVTAADTAVYYCARMELWSYYFDYWGQGTLVTVSS
	148 (VL)	EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGQA PRLLIYDTSKLASGIPARFSGSGSGTDFTLTISSLEPEDVAV YYCFQGSVYPFTFGQGTKLEIK
Blinatumomab (MT103, AMG103)	149 (VH1)	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPG QGLEWIGQIWPGDGDTNYNGKFKGKATLTADESSSTAYMQLS SLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSS
	150 (VL)	DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQ IPGQPPKLLIYDASNLVSGIPPRFSGSGSGTDFTLNIHPVEK VDAATYHCQQSTEDPWTFGGGTKLEIK
	151 (VH2)	DIKLQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQ GLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSS LTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSS

Exemplary CD19 scFv VH and VL sequences		
	152 (VL1)	DIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTS PKRWIYDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAAT YYCQQWSSNPLTFGAGTKLELK
Coltuximab ravtansine (SAR3419)	153 (VH)	QVQLVQPGAEVVKPGASVKLSCKTSGYTFTSNWMHWVKQAPG QGLEWIGEIDPSDSYTNYNQNFQGKAKLTVDKSTSTAYMEVS SLRSDDTAVYYCARGSNPYYYAMDYWGQGTSVTVSS
	154 (VL2)	EIVLTQSPAIMSASPGERVTMTCSASSGVNYMHWYQQKPGTS PRRWIYDTSKLASGVPARFSGSGSGTDYSLTISSMEPEDAAT YYCHQRGSYTFGGGTKLEIK
Loncastuximab tesirine (ADCT-402)	155 (VH)	QVQLVQPGAEVVKPGASVKLSCKTSGYTFTSNWMHWVKQAPG QGLEWIGEIDPSDSYTNYNQNFQGKAKLTVDKSTSTAYMEVS SLRSDDTAVYYCARGSNPYYYAMDYWGQGTSVTVSS
	156 (VL)	EIVLTQSPAIMSASPGERVTMTCSASSGVNYMHWYQQKPGTS PRRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEPEDAAT YYCHQRGSYTFGGGTKLEIK
FMC63, alt	157 (VH)	EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPR KGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNS LQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSS
	158 (VL)	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDG TVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIA TYFCQQGNTLPYTFGGGTKLEIT

[00355] In some embodiments, the CAR comprises a VH selected from SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, or SEQ ID NO: 157.

[00356] In some embodiments, the CAR comprises a VL selected from SEQ ID NO: 90, SEQ ID NO: 95, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, or SEQ ID NO: 158.

[00357] In some embodiments, the CAR comprises a VH selected from SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, or SEQ ID NO: 157 and a VL selected from SEQ ID NO: 90, SEQ ID NO: 95, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, or SEQ ID NO: 158.

[00358] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence as provided in the following table:

CAR ID No.	SEQ ID NO.	Sequence
CD19AB1HL	99	MALPVTALLLPLALLLHAARPGSEVQLVQSGAEVKKPG ESLKISCKGSGYSFSSSWIGWVRQMPGKGLEWMGIIYP DDSDTRYSPSFQGQVTISADKSIRTAYLQWSSLKASDTA MYYCARHVTMIWGVIIDFWGQGTLVTVSSGGGGSGGG GSGGGGSAIQLTQSPSSLSASVGDRVTITCRASQGISSAL AWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQFNSYPYTFGQGTKLEIKSGLDF VPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYC NHRNKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
CD19AB1HL	159	GSEVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIGW VRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADK SIRTAYLQWSSLKASDTAMYYCARHVTMIWGVIIDFW GQGTLVTVSSGGGGSGGGGSGGGGSAIQLTQSPSSLSAS VGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDAS SLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFN SYPYTFGQGTKLEIKSGLDFVPVFLPAKPTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAP AYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
CD19AB1HL	163	EVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIGWVR QMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADKSIR TAYLQWSSLKASDTAMYYCARHVTMIWGVIIDFWGQG TLVTVSSGGGGSGGGGSGGGGSAIQLTQSPSSLSASVGD RVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLES GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPY TFGQGTKLEIKSGLDFVPVFLPAKPTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR

CD19AB1LH	105	MALPVTALLLPLALLLHAARPGSAIQLTQSPSSLSASVG DRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLE SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYP YTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVQSGAE VKKPGESLKISCKGSGYSFSSSWIGWVRQMPGKGLEW MGIIYPDDSDTRYSPSFQGQVTISADKSIRTAYLQWSSL KASDTAMYYCARHVTMIWGVIIDFWGQGTLVTVSSSG LDFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITL YCNHRNKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
CD19AB1LH	160	GSAIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQ QKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQFNSYPYTFGQGTKLEIKGGGGSGGG GSGGGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFSSS WIGWVRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTI SADKSIRTAYLQWSSLKASDTAMYYCARHVTMIWGVII DFWGQGTLVTVSSSGLDFVPVFLPAKPTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALHMQALPPR
CD19AB1LH	164	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQK PGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQFNSYPYTFGQGTKLEIKGGGGSGGGGSG GGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIG WVRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISAD KSIRTAYLQWSSLKASDTAMYYCARHVTMIWGVIIDF WGQGTLVTVSSSGLDFVPVFLPAKPTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
CD19AB2HL	106	MALPVTALLLPLALLLHAARPGSQVQLVQSGAEVKKP GSSVKVSCKDSGGTFSSYAISWVRQAPGQGLEWMGGII PIFGTTNYAQQFQGRVTITADESTSTAYMELSSLRSEDT AVYYCAREAVAADWLDPWGQGTLVTVSSGGGGSGGG GSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIKSGL DFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITL

		YCNHRNKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
CD19AB2HL	161	GSQVQLVQSGAEVKKPGSSVKVSCKDSGGTFSSYAISW VRQAPGQGLEWMGGIIPIFGTTNYAQQFQGRVTITADES TSTAYMELSSLRSEDTAVYYCAREAVAADWLDPWGQ GTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSRFTFGPGTKVDIKSGLDFVPVFLPAKPTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAP AYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
CD19AB2HL	165	QVQLVQSGAEVKKPGSSVKVSCKDSGGTFSSYAISWVR QAPGQGLEWMGGIIPIFGTTNYAQQFQGRVTITADESTS TAYMELSSLRSEDTAVYYCAREAVAADWLDPWGQGT LVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGER ATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSR FTFGPGTKVDIKSGLDFVPVFLPAKPTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
CD19AB2LH	107	MALPVTALLLPLALLLHAARPGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSRFTFGPGTKVDIKGGGGSGGGGSGGGGSQVQLVQSG AEVKKPGSSVKVSCKDSGGTFSSYAISWVRQAPGQGLE WMGGIIPIFGTTNYAQQFQGRVTITADESTSTAYMELSS LRSEDTAVYYCAREAVAADWLDPWGQGTLVTVSSSGL DFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITL YCNHRNKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
CD19AB2LH	162	GSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWY QQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYCQQYGSSRFTFGPGTKVDIKGGGGSGG

		GGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKDSGGTF SSYAISWVRQAPGQGLEWMGGIIPIFGTTNYAQQFQGR VTITADESTSTAYMELSSLRSEDTAVYYCAREAVAADW LDPWGQGTLVTVSSSGLDFVPVFLPAKPTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAP AYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
CD19AB2LH	166	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRL EPEDFAVYYCQQYGSSRFTFGPGTKVDIKGGGGSGGGG SGGGGSQVQLVQSGAEVKKPGSSVKVSCKDSGGTFSSY AISWVRQAPGQGLEWMGGIIPIFGTTNYAQQFQGRVTIT ADESTSTAYMELSSLRSEDTAVYYCAREAVAADWLDP WGQGTLVTVSSSGLDFVPVFLPAKPTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR

[00359] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99:

MALPVTALLLPLALLLHAARPGSEVQLVQSGAEVKKPGESLKISCKGSGYSF SSSWIGWVRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADKSIRTAYL QWSSLKASDTAMYYCARHVTMIWGVIIDFWGQGTLVTVSSGGGGSGGGGSGG GGSAIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIY DASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPYTFGQG TKLEIKSGLDFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLY NELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR(SEQ ID NO: 99)

or is substantially similar to SEQ ID NO: 99, or is an active fragment of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ

ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 99.

[00360] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99.

[00361] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to

amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99.

[00362] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 99, the hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99,

the costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99.

[00363] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR

comprises an amino acid sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L corresponds to amino acids 160-266 of SEQ ID NO: 99, the hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 99.

[00364] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 92 and corresponds to amino acids 24-266 of SEQ ID NO: 99, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99.

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 101)

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR (SEQ ID NO: 102)

In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 92 and corresponds to amino acids 24-266 of SEQ ID NO: 99, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99, wherein

the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 92 and corresponds to amino acids 24-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 92 and corresponds to amino acids 24-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 92 and corresponds to amino acids 24-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99.

[00365] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 99, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 160-266 of SEQ ID NO: 99,

a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 99, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 160-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 99, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 160-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 99, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 160-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the

CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 99, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 24-144 of SEQ ID NO: 99 and the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 160-266 of SEQ ID NO: 99, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 99, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 99, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 99, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 99.

[00366] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105:

MALPVTALLLPLALLLHAARPGSAIQLTQSPSSLSASVGDRVTITCRASQGI
SSALAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQFNSYPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVQSGAEV
KKPGESLKISCKGSGYSFSSSWIGWVRQMPGKGLEWMGIIYPDDSDTRYSPS
FQGQVTISADKSIRTAYLQWSSLKASDTAMYYCARHVTMIWGVIIDFWGQGT
LVTVSSSGLDFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG
GAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIF
KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLY
NELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE
IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 105)

or is substantially similar to SEQ ID NO: 105, or is an active fragment of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105.

[00367] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105.

[00368] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105.

[00369] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR corresponds to amino acids 24-266 of SEQ ID NO: 105, the hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105.

[00370] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105, a hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-130 of

SEQ ID NO: 105 and the V_H corresponds to amino acids 146-266 of SEQ ID NO: 105, the hinge domain of the CAR corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR corresponds to amino acids 396-507 of SEQ ID NO: 105.

[00371] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 93 and corresponds to amino acids 24-266 of SEQ ID NO: 105, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 93 and corresponds to amino acids 24-266 of SEQ ID NO: 105, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 93 and corresponds to amino acids 24-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and

corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 93 and corresponds to amino acids 24-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 93 and corresponds to amino acids 24-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105.

[00372] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 105, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 146-266 of SEQ ID NO: 105, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds

to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 105, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 146-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 105, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 146-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 105, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 146-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 105, wherein the V_L comprises an

amino acid sequence of SEQ ID NO: 90 and corresponds to amino acids 24-130 of SEQ ID NO: 105 and the V_H comprises an amino acid sequence of SEQ ID NO: 89 and corresponds to amino acids 146-266 of SEQ ID NO: 105, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 271-325 of SEQ ID NO: 105, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 326-353 of SEQ ID NO: 105, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 354-395 of SEQ ID NO: 105, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 396-507 of SEQ ID NO: 105.

[00373] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106:

MALPVTALLLPLALLLHAARPGSQVQLVQSGAEVKKPGSSVKVSCKDSGGTF
SSYAISWVRQAPGQGLEWMGGIIPIFGTTNYAQQFQGRVTITADESTSTAYM
ELSSLRSEDTAVYYCAREAVAADWLDPWGQGTLVTVSSGGGGSGGGGSGGGG
SEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYG
ASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGT
KVDIKSGLDFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFK
QPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYN
ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 106)

or is substantially similar to SEQ ID NO: 106, or is an active fragment of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106.

[00374] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of

SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106.

[00375] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106.

[00376] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106, a hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, a transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, a costimulatory domain of the CAR

corresponds to amino acids 353-394 of SEQ ID NO: 106, and a signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106.

[00377] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106, a hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, a transmembrane domain

of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, a costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and a signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ

ID NO: 106, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 106.

[00378] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 96 and corresponds to amino acids 24-265 of SEQ ID NO: 106, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 96 and corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 96 and corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106, wherein the antigen

binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 96 and corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 96 and corresponds to amino acids 24-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106.

[00379] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 106, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 158-265 of SEQ ID NO: 106, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 106, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L comprises an amino acid sequence of SEQ ID NO: 95

and corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 106, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 106, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 106, wherein the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 24-142 of SEQ ID NO: 106 and the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 158-265 of SEQ ID NO: 106, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 106,

the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 106, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 106, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 106.

[00380] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107:

MALPVTALLLPLALLLHAARPGSEIVLTQSPGTLSLSPGERATLSCRASQSV
SSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEP
EDFAVYYCQQYGSSRFTFGPGTKVDIKGGGGSGGGGSGGGGSQVQLVQSGAE
VKKPGSSVKVSCKDSGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTTNYAQ
QFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAVAADWLDPWGQGTL
VTVSSSGLDFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFK
QPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYN
ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 107)

or is substantially similar to SEQ ID NO: 107, or is an active fragment of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107.

[00381] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ

ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107.

[00382] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107.

[00383] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107, a hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, a transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, a costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and a signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of

SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107.

[00384] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107, a hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, a transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, a costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and a signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ

ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR corresponds to amino acids 395-506 of SEQ ID NO: 107.

[00385] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 97 and corresponds to amino acids 24-265

of SEQ ID NO: 107, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 97 and corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 97 and corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 97 and corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and

corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises an amino acid sequence of SEQ ID NO: 97 and corresponds to amino acids 24-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107.

[00386] In some embodiments, the CAR comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence of SEQ ID NO: 107, wherein the antigen binding domain of the CAR comprises a V_H and a V_L, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 147-265 of SEQ ID NO: 107, a hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, a transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, a costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and a signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 90% identical to a sequence of SEQ ID NO: 107, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR

comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 95% identical to a sequence of SEQ ID NO: 107, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence that is at least 98% identical to a sequence of SEQ ID NO: 107, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107. In some embodiments, the CAR comprises an amino acid sequence of SEQ ID NO: 107, wherein the V_L comprises an amino acid sequence of SEQ ID NO: 95 and corresponds to amino acids 24-131 of SEQ ID NO: 107 and the V_H comprises an amino acid sequence of SEQ ID NO: 94 and corresponds to amino acids 147-265 of SEQ ID NO: 107, the hinge domain of the CAR comprises an amino acid sequence of SEQ ID NO: 59 and corresponds to amino acids 270-324 of SEQ ID NO: 107, the transmembrane domain of the CAR comprises an amino acid sequence of SEQ ID NO: 61 and corresponds to amino acids 325-352 of SEQ ID NO: 107, the costimulatory domain of the CAR comprises an amino acid sequence of SEQ ID NO: 101 and corresponds to amino acids 353-394 of SEQ ID NO: 107, and the signaling domain of the CAR comprises an amino acid sequence of SEQ ID NO: 102 and corresponds to amino acids 395-506 of SEQ ID NO: 107.

[00387] In any of the preceding embodiments, the antigen binding domain of the CAR may be directly fused to the hinge domain of the CAR. In any of the preceding embodiments, the antigen binding domain of the CAR may be connected to the hinge domain of the CAR through a polypeptide linker, such as those provided for herein. In some embodiments, the polypeptide linker comprises an amino acid sequence of SGLD (SEQ ID NO: 100). In some embodiments, the polypeptide linker connects the C-terminus of the antigen binding domain to the N-terminus of the hinge region. In some embodiments, the antigen binding domain comprises a V_H and a V_L and the polypeptide linker connects the C-terminus of the V_H to the N-terminus of the hinge region. In some embodiments, the antigen binding domain comprises a V_H and a V_L and the polypeptide linker connects the C-terminus of the V_L to the N-terminus of the hinge region.

[00388] These are merely illustrative in nature and are not limiting to the present embodiments and any chimeric antigen receptor can be delivered in conjunction with the viral particles and vectors provided for herein. These are non-limiting examples of CARs and any CAR construct could be encoded for by the nucleic acid molecule.

[00389] In some embodiments, the pseudotyped viral particle further comprises a heterologous nucleic acid molecule encoding a cargo of interest. The nucleic acid molecule may be useful for modulating the expression of a target gene. In some embodiments, the cargo can be used to modulate the activity of a cell or express a protein that is trafficked to the surface of the target cell. Therefore, in some embodiments, the nucleic acid may comprise an siRNA or an shRNA. The nucleic acid may also encode for a cargo of interest. Therefore, in some embodiments, the cargo of interest may comprise a polypeptide or portion thereof, a protein or portion thereof, a chimeric antigen receptor or portion thereof, or a tumor antigen or a portion thereof. In some embodiments, the cargo of interest is an antibody that is produced by the virus, which can then be secreted by the cell that is infected with the virus. The term "protein" can refer to any polypeptide that carries a native function in a cellular environment. Therefore, in some embodiments, the protein encoded by the nucleic acid cargo of interest may comprise an enzyme, a nuclear receptor, a transporter, a ribosomal protein, a membrane bound protein, a cytoplasmic protein, a G-protein coupled receptor, a voltage gated ion channel, a secretory protein, a mitochondria protein, a cytokine, a chimeric antigen receptor, a tumor antigen, or a portion or chimeric species thereof.

[00390] Without being bound to any particular theory, the viral particle comprising a heterologous viral glycoprotein as provided for herein and comprising a targeting moiety as provided for herein can be used to express the heterologous molecule of interest in the target cell. Thus, for example, the CAR can be expressed in a T cell that is targeted by a viral particle

pseudotyped with a VSV-G protein or a SVCV-G protein as provided for herein. Where the T cell is the intended target, the viral particle can comprise a targeting moiety that binds to a target on the surface of a T cell, such as, but not limited to CD2, CD3, CD4, CD5, CD7 or CD8. In some embodiments, the target is CD2. In some embodiments, the target is CD3. In some embodiments, the target is CD4. In some embodiments, the target is CD5. In some embodiments, the target is CD6. In some embodiments, the target is CD7. In some embodiments, the target is CD8. In some embodiments, the targeting moiety targeting CD7 is as provided for herein. In some embodiments, the targeting moiety targeting CD8 is as provided for herein.

[00391] In some embodiments, the pseudotyped viral particle is a recombinant lentivirus. In some embodiments, the recombinant pseudotyped viral particle is replication competent. In some embodiments, the recombinant pseudotyped viral particle is replication incompetent.

Exemplary viral particles comprising a targeting moiety comprising an Fc domain

[00392] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having a formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion, wherein the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53; wherein the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51; wherein the stalk portion S_1 comprises a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28; wherein the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A; wherein the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A; wherein the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A; and wherein the variant Fc protein further comprises a transmembrane domain comprising a sequence selected from SEQ ID NO: 61 or SEQ ID NO: 62. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 22. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 23. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 24. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 25. In some embodiments, the heterologous viral

glycoprotein comprises a sequence of SEQ ID NO: 52. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 53. In some embodiments, the targeting moiety comprises an amino acid sequence of SEQ ID NO: 38. In some embodiments, the targeting moiety comprises an amino acid sequence of SEQ ID NO: 39. In some embodiments, the targeting moiety comprises an amino acid sequence of SEQ ID NO: 50. In some embodiments, the targeting moiety comprises an amino acid sequence of SEQ ID NO: 51. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 26 and comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 27 and comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 28 and comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the transmembrane domain has an amino acid sequence of SEQ ID NO: 61. In some embodiments, the transmembrane domain has an amino acid sequence of SEQ ID NO: 62. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00393] In some embodiments, a viral particle is provided, said particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having a formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion, wherein the

heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53; wherein the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51; wherein the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1; wherein L_1 is a linker comprising a sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, or SEQ ID NO: 76, or is absent; Fc is a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28; wherein the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A; wherein the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A; wherein the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A; L_2 is a linker comprising a sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58. SEQ ID NO: 73 SEQ ID NO: 74, SEQ ID NO: 75, or SEQ ID NO: 76, or is absent; and X_1 is a polypeptide comprising a transmembrane domain having a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain having a sequence of SEQ ID NO: 59, SEQ ID NO: 60, or any fragment thereof, or is absent; T_M is a transmembrane domain having a sequence of SEQ ID NO: 61 or SEQ ID NO: 62 or any fragment thereof, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64 or the ICD is absent. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 22. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 23. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 24. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 25. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 52. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 53. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 38. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 39. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 50. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 51. In some embodiments, L_1 is absent. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 54. In some

embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 55. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 56. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 57. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 58. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 73. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 74. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 75. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 76. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 26 and comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 27 and comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 28 and comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A. In some embodiments, L_2 is absent. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 54. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 55. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 56. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 57. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 58. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 73. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 74. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 75. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 76. In some embodiments, ECD is absent. In some embodiments, ECD comprises an amino acid sequence of SEQ ID NO: 59. In some embodiments, ECD comprises an amino acid sequence of SEQ ID NO: 60. In some embodiments, T_M comprises an amino acid sequence of SEQ ID NO: 61. In some embodiments, T_M comprises an amino acid sequence of SEQ ID NO: 62. In some embodiments, ICD is absent. In some embodiments, ICD is present and the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, ICD is present and the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO:

99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00394] In some embodiments, a viral particle is provided, said particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having a formula $T\text{-}S_1$, wherein T is a target binding domain and S_1 is a stalk portion, wherein the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53; wherein the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51; wherein the stalk portion S_1 comprises a formula of $L_1\text{-}Fc\text{-}L_2\text{-}X_1$; wherein L_1 is a linker comprising a sequence of SEQ ID NO: 55 or is absent; Fc is a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28; wherein the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A; wherein the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A; wherein the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A; L_2 is a linker comprising a sequence of SEQ ID NO: 55 or is absent; and X_1 is a polypeptide comprising a transmembrane domain having a formula of $ECD\text{-}T_M\text{-}ICD$, wherein ECD is an extracellular domain having a sequence of SEQ ID NO: 60, or a fragment thereof, or is absent; T_M is a transmembrane domain having a sequence of SEQ ID NO: 62 or a fragment thereof, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64 or the ICD is absent. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 22. In some

embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 23. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 24. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 25. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 52. In some embodiments, the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 53. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 38. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 39. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 50. In some embodiments, T comprises an amino acid sequence of SEQ ID NO: 51. In some embodiments, L_1 is absent. In some embodiments, L_1 comprises an amino acid sequence of SEQ ID NO: 55. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 26 and comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 27 and comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A. In some embodiments, the variant Fc protein is a variant of SEQ ID NO: 28 and comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A. In some embodiments, L_2 is absent. In some embodiments, L_2 comprises an amino acid sequence of SEQ ID NO: 55. In some embodiments, ECD is absent. In some embodiments, ECD comprises an amino acid sequence of SEQ ID NO: 60. In some embodiments, T_M comprises an amino acid sequence of SEQ ID NO: 62. In some embodiments, ICD is absent. In some embodiments, ICD is present and the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, ICD is present and the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity

to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00395] In some embodiments, a viral particle is provided, said particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having a formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion, wherein the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 23 or SEQ ID NO: 25; wherein the target binding domain comprises a sequence of SEQ ID NO: 39; wherein the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1; wherein L_1 is a linker comprising a sequence of SEQ ID NO: 55; Fc is a variant Fc protein comprising a sequence fo SEQ ID NO: 104; L_2 is a linker and is absent; and X_1 is a polypeptide comprising a transmembrane domain having a formula of ECD-T_M-ICD, wherein ECD is an extracellular domain having a sequence of SEQ ID NO: 60; T_M is a transmembrane domain having a sequence of SEQ ID NO: 62, and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95%

identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00396] In some embodiments, a viral particle is provided, said particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 23 or SEQ ID NO: 25, having at least 95% identity to SEQ ID NO: 23 or SEQ ID NO: 25, having at least 99% identity to SEQ ID NO: 23 or SEQ ID NO: 25, or having at least 100% identity to SEQ ID NO: 23 or SEQ ID NO: 25; and the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00397] In some embodiments, a viral particle is provided, said particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 52 or SEQ ID NO: 53, having at least 95% identity to SEQ ID NO: 52 or SEQ ID NO: 53, having at least 99% identity to SEQ ID NO: 52 or SEQ ID NO: 53, or having at least 100% identity to SEQ ID NO: 52 or SEQ ID NO: 53; and the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98.

In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

Exemplary viral particles comprising a targeting moiety comprising a flexible polypeptide

[00398] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral structural protein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having a formula of T-S_1, wherein T is a target binding domain and S_1 is a stalk portion; wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 38 or SEQ ID NO: 39; wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein L_3 is a flexible peptide linker having an amino acid sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58; and X_1 is a polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein ECD is an extracellular domain having an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent; T_M is a transmembrane domain having an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif, said env incorporation motif having an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 38. In some embodiments, the target binding domain has an amino acid sequence

of SEQ ID NO: 39. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 54. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 55. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 56. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 57. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 58. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 59. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 60. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 61. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 62. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00399] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral structural protein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having a formula of T-S_1, wherein T is a target binding domain and S_1 is a stalk portion; wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 50 or SEQ ID NO: 51; wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein L_3 is a flexible peptide linker having an amino acid sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58; and X_1 is a polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein

ECD is an extracellular domain having an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent; T_M is a transmembrane domain having an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif, said env incorporation motif having an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 50. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 51. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 54. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 55. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 56. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 57. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 58. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 59. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 60. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 61. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 62. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00400] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral structural protein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having a formula of T-S_1, wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53; wherein T is a target binding domain and S_1 is a stalk portion, wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51; wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein L_3 is a flexible peptide linker having an amino acid sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58; and X_1 is a polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein ECD is an extracellular domain having an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or is a fragment thereof, or is absent; T_M is a transmembrane domain having an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif, said env incorporation motif having an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 22. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 23. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 24. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 25. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 52. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 53. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 38. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 39. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 50. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 51. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 54. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 55. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 56. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 57. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 58. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 59. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 60. In some embodiments, the T_M has

an amino acid sequence of SEQ ID NO: 61. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 62. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. At least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00401] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral structural protein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having a formula of T-S_1, wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52, or SEQ ID NO: 53; wherein T is a target binding domain and S_1 is a stalk portion, wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50, or SEQ ID NO: 51; wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein L_3 is a flexible peptide linker having an amino acid sequence of SEQ ID NO: 55; and X_1 is a polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein ECD is an extracellular domain having an amino acid sequence of SEQ ID NO: 59, or is a fragment thereof, or is absent; T_M is a transmembrane domain having an amino acid sequence of SEQ ID NO: 61, or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation

motif, said env incorporation motif having an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 22. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 23. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 24. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 25. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 52. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 53. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 38. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 39. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 50. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 51. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 55. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 59. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 61. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00402] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral structural protein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having a formula of T-S_1, wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 23 or SEQ ID NO: 25; wherein T is a target binding domain and S_1 is a stalk portion, wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 39; wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein L_3 is a flexible peptide linker having an amino acid sequence of SEQ ID NO: 55; and X_1 is a polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein ECD is an extracellular domain having an amino acid sequence of SEQ ID NO: 59, or is a fragment thereof, or is absent; T_M is a transmembrane domain having an amino acid sequence of SEQ ID NO: 61, or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif, said env incorporation motif having an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 23. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 25. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 39. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 55. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 59. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 61. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO:

106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00403] In some embodiments, a viral particle is provided, the viral particle comprising a heterologous viral structural protein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having a formula of T-S_1, wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 52 or SEQ ID NO: 53; wherein T is a target binding domain and S_1 is a stalk portion, wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 39; wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein L_3 is a flexible peptide linker having an amino acid sequence of SEQ ID NO: 55; and X_1 is a polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein ECD is an extracellular domain having an amino acid sequence of SEQ ID NO: 59, or is a fragment thereof, or is absent; T_M is a transmembrane domain having an amino acid sequence of SEQ ID NO: 61, or a fragment thereof; and ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif, said env incorporation motif having an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 52. In some embodiments, the heterologous viral structural protein comprises a sequence of SEQ ID NO: 53. In some embodiments, the target binding domain has an amino acid sequence of SEQ ID NO: 39. In some embodiments, L_3 has an amino acid sequence of SEQ ID NO: 55. In some embodiments, the ECD has an amino acid sequence of SEQ ID NO: 59. In some embodiments, the T_M has an amino acid sequence of SEQ ID NO: 61. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 63. In some embodiments, the env incorporation motif has an amino acid sequence of SEQ ID NO: 64. In some embodiments, the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest. In some embodiments, the heterologous molecule of interest is as provided for herein. In some embodiments, the heterologous molecule of interest is a CAR as provided for herein. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99. at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99. In some embodiments, the CAR

comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105. at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106. at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106. In some embodiments, the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107. at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00404] In some embodiments, a pharmaceutical composition is provided comprising the envelope pseudotyped viral particles or vectors as provided for herein, i.e. a particle that comprises a VSV-G mutant protein provided for herein.

[00405] In some embodiments, methods of delivering a cargo of interest to a cell are provided. In some embodiments, the methods comprise contacting the cell with the pseudotyped viral-like particles or viral vectors as provided for herein, or a pharmaceutical composition comprising the same.

[00406] In some embodiments, methods of delivering a cargo of interest to a cell in a subject are provided. In some embodiments, the methods comprise administering to the subject the pseudotyped viral-like particles or viral vectors as provided for herein, or a pharmaceutical composition comprising the same. In some embodiments, the cargo is a chimeric antigen receptor or as otherwise provided for herein.

[00407] In some embodiments, methods for of delivering a chimeric antigen receptor to a T-cell in a subject are provided. In some embodiments, the methods comprising administering to the subject the pseudotyped viral-like particles or viral vectors as provided for herein, or a pharmaceutical composition comprising the same, wherein the pseudotyped viral-like particle or viral vector comprises a heterologous nucleic acid molecule encoding the chimeric antigen receptor.

[00408] Also provided herein are nucleic acid molecules encoding a mutant VSV-G protein as provided for herein.

[00409] Methods of making the viral like particles or vectors comprising a mutant VSV-G protein are also provided. In some embodiments, the methods comprise transfecting or transducing a packaging cell line with the nucleic acid molecules encoding a mutant VSV-G protein as provided for herein under conditions sufficient to produce the pseudotyped viral-like

particles or viral vectors. In some embodiments, the methods comprise transfecting or transducing a packaging cell line with the plurality of nucleic acid molecules provided for herein under conditions sufficient to produce the pseudotyped viral-like particles or viral vectors. In some embodiments, methods further comprise isolating the pseudotyped viral-like particle or viral vector. In some embodiments, the nucleic acid molecules also comprise a nucleic acid molecule encoding a targeting moiety and/or a cargo that is to be delivered by the viral vector that is produced.

Methods of Treating a Disease or Disorder

[00410] Also provided for herein are methods of treating a disease or disorder in a s subject in need thereof. In some embodiments, the methods comprise administering to the subject the pseudotyped viral-like particles or viral vectors as provided for herein, or a pharmaceutical composition comprising the same, wherein the pseudotyped viral-like particle or viral vector comprises a heterologous nucleic acid molecule encoding the chimeric antigen receptor.

[00411] In some embodiments, the disease or disorder is any disease or disorder wherein a chimeric antigen receptor as provided for herein would be useful for the treatment of said disease or disorder. In some embodiments, the disease or disorder is cancer (e.g. such as a T cell or B cell disorder or other types of cancer as described herein), an immune disorder, an auto-immune disorder, metabolic disorder, and the like. In some embodiments, the immune disorder is selected from multiple sclerosis (MS), systemic lupus erythematosus (SLE), systemic sclerosis (SSc), lupus nephritis (LN), warm autoimmune hemolytic anemia (WAHA), primary sclerosing cholangitis (PSC), or IgG4-related disease (IGG4-RD). Immune disorders may also be selected from acute disseminated encephalomyelitis (ADEM), Evans' syndrome (ES), focal segmental glomerulosclerosis (FSGS), Mixed connective tissue disease (MCTD), Mooren's ulcer (MU), chronic inflammatory demyelinating polyneuropathy (CIDP), Membranous nephropathy (MN), or thyroid eye disease (TED). In some embodiments, the immune disorder is multiple sclerosis (MS). In some embodiments, the immune disorder is systemic lupus erythematosus (SLE). In some embodiments, the immune disorder is systemic sclerosis (SSc). In some embodiments, the immune disorder is lupus nephritis (LN). In some embodiments, the immune disorder is warm autoimmune hemolytic anemia (WAHA). In some embodiments, the immune disorder is primary sclerosing cholangitis (PSC). In some embodiments, the immune disorder is or IgG4-related disease (IGG4-RD). In some embodiments, the immune disorder is acute disseminated encephalomyelitis (ADEM). In some embodiments, the immune disorder is Evans' syndrome (ES). In some embodiments, the

immune disorder is focal segmental glomerulosclerosis (FSGS). In some embodiments, the immune disorder is Mixed connective tissue disease (MCTD). In some embodiments, the immune disorder is Mooren's ulcer (MU). In some embodiments, the immune disorder is chronic inflammatory demyelinating polyneuropathy (CIDP). In some embodiments, the immune disorder is Membranous nephropathy (MN). In some embodiments, the immune disorder is thyroid eye disease (TED).

[00412] Without being bound to any particular theory, the viral particles provided herein may be used to target CD7 positive T-cells and deliver a chimeric antigen receptor targeting CD19 (CD19 CAR) such as those provided for herein. The CD19 CAR cells then deplete the CD19 positive B-cell population, which results in treatment of immune/autoimmune diseases and disorders, as provided for herein.

[00413] Also provided for herein are methods of treating cancer in a subject. In some embodiments, the methods comprise administering to the subject the pseudotyped viral-like particles or viral vectors as provided for herein, or a pharmaceutical composition comprising the same, wherein the pseudotyped viral-like particle or viral vector comprises a heterologous nucleic acid molecule encoding the chimeric antigen receptor.

[00414] In some embodiments, the methods comprise administering to the subject immune cells that have been transduced by the pseudotyped viral-like particle or viral vectors as provided for herein. In some embodiments, the immune cells are first isolated from the subject prior to transduction by the pseudotyped viral-like particle or viral vectors as provided for herein.

[00415] Also provided herein are methods of treating a disease in a subject in need thereof.

[00416] In some embodiments, the methods provided include, but are not limited to, methods of treating a disease in a subject in need thereof, comprising administering to the subject the viral particle(s) provided herein to treat the disease.

[00417] In certain embodiments, the disease is a cancer. In addition, the compositions provided for herein can be used in methods for the treatment of any condition related to a cancer, such as a cell-mediated immune response against a tumor cell(s), where it is desirable to treat or alleviate the disease. The types of cancers to be treated include, but are not limited to, carcinoma, blastoma, sarcoma, certain leukemia or lymphoid malignancies, benign and malignant tumors, malignancies e.g., sarcomas, carcinomas, and melanomas. Other exemplary cancers include, but are not limited to, breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, colorectal cancer, renal cancer, liver cancer, brain cancer, lymphoma, leukemia, lung cancer, thyroid cancer, and the like. The cancers may be

non-solid tumors (such as hematological tumors) or solid tumors. Adult tumors/cancers and pediatric tumors/cancers are also included. In one embodiment, the cancer is a hematological tumor. In one embodiment, the cancer is a carcinoma. In one embodiment, the cancer is a sarcoma. In one embodiment, the cancer is a leukemia. In one embodiment, the cancer is lymphoma. In one embodiment the cancer is a solid tumor.

[00418] Solid tumors are abnormal masses of tissue that usually do not contain cysts or liquid areas. Solid tumors can be benign or malignant. Different types of solid tumors are named for the type of cells that form them (such as sarcomas, carcinomas, and lymphomas). Examples of solid tumors, such as sarcomas and carcinomas, include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, lymphoid malignancy, pancreatic cancer, breast cancer, lung cancers, ovarian cancer, prostate cancer, hepatocellular carcinoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, medullary thyroid carcinoma, papillary thyroid carcinoma, pheochromocytomas sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, Wilms' tumor, cervical cancer, testicular tumor, seminoma, bladder carcinoma, melanoma, CNS tumors (such as a glioma (such as brainstem glioma and mixed gliomas), glioblastoma (also known as glioblastoma multiforme) astrocytoma, CNS lymphoma, germinoma, medulloblastoma, Schwannoma craniopharyogioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, neuroblastoma, retinoblastoma and brain metastases).

[00419] Carcinomas that can be amenable to therapy by the methods disclosed herein include, but are not limited to, esophageal carcinoma, hepatocellular carcinoma, basal cell carcinoma (a form of skin cancer), squamous cell carcinoma (various tissues), bladder carcinoma, including transitional cell carcinoma (a malignant neoplasm of the bladder), bronchogenic carcinoma, colon carcinoma, colorectal carcinoma, gastric carcinoma, lung carcinoma, including small cell carcinoma and non-small cell carcinoma of the lung, adrenocortical carcinoma, thyroid carcinoma, pancreatic carcinoma, breast carcinoma, ovarian carcinoma, prostate carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinoma, cystadenocarcinoma, medullary carcinoma, renal cell carcinoma, ductal carcinoma in situ or bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical carcinoma, uterine carcinoma,

testicular carcinoma, osteogenic carcinoma, epithelial carcinoma, and nasopharyngeal carcinoma.

[00420] In certain exemplary embodiments, the compositions provided herein can be used in methods to treat a myeloma, or a condition related to myeloma. Examples of myeloma or conditions related thereto include, without limitation, light chain myeloma, non-secretory myeloma, monoclonal gamopathy of undertermined significance (MGUS), plasmacytoma (e.g., solitary, multiple solitary, extramedullary plasmacytoma), amyloidosis, and multiple myeloma. In some embodiments, methods of treating multiple myeloma are provided. In some embodiments, the multiple myeloma is refractory myeloma. In some embodiments, the multiple myeloma is relapsed myeloma.

[00421] In certain exemplary embodiments, the in vivo modified immune cells produced using the compositions provided herein are used to treat a melanoma, or a condition related to melanoma. Examples of melanoma or conditions related thereto include, without limitation, superficial spreading melanoma, nodular melanoma, lentigo maligna melanoma, acral lentiginous melanoma, amelanotic melanoma, or melanoma of the skin (e.g., cutaneous, eye, vulva, vagina, rectum melanoma). In some embodiments, the melanoma is cutaneous melanoma In some embodiments, the melanoma is refractory melanoma. In some embodiments, the melanoma is relapsed melanoma.

[00422] In some embodiments, the compositions provided herein are used to treat a sarcoma, or a condition related to sarcoma. Examples of sarcoma or conditions related thereto include, without limitation, angiosarcoma, chondrosarcoma, chordoma, endotheliosarcoma, Ewing's sarcoma, fibrosarcoma, gastrointestinal stromal tumor, leiomyosarcoma, liposarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, mesothelioma, malignant peripheral nerve sheath tumor, myxosarcoma, osteogenic sarcoma, osteosarcoma, pleomorphic sarcoma, rhabdomyosarcoma, synovioma, synovial sarcoma, and other soft tissue sarcomas. In some embodiments, the sarcoma is synovial sarcoma. In some embodiments, the sarcoma is liposarcoma such as myxoid/round cell liposarcoma, differentiated/dedifferentiated liposarcoma, or pleomorphic liposarcoma. In some embodiments, the sarcoma is myxoid/round cell liposarcoma. In some embodiments, the sarcoma is refractory sarcoma. In some embodiments, the sarcoma is relapsed sarcoma.

[00423] In some embodiments, the subject has been treated with a therapeutic agent targeting the disease or condition, e.g. the tumor, prior to administration of the composition. In some aspects, the subject is refractory or non-responsive to the other therapeutic agent. In some embodiments, the subject has persistent or relapsed disease, e.g., following treatment with

another therapeutic intervention, including chemotherapy, radiation, and/or hematopoietic stem cell transplantation (HSCT), e.g., allogenic HSCT. In some embodiments, the administration effectively treats the subject despite the subject having become resistant to another therapy.

[00424] In some embodiments, the subject is responsive to the other therapeutic agent, and treatment with the therapeutic agent reduces disease burden. In some aspects, the subject is initially responsive to the therapeutic agent, but exhibits a relapse of the disease or condition over time. In some embodiments, the subject has not relapsed. In some such embodiments, the subject is determined to be at risk for relapse, such as at a high risk of relapse, and thus the composition is administered prophylactically, e.g., to reduce the likelihood of or prevent relapse. In some aspects, the subject has not received prior treatment with another therapeutic agent.

[00425] The administration of the compositions may be carried out in any convenient manner known to those of skill in the art. For example, the compositions may be administered to a subject by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient transarterially, subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous (i.v.) injection, intraperitoneally, intranasally, intracranially, or intraosseously. In other instances, the compositions is injected directly into a site of a local disease site in the subject, a lymph node, an organ, a tumor, and the like.

[00426] For the prevention or treatment of disease, the appropriate dosage may depend on the type of disease to be treated, the severity and course of the disease, whether the composition is administered for preventive or therapeutic purposes, previous therapy, the subject's clinical history and response to the treatment, and the discretion of the attending physician. The composition is, in some embodiments, suitably administered to the subject at one time or over a series of treatments.

[00427] In some embodiments, the composition is administered as part of a combination treatment, such as simultaneously with or sequentially with, in any order, another therapeutic intervention, such as an antibody or produced cell or receptor or agent, such as a cytotoxic or therapeutic agent. The composition(s), in some embodiments, is co-administered with one or more additional therapeutic agents or in connection with another therapeutic intervention, either simultaneously or sequentially in any order. In some contexts, the composition is co-administered with another therapy sufficiently close in time such that the composition enhances the effect of one or more additional therapeutic agents, or vice versa. In some embodiments,

the composition is administered prior to the one or more additional therapeutic agents. In some embodiments, the composition is administered after the one or more additional therapeutic agents. In some embodiments, the one or more additional agents includes a cytokine, such as IL-2, for example, to enhance persistence. In some embodiments, the methods comprise administration of a chemotherapeutic agent. In some embodiments, the methods do not comprise the administration of a chemotherapeutic agent.

[00428] In certain embodiments, the compositions may be administered to a subject in combination with an immune checkpoint antibody (e.g., an anti-PD1, anti-CTLA-4, or anti-PDL1 antibody). For example, viral vectors may be administered in combination with an antibody or antibody fragment targeting, for example, PD-1 (programmed death 1 protein). Examples of anti-PD-1 antibodies include, but are not limited to, pembrolizumab (KEYTRUDA®, formerly lambrolizumab, also known as MK-3475), and nivolumab (BMS-936558, MDX-1106, ONO-4538, OPDIVO®) or an antigen-binding fragment thereof. In certain embodiments, the compositions may be administered in combination with an anti-PD-L1 antibody or antigen-binding fragment thereof. Examples of anti-PD-L1 antibodies include, but are not limited to, BMS-936559, MPDL3280A (TECENTRIQ®, Atezolizumab), and MEDI4736 (Durvalumab, Imfinzi). In certain embodiments, the composition may be administered in combination with an anti-CTLA-4 antibody or antigen-binding fragment thereof. An example of an anti- CTLA-4 antibody includes, but is not limited to, Ipilimumab (trade name Yervoy). Other types of immune checkpoint modulators may also be used including, but not limited to, small molecules, siRNA, miRNA, and CRISPR systems. Immune checkpoint modulators may be administered before, after, or concurrently with the viral vector. In certain embodiments, combination treatment comprising an immune checkpoint modulator may increase the therapeutic efficacy of a therapy comprising a composition as provided herein. The other therapeutic can be administered simultaneously, before, or after the compositions provided herein are administered to the subject.

[00429] In certain embodiments, the subject is provided a secondary treatment. Secondary treatments include but are not limited to chemotherapy, radiation, surgery, and medications. In some embodiments, the subject is not provided a secondary treatment.

[00430] In some embodiments, the methods are performed without a lymphodepletion step, such as the administration of cyclophosphamide and/or fludarabine.

[00431] In some embodiments, the subject can be administered a conditioning therapy after the administration of the compositions to kill certain immune cells that are not transduced with the CAR encoded by the compositions. This can be done by including a selection marker that

is encoded by the nucleic acid cargo of interest. In some embodiments, the conditioning therapy comprises administering an effective amount of cyclophosphamide to the subject. In some embodiments, the conditioning therapy comprises administering an effective amount of fludarabine to the subject. In some embodiments, the conditioning therapy comprises administering an effective amount of a combination of cyclophosphamide and fludarabine to the subject.

[00432] In some embodiments, a specific dosage regimen of the present disclosure includes a lymphodepletion step after the administration of the composition. In an exemplary embodiment, the lymphodepletion step includes administration of cyclophosphamide and/or fludarabine.

[00433] In some embodiments, the lymphodepletion step includes administration of cyclophosphamide at a dose of between about 200 mg/m^2/day and about 2000 mg/m^2/day (e.g., 200 mg/m^2/day, 300 mg/m^2/day, or 500 mg/m^2/day). In an exemplary embodiment, the dose of cyclophosphamide is about 300 mg/m^2/day. In some embodiments, the lymphodepletion step includes administration of fludarabine at a dose of between about 20 mg/m^2/day and about 900 mg/m^2/day (e.g., 20 mg/m^2/day, 25 mg/m^2/day, 30 mg/m^2/day, or 60 mg/m^2/day). In an exemplary embodiment, the dose of fludarabine is about 30 mg/m^2/day.

[00434] In some embodiment, the lymphodepletion step includes administration of cyclophosphamide at a dose of between about 200 mg/m^2/day and about 2000 mg/m^2/day (e.g., 200 mg/m^2/day, 300 mg/m^2/day, or 500 mg/m^2/day), and fludarabine at a dose of between about 20 mg/m^2/day and about 900 mg/m^2/day (e.g., 20 mg/m^2/day, 25 mg/m^2/day, 30 mg/m^2/day, or 60 mg/m^2/day). In an exemplary embodiment, the lymphodepletion step includes administration of cyclophosphamide at a dose of about 300 mg/m^2/day, and fludarabine at a dose of about 30 mg/m^2/day.

[00435] In an exemplary embodiment, the dosing of cyclophosphamide is 300 mg/m^2/day over three days, and the dosing of fludarabine is 30 mg/m^2/day over three days.

[00436] It is known in the art that one of the adverse effects of the use of CAR T cells can be the onset of immune activation, known as cytokine release syndrome (CRS). CRS is immune activation resulting in elevated inflammatory cytokines. CRS is a known on-target toxicity, development of which likely correlates with efficacy. Clinical and laboratory measures range from mild CRS (constitutional symptoms and/or grade-2 organ toxicity) to severe CRS (sCRS; grade $\geq$3 organ toxicity, aggressive clinical intervention, and/or potentially life threatening). Clinical features include: high fever, malaise, fatigue, myalgia, nausea, anorexia, tachycardia/hypotension, capillary leak, cardiac dysfunction, renal impairment, hepatic failure,

and disseminated intravascular coagulation. Dramatic elevations of cytokines including interferon-gamma, granulocyte macrophage colony-stimulating factor, IL-10, and IL-6 have been shown following CAR T-cell infusion. One CRS signature is elevation of cytokines including IL-6 (severe elevation), IFN-gamma, TNF-alpha (moderate), and IL-2 (mild). Elevations in clinically available markers of inflammation including ferritin and C-reactive protein (CRP) have also been observed to correlate with the CRS syndrome. The presence of CRS generally correlates with expansion and progressive immune activation of adoptively transferred cells. It has been demonstrated that the degree of CRS severity is dictated by disease burden at the time of infusion as patients with high tumor burden experience a more sCRS.

[00437] Accordingly, in some embodiments, the methods comprise, following the diagnosis of CRS, appropriate CRS management strategies to mitigate the physiological symptoms of uncontrolled inflammation without dampening the antitumor efficacy of the in vivo generated cells (e.g., CAR T cells). CRS management strategies are known in the art. For example, systemic corticosteroids may be administered to rapidly reverse symptoms of sCRS (e.g., grade 3 CRS) without compromising initial antitumor response.

[00438] In some embodiments, an anti-IL-6R antibody may be administered. An example of an anti-IL-6R antibody is the Food and Drug Administration-approved monoclonal antibody tocilizumab, also known as atlizumab (marketed as Actemra, or RoActemra). Tocilizumab is a humanized monoclonal antibody against the interleukin-6 receptor (IL-6R). Administration of tocilizumab has demonstrated near-immediate reversal of CRS.

[00439] CRS is generally managed based on the severity of the observed syndrome and interventions are tailored as such. CRS management decisions may be based upon clinical signs and symptoms and response to interventions, not solely on laboratory values alone.

[00440] Mild to moderate cases generally are treated with symptom management with fluid therapy, non-steroidal anti-inflammatory drug (NSAID) and antihistamines as needed for adequate symptom relief. More severe cases include patients with any degree of hemodynamic instability; with any hemodynamic instability, the administration of tocilizumab is recommended. The first-line management of CRS may be tocilizumab, in some embodiments, at the labeled dose of 8 mg/kg IV over 60 minutes (not to exceed 800 mg/dose); tocilizumab can be repeated Q8 hours. If suboptimal response to the first dose of tocilizumab, additional doses of tocilizumab may be considered. Tocilizumab can be administered alone or in combination with corticosteroid therapy. Patients with continued or progressive CRS symptoms, inadequate clinical improvement in 12-18 hours or poor response to tocilizumab,

may be treated with high-dose corticosteroid therapy, generally hydrocortisone 100 mg IV or methylprednisolone 1-2 mg/kg. In patients with more severe hemodynamic instability or more severe respiratory symptoms, patients may be administered high-dose corticosteroid therapy early in the course of the CRS. CRS management guidance may be based on published standards (Lee et al. (2019) Biol Blood Marrow Transplant, doi.org/10.1016/j.bbmt.2018.12.758; Neelapu et al. (2018) Nat Rev Clin Oncology, 15:47; Teachey et al. (2016) Cancer Discov, 6(6):664-679).

[00441] Features consistent with Macrophage Activation Syndrome (MAS) or Hemophagocytic lymphohistiocytosis (HLH) have been observed in patients treated with CAR-T therapy (Henter, 2007), coincident with clinical manifestations of the CRS. MAS appears to be a reaction to immune activation that occurs from the CRS, and should therefore be considered a manifestation of CRS. MAS is similar to HLH (also a reaction to immune stimulation). The clinical syndrome of MAS is characterized by high grade non-remitting fever, cytopenias affecting at least two of three lineages, and hepatosplenomegaly. It is associated with high serum ferritin, soluble interleukin-2 receptor, and triglycerides, and a decrease of circulating natural killer (NK) activity.

[00442] In some embodiments, methods of treating cancer in a subject in need thereof are provided, the methods comprising administering to the subject any of the compositions, such as the viral particle(s), provided herein.

[00443] The compositions disclosed herein can comprise a pharmaceutical composition, and for example include a pharmaceutically acceptable carrier, and/or a pharmaceutical formulation.

[00444] The term "pharmaceutical formulation" refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered. A "pharmaceutically acceptable carrier" refers to an ingredient in a pharmaceutical formulation, other than an active ingredient, which is nontoxic to a subject. A pharmaceutically acceptable carrier includes, but is not limited to, a buffer, excipient, stabilizer, or preservative. In some aspects, the choice of carrier is determined in part by the particular cell and/or by the method of administration. Accordingly, there are a variety of suitable formulations. For example, the pharmaceutical composition can contain preservatives. Suitable preservatives may include, for example, methylparaben, propylparaben, sodium benzoate, and benzalkonium chloride. In some aspects, a mixture of two or more preservatives is used. The preservative or mixtures thereof are typically present in an amount

of about 0.0001% to about 2% by weight of the total composition. Carriers are described, e.g., by Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980). Pharmaceutically acceptable carriers are generally nontoxic to recipients at the dosages and concentrations employed, and include, but are not limited to: buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride; benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as polyethylene glycol (PEG).

[00445] Buffering agents in some aspects are included in the compositions. Suitable buffering agents include, for example, citric acid, sodium citrate, phosphoric acid, potassium phosphate, and various other acids and salts. In some aspects, a mixture of two or more buffering agents is used. The buffering agent or mixtures thereof are typically present in an amount of about 0.001% to about 4% by weight of the total composition. Methods for preparing administrable pharmaceutical compositions are known. Exemplary methods are described in more detail in, for example, Remington: The Science and Practice of Pharmacy, Lippincott Williams & Wilkins; 21st ed. (May 1, 2005).

[00446] The formulations can include aqueous solutions. The formulation or composition may also contain more than one active ingredient useful for the particular indication, disease, or condition being treated with the composition, preferably those with activities complementary to the composition, where the respective activities do not adversely affect one another. Such active ingredients are suitably present in combination in amounts that are effective for the purpose intended. Thus, in some embodiments, the pharmaceutical composition further includes other pharmaceutically active agents or drugs, such as chemotherapeutic agents, e.g., asparaginase, busulfan, carboplatin, cisplatin, daunorubicin, doxorubicin, fluorouracil, gemcitabine, hydroxyurea, methotrexate, paclitaxel, rituximab, vinblastine, and/or vincristine. The pharmaceutical composition in some embodiments contains the composition in amounts effective to treat or prevent the disease or condition, such as a therapeutically effective or

prophylactically effective amount. Therapeutic or prophylactic efficacy in some embodiments is monitored by periodic assessment of treated subjects. The desired dosage can be delivered by a single bolus administration of the composition, by multiple bolus administrations of the composition, or by continuous infusion administration of the composition. In some embodiments, the pharmaceutical composition does not include a chemotherapeutic.

[00447] Formulations include those for oral, intravenous, intraperitoneal, subcutaneous, pulmonary, transdermal, intramuscular, intranasal, buccal, sublingual, or suppository administration. In some embodiments, the composition is administered parenterally. The term "parenteral," as used herein, includes intravenous, intramuscular, subcutaneous, rectal, vaginal, and intraperitoneal administration. In some embodiments, the composition is administered to the subject using peripheral systemic delivery by intravenous, intraperitoneal, or subcutaneous injection. Compositions in some embodiments are provided as sterile liquid preparations, e.g., isotonic aqueous solutions, suspensions, emulsions, dispersions, or viscous compositions, which may in some aspects be buffered to a selected pH. Liquid preparations are normally easier to prepare than gels, other viscous compositions, and solid compositions. Additionally, liquid compositions are somewhat more convenient to administer, especially by injection. Viscous compositions, on the other hand, can be formulated within the appropriate viscosity range to provide longer contact periods with specific tissues. Liquid or viscous compositions can comprise carriers, which can be a solvent or dispersing medium containing, for example, water, saline, phosphate buffered saline, polyol (for example, glycerol, propylene glycol, liquid polyethylene glycol) and suitable mixtures thereof.

[00448] Sterile injectable solutions can be prepared by incorporating the composition in a solvent, such as in admixture with a suitable carrier, diluent, or excipient such as sterile water, physiological saline, glucose, dextrose, or the like. The compositions can contain auxiliary substances such as wetting, dispersing, or emulsifying agents (e.g., methylcellulose), pH buffering agents, gelling or viscosity enhancing additives, preservatives, flavoring agents, and/or colors, depending upon the route of administration and the preparation desired. Standard texts may in some aspects be consulted to prepare suitable preparations.

[00449] Various additives which enhance the stability and sterility of the compositions, including antimicrobial preservatives, antioxidants, chelating agents, and buffers, can be added. Prevention of the action of microorganisms can be ensured by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, and sorbic acid. Prolonged absorption of the injectable pharmaceutical form can be brought about by the use of agents delaying absorption, for example, aluminum monostearate and gelatin.

[00450] The formulations to be used for in vivo administration are generally sterile. Sterility may be readily accomplished, e.g., by filtration through sterile filtration membranes.

[00451] The embodiments provided for herein can be used for many purposes, since the a pseudotyped virus capable of fusing with a target cell can be used to deliver a gene or other heterologous sequence of interest.

Enumerated Embodiments

[00452] In some embodiments, the following embodiments are provided:

1. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion.
2. The viral particle of embodiment 1, wherein the stalk portion S_1 comprises a variant Fc protein, wherein the variant Fc protein comprises a transmembrane domain and an effector mutation, wherein the effector mutation inhibits the interaction between the Fc protein and a Fc interacting protein, such as FcγR, C1q, FcRβ, or FcRn.
3. The viral particle of embodiment 2, wherein the S_1 stalk portion is attached to the surface of the viral particle through the transmembrane domain.
4. The viral particle of embodiments 2 or 3, wherein the Fc protein is a IgG1 Fc, IgG2 Fc or IgG4 Fc protein.
5. The viral particle of any one of embodiments 2-4, wherein the variant Fc protein comprises a variant of a sequence of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28.
6. The viral particle of any one of embodiments 2-5, wherein the variant Fc protein is a variant IgG1 Fc protein.
7. The viral particle of embodiment 6, wherein the variant IgG1 Fc protein comprises one or more of the mutations selected from the group consisting of: L234A, L235A, N297A, P329G, I253A, H310A, and H435A.
8. The viral particle of embodiments 6 or 7, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to L234A and L235A of SEQ ID NO: 26.
9. The viral particle of any one of embodiments 6-8, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to N297A of SEQ ID NO: 26.
10. The viral particle of any one of embodiments 6-9, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to P329G of SEQ ID NO: 26.

11. The viral particle of any one of embodiments 6-10, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to L234A, L235A, N297A, and P329G of SEQ ID NO: 26.

12. The viral particle of any one of embodiments 6-11, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to I253A of SEQ ID NO: 26.

13. The viral particle of any one of embodiments 6-12, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to H310A of SEQ ID NO: 26.

14. The viral particle of any one of embodiments 6-13, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to H435A of SEQ ID NO: 26.

15. The viral particle of any one of embodiments 6-14, wherein the variant IgG1 Fc protein comprises a mutation that corresponds to I253A, H310A, and H435A of SEQ ID NO: 26.

16. The viral particle of any one of embodiments 6-15, wherein the variant IgG1 Fc protein comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 103 and further comprises one or more mutations that correspond to L19A, L20A, N82A, P114G, I38A, H95A, and/or H220A of SEQ ID NO: 103.

17. The viral particle of any one of embodiments 6-16, wherein the variant IgG1 Fc protein comprises an amino acid sequence having at least 80% identity to SEQ ID NO: 104, at least 85% identity to SEQ ID NO: 104, at least 90% identity to SEQ ID NO: 104, at least 95% identity to SEQ ID NO: 104, at least 98% identity to SEQ ID NO: 104, or at least 100% identity to SEQ ID NO: 104.

18. The viral particle of any one of embodiments 2-5, wherein the variant Fc protein is a variant IgG2 Fc protein.

19. The viral particle of embodiment 18, wherein the variant IgG2 Fc protein comprises one or more mutations selected from the group consisting of: N297A, P329G, I253A, H310A, and H435A.

20. The viral particle of embodiments 18 or 19, wherein the IgG2 Fc protein comprises a mutation that corresponds to N297A of SEQ ID NO: 27.

21. The viral particle of embodiments 18 or 19, wherein the IgG2 Fc protein comprises a mutation that corresponds to P329G of SEQ ID NO: 27.

22. The viral particle of any one of embodiments 18-21, wherein the IgG2 Fc protein comprises a mutation that corresponds to N297A and P329G of SEQ ID NO: 27.

23. The viral particle of any one of embodiments 18-22, wherein the variant IgG2 Fc protein comprises a mutation that corresponds to I253A of SEQ ID NO: 27.

24. The viral particle of any one of embodiments 18-23, wherein the variant IgG2 Fc protein comprises a mutation that corresponds to H310A of SEQ ID NO: 27.

25. The viral particle of any one of embodiments 18-24, wherein the IgG2 Fc protein comprises a mutation that corresponds to H435A of SEQ ID NO: 27.

26. The viral particle of any one of embodiments 18-25, wherein the variant IgG2 Fc protein comprises a mutation that corresponds to I253A, H310A, and H435A of SEQ ID NO: 27.

27. The viral particle of any one of embodiments 2-5, wherein the variant Fc protein is a variant IgG4 Fc protein.

28. The viral particle of embodiment 27, wherein the variant IgG4 Fc protein comprises one or more mutations selected from the group consisting of: S228P, L235E, N297A, P329G, I253A, H310A, and H435A.

29. The viral particle of embodiments 27 or 28, wherein the IgG4 Fc protein comprises a mutation that corresponds to S228P of SEQ ID NO: 28.

30. The viral particle of any one of embodiments 27-29, wherein the IgG4 Fc protein comprises a mutation that corresponds to L235E of SEQ ID NO: 28.

31. The viral particle of any one of embodiments 27-30, wherein the IgG4 Fc protein comprises a mutation that corresponds to N297A of SEQ ID NO: 28.

32. The viral particle of any one of embodiments 27-31, wherein the IgG4 Fc protein comprises a mutation that corresponds to P329G of SEQ ID NO: 28.

33. The viral particle of any one of embodiments 27-32, wherein the IgG4 Fc protein comprises a mutation that corresponds to S228P, L235E, N297A, and P329G of SEQ ID NO: 28.

34. The viral particle of any one of embodiments 37-33, wherein the variant IgG4 Fc protein comprises a mutation that corresponds to I253A of SEQ ID NO: 28.

35. The viral particle of any one of embodiments 27-34, wherein the variant IgG4 Fc protein comprises a mutation that corresponds to H310A of SEQ ID NO: 28.

36. The viral particle of any one of embodiments 27-35, wherein the IgG4 Fc protein comprises a mutation that corresponds to H435A of SEQ ID NO: 28.

37. The viral particle of any one of embodiments 27-36, wherein the variant IgG4 Fc protein comprises a mutation that corresponds to I253A, H310A, and H435A of SEQ ID NO: 28.

38. The viral particle of any one of embodiments 2-37, wherein the targeting moiety having the formula T-S_1 comprises a stalk portion S_1 having a formula of L_1-Fc-L_2-X_1, wherein:

L_1 is a linker or absent;

Fc is a variant Fc protein;

L_2 is a linker or absent; and

X_1 is a polypeptide comprising the transmembrane domain,

wherein the targeting moiety having the formula T-S_1 has a formula of T-L_1-Fc-L_2-X_1.

39. The viral particle of embodiment 38, wherein L_1 and L_2 are each, independently, a polypeptide linker.

40. The viral particle of embodiment 39, wherein the polypeptide linker comprises $(GGGGA)_n$ (SEQ ID NO: 54), $(GGGGS)_n$ (SEQ ID NO: 55), $(EAAAK)_n$ (SEQ ID NO: 73), $A(EAAAK)_nA$ (SEQ ID NO: 74), $(XP)_n$ (SEQ ID NO: 75), wherein X is Ala, Lys, or Glu, GSAGSAAGSGEF (SEQ ID NO: 56), KESGSVSSEQLAQFRSLD (SEQ ID NO: 57), EGKSSGSGSESKST (SEQ ID NO: 58), AEAAAKEAAAKA (SEQ ID NO: 76), or a combination thereof, wherein each n is, independently, 1-5.

41. The viral particle of any one of embodiments 38-40, wherein L_1 is absent.

42. The viral particle of any one of embodiments 38-40, wherein L_1 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), and

wherein each n is, independently, 1-5.

43. The viral particle of any one of embodiments 38-42, wherein L_2 is absent.

44. The viral particle of any one of embodiments 38-42, wherein L_2 is $(GGGGA)_n$ (SEQ ID NO: 54) or $(GGGGS)_n$ (SEQ ID NO: 55), and

wherein each n is, independently, 1-5.

45. The viral particle of any one of embodiments 38-44, wherein X_1 comprises a polypeptide having a formula of ECD-T_M-ICD, wherein:

ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or absent;

T_M is a transmembrane domain of a transmembrane protein; and

ICD is an intracellular domain or a protein that facilitates incorporation of the targeting moiety into the envelope of the viral particle, or absent,

wherein the targeting moiety having the formula of T-L_1-Fc-L_2-X_1 has a formula of T-L_1-Fc-L_2-ECD-T_M-ICD.

46. The viral particle of embodiment 45, wherein the ECD is absent.

47. The viral particle of embodiment 45, wherein the ECD is an extracellular domain, or fragment thereof, of CD8 or CD28.

48. The viral particle of embodiment 47, wherein the ECD comprises an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60.

49. The viral particle of embodiment 47, wherein the ECD comprises an amino acid sequence of SEQ ID NO: 60.

50. The viral particle of any one of embodiments 45-49, wherein T_M is a transmembrane domain, or a fragment thereof, of CD8 or CD28.

51. The viral particle of embodiment 50, wherein the T_M comprises an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62.

52. The viral particle of embodiment 50, wherein the T_M comprises an amino acid sequence of SEQ ID NO: 62.

53. The viral particle of any one of embodiments 45-52, wherein the ICD is absent.

54. The viral particle of any one of embodiments 45-52, wherein the ICD comprises an Env incorporation motif.

55. The viral particle of embodiment 54, wherein the Env incorporation motif comprises an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

56. The viral particle of embodiment 1, wherein the stalk portion S_1 comprises a formula of L_3-X_1, wherein:

L_3 is a flexible peptide linker, and

X_1 is a polypeptide comprising a transmembrane domain,

wherein the targeting moiety having the formula T-S_1 has a formula of T-L_3-X_1.

57. The viral particle of embodiment 56, wherein L_3 comprises a polypeptide having a sequence of $(GGGGA)_n$ (SEQ ID NO: 54), $(GGGGS)_n$ (SEQ ID NO: 55), GSAGSAAGSGEF (SEQ ID NO: 56), KESGSVSSEQLAQFRSLD (SEQ ID NO: 57), EGKSSGSGSESKST (SEQ ID NO: 58), or any combination thereof, wherein each n is, independently, 1-4.

58. The viral particle of embodiment 57, wherein n is 1, 2, or 4.

59. The viral particle of any one of embodiments 56-58, wherein X_1 comprises a polypeptide having a formula of ECD-T_M-ICD, wherein:

ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or absent;

T_M is a transmembrane domain of a transmembrane protein; and

ICD is an intracellular domain or a protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, or absent,

wherein the targeting moiety having the formula of T-L_3-X_1 has a formula of T-L_3-ECD-T_M-ICD.

60. The viral particle of embodiment 59, wherein the ECD is absent.

61. The viral particle of embodiment 59, wherein the ECD is an extracellular domain, or fragment thereof, or CD8 or CD28.

62. The viral particle of embodiment 61, wherein the ECD comprises an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60.

63. The viral particle of embodiment 61, wherein the ECD comprises an amino acid sequence of SEQ ID NO: 59.

64. The viral particle of any one of embodiments 59-63, wherein T_M is a transmembrane domain, or a fragment thereof, of CD8 or CD28.

65. The viral particle of embodiment 64, wherein the T_M comprises an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62.

66. The viral particle of embodiment 64, wherein the T_M comprises an amino acid sequence of SEQ ID NO: 61.

67. The viral particle of any one of embodiments 59-66, wherein the ICD is absent.

68. The viral particle of any one of embodiments 59-66, wherein the ICD comprises an Env incorporation motif.

69. The viral particle of embodiment 68, wherein the Env incorporation motif comprises an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

70. The viral particle of any one of embodiments 1-69, wherein the target binding domain (T) binds to an immune cell, wherein the immune cell is any of a T cell, B cell; NK cell, dendritic cell, neutrophils, macrophages, a cancer cell; or, for example, CD3+ T cell; CD4+ T cell; CD7+ T cell, CD8+ T cell; CD19+ B cell; CD19+ cancer cell; CD20+ B cell; CD20+ cancer cell, CD30+ lung epithelial cell; CD34+ haematopoietic stem cell; CD105+ endothelial cell; CD105+ haematopoietic stem cell; CD117+ haematopoietic stem cell; CD133+ cancer cell; EpCAM+ cancer cell; GluA2+ neuron; GluA4+ neuron; Haematopoietic stem cell; Hepatocyte; Her2/Neu+ cancer cell; NKG2D+ natural killer cell; SLC1A3+ astrocyte; SLC7A10+ adipocyte; or progenitor cells.

71. The viral particle of any one of embodiments 1-70, wherein the target binding domain (T) binds to CD7, CD8, cKit (CD117), CD4, CD3, CD5, CD6, CD2, TCR alpha, TCR beta, TCR gamma, TCR delta, CD10, CD34, CD110, CD33, CD14, CD68, CCR7, CD62L, CD25, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, or CXCR3, A glycosylated CD43 epitope expressed on acute leukemia or lymphoma but not on hematopoietic progenitors; A

glycosylated CD43 epitope expressed on non-hematopoietic cancers; A kinase anchor protein 4 (AKAP-4); Adrenoceptor beta 3 (ADRB3); AFP; Anaplastic lymphoma kinase (ALK); Androgen receptor; Angiopoietin-binding cell surface receptor 2 (Tie 2); Auto antibody to desmoglein 1 (Dsgl); Auto antibody to desmoglein 3 (Dsg3); B7H3 (CD276); Biotin; Bone marrow stromal cell antigen 2 (BST2); BST1/CD157; Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-la); Carbonic anhydrase IX (CA1X); Carcinoembryonic antigen (CEA); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS or Brother of the Regulator of lmprinted Sites); CCR4; CD5; CD19; CD20; CD22; CD24; CD30; CD32 (FCGR2A); CD33; CD34; CD38; CD44v6; CD72; CD79a; CD79b; CD97; CD99; CD123; CD171; CD179a; CD179b-IGLll; CD200R; CD276/B7H3; CD300 molecule-like family member f (CD300LF); CDH1-CD324; CDH6; CDH17; CDH19; Chromosome X open reading frame 61 (CXORF61); Claudin 6 (CLDN6); Claudinl8.2 (CLD18A2 or CLDN18A.2); CMV pp65; C-MYC epitope Tag; Cripto; CS1 (also referred to as CD2 subset 1 or CRACC or SLAMF7 or CD319 or 19A24); CSF2RA (GM-CSFR-alpha); C-type lectin domain family 12 member A (CLEC12A); C-type lectin-like molecule-1 (CLL-1 or CLECL1); Cyclin Bl; Cytochrome P450 IB 1 (CYP1B 1); DLL3; EBV-EBNA3c; EGF-bke module- containing mucin-like hormone receptor-like 2 (EMR2); Elongation factor 2 mutated (ELF2M); Ephrin B2; Ephrin type-A receptor 2 (EphA2); Epidermal growth factor receptor (EGFR); Epidermal growth factor receptor variant III (EGFRviii); Epithelial cell adhesion molecule (EPCAM); ERG; ETS translocation-variant gene 6 located on chromosome 12p (ETV6-AML); Fc fragment of IgA receptor (FCAR or CD89); Fc receptor-like 5 (FCRL5); Fibroblast activation protein alpha (FAP); FITC; Fms Like Tyrosine Kinase 3 (FLT3); Folate receptor alpha (Fra or FR1); Folate receptor beta (FRb); Follicle stimulating hormone receptor (FSHR); Fos-related antigen 1; Fucosyl-GMl; G protein coupled receptor class C group 5 member D (GPRC5D); G protein-coupled receptor 20 (GPR20); GAD; Ganglioside G2 (GD2) ; Ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); Ganglioside GM3 (aNeu5Ac(2-3)bDClalp(l- 4)bDGlcp(l-l)Cer); GD3; GFRalpha4; Glycoprotein 100 (gplOO); Glypican-3 (GPC3); Gonadotropin Hormone receptor (CGHR or GR); GpA33; GpNMB; GPRC5D; Guanylyl cyclase C (GCC); Heat shock protein 70-2 mutated (mut hsp70-2); Hepatitis A virus cellular receptor 1 (HAVCR1); Hexasaccharide portion of globoH glycoceramide (GloboH); High molecular weight-melanoma associated antigen (HMWMAA); HIV1 envelope glycoprotein; HLA; HLA-DOA; HLA-A; HLA-A2; HLA-B; HLA-C; HLA-DM; HLA-DOB; HLA-DP; HLA-DQ; HLA-DR; HLA-G; HTLVl-Tax; Human papilloma virus E6 (HPV E6); Human papilloma virus E7 (HPV E7); Human Telomerase reverse transcriptase (hTERT); IgE;

IL13Ra2; Ill lRa; Immunoglobulin lambda-like polypeptide 1 (IGLL1); Influenza A hemagglutinin (HA); Insulin-like growth factor 1 receptor (IGF-I receptor); Interleukin 11 receptor alpha (IL-llRa); Interleukin- 13 receptor subunit alpha-2 (IL-13Ra2 or CD213A2); Intestinal carboxyl esterase; KIT (CD117); KSHV K8.1; KSHV-gH; LAMP1 ; Legumain; Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Leutenizing hormone receptor (LHR); Lewis(Y) antigen; Lews Ag; Livl; Locus K 9 (LY6K); Low conductance chloride channel; Lymphocyte antigen 6 complex; Lymphocyte antigen 75 (LY75); Lymphocyte-specific protein tyrosine kinase (LCK); Mammary gland differentiation antigen (NY-BR-1); Melanoma antigen recognized by T cells 1 (MelanA or MARTI); Melanoma- associated antigen 1 (MAGE-A1); Melanoma cancer testis antigen-1 (MAD-CT-1); Melanoma cancer testis antigen-2 (MAD-CT-2); Melanoma inhibitor of apoptosis (ML-IAP); Mesothelin; MPL; Mucin 1 cell surface associated (MUC1); N-Acetyl glucosaminyl-transferase V (NA17); Nectin-4; Neural cell adhesion molecule (NCAM); NKG2D; NYBR1; O-acetyl-GD2 ganglioside (OacGD2); Olfactory receptor 51E2 (OR51E2); Oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); P53 mutant; Paired box protein Pax-3 (PAX3); Paired box protein Pax-5 (PAX5); Pannexin 3 (PANX3); PDL1; P-glycoprotein; Placenta-specific 1 (PLAC1); Platelet-derived growth factor receptor beta (PDGFR-beta); Polysialic acid; Proacrosin binding protein sp32 (OY-TES1); Prostase; Prostate carcinoma tumor antigen-1 (PCT A-l or Galectin 8); Prostate stem cell antigen (PSCA); Prostate-specific membrane antigen (PSMA); Prostatic acid phosphatase (PAP); Prostein; Protease Serine 21 (Testisin or PRSS21); Proteasome (Prosome Macropain) Subunit Beta Type 9 (LMP2); PTK7; Ras G12V; Ras Homolog Family Member C (RhoC); Rat sarcoma (Ras) mutant; Receptor for Advanced Gly cation Endproducts (RAGE-1); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Receptor tyrosine-protein kinase ERBB2 or Her-22/neu; Renal ubiquitous 1 (RU1); Renal ubiquitous 2 (RU2); Sarcoma translocation breakpoints; Serine 2 (TMPRSS2) ETS fusion gene; Sialyl Lewis adhesion molecule (sLe); SLAMF4; SLAMF6; Slea (CA19.9 or Sialyl Lewis Antigen); Sperm protein 17 (SPA17); Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Stage-specific embryonic antigen-4 (SSEA-4); STEAP1; Survivin; Synovial sarcoma X breakpoint 2 (SSX2); TCR Gamma Alternate Reading Frame Protein (TARP); TCR-beta1 chain; TCR-beta2 chain; TCR-delta chain; TCR-gamma chain; TCRgamma-delta; Telomerase; TGFbetaR2; The antigen recognized by TNT antibody; Thyroid stimulating hormone receptor (TSHR); Timl-/HVCR1; Tissue Factor 1 (TF1); Tn ag; Tn antigen ((Tn Ag) or (GalNAca-Ser/Thr)); TNF

receptor family member B cell maturation (BCMA); Transglutaminase 5 (TGS5); Transmembrane protease; TROP2; Tumor endothelial marker 1 (TEM1/CD248); Tumor endothelial marker 7-related (TEM7R); Tumor protein p53 (p53); Tumor-associated glycoprotein 72 (TAG72); Tyrosinase; Tyrosinase-related protein 2 (TRP-2); Uroplakin 2 (UPK2); Vascular endothelial growth factor receptor 2 (VEGFR2); V-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Wilms tumor protein (WT1); or X Antigen Family Member 1A (XAGE1).

72. The viral particle of embodiment 71, wherein the target binding domain (T) binds to CD7.

73. The viral particle of embodiment 72, wherein the target binding domain (T) comprises a polypeptide comprising: (i) a heavy chain variable region comprising heavy chain CDRl, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 30; the heavy chain CDR2 has the amino acid sequence of SEQ ID NO: 31; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 32, or variants of any of the foregoing; and (ii) a light chain variable region comprising light chain CDR1, CDR2, and CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 33; the light chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 34; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 35; or variants of any of the foregoing.

74. The viral particle of embodiment 73, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 36, wherein the polypeptide comprises the sequences of HCDR1 as set forth in SEQ ID NO: 30; HCDR2 as set forth in SEQ ID NO: 31; and HCDR3 as set forth in SEQ ID NO: 32.

75. The viral particle of embodiments 73 or 74, wherein the light chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 37, wherein the polypeptide comprises the sequences of LCDR1 as set forth in SEQ ID NO: 33; LCDR2 as set forth in SEQ ID NO: 34; and LCDR3 as set forth in SEQ ID NO: 35.

76. The viral particle of any one of embodiments 73-75, wherein the polypeptide comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 36, and the light chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 37, wherein polypeptide comprises the sequences of HCDR1 as set forth in SEQ ID NO: 30; HCDR2 as set forth in SEQ ID NO: 31;

HCDR3 as set forth in SEQ ID NO: 32; LCDR1 as set forth in SEQ ID NO: 33; LCDR2 as set forth in SEQ ID NO: 34; and LCDR3 as set forth in SEQ ID NO: 35.

77. The viral particle of any one of embodiments 73-76, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 36; and the light chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 37.

78. The viral particle of any one of embodiments 73-77, wherein the heavy chain variable region comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 36; and the light chain variable region comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 37.

79. The viral particle of any one of embodiments 73-78, wherein the heavy chain variable region comprises an amino acid sequence having at least 99% sequence identity to SEQ ID NO: 36; and the light chain variable region comprises an amino acid sequence having at least 99% sequence identity to SEQ ID NO: 37.

80. The viral particle of any one of embodiments 73-79, wherein the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 36, and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 37.

81. The viral particle of any one of embodiments 73-80, wherein the heavy chain variable region and the light chain variable region are linked by a linker, such as a peptide linker, which can be for example, a glycine/serine linker.

82. The viral particle of embodiment 81, wherein the peptide linker comprises a sequence of $(GGGGS)_n$, wherein n is independently 1-5.

83. The viral particle of any one of embodiments 73-80, wherein the heavy chain variable region and the light chain variable region are directly linked to one another and are not linked by a linker.

84. The viral particle of any one of embodiments 72-82, wherein the target binding domain (T) that binds to CD7 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 38, at least 95% sequence identity to SEQ ID NO: 38, at least 99% sequence identity to SEQ ID NO: 38, or a sequence as set forth in SEQ ID NO: 38.

85. The viral particle of any one of embodiments 72-82, wherein the target binding domain (T) that binds to CD7 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 39, having at least 95% sequence identity to SEQ ID NO: 39, having at least 99% sequence identity to SEQ ID NO: 39, or a sequence as set forth in SEQ ID NO: 39.

86. The viral particle of embodiment 71, wherein the target binding domain (T) binds to CD8.

87. The viral particle of embodiment 86, wherein the target binding domain (T) comprises a polypeptide that comprises: a heavy chain variable region comprising heavy chain CDRl, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 42; the heavy chain CDR2 has the amino acid sequence of SEQ ID NO: 43; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 44, or variants of any of the foregoing; and (ii) a light chain variable region comprising light chain CDR1, CDR2, and CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 45; the light chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 46; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 47; or variants of any of the foregoing.

88. The viral particle of embodiment 87, wherein the target binding domain (T) comprises a heavy chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 48, wherein the polypeptide comprises the sequences of HCDR1 as set forth in SEQ ID NO: 42; HCDR2 as set forth in SEQ ID NO: 43; and HCDR3 as set forth in SEQ ID NO: 44.

89. The viral particle of embodiment 87 or 88, wherein the target binding domain (T) comprises a light chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 49, wherein the polypeptide comprises the sequences of LCDR1 as set forth in SEQ ID NO: 45; LCDR2 as set forth in SEQ ID NO: 46; and LCDR3 as set forth in SEQ ID NO: 47.

90. The viral particle of any one of embodiments 87-89, wherein the target binding domain (T) comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 48, and the light chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 49, wherein polypeptide comprises the sequences of HCDR1 as set forth in SEQ ID NO: 42; HCDR2 as set forth in SEQ ID NO: 43; HCDR3 as set forth in SEQ ID NO: 44; LCDR1 as set forth in SEQ ID NO: 45; LCDR2 as set forth in SEQ ID NO: 46; and LCDR3 as set forth in SEQ ID NO: 47.

91. The viral particle of any one of embodiments 87-90, wherein the target binding domain (T) comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, where the heavy chain variable region comprises an amino acid sequence having at

least 90% sequence identity to SEQ ID NO: 48; and the light chain variable region comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 49.

92. The viral particle of any one of embodiments 87-90, wherein the target binding domain (T) comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 48; and the light chain variable region comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 49.

93. The viral particle of any one of embodiments 87-90, wherein the target binding domain (T) comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 99% sequence identity to SEQ ID NO: 48; and the light chain variable region comprises an amino acid sequence having at least 99% sequence identity to SEQ ID NO: 49.

94. The viral particle of embodiment 86, wherein the target binding domain (T) comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 48, and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 49.

95. The viral particle of any one of embodiments 87-94, wherein the heavy chain variable region and the light chain variable region are linked by a linker, such as a peptide linker.

96. The viral particle of embodiment 95, wherein the peptide linker is a glycine/serine linker.

97. The viral particle of embodiments 95 or 96, wherein the peptide linker comprises a sequence of $(GGGGS)_n$ (SEQ ID NO: 55), wherein each n is independently 1-5.

98. The viral particle of any one of embodiments 87-94, wherein the heavy chain variable region and the light chain variable region are directly linked to one another and are not linked by a linker.

99. The viral particle of any one of embodiments 86-97, wherein the target binding domain (T) that binds to CD8 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 50, at least 95% sequence identity to SEQ ID NO: 50, at least 99% sequence identity to SEQ ID NO: 50, or a sequence as set forth in SEQ ID NO: 50.

100. The viral particle of any one of embodiments 86-97, wherein the target binding domain (T) that binds to CD8 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 51, having at least 95% sequence identity to SEQ ID NO: 51, having at least 99% sequence identity to SEQ ID NO: 51, or a sequence as set forth in SEQ ID NO: 51.

101. The viral particle of any one of embodiments 1-100, wherein the target binding domain (T) is an antibody, or an antigen-binding fragment thereof, such as scFv antibody.

102. The viral particle of any one of embodiments 1-101, wherein the heterologous viral glycoprotein is a SVCV-G polypeptide.

103. The viral particle of embodiment 102, wherein the SVCV-G polypeptide comprises a polypeptide having at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO: 52 or SEQ ID NO: 53.

104. The viral particle of embodiment 102 or 103, wherein the SVCV-G polypeptide comprises a polypeptide having at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO: 52.

105. The viral particle of embodiment 102 or 103, wherein the SVCV-G polypeptide comprises a polypeptide having at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO: 53.

106. The viral particle of embodiment 102 or 103, wherein the SVCV-G polypeptide comprises SEQ ID NO: 52 or SEQ ID NO: 53.

107. The viral particle of any one of embodiments 102, 103, or 106, wherein the SVCV-G polypeptide comprises SEQ ID NO: 52.

108. The viral particle of any one of embodiments 102, 103, or 106, wherein the SVCV-G polypeptide comprises SEQ ID NO: 53.

109. The viral particle of any one of embodiments 1-101, wherein the heterologous viral glycoprotein is a VSV-G polypeptide.

110. The viral particle 109, wherein the VSV-G polypeptide comprises a polypeptide of SEQ ID NO: 2 comprising a mutation that corresponds to a mutation at position 182 of SEQ ID NO: 2.

111. The viral particle 109, wherein the VSV-G polypeptide comprises an amino acid sequence having at least 70% identity to SEQ ID NO: 2 and comprising a mutation at position 182 as compared to SEQ ID NO: 2.

112. The viral particle of embodiment 110 or 111, wherein the VSV-G polypeptide comprises a I182E or I182D mutation as compared to SEQ ID NO: 2.

113. The viral particle of any one of embodiments 109-112, wherein the VSV-G polypeptide comprises the sequence having at least 70% identity to SEQ ID NO: 1 and comprising a mutation at position 198 as compared to SEQ ID NO: 1.

114. The viral particle of any one of embodiments 109-113, wherein the VSV-G polypeptide comprises a mutation that corresponds to I182D or I182E as compared to a sequence of SEQ ID NO: 2.

115. The viral particle of any one of embodiments 109-114, wherein the VSV-G polypeptide comprises a sequence at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% to a sequence of SEQ ID NO: 4.

116. The viral particle of any one of embodiments 109-114, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 4.

117. The viral particle of any one of embodiments 109-114, wherein the VSV-G polypeptide comprises a sequence at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% to a sequence of SEQ ID NO: 5.

118. The viral particle of any one of embodiments 109-114, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 5.

119. The viral particle of any one of embodiments 109-111 or 113, wherein the VSV-G polypeptide comprises a sequence at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% to a sequence of SEQ ID NO: 3.

120. The viral particle of any one of embodiments 109-111 or 113, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 3.

121. The viral particle of any one of embodiments 109-120, wherein the VSV-G polypeptide further comprises a mutation in the VSV-G protein that corresponds to a mutation as described in US 2020/0216502.

122. The viral particle of any one of embodiments 109-121, wherein the VSV-G polypeptide further comprises a mutation in the VSV-G protein that corresponds to a position of 8, 10, 47, 209 and/or 354 as compared to SEQ ID NO: 2.

123. The viral particle of any one of embodiments 109-122, wherein the VSV-G polypeptide further comprises a mutation that corresponds to a position 8 in SEQ ID NO: 2, wherein the mutation any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except Y.

124. The viral particle of any one of embodiments 109-123, wherein the VSV-G polypeptide further comprises a mutation that corresponds to a position 209 in SEQ ID NO: 2, wherein the mutation any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except H.

125. The viral particle of any one of embodiments 109-124, wherein the VSV-G polypeptide further comprises a mutation that corresponds to a position 47 in SEQ ID NO: 2, wherein the mutation any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except K or R.

126. The viral particle of any one of embodiments 109-125, wherein the VSV-G polypeptide further comprises a mutation that corresponds to a position 354 in SEQ ID NO: 2, wherein the mutation any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except K or R.

127. The viral particle of any one of embodiments 109-126, wherein the VSV-G polypeptide further comprises a mutation that corresponds to a position 10 in SEQ ID NO: 2, wherein the mutation any amino acid different from the amino acid indicated at that position in the sequence SEQ ID NO: 2, except Q or N.

128. The viral particle of any one of embodiments 109-127, wherein the VSV-G protein comprises a substitution at position 47 or at position 354, or at both positions 47 and 354, wherein each position is, independently, substituted by A, G, F, Q, or N.

129. The viral particle of any one of embodiments 109-128, wherein the VSV-G protein comprises a substitution at position 8, wherein the substitution is H8A, H8I, H8V, H8L, H8C, H8D, H8E, H8F, H8G, H8K, H8M, H8N, H8P, H8Q, H8R, H8S, H8T, H8W, or H8Y.

130. The viral particle of any one of embodiments 109-129, wherein the VSV-G protein comprises a substitution at position 47, wherein the substitution is K47Q or K47N.

131. The viral particle of any one of embodiments 109-130, wherein the VSV-G protein comprises a substitution H8A and/or K47Q mutation.

132. The viral particle of any one of embodiments 109-131, wherein the VSV-G protein comprises a substitution at position 10, such as Q10A, Q10R, or Q10K substitution.

133. The viral particle of any one of embodiments 109-132, wherein the VSV-G protein further comprises a mutation that corresponds to a mutation at positions 214 and/or 352 of SEQ ID NO: 2.

134. The viral particle of embodiment 133, wherein the VSV-G polypeptide comprises a T214N and/or T352A mutation.

135. The viral particle of embodiment 109, wherein the VSV-G polypeptide comprises a substitution at positions I182 and at least one of T214, and T352 of SEQ ID NO: 2.

136. The viral particle of embodiment 135, wherein the VSV-G polypeptide comprises substitutions at positions I182, T214, and T352 of SEQ ID NO: 2.

137. The viral particle of embodiments 135 or 136, wherein the substitution at position 182 is I182D or I182E, the substitution at position 214 is T214N, and the substitution at position 352 is T352A.

138. The viral particle of any one of embodiments 135-137, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24 or SEQ ID NO: 25.

139. The viral particle of any one of embodiments 135-137, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 22.

140. The viral particle of any one of embodiments 135-137, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 23.

141. The viral particle of any one of embodiments 135-137, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 24.

142. The viral particle of any one of embodiments 135-137, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 25.

143. The viral particle of any one of embodiments 1-142, wherein the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest.

144. The viral particle of embodiment 141, wherein the heterologous molecule of interest is an siRNA, an shRNA, a non-coding RNA (e.g. a guide RNA for a CRISPR system), a peptide, a polypeptide, a protein, a viral payload, a viral genome, or a combination thereof.

145. The viral particle of embodiments 143 or 144, wherein the heterologous molecule of interest is a chimeric antigen receptor ("CAR").

146. The viral particle of embodiment 145, wherein the CAR comprises an antigen binding domain comprising an antibody, or a fragment thereof.

147. The viral particle of embodiment 146, wherein the antibody, or fragment thereof is an antibody, a scFv antibody, an antigen binding domain, an ankyrin repeat, a VHH domain antibody, a nanobody, a single domain antibody, or an FN3 antibody.

148. The viral particle of embodiment 146 or 147, wherein the antigen binding domain of the CAR binds to CD19.

149. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a heavy chain variable region comprising the sequences

of HCDR1 as set forth in SEQ ID NO: 108; HCDR2 as set forth in SEQ ID NO: 109, and HCDR3 as set forth in SEQ ID NO: 110.

150. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a light chain variable region comprising the sequences of LCDR1 as set forth in SEQ ID NO: 111; LCDR2 as set forth in SEQ ID NO: 112, and LCDR3 as set forth in SEQ ID NO: 113.

151. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 89, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 108; HCDR2 as set forth in SEQ ID NO: 109, and HCDR3 as set forth in SEQ ID NO: 110.

152. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a light chain variable region comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 90, wherein the light chain variable region comprises the sequences of LCDR1 as set forth in SEQ ID NO: 111; LCDR2 as set forth in SEQ ID NO: 112, and LCDR3 as set forth in SEQ ID NO: 113.

153. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 89; and a light chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 90, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 108; HCDR2 as set forth in SEQ ID NO: 109, HCDR3 as set forth in SEQ ID NO: 110; LCDR1 as set forth in SEQ ID NO: 111; LCDR2 as set forth in SEQ ID NO: 112, and LCDR3 as set forth in SEQ ID NO: 113.

154. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 89; and the light chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 90.

155. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence

having at least 95% identity to an amino acid sequence of SEQ ID NO: 89; and the light chain variable region comprises an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO: 90.

156. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 99% identity to an amino acid sequence of SEQ ID NO: 89; and the light chain variable region comprises an amino acid sequence having at least 99% identity to an amino acid sequence of SEQ ID NO: 90.

157. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 89; and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 90.

158. The viral particle of any one of embodiments 149-157, wherein the heavy chain variable region and the light chain variable region are directly linked to one another and are not linked by a linker.

159. The viral particle of embodiments any one of embodiments 149-157, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 92, at least 95% sequence identity to SEQ ID NO: 92, at least 99% sequence identity to SEQ ID NO: 92, or a sequence as set forth in SEQ ID NO: 92.

160. The viral particle of embodiments any one of embodiments 149-157, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 93, at least 95% sequence identity to SEQ ID NO: 93, at least 99% sequence identity to SEQ ID NO: 93, or a sequence as set forth in SEQ ID NO: 93.

161. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a heavy chain variable region comprising the sequences of HCDR1 as set forth in SEQ ID NO: 114; HCDR2 as set forth in SEQ ID NO: 115, and HCDR3 as set forth in SEQ ID NO: 116.

162. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a light chain variable region comprising the sequences of

LCDR1 as set forth in SEQ ID NO: 117; LCDR2 as set forth in SEQ ID NO: 118, and LCDR3 as set forth in SEQ ID NO: 119.

163. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a heavy chain variable region comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 94, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 114; HCDR2 as set forth in SEQ ID NO: 115, and HCDR3 as set forth in SEQ ID NO: 116.

164. The viral particle of embodiment 148, wherein the antigen binding domain of the CAR that binds to CD19 comprises a light chain variable region comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 95, wherein the light chain variable region comprises the sequences of LCDR1 as set forth in SEQ ID NO: 117; LCDR2 as set forth in SEQ ID NO: 118, and LCDR3 as set forth in SEQ ID NO: 119.

165. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 94; and the light chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 95, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 114; HCDR2 as set forth in SEQ ID NO: 115, HCDR3 as set forth in SEQ ID NO: 116; LCDR1 as set forth in SEQ ID NO: 117; LCDR2 as set forth in SEQ ID NO: 118, and LCDR3 as set forth in SEQ ID NO: 119.

166. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 94; and the light chain variable region comprises an amino acid sequence having at least 90% identity to an amino acid sequence of SEQ ID NO: 95.

167. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO: 94; and the light

chain variable region comprises an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO: 95.

168. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 99% identity to an amino acid sequence of SEQ ID NO: 94; and the light chain variable region comprises an amino acid sequence having at least 99% identity to an amino acid sequence of SEQ ID NO: 95.

169. The viral particle of embodiment 148, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 94; and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 95.

170. The viral particle of any one of embodiments 161-169, wherein the heavy chain variable region and the light chain variable region are directly linked to one another and are not linked by a linker.

171. The viral particle of embodiments any one of embodiments 161-169, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 96, at least 95% sequence identity to SEQ ID NO: 96, at least 99% sequence identity to SEQ ID NO: 96, or a sequence as set forth in SEQ ID NO: 96.

172. The viral particle of embodiments any one of embodiments 161-169, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to SEQ ID NO: 97, at least 95% sequence identity to SEQ ID NO: 97, at least 99% sequence identity to SEQ ID NO: 97, or a sequence as set forth in SEQ ID NO: 97.

173. The viral particle of any one of embodiments 145-172, wherein the CAR further comprises a hinge domain, a transmembrane domain, a costimulatory domain, and a signaling domain.

174. The viral particle of embodiment 173, wherein the hinge domain comprises an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to an amino acid sequence of SEQ ID NO: 59.

175. The viral particle of embodiment 173 or 174, wherein the transmembrane domain comprises an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to an amino acid sequence of SEQ ID NO: 61.

176. The viral particle of any one of embodiments 173-175, wherein the costimulatory domain comprises an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to an amino acid sequence of SEQ ID NO: 101.

177. The viral particle of any one of embodiments 173-176, wherein the signaling domain comprises an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to an amino acid sequence of SEQ ID NO: 102.

178. The viral particle of embodiment 148, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99, at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99.

179. The viral particle of embodiment 148, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105, at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105.

180. The viral particle of embodiment 148, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106, at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106.

181. The viral particle of embodiment 148, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107, at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

182. A method of infecting a cell, the method comprising contacting the cell with a viral particle of any one of embodiments 1-181.

183. A method of infecting a cell in a subject, the method comprising administering to the subject a pharmaceutical composition comprising a viral particle of any one of embodiments 1-181.

184. A method of delivering a heterologous molecule of interest to a cell, the method comprising contacting the cell with a viral particle of any one of embodiments 1-181, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous

molecule of interest.

185. A method of delivering a heterologous molecule of interest to a cell in a subject, the method comprising administering to the subject a viral particle of any one of embodiments 1-181, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest.

186. The method of any one of embodiments 182-185, wherein the cell is an immune cell.

187. The method of any one of embodiments 182-186, wherein the cell is a T cell, B cell; NK cell, dendritic cell, neutrophils, macrophages, a cancer cell; or, for example, CD3+ T cell; CD4+ T cell; CD7+ T cell, CD8+ T cell; CD19+ B cell; CD19+ cancer cell; CD20+ B cell; CD20+ cancer cell, CD30+ lung epithelial cell; CD34+ haematopoietic stem cell; CD105+ endothelial cell; CD105+ haematopoietic stem cell; CD117+ haematopoietic stem cell; CD133+ cancer cell; EpCAM+ cancer cell; GluA2+ neuron; GluA4+ neuron; Haematopoietic stem cell; Hepatocyte; Her2/Neu+ cancer cell; NKG2D+ natural killer cell; SLC1A3+ astrocyte; SLC7A10+ adipocyte.

188. A method of treating a disease or disorder in a subject, the method comprising administering to the subject a viral particle of any one of embodiments 1-181, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest to treat the disease or disorder.

189. The method of embodiment 188, wherein the disease or disorder is cancer (e.g. such as a T cell or B cell disorder or other type of cancer as described herein), an immune disorder, an auto-immune disorder, metabolic disorder, and the like.

190. The method of embodiment 189, wherein the immune disorder is multiple sclerosis (MS), systemic lupus erythematosus (SLE), systemic sclerosis (SSc), lupus nephritis (LN), warm autoimmune hemolytic anemia (WAHA), primary sclerosing cholangitis (PSC), IgG4-related disease (IGG4-RD), acute disseminated encephalomyelitis (ADEM), Evans' syndrome (ES), focal segmental glomerulosclerosis (FSGS), Mixed connective tissue disease (MCTD), Mooren's ulcer (MU), chronic inflammatory demyelinating polyneuropathy (CIDP), Membranous nephropathy (MN), or thyroid eye disease (TED).

191. The method of embodiment 189, wherein the immune disorder is multiple sclerosis (MS), systemic lupus erythematosus (SLE), systemic sclerosis (SSc), lupus nephritis (LN), warm autoimmune hemolytic anemia (WAHA), primary sclerosing cholangitis (PSC), or IgG4-related disease (IGG4-RD).

192. The method of embodiment 189, wherein the immune disorder is multiple sclerosis (MS), systemic lupus erythematosus (SLE), systemic sclerosis (SSc), or lupus nephritis (LN).

193. The method of embodiment 189, wherein the immune disorder is warm autoimmune hemolytic anemia (WAHA), primary sclerosing cholangitis (PSC), or IgG4-related disease (IGG4-RD).

194. A method of delivering a heterologous molecule to a target cell, the method comprising contacting the cell with a viral vector or particle of any one of embodiments 1-181, wherein the particle comprises a nucleic acid molecule encoding the heterologous molecule.

195. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1,

wherein T is a target binding domain and S_1 is a stalk portion,

wherein the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52 or SEQ ID NO: 53;

wherein the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50 or SEQ ID NO: 51;

wherein the stalk portion S_1 comprises a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28;

wherein the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A;

wherein the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A;

wherein the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A; and

wherein the variant Fc protein further comprises a transmembrane domain comprising a sequence selected from SEQ ID NO: 61 or SEQ ID NO: 62.

196. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1,

wherein T is a target binding domain and S_1 is a stalk portion,

wherein the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52 or SEQ ID NO: 53;

wherein the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50 or SEQ ID NO: 51;

wherein the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1, wherein:

L_1 is a linker comprising a sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, or SEQ ID NO: 76 or is absent;

Fc is a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28;

wherein the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A;

wherein the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A;

wherein the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A;

L_2 is a linker comprising a sequence selected from SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, or SEQ ID NO: 76 or is absent; and

X_1 is a polypeptide comprising a transmembrane domain having a formula of ECD-T_M-ICD, wherein:

ECD is an extracellular domain having a sequence selected from SEQ ID NO: 59 or SEQ ID NO: 60 or a fragment thereof or is absent;

T_M is a transmembrane domain having a sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64 or the ICD is absent.

197. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1,

wherein T is a target binding domain and S_1 is a stalk portion,

wherein the heterologous viral glycoprotein comprises a sequence selected from SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52 or SEQ ID NO: 53;

wherein the target binding domain comprises a sequence selected from SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50 or SEQ ID NO: 51;

wherein the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1, wherein:

L_1 is a linker comprising a sequence of SEQ ID NO: 55 or is absent;

Fc is a variant Fc protein comprising a sequence that is a variant of SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 28;

wherein the variant of SEQ ID NO: 26 comprises one or more mutations selected from the group consisting of L234A, L235A, N297A, P329G, I253A, H310A, and H435A;

wherein the variant of SEQ ID NO: 27 comprises one or more mutations selected from the group consisting of N297A, P329G, I253A, H310A, and H435A;

wherein the variant of SEQ ID NO: 28 comprises one or more mutations selected from the group consisting of S228P, L235E, N297A, P329G, I253A, H310A, and H435A;

L_2 is a linker comprising a sequence of SEQ ID NO: 55 or is absent; and

X_1 is a polypeptide comprising a transmembrane domain having a formula of ECD-T_M-ICD, wherein:

ECD is an extracellular domain having a sequence of SEQ ID NO: 60 or a fragment thereof or is absent;

T_M is a transmembrane domain having a sequence of SEQ ID NO: 62, or a fragment thereof; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64 or the ICD is absent.

198. The viral particle of any one of embodiments 195-197, wherein the variant Fc protein comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 104, at least 90% identity to SEQ ID NO: 104, at least 95% identity to SEQ ID NO: 104, at least 98% identity to SEQ ID NO: 104, or comprises the amino acid sequence of SEQ ID NO: 104.

199. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety comprising a polypeptide having the formula T-S_1,

wherein T is a target binding domain and S_1 is a stalk portion,

wherein the heterologous viral glycoprotein comprises a sequence of SEQ ID NO: 23 or SEQ ID NO: 25;

wherein the target binding domain comprises a sequence of SEQ ID NO: 39;

wherein the stalk portion S_1 comprises a formula of L_1-Fc-L_2-X_1, wherein:

L_1 is a linker comprising a sequence of SEQ ID NO: 55;

Fc is a variant Fc protein comprising a sequence of SEQ ID NO: 104;

L_2 is a linker and is absent;

X_1 is a polypeptide comprising a transmembrane domain having a formula of ECD-T_M-ICD, wherein:

ECD is an extracellular domain having a sequence of SEQ ID NO: 60;

T_M is a transmembrane domain having a sequence of SEQ ID NO: 62; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63.

200. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein;

the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 23 or SEQ ID NO: 25, having at least 95% identity of SEQ ID NO: 23 or SEQ ID NO: 25, having at least 99% identity to SEQ ID NO: 23 or SEQ ID NO: 25, or having at least 100% identity to SEQ ID NO: 23 or SEQ ID NO: 25; and

the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98.

201. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein;

the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to of SEQ ID NO: 52 or SEQ ID NO: 53, having at least 95% identity to SEQ ID NO: 52 or SEQ ID NO: 53, having at least 99% identity to SEQ ID NO: 52 or

SEQ ID NO: 53, or having at least 100% identity to SEQ ID NO: 52 or SEQ ID NO: 53; and

the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98.

202. A viral particle comprising a heterologous viral structural protein and a targeting moiety comprising a polypeptide having the formula T-S_1,

wherein T is a target binding domain and S_1 is a stalk portion;

wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 38 or SEQ ID NO: 39;

wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein

L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58; and

X_1 is polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein:

ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or a fragment thereof, or is absent;

T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif comprising an amino acid comprising a sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

203. The viral particle of embodiment 202, wherein:

T comprises an amino acid sequence of SEQ ID NO: 38;

L_3 comprises an amino acid sequence of SEQ ID NO: 55;

ECD comprises an amino acid sequence of SEQ ID NO: 59;

T_M comprises an amino acid sequence of SEQ ID NO: 61; and

the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

204. The viral particle of embodiment 202, wherein:

T comprises an amino acid sequence of SEQ ID NO: 39;

L_3 comprises an amino acid sequence of SEQ ID NO: 55;

ECD comprises an amino acid sequence of SEQ ID NO: 59;

T_M comprises an amino acid sequence of SEQ ID NO: 61; and

the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

205. A viral particle comprising a heterologous viral structural protein and a targeting moiety comprising a polypeptide having the formula T-S_1,

wherein T is a target binding domain and S_1 is a stalk portion;

wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 50 or SEQ ID NO: 51;

wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein

L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58; and

X_1 is polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein:

ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or a fragment thereof, or is absent;

T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif comprising an amino acid comprising a sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

206. The viral particle of embodiment 205, wherein:

T comprises an amino acid sequence of SEQ ID NO: 50;

L_3 comprises an amino acid sequence of SEQ ID NO: 55;

ECD comprises an amino acid sequence of SEQ ID NO: 59;

T_M comprises an amino acid sequence of SEQ ID NO: 61; and

the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

207. The viral particle of embodiment 205, wherein:

T comprises an amino acid sequence of SEQ ID NO: 51;

L_3 comprises an amino acid sequence of SEQ ID NO: 55;

ECD comprises an amino acid sequence of SEQ ID NO: 59;

T_M comprises an amino acid sequence of SEQ ID NO: 61; and

the ICD comprises an env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

208. A viral particle comprising a heterologous viral structural protein and a targeting moiety comprising a polypeptide having the formula T-S_1;

wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52 or SEQ ID NO: 53;

wherein T is a target binding domain and S_1 is a stalk portion;

wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50 or SEQ ID NO: 51;

wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein

L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, or SEQ ID NO: 58; and

X_1 is polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein:

ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60, or a fragment thereof, or is absent;

T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62, or a fragment thereof; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid comprising a sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

209. A viral particle comprising a heterologous viral structural protein and a targeting moiety comprising a polypeptide having the formula T-S_1;

wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 52 or SEQ ID NO: 53;

wherein T is a target binding domain and S_1 is a stalk portion;

wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 50 or SEQ ID NO: 51;

wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein

L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 55; and

X_1 is polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein:

ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59 or a fragment thereof, or is absent;

T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61 or a fragment thereof; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle or is absent, wherein the ICD comprises an env incorporation motif comprising an amino acid comprising a sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

210. A viral particle comprising a heterologous viral structural protein and a targeting moiety comprising a polypeptide having the formula T-S_1;

wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 23 or SEQ ID NO: 25;

wherein T is a target binding domain and S_1 is a stalk portion;

wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 39;

wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein

L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 55; and

X_1 is polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein:

ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59;

T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral

particle, wherein the ICD comprises an env incorporation motif comprising an amino acid comprising a sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

211. A viral particle comprising a heterologous viral structural protein and a targeting moiety comprising a polypeptide having the formula T-S_1;

wherein the heterologous viral structural protein comprises a sequence of SEQ ID NO: 52 or SEQ ID NO: 53;

wherein T is a target binding domain and S_1 is a stalk portion;

wherein the target binding domain comprises an amino acid sequence of SEQ ID NO: 39;

wherein the stalk portion S_1 comprises a formula of L_3-X_1; wherein

L_3 is a flexible peptide linker comprising an amino acid sequence of SEQ ID NO: 55; and

X_1 is polypeptide comprising a transmembrane domain having a formula ECD-T_M-ICD, wherein:

ECD is an extracellular domain comprising an amino acid sequence of SEQ ID NO: 59;

T_M is a transmembrane domain comprising an amino acid sequence of SEQ ID NO: 61; and

ICD is an intracellular domain or protein that facilitates the incorporation of the targeting moiety into the envelope of the viral particle, wherein the ICD comprises an env incorporation motif comprising an amino acid comprising a sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

212. The viral particle of any one of embodiments 196-211, wherein the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest.

213. The viral particle of embodiment 212, wherein the heterologous molecule of interest is a CAR.

214. The viral particle of embodiment 213, wherein the antigen binding domain of the CAR binds to CD19.

215. The viral particle of embodiment 214, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 99, at least 90% identity to SEQ ID NO: 99, at least 95% identity to SEQ ID NO: 99, at least 99% identity to SEQ ID NO: 99, or at least 100% identity to SEQ ID NO: 99.

216. The viral particle of embodiment 214, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 105, at least 90% identity to SEQ ID NO: 105, at least 95% identity to SEQ ID NO: 105, at least 99% identity to SEQ ID NO: 105, or at least 100% identity to SEQ ID NO: 105.

217. The viral particle of embodiment 214, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 106, at least 90% identity to SEQ ID NO: 106, at least 95% identity to SEQ ID NO: 106, at least 99% identity to SEQ ID NO: 106, or at least 100% identity to SEQ ID NO: 106.

218. The viral particle of embodiment 214, wherein the CAR comprises an amino acid sequence having at least 85% identity to SEQ ID NO: 107, at least 90% identity to SEQ ID NO: 107, at least 95% identity to SEQ ID NO: 107, at least 99% identity to SEQ ID NO: 107, or at least 100% identity to SEQ ID NO: 107.

[00453] The following examples are illustrative, but not limiting, of the compounds, compositions and methods described herein. Other suitable modifications and adaptations known to those skilled in the art are within the scope of the following embodiments.

Examples

[00454] Example 1: Mutation at position 182 of VSV-G abrogates LDL-R interaction, but retains fusing properties. Plasmids/Sequences. All VSV-G plasmids were derived from pCMV-VSV-G Envelope Vector (Cell Bio Labs, catalog RV-110). Point mutations and combinations thereof were introduced using site directed mutagenesis (New England Biolabs). Individual mutations H8A and K47Q were previously shown to partially "blind" VSV-G, reducing its binding to LDL-R, the native cellular receptor for VSV (PMID: 29531262, DOI: 10.1038/s41467-018-03432-4). In this experiment, a single binder molecule consisting of a CD7-targeting scFv (clone MT701) fused to an IgG "stalk" bearing a CD28 transmembrane domain was used.

[00455] Cells. HEK293T cells were grown in DMEM with 10% FBS. SupT1 cells were maintained in RPMI media with 10% FBS. Human PBMCs were purchased from AllCells and cultured in X-Vivo 10 (Lonza) supplemented with 20ng/mL IL-2 (Peprotech). PBMCs were activated 48 hours prior to transduction using anti-CD3/CD28 Dynabeads (Cell Therapy Systems).

[00456] Generation of lentiviral particles. The recombinant lentiviral particles co-expressing VSV-G glycoprotein and binder molecules were generated by plasmid transection into HEK293T cells using Lipofectamine 3000 (ThermoFisher Scientific). A total of 5 plasmids

were transfected: (1) plasmid expressing the VSV-G glycoprotein, (2) plasmid expressing the binder protein (3) plasmid expressing the lentiviral transfer genome encoding for eGFP, (4) plasmid expressing gag-pol, and (5) plasmid expressing rev. Transfected cell supernatant was harvested 48 hours later. Virus in the cell supernatant was concentrated by centrifugation through a sucrose cushion and resuspended in PBS. Lentiviral particle titer was determined using the Lenti-X p24 Rapid Titer Kit (Takara Bio, San Jose, CA).

[00457] Lentivirus transduction assay. A series of 10-fold dilutions (in cell culture media) of the concentrated lentivirus was performed and used to infect SupT1 and activated human PBMCs. Media was replaced 6 hours later, and the transduced cells were analyzed by flow cytometry on days 4 and 7 after transduction. Cells were stained with a viability stain and an anti-CD7 antibody to detect CD7 positive cells (PeCy7 mouse-anti-human CD7, clone CD7-6B7, BD Biosciences). Expression of eGFP was measured to calculate transduction efficiency.

[00458] Structure-guided design of novel blinding mutations. Using a published crystal structures of VSV-G bound to CR2 and CR3 of the LDL-R (pdb 50YL and 50Y9, respectively), two putative positions in VSV-G with side chains oriented toward the binding interface on LDL-R were identified (FIG. 1). Residue Q10 (SEQ ID NO: 2) appeared to form several interactions with residues in both CR2 and CR3. In CR3, this included interactions with a positively charged arginine residue. Thus, three substitutions were tested: Q10A to reduce side-chain interactions that potentially stabilize LDL-R binding and Q10R and Q10K to create electrostatic repulsion.

[00459] Residue I182 (SEQ ID NO: 2) appeared to contact several residues in both CR2 and CR3 as well. Three substitutions were tested: I182A to reduce side-chain interactions that potentially stabilize LDL-R binding and I182D and I182E to create electrostatic repulsion against the primary binding interfaces on LDL-R.

[00460] Addition of negative charges in the binding interface ablate native tropism without altering fusogenicity. Titration of viral supernatants on the CD7+ T cell line SupT1 validated the structural predictions for residue I182. In the absence of any compensatory binder molecule, WT VSV-G reached titers of 3.0e8 while both I182D and I182E were ~3 orders of magnitude lower (Fig 2). Substitutions at residue I182 preserved fusogenicity, as titers were restored to 1e8 in the presence of a binder redirecting the virions to CD7.

[00461] The data is illustrated in FIG. 2, which shows that the addition of negative charges in the binding interface ablate native tropism without altering fusogenicity. FIG. 2A shows the titration of VSV-G constructs on SupT1 cells. Plotted is the percentage of SupT1 cells expressing GFP at each amount of viral input in terms of p24 antigen. Dashed lines/open circles

indicate VSV-G constructs alone, solid lines/filled circles indicate the same construct with a CD7 targeting molecule expressed in trans. FIG. 2B illustrates Functional titer of each construct calculated from the titration in A, expressed as transducing units per mL of concentrated virus supernatant (TU/mL).

[00462] Thus these examples demonstrate that a mutation position 182 is sufficient to abrogate the LDL-R interaction, but retain fusogenic properties when combining with a targeting moiety that binds to a target on the target cell.

[00463] Example 2: Serum Stable VSV-G Protein

[00464] WT VSV-G is reported to be sensitive to inactivation by naïve human serum, with inactivation ranging from minimal change to about 100-fold decrease depending on study parameters. Accordingly, it was assessed i) whether substitution at position I182 produced a variant VSV-G with similar sensitivity to serum and ii) whether incorporation of known serum stabilizing VSV-G mutations into the I182 substituted constructs had an effect on the serum stability of the constructs.

[00465] WT VSV-G, Serum Stable VSV-G (T214N, T352A), LDL-R de-targeted VSV-G (I182E), and LDL-R de-targeted serum stable VSV-G (I182E, T214N, T352A) were tested for their ability to infect SupT1 cells in the presence or absence of naïve serum or heat inactivated serum (HI) (FIG. 4). As expected WT VSV-G had a dramatic decrease in percent infectivity when administered in the presence of serum with a mild rescue of infectivity if serum was heat inactivated (FIG. 4, columns 1-3). The inclusion of the CD7 targeting moiety on an IgG1 Fc stalk (WT) did not rescue the serum inactivation (FIG. 4, columns 4-6). The VSV-G constructs harboring the T214N and T352A mutations showed a similar reduction in infectivity in the presence of serum with no distinction between naïve or HI serum (FIG. 4, columns 7-9). However, the inclusion of the targeting moiety was able to partially rescue the inactivation in either serum condition (FIG. 4, columns 10-12). Surprisingly, the LDL-R de-targeted VSV-G (I182E) showed no reduction in infectivity percentage in the presence of either serum condition (FIG. 4, columns 13-15), but rather showed increased infectivity in the presence of naïve serum as compared to serum free or HI serum conditions. Further inclusion of the known serum stable mutations into VSV-G (I182E, T214N, T352A) also demonstrated increased infectivity in the presence of serum as compared to serum free conditions (FIG. 4, columns 16-18). Further, the I182E, T214N, T352A construct also demonstrates increased infectivity in the presence of HI serum (FIG. 4, column 18), which indicates that the triple mutant construct has a higher degree of serum stability than the other constructs examined.

[00466] To further characterize the effect of including serum stabilizing mutations in the viral constructs of the present application, WT VSV-G, VSV-G (I182E), and VSV-G (I182E, T230N, T352A) were assessed at a lower dose of vector (FIG. 5). In agreement with the previous assessment, WT VSV-G showed decreased infectivity in serum as compared to no-serum conditions (FIG. 5, columns 1 and 2). However, heat inactivation (HI) of serum did appear to have a rescuing effect on WT VSV-G infectivity (FIG. 5, column 3). In further agreement with the previous assessment, VSV-G (I182E) demonstrated enhanced infectivity in the presence of serum as compared to no serum conditions (FIG. 5, columns 4 and 5). The presence of HI serum also resulted in an increased infectivity compared to no serum, with a smaller effect than naïve serum (FIG. 5, column 6). VSV-G (I182E, T214N, T352A) also demonstrated increased infectivity in serum and HI serum conditions as compared to no serum conditions (FIG. 5, columns 7-9), in agreement with the previous assessment. Further, when compared to the respective no serum condition, VSV-G (I182E, T230N, T352A) results in a greater percent increased infectivity compared to VSV-G (I182E), suggesting that inclusion of all three mutations results in greater serum stability than just I182E alone.

[00467] Thus, these examples demonstrate that i) the LDL-R detargeting mutation I182E affords an unexpected level of protection against the serum inactivation observed for WT VSV-G, ii) the LDL-R detargeting mutation I182E does not abrogate the serum stabilizing effect of the T230N + T352A mutations, and iii) the combined mutation construct VSV-G (I182E, T230N, T352A) appears to have a greater serum stabilizing effect than either I182E alone or T230N + T352A alone. Thus, VSV-G (I182E, T230N, T352A) is able to ablate native tropoism without alternating fusogenicity and additionally demonstrates a more stable profile and is not neutralized in serum.

[00468] Example 3: Spring viremia of carp virus G protein can facilitate cell specific fusion.

[00469] Methods

[00470] Plasmids/Sequences. All rhabdovirus GP sequences were codon optimized and synthesized by Genscript. Sequences are shown below, with accession numbers found in the following table, which are hereby incorporated by reference in its entirety, Table 1:

Table 1. Rhadovirus glycoprotein sequences used.

Rhabdovirus	Genbank Accession
Spodoptera frugiperda rhabdovirus isolate Sf - G	KF947078.1
Drosophila obscura sigma virus 10A - G	GQ410979.1
Wuhan insect virus 7 - G	YP_009301742.1
Perch rhabdovirus - G	YP_007641366.1

Spring viremia of carp virus - G	CAA85735.1

[00471] The targeting moiety comprises an anti-CD7 antibody (clone MT701, in single chain format) anchored to the membrane via an IgG based Fc stalk, which comprises a CD28 transmembrane domain.

[00472] **Cells.** HEK293T cells were grown in DMEM with 10% FBS. SupT1 cells were maintained in RPMI media with 10% FBS. Human PBMCs were purchased from AllCells and cultured in X-Vivo 10 (Lonza) supplemented with 20ng/mL IL-2 (Peprotech). PBMCs were activated 48 hours prior to transduction using anti-CD3/CD28 Dynabeads (Cell Therapy Systems).

[00473] **Generation of lentiviral particles.** The recombinant lentiviral particles co-expressing rhabdovirus-G glycoproteins and binder molecules were generated by plasmid transection into HEK293T cells using Lipofectamine 3000 (ThermoFisher Scientific). A total 5 plasmids were transfected: (1) plasmid expressing the rhabdovirus G glycoprotein, (2) plasmid expressing the binder protein (where indicated), (3) plasmid expressing the lentiviral transfer genome encoding for CAR20, (4) plasmid expressing gag-pol, and (5) plasmid expressing rev. Transfected cell supernatant was harvested 48 hours later. Virus in the cell supernatant was concentrated by centrifugation through a sucrose cushion and resuspended in x-vivo medium. Lentiviral particle titer was determined using the Lenti-X p24 Rapid Titer Kit (Takara Bio, San Jose, CA).

[00474] **Lentivirus transduction assay.** A series of 5-fold dilutions (in cell culture media) of the concentrated lentivirus was performed and used to infect SupT1 and activated human PBMCs. Media was replaced 6 hours later, and the transduced cells were analyzed by flow cytometry on days 4 and 7 after transduction. Cells were stained with a viability stain, an anti-CD7 antibody to detect CD7 positive cells, and an anti-CAR antibody to detect CAR20 expression as a measure of transduction efficiency.

[00475] Results:

[00476] **SVCV-G mediates fusion into human cells.** Most non-mammalian rhabdovirus G proteins failed to mediate transduction in human cells, with the exception of Spring viremia of carp virus G (SVCV-G). This glycoprotein did not target SupT1 or human PBMC cells on its own as transduction was very inefficient (~1 log lower than blinded VSV-G I182E) in the absence of the CD7 binder. Targeted transduction mediated by the CD7 binder reached comparable titers to retargeted VSV-G I182E.

[00477] This surprising and unexpected result demonstrates that a viral structural protein that cannot infect an immune cell on its own can be used to infect a cell when the virus also

expresses a targeting moiety, such as one that comprises an anti-CD7 scFv. This result could not have been predicted and is shown not to be an effect of the anti-CD7 scFv on its own as the presence of the anti-CD7 scFv targeting moiety was not sufficient to induce infections utilizing other non-human rhabdovirus GP proteins. The data is illustrated in FIG. 6.

[00478] Example 4: CD7 Targeting Moiety can be linked to a Fc stalk to transduce PBMCs.

[00479] Generation of Plasmids and Sequences.

[00480] The amino acid sequence including CDRs of the CD7 binder was determined via mass spectrometry (Rapid Novor). CD7 binder sequences were synthesized by IDT or GenScript (Piscataway, NJ) using codon optimization for human expression and inserted onto viral glycoprotein or IgG-based stalks and flanked by a G4S linker. An example viral glycoprotein is a Nipah-G protein with the CD7 binder attached to the extracellular region. An example IgG-based stalk was a human IgG1 Fc dimer with a CD8 or CD28 transmembrane region and an envelope incorporating motif with the CD7 binder attached to the extracellular region. The resulting binders were expressed under the direction of a CMV promoter.

[00481] Generation of Engineered Lentiviral Particles.

[00482] The recombinant lentiviral particles expressing the CD7 binder incorporated on the surface were generated by plasmid transection into HEK293T cells using Lipofectamine 3000 (ThermoFisher Scientific). In some embodiments, a total of 5 plasmids were transfected: (1) plasmid expressing the CD7 binder with the IgG stalk or a plasmid expressing the CD7 binder on a Nipah-G protein, (2) plasmid expressing a detargeted-VSV-G protein, (3) lentiviral genome expressing eGFP, (4) plasmid expressing gag-pol, (5) plasmid expressing rev.In some embodiments, a total of 5 plasmids were transfected: (1) plasmid expressing the CD7 binder with the Nipah-G protein, (2) plasmid expressing Nipah-F protein, (3) lentiviral genome expressing eGFP, (4) plasmid expressing gag-pol, (5) plasmid expressing rev. Media was changed 6 hours after transfection and cells were harvested 48 hours later. Virus in the media was concentrated by centrifugation through a sucrose cushion and resuspended in media. Lentiviral particle titer was determined using the Lenti-X p24 Rapid Titer Kit (Takara Bio, San Jose, CA)

[00483] CD7 binders attach to both human and non-human primate PBMCs, leading to CD7+ cell transduction.

[00484] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated

lentivirus was used to infect human and non-human primate cells. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on days 4 and 7 after transduction. Cells were stained with an anti-CD7 antibody to detect CD7 positive cells (PE-Cy7 mouse-anti-human CD7, clone MT-701, Biolegend) as well as GFP expression. Cell viability was also determined. CD7 binders adhered to Paramyxoviridae glycoproteins, such as Nipah-G with Nipah-(FIG. 7A-D and FIG. 8A-D) or with Rhabdoviridae glycoproteins, such as VSV-G (FIG. 7I-L and FIG. 8I-L) successfully transduced human PBMCs (FIG. 7A-L) or NHP PBMCs (FIG. 8A-L) compared to the binder alone (FIG. 7E-H and FIG. 8E-H) which shows no transduction. When CD7 with an IgG stalk was tested, the binder alone (top row) again did not transduce human (FIG. 7M) or NHP PBMCs (FIG. 8M) but when administered with blinded VSV-G, transduction was seen in both human (FIG. 7M, bottom panel) and NHP PBMCs (FIG. 8M, bottom panel).

[00485] These examples and embodiments demonstrate that the polypeptides can be used to bind to CD7 and target viral particles to cells expressing CD7 to transduce the cells expressing CD7.

[00486] Example 5: CD8 Targeting Moiety can be linked to a Fc stalk to transduce PBMCs.

[00487] Generation of Plasmids and Sequences.

[00488] The amino acid sequence including CDRs of the CD8 binder was determined via mass spectrometry (Rapid Novor). CD8 binder sequences were synthesized by IDT or GenScript (Piscataway, NJ) using codon optimization for human expression and inserted onto viral glycoprotein or IgG-based stalks and flanked by a G4S linker. An example viral glycoprotein is a Nipah-G protein with the CD8 binder attached to the extracellular region. An example IgG-based stalk was a human IgG1 Fc dimer with a CD8 or CD28 transmembrane region and an envelope incorporating motif with the CD8 binder attached to the extracellular region. The resulting binders were expressed under the direction of a CMV promoter.

[00489] Generation of Engineered Lentiviral Particles.

[00490] The recombinant lentiviral particles expressing the CD8 binder incorporated on the surface were generated by plasmid transection into HEK293T cells using Lipofectamine 3000 (ThermoFisher Scientific). In some embodiments, a total of 5 plasmids were transfected: (1) plasmid expressing the CD8 binder with the IgG stalk, (2) plasmid expressing a detargeted-VSV-G protein, (3) lentiviral genome expressing eGFP, (4) plasmid expressing gag-pol, (5) plasmid expressing rev. In some embodiments, the lentiviral genome expressing eGFP was replaced with a CAR molecule. Media was changed 6 hours after transfection and cells were

harvested 48 hours later. Virus in the media was concentrated by centrifugation through a sucrose cushion and resuspended in media. Lentiviral particle titer was determined using the Lenti-X p24 Rapid Titer Kit (Takara Bio, San Jose, CA).

[00491] CD8 binders attach to both human and non-human primate PBMCs, leading to CD8+ cell transduction.

[00492] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 6 after transduction. Cells were stained with an anti-CD8 antibody to detect CD8 positive cells (BV421 mouse-anti-human CD8, clone RPA-T8, Biolegend) as well as GFP or CAR20 expression. The CD20 CAR construct was as described in U.S. Patent Application No. 18/066,420; U.S. Patent Application No. 18/157,421; and U.S. Patent Application No. 18/167,444; each of which are incorporated herein by reference in their entirety. Cell viability was also determined. CD8 binders with detargeted VSV-G successfully transduced human PBMCs (FIG. 9A) or NHP PBMCs (FIG. 9B) with GFP (FIG. 9A-9B, top row) and CAR20 (FIG. 9A-9B, bottom row).

[00493] These examples and embodiments demonstrate that the polypeptides can be used to bind to CD8 and target viral particles to cells expressing CD8 to transduce the cells expressing CD8.

[00494] Example 6: VSV-G* pseudotyped lentiviruses harboring Fc stalk binder transduce PBMCs.

[00495] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. The binder constructs utilized for VSV-G* pseudotyped lentiviruses in the present example are the same as the CD7 binder constructs utilized in previous examples. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine CAR transduction. The CAR was a CD20 CAR construct was as provided for in Example 5. CAR expression was observed in all human and non-human primate PBMCs assessed (FIG.

10A) compared to the binder alone (FIG. 10B) which shows no transduction. Data are also presented as percent CAR expression vs multiplicity of infection (FIG. 10C).

[00496] These examples and embodiments demonstrate that the VSV-G* pseudotyped lentiviruses are able to successfully transduce a variety of human and non-human primate PMBCs.

[00497] Example 7: CD7 Targeting Moiety can be linked to a flexible stalk to transduce PBMCs.

[00498] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine CAR transduction. The CAR was a CD20 CAR construct was as provided for in Example 5. CAR expression was observed in all human and non-human primate PBMCs assessed (FIG. 11A) compared to no binder (FIG. 11B) which shows no transduction. Data are also presented as percent CAR expression vs multiplicity of infection (FIG. 11C).

[00499] These examples and embodiments demonstrate that a CD7 binder with a flexible stalk is able to successfully transduce human and non-human primate PBMCs. This represents a surprising and unexpected result in light of a recent report by Dobson and colleagues (Dobson CS, Reich AN, Gaglione S, Smith BE, Kim EJ, Dong J, Ronsard L, Okonkwo V, Lingwood D, Dougan M, Dougan SK, Birnbaum ME. Antigen identification and high-throughput interaction mapping by reprogramming viral entry. Nat Methods. 2022 Apr;19(4):449-460. doi: 10.1038/s41592-022-01436-z. Epub 2022 Apr 8. PMID: 35396484; PMCID: PMC9012700) which showed that a VSVG (K47Q, R354A) psuedotyped virus utilizing IL-13 as a target binding domain was unable to transduce IL-13Rα1-expressing cells when utilizing a flexible $(G_4S)_3$ surface architecture. To determine whether the number of G_4S repeats is an essential variable for transduction, various constructs were utilized harboring between 0 and 4 G_4S repeats (FIG. 12). Viruses comprising the various G_4S stalks each with an anti-CD7 binding domain were transfected along with a packaging plasmid set consisting of VSV-G*, xHIV packaging, rev, and a SIN lentivector genome encoding an anti-CD20 CAR (CAR20) in

HEK293T cells. Control samples were either the packaging set alone without a binder, the packaging set with an IgG Fc stalk with an anti-CD7 binding domain, or the packaging set without a binder substituting VSV-G* with VSV-G wild-type. Viral supernatant was purified by centrifugation over a 20% sucrose cushion and resuspended in X-Vivo media. Resuspended virus was analyzed by a p24 assay to determine viral protein content in solution. 10-fold dilutions by p24 mass of virus were administered to SupT1 and human PBMCs as indicated. Flow cytometry was utilized to assess the fraction of cells with CAR20 protein on the surface at seven days after transduction. In SupT1 cells (FIG. 12A), $(G_4S)_1$ resulted in greater CAR expression than $(G_4S)_2$ or $(G_4S)_3$ constructs. Surprisingly, constructs harboring a $(G_4S)_4$ flexible stalk did not follow the trend established for $(G_4S)_{1-3}$ and instead the $(G_4S)_4$ flexible stalk constructs resulted in greater CAR expression than any of the other $(G_4S)_n$ constructs tested. A similar result was found in human PBMCs (FIG. 12B).

[00500] Example 8: SVCV-G pseudotyped lentiviruses harboring Fc stalk binder transduce PBMCs.

[00501] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. The CD7 binder constructs utilized for SVCV-G pseudotyped lentiviruses of the present example are the same as those utilized in previous examples. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine CAR transduction. The CAR was a CD20 CAR construct was as provided for in Example 5. CAR expression was observed in all human and non-human primate PBMCs assessed (FIG. 13A) compared to no binder (FIG. 13B) which shows no transduction. Data are also presented as percent CAR expression vs multiplicity of infection (FIG. 13C).

[00502] These examples and embodiments demonstrate that the i) SVCV-G pseudotyped lentiviruses are able to successfully transduce PMBCs and ii) the variant Fc stalks of the present disclosure are not limited to just VSV-G pseudotyped embodiments.

[00503] Example 9: SVCV-G pseudotyped lentiviruses harboring a CD7/flexible stalk binder transduce PBMCs.

[00504] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. The binder constructs

utilized for SVCV-G pseudotyped lentiviruses are the same as those utilized in previous example 4. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine CAR transduction. The CAR was a CD20 CAR construct was as provided for in Example 5. CAR expression was observed in all human and non-human primate PBMCs assessed (FIG. 14A) compared to no binder (FIG. 14B) which shows no transduction. Data are also presented as percent CAR expression vs multiplicity of infection (FIG. 14C).

[00505] These examples and embodiments demonstrate that the i) SVCV-G pseudotyped lentiviruses are able to successfully transduce PMBCs and ii) the flexible stalk constructs are not limited to just VSV-G pseudotyped embodiments.

[00506] Example 10: SVCV-G pseudotyped lentiviruses are comparable to VSV-G* pseudotyped lentiviruses.

[00507] The transduction efficiency of SVCV-G and VSV-G* pseudotyped lentiviruses harboring a CD7 binder with a Fc stalk were compared. Lentivirus generation and cell transduction assays were performed as in the previous examples. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine CAR transduction. The CAR was a CD20 CAR construct was as provided for in Example 5. CAR expression was comparable between VSV-G* and SVCV-G pseudotyped constructs across in SupT1 cells as well as several human PBMC lines and non-human primate PBMC lines (FIG. 15).

[00508] The transduction efficiency of SVCV-G and VSV-G* pseudotyped lentiviruses harboring a CD7 binder with a flexible stalk were also compared. Lentivirus generation and cell transduction assays were performed as in the previous examples. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM

Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine CAR transduction. The CAR was a CD20 CAR construct was as provided for in Example 5. CAR expression was comparable between VSV-G* and SVCV-G pseudotyped constructs across in SupT1 cells as well as several human PBMC lines and non-human primate PBMC lines (FIG. 16).

[00509] These examples and embodiments demonstrate that both VSV-G* and SVCV-G pseudotyped viral particles are able to transduce SupT1 and PBMC cells with similar potency when using a CD7 binder with either the variant Fc stalks of the present disclosure or the flexible peptide stalks of the present disclosure, suggesting that both VSV-G* and SVCV-G constructs may be useful in transducing a wide array of cell types.

[00510] Example 11: VSV-G* pseudotyped lentiviruses harboring a CD7/Fc stalk binder transduce PBMCs with CD19 CAR construct.

[00511] Human PBMC cells were maintained in X-Vivo10 media with 5% human serum and 20ng/mL of human IL-2. Non-human primate cells were maintained in RPMI media with 10% FBS, 1% Pen/Strep with 1mM Sodium Pyruvate and 100units/mL hIL-2. Concentrated lentivirus was used to infect human and non-human primate cells. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. Media was replaced 24 hours later, and the transduced cells were analyzed by flow cytometry on day 6 after transduction to determine CAR transduction. CAR transduction was determined via detection of the G_4S linker within each CAR construct. Results are provided in the table below:

	Construct					
	Non-transduced	CD20 CAR	CD19 CAR (SEQ ID NO: 99)	CD19 CAR (SEQ ID NO: 105)	CD19 CAR (SEQ ID NO: 106)	CD19 CAR (SEQ ID NO: 107)
Percent CAR + cells	0.022	16.0	61.4	58.3	51.4	54.0

[00512] The non-transduced control exhibited no G_4S staining as expected. As a positive control, PBMCs were transduced with a CD20 CAR construct known to transduce PBMCs (as described in U.S. Patent No. 11,767,366; U.S. Patent Publication No. 2023/0279363; U.S. Patent Publication No. 2023/0293688; and U.S. Patent Publication No. 2024/0059744; each of which are incorporated herein by reference in their entirety). The CD20 CAR construct

exhibited a modest transduction of the PBMCs. Each CD19 CAR construct tested was robustly transduced, with each construct being detected in at least 50% of the PBMCs. The difference in transduction between the CD19 and CD20 CAR constructs may be attributed to the detection method, using an antibody against G_4S rather than against CD20. Nonetheless, these examples and embodiments demonstrate that the CD19 CAR constructs of the present disclosure are successfully delivered and transduced by the viral particles of the present disclosure.

[00513] Example 12: VSV-G pseudotyped lentiviruses delivering various CAR transgenes exhibit minimal off target transduction.

[00514] The off target transduction of B-cells via VSV-G* pseudotyped lentiviral constructs utilizing Fc binder stalks and delivering various CAR transgene payloads was assessed in several B-cell populations. CAR transgenes assessed were a CD20 targeted CAR (CAR20), CD19 targeted CARs comprising the amino acid sequences of SEQ ID NO: 107, SEQ ID NO: 105, or SEQ ID NO: 132, and a control CAR. The CD19 CAR comprising SEQ ID NO: 132 represents a unique CD19 antigen binding domain as compared to SEQ ID NO: 107 or 105 and is of murine origin. In contrast, the CD19 CARs corresponding to SEQ ID NO: 107 and 105 are fully human antibody-derived antigen binding domains. The V_H and V_L domains of the SEQ ID NO: 132 CD19 CAR correspond to SEQ ID NOs: 133 and 134, respectively. All CAR transgenes also contained a GFP reporter separated from the CAR by a T2A sequence. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. Cell lines were maintained in RPMI 1640 supplemented with 10% FBS and Pen/Strep. Concentrated lentivirus was used to transduce the various B-cell populations. The CD7 binder constructs utilized for the pseudotyped lentiviruses are the same as those utilized in previous examples. Media was replaced approximately 6 hours later, and the transduced cells were analyzed by flow cytometry on day 7 after transduction to determine GFP transduction. As a control, SupT1 cells were also infected with the same lentiviral constructs.

[00515] As expected, all CAR constructs were successfully transduced in SupT1 cells (FIG. 17A). Low levels of off target transduction were detected in Raji cells for CD19 CAR constructs SEQ ID NO: 107 and SEQ ID NO: 132 (FIG. 17B). Appreciable levels of off target transduction were detected in Rec1 cells for CD19 CAR constructs SEQ ID NO: 107 and SEQ ID NO: 132 (FIG. 17E). However, the CD19 CAR construct of SEQ ID NO: 105 did not show any appreciable level of off target transduction across any of the B-cell lines tested (FIG. 17B-H).

[00516] Example 13: VSV-G* pseudotyped lentiviruses with CD19-CAR transgene payload kills CD19 positive lymphoma cells *in vitro*

[00517] The ability of VSV-G* pseudotyped lentiviral constructs with a CD19-CAR transgene to kill CD19 positive lymphoma cells *in vitro* was assessed. The VSV-G* pseudotyped lentiviral constructs utilized CD7 binders as provided for herein. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23), as provided for herein. Human PBMCs were transduced with a lentiviral construct carrying a CD19-CAR (CAR19) transgene. The CAR19 transgenes comprised antigen binding domains of SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 96, or SEQ ID NO: 97. These corresponded to CD19 CAR constructs of SEQ ID NO: 99, SEQ ID NO: 105, SEQ ID NO: 106, or SEQ ID NO: 107. CAR+ PBMCs were mixed with target CD19-expressing B cells at known Effector:Target (E:T) ratios. After a 2 day coculture, flow cytometry was used to determine the frequency of B cells remaining and normalized to controls using non-transduced PBMCs. All lentiviral constructs tested produced a dose dependent killing of CD19 positive lymphoma cells (FIG 18A and FIG. 18B)

[00518] These examples and embodiments demonstrate that the VSV-G* pseudotyped lentiviruses utilizing the CD7 binders of the present disclosure not only transduce the appropriate target cells as demonstrated by the previous examples, but also produce robust and dose dependent killing of CD19 positive lymphoma cells *in vitro*.

[00519] Example 14: B-cell killing by CD19 CAR expressing PBMCs is CD19 dependent.

[00520] The selective killing of CD19 positive B-cells was assessed. Raji B-cells were modified to express GPF and knock out CD19 (Raji-GFPΔCD19), express GFP and knock out CD20 (Raji-GFPΔCD20) or just express GFP (Raji-GFP). Human PBMC were transduced with lentiviral constructs as provided for herein carrying either a CD19 CAR transgene (SEQ ID NO: 105 or SEQ ID NO: 107) or a CD20-CAR (CAR20) transgene. The modified Raji cells were then added to the CAR modified PBMCs at a given effector to target ratio (E:T). After a 2 day coculture, flow cytometry was used to determine the frequency of B cells remaining and normalized to controls using non-transduced PBMCs. The CD19-CAR positive PBMCs produced a dose dependent killing of the Raji-GFP and Raji-GFPΔCD20 cells, but not the Raji-GFPΔCD19 cells (FIG. 19A and 19B) indicating that the PBMC killing of the Raji cells was CD19 dependent. Similarly, the control CAR20 positive PBMCs produced a dose dependent killing of the Raji-GFP and Raji-GFPΔCD19 cells, but not the Raji-GFPΔCD20 cells (FIG. 19C), indicating that the PBMC killing of the Raji cells was CD20 dependent.

[00521] Example 15: Assessment of potential for generation of CAR resistant B-cells.

[00522] An experiment was performed to assess the risk of unintended B cell transduction resulting in CAR-resistance B cells. Naïve Rec-1 lymphoblast B cells were first transduced with viral constructs as provided for herein to generate B cells harboring a CAR19 transgene (SEQ ID NO: 105) or GFP. Then, the generated B cells as well as unmodified B cells were exposed to CAR19 positive PBMCs at a given effector to target ratio (E:T). After a 2 day coculture, flow cytometry was used to determine the frequency of B cells remaining and normalized to controls using non-transduced PBMCs. The ability of the CAR19 positive PBMCs to kill both cell lines as well as the possibility of enriching for transgene positive B cells was assessed. CAR19 positive PBMCs were generated as described in previous examples with a VSV-G* pseudotyped lentiviral constructs utilizing a CD7 binder having the sequence of SEQ ID NO: 98 and delivering a CAR transgene having the sequence of SEQ ID NO: 105. The results are illustrated in FIG. 20A and 20B.

[00523] As shown in FIG. 20A, the CAR19 positive PBMCs were still able to kill the CAR19 positive B cells (+ SEQ ID NO: 105) at a similar potency to the killing of B cells not expressing the CAR19 transgene (-SEQ ID NO: 105). As expected, PBMCs that were not transduced with the CAR transgene did not produce appreciable cell killing. As shown in FIG. 20B, the CAR19 positive B cells were not selectively spared from CAR19 positive PBMCs, as demonstrated by the lack of enrichment for CAR19 positive B-cells across the E:T ratios.

[00524] The data of the present example further highlight the favorable risk profile of the viral particles provided for herein. As demonstrated in previous examples, the viral particles provided for herein and delivering a CD19 CAR transgene of SEQ ID NO: 105 have minimal off target transduction of B-cells. The data of the present example demonstrate that even if B-cells were unintentionally transduced, this transduction does not confer resistance to the B-cells, which are still susceptible to the CAR19 positive PBMCs.

[00525] Example 16: VSV-G* pseudotyped lentiviruses deplete B-cells in mice.

[00526] The ability of VSV-G* pseudotyped lentiviral constructs to deplete B-cell populations *in vivo* was assessed. The VSV-G* pseudotyped lentiviral constructs utilized CD7 binders as provided for herein. The VSV-G protein utilized was a variant VSV-G protein harboring a mutation to prevent binding of VSV-G to the LDL-R. The variant VSV-G is denoted VSV-G* and corresponds to VSV-G (I182E, T214N, T352A) (e.g. SEQ ID NO: 23, SEQ ID NO: 25), as provided for herein. Treated mice were injected with lentiviral particles expressing a CD19-CAR transgene (SEQ ID NO: 105 or SEQ ID NO: 107) and then assessed for various experimental outputs including B-cell depletion and detection of CAR19 in the

blood (FIG. 21A). Control mice ("no vector" FIGs 21-23) did not receive any injection. The mice utilized are huCD34 NSG mice which have circulating human T and B cells.

[00527] First, mice were assessed to determine if circulating CAR19 transgene was detectable (FIG. 21B). Blood was collected at set intervals and assessed by flow cytometry for CAR19 transgene expression. As shown in FIG. 21B, the CAR19 transgene corresponding to SEQ ID NO: 105 was readily detected in the blood by day 21 post vector administration. The CAR19 transgene corresponding to SEQ ID NO: 107 was not readily detected over the course of the assessment.

[00528] B cell depletion was assessed via flow cytometry interrogation with a primary B cell marker of CD19 and a secondary B cell marker for CD20. Mice receiving either CD19 CAR construct saw a dramatic and sustained loss of B cells for 70 days post administration (FIG. 22A and 22B). Upon study termination, the spleen and bone marrow of treated mice were also assessed for evidence of B cell depletion. As shown in FIG. 23A and 23B, both CD19 CAR constructs resulted in extensive B cell depletion in both the spleen and bone marrow.

[00529] The data of the present example demonstrate the ability of the viral particles provided for herein to generate CAR19+ cells *in vivo*, resulting in *in vivo* depletion of B cells. Further, the detection of sustained CAR19+ cells in the blood indicate that in the absence of an immune response against the CAR molecule, the CAR19+ cells generated by the viral particles are maintained and active.

[00530] Example 17: VSV-G* pseudotyped lentiviruses eliminate established tumors in mice

[00531] To further characterize the *in vivo* efficacy of the viral particles, the ability of VSV-G* pseudotyped lentiviral constructs to prevent tumor formation will be assessed. The mice utilized are huCD34 NSG mice which have circulating human T and B cells. Mice are injected with viral particles expressing a GFP transgene or a CD19-CAR transgene on protocol Day 1. On Day 9, mice are infused with Raji tumor cells and tumor progression is monitored. Mice receiving no treatment or lentiviral constructs expressing GFP are expected to demonstrate progressive tumor development and spread as determined by IVIS imaging. In contrast, mice receiving lentiviral constructs expressing the CD19-CAR transgene are expected to demonstrate no tumor development after Raji cell infusion.

[00532] The ability of the viral particles to affect established tumors *in vivo* will also be assessed. Mice are infused with Raji tumor cells on protocol Day 0. Mice are humanized via human PBMC engraftment on protocol Day 5, and mice are either not injected with viral particles (control) or injected with viral particles expressing a CD19-CAR transgene on

protocol Day 6. Tumor progression will be monitored through protocol Day 30. Control and virus treated mice are expected to demonstrate comparable tumor load on Day 5 (prior to virus administration), Day 7, and Day 8 as determined by IVIS imaging, which will demonstrate that Raji tumors are successfully established in both groups. At Day 12, control mice are expected to continue to exhibit increased tumor load, whereas virus treated mice are expected to exhibit a dramatic decrease in tumor load.

[00533] This specification contains numerous citations to patents, patent applications, and publications. Each is hereby incorporated by reference for all purposes.

[00534] The specification also makes reference to various sequences, such as those provided herein and below.

VSV-G Indiana Full length WT:
MKCLLYLAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMC
HASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHV
LVDEYTGEWVDSQFINGKCSNYICPTVHNSTTWHSDYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNY
FAYETGGKACKMQYCKHWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLC
QETWSKIRAGLPISPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDD
WAPYEDVEIGPNGVLRTSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNP
IELVEGWFSSWKSSIASFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO:
1)

VSV-G Indiana Ectodomain WT:
KFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 2)

VSV-G Indiana ectodomain I182A:
KFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLASMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 3)

VSV-G Indiana ectodomain I182D:
KFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLDSMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 4)

VSV-G Indiana ectodomain I182E:
KFTIVFPHNQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN

GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLESMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 5)

VSV-G Indiana ectodomain H8A + K47Q:
KFTIVFPANQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPQSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 6)

VSV-G Indiana ectodomain Q10A:
KFTIVFPHNAKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 7)

VSV-G Indiana ectodomain Q10R:
KFTIVFPHNRKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 8)

VSV-G Indiana ectodomain Q10K:
KFTIVFPHNKKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGP
KYITHSIRSFTPSVEQCKESIEQTKQGTWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIN
GKCSNYICPTVHNSTTWHSDYKVKGLCDSNLISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCK
HWGVRLPSGVWFEMADKDLFAAARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLPISPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTERELWDDWAPYEDVEIGPNGVLR
TSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQLPDDESLFFGDTGLSKNPIELVEGWFSSWKSSIA
SFFFIIGLIIGLFLVLRVGIHLCIKLKHTKKRQIYTDIEMNRLGK (SEQ ID NO: 9)

VSV-G New Jersey Full length WT:
MLSYLIFALVVSPILGKIEIVFPQHTTGDWKRVPHEYNYCPTSADKNSHGTQTGIPVELTMPKGLTTHQVDGFMC
HSALWMTTCDFRWYGPKYITHSIHNEEPTDYQCLEAIKAYKDGVSFNPGFPPQSCGYGTVTDAEAHIVTVTPHSV
KVDEYTGEWIDPHFIGGRCKGQICETVHNSTKWFTSSDGESVCSQLFTLVGGTFFSDSEEITSMGLPETGIRSNY
FPYVSTEGICKMPFCRKPGYKLKNDLWFQITDPDLDKTVRDLPHIKDCDLSSSIVTPGEHATDISLISDVERILD
YALCQNTWSKIEAGEPITPVDLSYLGPKNPGAGPVFTIINGSLHYFMSKYLRVELESPVIPRMEGKVAGTRIVRQ
LWDQWFPFGEVEIGPNGVLKTKQGYKFPLHIIGTGEVDNDIKMERIVKHWEHPHIEAAQTFLKKDDTEEVLYYGD
TGVSKNPVELVEGWFSGWRSSIMGVLAVIIGFVILIFLIRLIGVLSSLFRQKRRPIYKSDVEMAHFR (SEQ ID
NO: 10)

VSV-G New Jersey ectodomain WT:
KIEIVFPQHTTGDWKRVPHEYNYCPTSADKNSHGTQTGIPVELTMPKGLTTHQVDGFMCHSALWMTTCDFRWYGP
KYITHSIHNEEPTDYQCLEAIKAYKDGVSFNPGFPPQSCGYGTVTDAEAHIVTVTPHSVKVDEYTGEWIDPHFIG
GRCKGQICETVHNSTKWFTSSDGESVCSQLFTLVGGTFFSDSEEITSMGLPETGIRSNYFPYVSTEGICKMPFCR
KPGYKLKNDLWFQITDPDLDKTVRDLPHIKDCDLSSSIVTPGEHATDISLISDVERILDYALCQNTWSKIEAGEP
ITPVDLSYLGPKNPGAGPVFTIINGSLHYFMSKYLRVELESPVIPRMEGKVAGTRIVRQLWDQWFPFGEVEIGPN

GVLKTKQGYKFPLHIIGTGEVDNDIKMERIVKHWEHPHIEAAQTFLKKDDTEEVLYYGDTGVSKNPVELVEGWFS
GWRSSIMGVLAVIIGFVILIFLIRLIGVLSSLFRQKRRPIYKSDVEMAHFR (SEQ ID NO: 11)

VSV-G Marraba Full length WT:
MLRLFLFCFLALGAHSKFTIVFPHHQKGNWKNVPSTYHYCPSSSDQNWHNDLTGVSLHVKIPKSHKAIQADGWMC
HAAKWVTTCDFRWYGPKYITHSIHSMSPTLEQCKTSIEQTKQGVWINPGFPPQSCGYATVTDAEVVVVQATPHHV
LVDEYTGEWIDSQLVGGKCSKEVCQTVHNSTVWHADYKITGLCESNLASVDITFFSEDGQKTSLGKPNTGFRSNH
FAYESGEKACRMQYCTQWGIRLPSGVWFELVDKDLFQAAKLPECPRGSSISAPSQTSVDVSLIQDVERILDYSLC
QETWSKIRAKLPVSPVDLSYLAPKNPGSGPAFTIINGTLKYFETRYIRVDISNPIIPHMVGTMSGTTTERELWND
WYPYEDVEIGPNGVLKTPTGFKFPLYMIGHGMLDSDLHKSSQAQVFEHPHAKDAASQLPDDETLFFGDTGLSKNP
VELVEGWFSSWKSTLASFFLIIGLGVALIFIIRIIVAIRYKYKGRKTQKIYNDVEMSRLGNK (SEQ ID NO:
12)

VSV-G Marraba ectodomain WT:
KFTIVFPHHQKGNWKNVPSTYHYCPSSSDQNWHNDLTGVSLHVKIPKSHKAIQADGWMCHAAKWVTTCDFRWYGP
KYITHSIHSMSPTLEQCKTSIEQTKQGVWINPGFPPQSCGYATVTDAEVVVVQATPHHVLVDEYTGEWIDSQLVG
GKCSKEVCQTVHNSTVWHADYKITGLCESNLASVDITFFSEDGQKTSLGKPNTGFRSNHFAYESGEKACRMQYCT
QWGIRLPSGVWFELVDKDLFQAAKLPECPRGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAKLPVSPV
DLSYLAPKNPGSGPAFTIINGTLKYFETRYIRVDISNPIIPHMVGTMSGTTTERELWNDWYPYEDVEIGPNGVLK
TPTGFKFPLYMIGHGMLDSDLHKSSQAQVFEHPHAKDAASQLPDDETLFFGDTGLSKNPVELVEGWFSSWKSTLA
SFFLIIGLGVALIFIIRIIVAIRYKYKGRKTQKIYNDVEMSRLGNK (SEQ ID NO: 13)

VSV-G Carajas Full length WT:
MKMKMVIAGLILCIGILPAIGKITISFPQSLKGDWRPVPKGYNYCPTSADKNLHGDLIDIGLRLRAPKSFKGISA
DGWMCHAARWITTCDFRWYGPKYITHSIHSFRPSNDQCKEAIRLTNEGNWINPGFPPQSCGYASVTDSESVVVTV
TKHQVLVDEYSGSWIDSQFPGGSCTSPICDTVHNSTLWHADHTLDSICDQEFVAMDAVLFTESGKFEEFGKPNSG
IRSNYFPYESLKDVCQMDFCKRKGFKLPSGVWFEIEDAEKSHKAQVELKIKRCPHGAVISAPNQNAADINLIMDV
ERILDYSLCQATWSKIQNKEALTPIDISYLGPKNPGPGPAFTIINGTLHYFNTRYIRVDIAGPVTKEITGFVSGT
STSRVLWDQWFPYGENSIGPNGLLKTASGYKYPLFMVGTGVLDADIHKLGEATVIEHPHAKEAQKVVDDSEVIFF
GDTGVSKNPVEVVEGWFSGWRSSLMSIFGIILLIVCLVLIVRILIALKYCCVRHKKRTIYKEDLEMGRIPRRA
(SEQ ID NO: 14)

VSV-G Carajas ectodomain WT:
KITISFPQSLKGDWRPVPKGYNYCPTSADKNLHGDLIDIGLRLRAPKSFKGISADGWMCHAARWITTCDFRWYGP
KYITHSIHSFRPSNDQCKEAIRLTNEGNWINPGFPPQSCGYASVTDSESVVVTVTKHQVLVDEYSGSWIDSQFPG
GSCTSPICDTVHNSTLWHADHTLDSICDQEFVAMDAVLFTESGKFEEFGKPNSGIRSNYFPYESLKDVCQMDFCK
RKGFKLPSGVWFEIEDAEKSHKAQVELKIKRCPHGAVISAPNQNAADINLIMDVERILDYSLCQATWSKIQNKEA
LTPIDISYLGPKNPGPGPAFTIINGTLHYFNTRYIRVDIAGPVTKEITGFVSGTSTSRVLWDQWFPYGENSIGPN
GLLKTASGYKYPLFMVGTGVLDADIHKLGEATVIEHPHAKEAQKVVDDSEVIFFGDTGVSKNPVEVVEGWFSGWR
SSLMSIFGIILLIVCLVLIVRILIALKYCCVRHKKRTIYKEDLEMGRIPRRA (SEQ ID NO: 15)

VSV-G Alagoa Full length WT:
MTPAFILCMLLAGSSWAKFTIVFPQSQKGDWKDVPPNYRYCPSSADQNWHGDLLGVNIRAKMPKVHKAIKADGWM
CHAAKWVTTCDYRWYGPQYITHSIHSFIPTKAQCEESIKQTKEGVWINPGFPPKNCGYASVSDAESIIVQATAHS
VMIDEYSGDWLDSQFPTGRCTGSTCETIHNSTLWYADYQVTGLCDSALVSTEVTFYSEDGLMTSIGRQNTGYRSN
YFPYEKGAAACRMKYCTHEGIRLPSGVWFEMVDKELLESVQMPECPAGLTISAPTQTSVDVSLILDVERMLDYSL
CQETWSKVHSGLPISPVDLGYIAPKNPGAGPAFTIVNGTLKYFDTRYLRIDIEGPVLKKMTGKVSGTPTKRELWT
EWFPYDDVEIGPNGVLKTPEGYKFPLYMIGHGLLDSDLQKTSQAEVFHHPQIAEAVQKLPDDETLFFGDTGISKN
PVEVIEGWFSNWRSSVMAIVFAILLLVITVLMVRLCVAFRHFCCQKRHKIYNDLEMNQLRR (SEQ ID NO:
16)

VSV-G Alagoa ectodomain WT:
KFTIVFPQSQKGDWKDVPPNYRYCPSSADQNWHGDLLGVNIRAKMPKVHKAIKADGWMCHAAKWVTTCDYRWYGP
QYITHSIHSFIPTKAQCEESIKQTKEGVWINPGFPPKNCGYASVSDAESIIVQATAHSVMIDEYSGDWLDSQFPT
GRCTGSTCETIHNSTLWYADYQVTGLCDSALVSTEVTFYSEDGLMTSIGRQNTGYRSNYFPYEKGAAACRMKYCT

HEGIRLPSGVWFEMVDKELLESVQMPECPAGLTISAPTQTSVDVSLILDVERMLDYSLCQETWSKVHSGLPISPV
DLGYIAPKNPGAGPAFTIVNGTLKYFDTRYLRIDIEGPVLKKMTGKVSGTPTKRELWTEWFPYDDVEIGPNGVLK
TPEGYKFPLYMIGHGLLDSDLQKTSQAEVFHHPQIAEAVQKLPDDETLFFGDTGISKNPVEVIEGWFSNWRSSVM
AIVFAILLLVITVLMVRLCVAFRHFCCQKRHKIYNDLEMNQLRR (SEQ ID NO: 17)

VSV-G Cocal Full length WT:
MNFLLLTFIVLPLCSHAKFSIVFPQSQKGNWKNVPSSYHYCPSSSDQNWHNDLLGITMKVKMPKTHKAIQADGWM
CHAAKWITTCDFRWYGPKYITHSIHSIQPTSEQCKESIKQTKQGTWMSPGFPPQNCGYATVTDSVAVVVQATPHH
VLVDEYTGEWIDSQFPNGKCETEECETVHNSTVWYSDYKVTGLCDATLVDTEITFFSEDGKKESIGKPNTGYRSN
YFAYEKGDKVCKMNYCKHAGVRLPSGVWFEFVDQDVYAAAKLPECPVGATISAPTQTSVDVSLILDVERILDYSL
CQETWSKIRSKQPVSPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRIDIDNPIISKMVGKISGSQTERELWT
EWFPYEGVEIGPNGILKTPTGYKFPLFMIGHGMLDSDLHKTSQAEVFEHPHLAEAPKQLPEEETLFFGDTGISKN
PVELIEGWFSSWKSTVVTFFFAIGVFILLYVVARIVIAVRYRYQGSNNKRIYNDIEMSRFRK (SEQ ID NO:
18)

VSV-G Cocal ectodomain WT:
KFSIVFPQSQKGNWKNVPSSYHYCPSSSDQNWHNDLLGITMKVKMPKTHKAIQADGWMCHAAKWITTCDFRWYGP
KYITHSIHSIQPTSEQCKESIKQTKQGTWMSPGFPPQNCGYATVTDSVAVVVQATPHHVLVDEYTGEWIDSQFPN
GKCETEECETVHNSTVWYSDYKVTGLCDATLVDTEITFFSEDGKKESIGKPNTGYRSNYFAYEKGDKVCKMNYCK
HAGVRLPSGVWFEFVDQDVYAAAKLPECPVGATISAPTQTSVDVSLILDVERILDYSLCQETWSKIRSKQPVSPV
DLSYLAPKNPGTGPAFTIINGTLKYFETRYIRIDIDNPIISKMVGKISGSQTERELWTEWFPYEGVEIGPNGILK
TPTGYKFPLFMIGHGMLDSDLHKTSQAEVFEHPHLAEAPKQLPEEETLFFGDTGISKNPVELIEGWFSSWKSTVV
TFFFAIGVFILLYVVARIVIAVRYRYQGSNNKRIYNDIEMSRFRK (SEQ ID NO: 19)

VSV-G Morreton Full length WT:
MLVLYLLLSLLALGAQCKFTIVFPHNQKGNWKNVPANYQYCPSSSDLNWHNGLIGTSLQVKMPKSHKAIQADGWM
CHAAKWVTTCDFRWYGPKYVTHSIKSMIPTVDQCKESIAQTKQGTWLNPGFPPQSCGYASVTDAEAVIVKATPHQ
VLVDEYTGEWVDSQFPTGKCNKDICPTVHNSTTWHSDYKVTGLCDANLISMDITFFSEDGKLTSLGKEGTGFRSN
YFAYENGDKACRMQYCKHWGVRLPSGVWFEMADKDIYNDAKFPDCPEGSSIAAPSQTSVDVSLIQDVERILDYSL
CQETWSKIRAHLPISPVDLSYLSPKNPGTGPAFTIINGTLKYFETRYIRVDIAGPIIPQMRGVISGTTTERELWT
DWYPYEDVEIGPNGVLKTATGYKFPLYMIGHGMLDSDLHISSKAQVFEHPHIQDAASQLPDDETLFFGDTGLSKN
PIELVEGWFSGWKSTIASFFFIIGLVIGLYLVLRIGIALCIKCRVQEKRPKIYTDVEMNRLDR (SEQ ID NO:
20)

VSV-G Morreton ectodomain WT:
KFTIVFPHNQKGNWKNVPANYQYCPSSSDLNWHNGLIGTSLQVKMPKSHKAIQADGWMCHAAKWVTTCDFRWYGP
KYVTHSIKSMIPTVDQCKESIAQTKQGTWLNPGFPPQSCGYASVTDAEAVIVKATPHQVLVDEYTGEWVDSQFPT
GKCNKDICPTVHNSTTWHSDYKVTGLCDANLISMDITFFSEDGKLTSLGKEGTGFRSNYFAYENGDKACRMQYCK
HWGVRLPSGVWFEMADKDIYNDAKFPDCPEGSSIAAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAHLPISPV
DLSYLSPKNPGTGPAFTIINGTLKYFETRYIRVDIAGPIIPQMRGVISGTTTERELWTDWYPYEDVEIGPNGVLK
TATGYKFPLYMIGHGMLDSDLHISSKAQVFEHPHIQDAASQLPDDETLFFGDTGLSKNPIELVEGWFSGWKSTIA
SFFFIIGLVIGLYLVLRIGIALCIKCRVQEKRPKIYTDVEMNRLDR (SEQ ID NO: 21)

Fc IgG1 (Accession No. P01857)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 26)

Fc IgG2 (Accession No. AAN76043)

STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL
GTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

VQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 27)

Fc IgG4 (Accession No. AAB59394)
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL
GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDP
EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREP
QVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN
VFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 28)

CD19 CAR:
DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTI
SNLEQEDIATYFCQQGNTLPYTFGGGTKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVS
LPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGG
SYAMDYWGQGTSVTVSSSGLDFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC
DIYIWAPLAGTCGVLLLSLVITLYCNHRNKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF
SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 132)

CD19 CAR VH:
EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSK
SQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSS (SEQ ID NO: 133)

CD19 CAR VL:
DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTI
SNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT (SEQ ID NO: 134)

TABLE OF ADDITIONAL CDR SEQUENCES

SEQ ID NO	Sequence	Description
77	SYWIH	CD7AB1 HCDR1- Kabat
78	RIDPNSGDTKYNEKFKN	CD7AB1 HCDR2- Kabat
32	SPYYSNDNSMDY	CD7AB1 HCDR3- Kabat
33	RASQSIGTSIH	CD7AB1 LCDR1- Kabat
34	YASESIS	CD7AB1 LCDR2- Kabat
35	QQSNSWPTT	CD7AB1 LCDR3- Kabat
79	GYPFTSYW	CD7AB1 HCDR1- IMGT
80	IDPNSGDT	CD7AB1 HCDR2- IMGT
81	ARSPYYSNDNSMDY	CD7AB1 HCDR3- IMGT
82	QSIGTS	CD7AB1 LCDR1- IMGT
-	YA	CD7AB1 LCDR2- IMGT
35	QQSNSWPTT	CD7AB1 LCDR3- IMGT
83	DYNLH	CD8AB1 HCDR1- Kabat
84	FIYPYNGGTGYNQKFKN	CD8AB1 HCDR2- Kabat
44	DHRYNEGVSFDY	CD8AB1 HCDR3- Kabat
45	RASESVDGFGNSFMN	CD8AB1 LCDR1- Kabat
46	LASNLES	CD8AB1 LCDR2- Kabat
47	QQNNEDPYT	CD8AB1 LCDR3- Kabat
85	RYTFTDYN	CD8AB1 HCDR1- IMGT
86	IYPYNGGT	CD8AB1 HCDR2- IMGT
87	ARDHRYNEGVSFDY	CD8AB1 HCDR3- IMGT
88	ESVDGFGNSF	CD8AB1 LCDR1- IMGT
-	LA	CD8AB1 LCDR2- IMGT
47	QQNNEDPYT	CD8AB1 LCDR3- IMGT
120	SSWIG	CD19AB1 HCDR1 Kabat
121	IIYPDDSDTRYSPSFQG	CD19AB1 HCDR2 Kabat
110	HVTMIWGVIIDF	CD19AB1 HCDR3 Kabat

SEQ ID NO	Sequence	Description
111	RASQGISSALA	CD19AB1 LCDR1 Kabat
112	DASSLES	CD19AB1 LCDR2 Kabat
113	QQFNSYPYT	CD19AB1 LCDR3 Kabat
122	GYSFSSSW	CD19AB1 HCDR1 IMGT
123	IYPDDSDT	CD19AB1 HCDR2 IMGT
124	ARHVTMIWGVIIDF	CD19AB1 HCDR3 IMGT
125	QGISSA	CD19AB1 LCDR1 IMGT
-	DA	CD19AB1 LCDR2 IMGT
113	QQFNSYPYT	CD19AB1 LCDR3 IMGT
126	SYAIS	CD19AB2 HCDR1 Kabat
127	GIIPIFGTTNYAQQFQG	CD19AB2 HCDR2 Kabat
116	EAVAADWLDP	CD19AB2 HCDR3 Kabat
117	RASQSVSSSYLA	CD19AB2 LCDR1 Kabat
118	GASSRAT	CD19AB2 LCDR2 Kabat
119	QQYGSSRFT	CD19AB2 LCDR3 Kabat
128	GGTFSSYA	CD19AB2 HCDR1 IMGT
129	IIPIFGIT	CD19AB2 HCDR2 IMGT
130	AREAVAADWLDP	CD19AB2 HCDR3 IMGT
131	QSVSSSY	CD19AB2 LCDR1 IMGT
-	GA	CD19AB2 LCDR2 IMGT
119	QQYGSSRFT	CD19AB2 LCDR3 IMGT

What is Claimed:

1. A viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having the formula T-S_1, wherein T is a target binding domain and S_1 is a stalk portion.

2. The viral particle of claim 1, wherein the viral particle further comprises a nucleic acid molecule encoding a heterologous molecule of interest.

3. The viral particle of claim 2, wherein the heterologous molecule of interest is a chimeric antigen receptor ("CAR") comprising an antigen binding domain comprising an antibody, or a fragment thereof. wherein the antigen binding domain of the CAR binds to CD19.

4. The viral particle of claim 3, wherein the antibody, or fragment thereof is an antibody, a scFv antibody, an antigen binding domain, an ankyrin repeat, a VHH domain antibody, a nanobody, a single domain antibody, or an FN3 antibody.

5. The viral particle of claim 3, wherein the antigen binding domain of the CAR that binds to CD19 comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 108; HCDR2 as set forth in SEQ ID NO: 109, and HCDR3 as set forth in SEQ ID NO: 110, and wherein the light chain variable region comprises the sequences of LCDR1 as set forth in SEQ ID NO: 111; LCDR2 as set forth in SEQ ID NO: 112, and LCDR3 as set forth in SEQ ID NO: 113.

6. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 89; and wherein the light chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 90, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 108; HCDR2 as set forth in SEQ ID NO: 109, HCDR3 as set forth in SEQ ID NO: 110; and wherein the light chain variable region

comprises the sequences of LCDR1 as set forth in SEQ ID NO: 111; LCDR2 as set forth in SEQ ID NO: 112, and LCDR3 as set forth in SEQ ID NO: 113.

7. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 89; and the light chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 90.

8. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 89; and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 90.

9. The viral particle of any one of claims 5-8, wherein the heavy chain variable region and the light chain variable region are directly linked to one another and are not linked by a linker.

10. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 92, at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 92, at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 92, or a sequence as set forth in SEQ ID NO: 92.

11. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 93, at least 95% sequence identity to the amino acid

sequence of SEQ ID NO: 93, at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 93, or a sequence as set forth in SEQ ID NO: 93.

12. The viral particle of claim 3, wherein the antigen binding domain of the CAR that binds to CD19 comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 114; HCDR2 as set forth in SEQ ID NO: 115, and HCDR3 as set forth in SEQ ID NO: 116, and wherein the light chain variable region comprises the sequences of LCDR1 as set forth in SEQ ID NO: 117; LCDR2 as set forth in SEQ ID NO: 118, and LCDR3 as set forth in SEQ ID NO: 119.

13. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 94; and the light chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 95, wherein the heavy chain variable region comprises the sequences of HCDR1 as set forth in SEQ ID NO: 114; HCDR2 as set forth in SEQ ID NO: 115, HCDR3 as set forth in SEQ ID NO: 116; LCDR1 as set forth in SEQ ID NO: 117; LCDR2 as set forth in SEQ ID NO: 118, and LCDR3 as set forth in SEQ ID NO: 119.

14. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 94; and the light chain variable region comprises an amino acid sequence having at least 90% identity to the amino acid sequence of SEQ ID NO: 95.

15. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises the amino acid sequence of SEQ

ID NO: 94; and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 95.

16. The viral particle of any one of claims 12-15, wherein the heavy chain variable region and the light chain variable region are linked via a polypeptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, or SEQ ID NO: 76.

17. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 96, at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 96, at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 96, or the sequence as set forth in SEQ ID NO: 96.

18. The viral particle of claim 3, wherein the antigen binding domain that binds to CD19 comprises a polypeptide comprising a sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 97, at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 97, at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 97, or the sequence as set forth in SEQ ID NO: 97.

19. The viral particle of any one of claims 3-18, wherein the CAR further comprises a hinge domain, a transmembrane domain, a costimulatory domain, and a signaling domain.

20. The viral particle of claim 3, wherein the CAR comprises an amino acid sequence having at least 85% identity to the amino acid sequence of SEQ ID NO: 99, at least 90% identity to the amino acid sequence of SEQ ID NO: 99, at least 95% identity to the amino acid sequence of SEQ ID NO: 99, at least 99% identity to the amino acid sequence of SEQ ID NO: 99, or at least 100% identity to the amino acid sequence of SEQ ID NO: 99.

21. The viral particle of claim 3, wherein the CAR comprises an amino acid sequence having at least 85% identity to the amino acid sequence of SEQ ID NO: 105, at least 90% identity to the amino acid sequence of SEQ ID NO: 105, at least 95% identity to the amino acid

sequence of SEQ ID NO: 105, at least 99% identity to the amino acid sequence of SEQ ID NO: 105, or at least 100% identity to the amino acid sequence of SEQ ID NO: 105.

22. The viral particle of claim 3, wherein the CAR comprises an amino acid sequence having at least 85% identity to the amino acid sequence of SEQ ID NO: 106, at least 90% identity to the amino acid sequence of SEQ ID NO: 106, at least 95% identity to the amino acid sequence of SEQ ID NO: 106, at least 99% identity to the amino acid sequence of SEQ ID NO: 106, or at least 100% identity to the amino acid sequence of SEQ ID NO: 106.

23. The viral particle of claim 3, wherein the CAR comprises an amino acid sequence having at least 85% identity to the amino acid sequence of SEQ ID NO: 107, at least 90% identity to the amino acid sequence of SEQ ID NO: 107, at least 95% identity to the amino acid sequence of SEQ ID NO: 107, at least 99% identity to the amino acid sequence of SEQ ID NO: 107, or at least 100% identity to the amino acid sequence of SEQ ID NO: 107.

24. The viral particle of claim 3, wherein the stalk portion S_1 comprises a variant Fc protein, wherein the variant Fc protein comprises a transmembrane domain and an effector mutation, wherein the effector mutation inhibits the interaction between the Fc protein and a Fc interacting protein, such as FcγR, C1q, FcRβ, or FcRn.

25. The viral particle of claim 24, wherein the S_1 stalk portion is attached to the surface of the viral particle through the transmembrane domain.

26. The viral particle of claim 24, wherein the variant Fc protein is a variant IgG1 Fc protein.

27. The viral particle of claim 26, wherein the variant IgG1 Fc protein comprises one or more of the mutations selected from the group consisting of: L234A, L235A, N297A, P329G, I253A, H310A, and H435A.

28. The viral particle of claim 26, wherein the variant IgG1 Fc protein comprises an amino acid sequence having at least 80% identity to SEQ ID NO: 104, at least 85% identity to SEQ ID NO: 104, at least 90% identity to SEQ ID NO: 104, at least 95% identity to SEQ ID NO: 104, at least 98% identity to SEQ ID NO: 104, or at least 100% identity to SEQ ID NO: 104.

29. The viral particle of any one of claims 2-37, wherein the targeting moiety having the formula T-S_1 comprises a stalk portion S_1 having a formula of L_1-Fc-L_2-X_1, wherein:

L_1 is a linker or absent;

Fc is a variant Fc protein;

L_2 is a linker or absent; and

X_1 is a polypeptide comprising the transmembrane domain,

wherein the targeting moiety having the formula T-S_1 has a formula of T-L_1-Fc-L_2-X_1.

30. The viral particle of claim 29, wherein L_1 and L_2 are each, independently, absent or a polypeptide linker comprising an amino acid sequence of SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, or SEQ ID NO: 76.

31. The viral particle of claim 29, wherein X_1 comprises a polypeptide having a formula of ECD-T_M-ICD, wherein:

ECD is an extracellular domain, or a fragment thereof, of a cell surface protein, or absent;

T_M is a transmembrane domain of a transmembrane protein; and

ICD is an intracellular domain or a protein that facilitates incorporation of the targeting moiety into the envelope of the viral particle, or absent,

wherein the targeting moiety having the formula of T-L_1-Fc-L_2-X_1 has a formula of T-L_1-Fc-L_2-ECD-T_M-ICD.

32. The viral particle of claim 31, wherein the ECD comprises an amino acid sequence of SEQ ID NO: 59 or SEQ ID NO: 60.

33. The viral particle of claim 31, wherein the T_M comprises an amino acid sequence of SEQ ID NO: 61 or SEQ ID NO: 62.

34. The viral particle of any one of claims 31-33, wherein the ICD comprises an Env incorporation motif comprising an amino acid sequence of SEQ ID NO: 63 or SEQ ID NO: 64.

35. The viral particle of claim 3, wherein the target binding domain (T) binds to CD7, CD8, cKit (CD117), CD4, CD3, CD5, CD6, CD2, TCR alpha, TCR beta, TCR gamma, TCR delta, CD10, CD34, CD110, CD33, CD14, CD68, CCR7, CD62L, CD25, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, or CXCR3, A glycosylated CD43 epitope expressed on acute leukemia or lymphoma but not on hematopoietic progenitors; A glycosylated CD43 epitope expressed on non-hematopoietic cancers; A kinase anchor protein 4 (AKAP-4); Adrenoceptor beta 3 (ADRB3); AFP; Anaplastic lymphoma kinase (ALK); Androgen receptor; Angiopoietin-binding cell surface receptor 2 (Tie 2); Auto antibody to desmoglein 1 (Dsgl); Auto antibody to desmoglein 3 (Dsg3); B7H3 (CD276); Biotin; Bone marrow stromal cell antigen 2 (BST2); BST1/CD157; Cancer/testis antigen 1 (NY-ESO-1); Cancer/testis antigen 2 (LAGE-la); Carbonic anhydrase IX (CA1X); Carcinoembryonic antigen (CEA); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS or Brother of the Regulator of lmprinted Sites); CCR4; CD5; CD19; CD20; CD22; CD24; CD30; CD32 (FCGR2A); CD33; CD34; CD38; CD44v6; CD72; CD79a; CD79b; CD97; CD99; CD123; CD171; CD179a; CD179b-IGLll; CD200R; CD276/B7H3; CD300 molecule-like family member f (CD300LF); CDH1-CD324; CDH6; CDH17; CDH19; Chromosome X open reading frame 61 (CXORF61); Claudin 6 (CLDN6); Claudinl8.2 (CLD18A2 or CLDN18A.2); CMV pp65; C-MYC epitope Tag; Cripto; CS1 (also referred to as CD2 subset 1 or CRACC or SLAMF7 or CD319 or 19A24); CSF2RA (GM-CSFR-alpha); C-type lectin domain family 12 member A (CLEC12A); C-type lectin-like molecule-1 (CLL-1 or CLECL1); Cyclin Bl; Cytochrome P450 IB 1 (CYP1B 1); DLL3; EBV-EBNA3c; EGF-bke module- containing mucin-like hormone receptor-like 2 (EMR2); Elongation factor 2 mutated (ELF2M); Ephrin B2; Ephrin type-A receptor 2 (EphA2); Epidermal growth factor receptor (EGFR); Epidermal growth factor receptor variant III (EGFRviii); Epithelial cell adhesion molecule (EPCAM); ERG; ETS translocation-variant gene 6 located on chromosome 12p (ETV6-AML); Fc fragment of IgA receptor (FCAR or

CD89); Fc receptor-like 5 (FCRL5); Fibroblast activation protein alpha (FAP); FITC; Fms Like Tyrosine Kinase 3 (FLT3); Folate receptor alpha (Fra or FR1); Folate receptor beta (FRb); Follicle stimulating hormone receptor (FSHR); Fos-related antigen 1; Fucosyl-GMl; G protein coupled receptor class C group 5 member D (GPRC5D); G protein-coupled receptor 20 (GPR20); GAD; Ganglioside G2 (GD2) ; Ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); Ganglioside GM3 (aNeu5Ac(2-3)bDClalp(l- 4)bDGlcp(l-l)Cer); GD3; GFRalpha4; Glycoprotein 100 (gplOO); Glypican-3 (GPC3); Gonadotropin Hormone receptor (CGHR or GR); GpA33; GpNMB; GPRC5D; Guanylyl cyclase C (GCC); Heat shock protein 70-2 mutated (mut hsp70-2); Hepatitis A virus cellular receptor 1 (HAVCR1); Hexasaccharide portion of globoH glycoceramide (GloboH); High molecular weight-melanoma associated antigen (HMWMAA); HIV1 envelope glycoprotein; HLA; HLA-DOA; HLA-A; HLA-A2; HLA-B; HLA-C; HLA-DM; HLA-DOB; HLA-DP; HLA-DQ; HLA-DR; HLA-G; HTLVl-Tax; Human papilloma virus E6 (HPV E6); Human papilloma virus E7 (HPV E7); Human Telomerase reverse transcriptase (hTERT); IgE; IL13Ra2; Ill lRa; Immunoglobulin lambda-like polypeptide 1 (IGLL1); Influenza A hemagglutinin (HA); Insulin-like growth factor 1 receptor (IGF-I receptor); Interleukin 11 receptor alpha (IL-llRa); Interleukin- 13 receptor subunit alpha-2 (IL-13Ra2 or CD213A2); Intestinal carboxyl esterase; KIT (CD117); KSHV K8.1; KSHV-gH; LAMP1 ; Legumain; Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Leutenizing hormone receptor (LHR); Lewis(Y) antigen; Lews Ag; Livl; Locus K 9 (LY6K); Low conductance chloride channel; Lymphocyte antigen 6 complex; Lymphocyte antigen 75 (LY75); Lymphocyte-specific protein tyrosine kinase (LCK); Mammary gland differentiation antigen (NY-BR-1); Melanoma antigen recognized by T cells 1 (MelanA or MARTI); Melanoma- associated antigen 1 (MAGE-A1); Melanoma cancer testis antigen-1 (MAD-CT-1); Melanoma cancer testis antigen-2 (MAD-CT-2); Melanoma inhibitor of apoptosis (ML-IAP); Mesothelin; MPL; Mucin 1 cell surface associated (MUC1); N-Acetyl glucosaminyl-transferase V (NA17); Nectin-4; Neural cell adhesion molecule (NCAM); NKG2D; NYBR1; O-acetyl-GD2 ganglioside (OacGD2); Olfactory receptor 51E2 (OR51E2); Oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); P53 mutant; Paired box protein Pax-3 (PAX3); Paired box protein Pax-5 (PAX5); Pannexin 3 (PANX3); PDL1; P-glycoprotein; Placenta-specific 1 (PLAC1); Platelet-derived growth factor receptor beta (PDGFR-beta); Polysialic acid; Proacrosin binding protein sp32 (OY-TES1); Prostase; Prostate carcinoma tumor antigen-1 (PCT A-1 or Galectin 8); Prostate stem cell antigen (PSCA); Prostate-specific

membrane antigen (PSMA); Prostatic acid phosphatase (PAP); Prostein; Protease Serine 21 (Testisin or PRSS21); Proteasome (Prosome Macropain) Subunit Beta Type 9 (LMP2); PTK7; Ras G12V; Ras Homolog Family Member C (RhoC); Rat sarcoma (Ras) mutant; Receptor for Advanced Gly cation Endproducts (RAGE-1); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Receptor tyrosine-protein kinase ERBB2 or Her-22/neu; Renal ubiquitous 1 (RU1); Renal ubiquitous 2 (RU2); Sarcoma translocation breakpoints; Serine 2 (TMPRSS2) ETS fusion gene; Sialyl Lewis adhesion molecule (sLe); SLAMF4; SLAMF6; Slea (CA19.9 or Sialyl Lewis Antigen); Sperm protein 17 (SPA17); Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Stage-specific embryonic antigen-4 (SSEA-4); STEAP1; Survivin; Synovial sarcoma X breakpoint 2 (SSX2); TCR Gamma Alternate Reading Frame Protein (TARP); TCR-beta1 chain; TCR-beta2 chain; TCR-delta chain; TCR-gamma chain; TCRgamma-delta; Telomerase; TGFbetaR2; The antigen recognized by TNT antibody; Thyroid stimulating hormone receptor (TSHR); Timl-/HVCR1; Tissue Factor 1 (TF1); Tn ag; Tn antigen ((Tn Ag) or (GalNAca-Ser/Thr)); TNF receptor family member B cell maturation (BCMA); Transglutaminase 5 (TGS5); Transmembrane protease; TROP2; Tumor endothelial marker 1 (TEM1/CD248); Tumor endothelial marker 7-related (TEM7R); Tumor protein p53 (p53); Tumor-associated glycoprotein 72 (TAG72); Tyrosinase; Tyrosinase-related protein 2 (TRP-2); Uroplakin 2 (UPK2); Vascular endothelial growth factor receptor 2 (VEGFR2); V-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Wilms tumor protein (WT1); or X Antigen Family Member 1A (XAGE1).

36. The viral particle of claim 35, wherein the target binding domain (T) binds to CD7.

37. The viral particle of claim 36, wherein the target binding domain (T) comprises a polypeptide comprising: (i) a heavy chain variable region comprising heavy chain CDRl, CDR2, and CDR3 sequences, wherein the heavy chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 30; the heavy chain CDR2 has the amino acid sequence of SEQ ID NO: 31; and the heavy chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 32, or variants of any of the foregoing; and (ii) a light chain variable region comprising light chain CDR1, CDR2, and CDR3 sequences, wherein the light chain CDR1 sequence has the amino acid sequence of SEQ ID NO: 33; the light chain CDR2 sequence has the amino acid sequence of SEQ ID NO: 34; and the light chain CDR3 sequence has the amino acid sequence of SEQ ID NO: 35; or variants of any of the foregoing.

38. The viral particle of claim 36 or 37, wherein the target binding domain (T) comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 36, and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 37.

39. The viral particle of any one of claims 36-38, wherein the target binding domain (T) that binds to CD7 comprises a polypeptide comprising a sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 38 or SEQ ID NO: 39, at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 38 or SEQ ID NO: 39, at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 38 or SEQ ID NO: 39, or a sequence as set forth in SEQ ID NO: 38 or SEQ ID NO: 39.

40. The viral particle of any one of claims 1-39, wherein the target binding domain (T) is an antibody, or an antigen-binding fragment thereof, such as scFv antibody.

41. The viral particle of claim 1, wherein the heterologous viral glycoprotein is a VSV-G polypeptide.

42. The viral particle of claim 41, wherein the VSV-G polypeptide comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24 or SEQ ID NO: 25.

43. A method of infecting a cell, the method comprising contacting the cell with a viral particle of any one of claims 1-42.

44. A method of infecting a cell in a subject, the method comprising administering to the subject a pharmaceutical composition comprising a viral particle of any one of claims 1-42.

45. A method of delivering a heterologous molecule of interest to a cell, the method comprising contacting the cell with a viral particle of any one of claims 1-42, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest.

46. A method of delivering a heterologous molecule of interest to a cell in a subject, the method comprising administering to the subject a viral particle of any one of claims 1-42, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest.

47. A method of treating a disease or disorder in a subject, the method comprising administering to the subject a viral particle of any one of claims 1-42, wherein the viral particle comprises a nucleic acid molecule encoding the heterologous molecule of interest to treat the disease or disorder.

48. The method of claim 47, wherein the disease or disorder is cancer (e.g. such as a T cell or B cell disorder or other type of cancer as described herein), an immune disorder, an auto-immune disorder, metabolic disorder, and the like.

49. The method of claim 48, wherein the immune disorder is multiple sclerosis (MS), systemic lupus erythematosus (SLE), systemic sclerosis (SSc), lupus nephritis (LN), warm autoimmune hemolytic anemia (WAHA), primary sclerosing cholangitis (PSC), IgG4-related disease (IGG4-RD), acute disseminated encephalomyelitis (ADEM), Evans' syndrome (ES), focal segmental glomerulosclerosis (FSGS), Mixed connective tissue disease (MCTD), Mooren's ulcer (MU), chronic inflammatory demyelinating polyneuropathy (CIDP), Membranous nephropathy (MN), or thyroid eye disease (TED).

50. A viral particle comprising a heterologous viral glycoprotein, a targeting moiety, and a nucleic acid molecule encoding for a heterologous molecule of interest, wherein;

the heterologous viral glycoprotein comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 23 or SEQ ID NO: 25, having at least 95% identity of SEQ ID NO: 23 or SEQ ID NO: 25, having at least 99% identity to SEQ ID NO: 23 or SEQ ID NO: 25, or having at least 100% identity to SEQ ID NO: 23 or SEQ ID NO: 25;

the targeting moiety comprises an amino acid sequence having at least 90% identity to SEQ ID NO: 98, at least 95% identity to SEQ ID NO: 98, at least 99% identity to SEQ ID NO: 98, or at least 100% identity to SEQ ID NO: 98; and

the heterologous molecule of interest is a chimeric antigen receptor ("CAR") comprising an antigen binding domain that binds to CD19, wherein the antigen binding domain comprises an amino acid sequence having at least 85%, 90%, 95%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO: 99, SEQ ID NO: 105, SEQ ID NO: 106, or SEQ ID NO: 107..

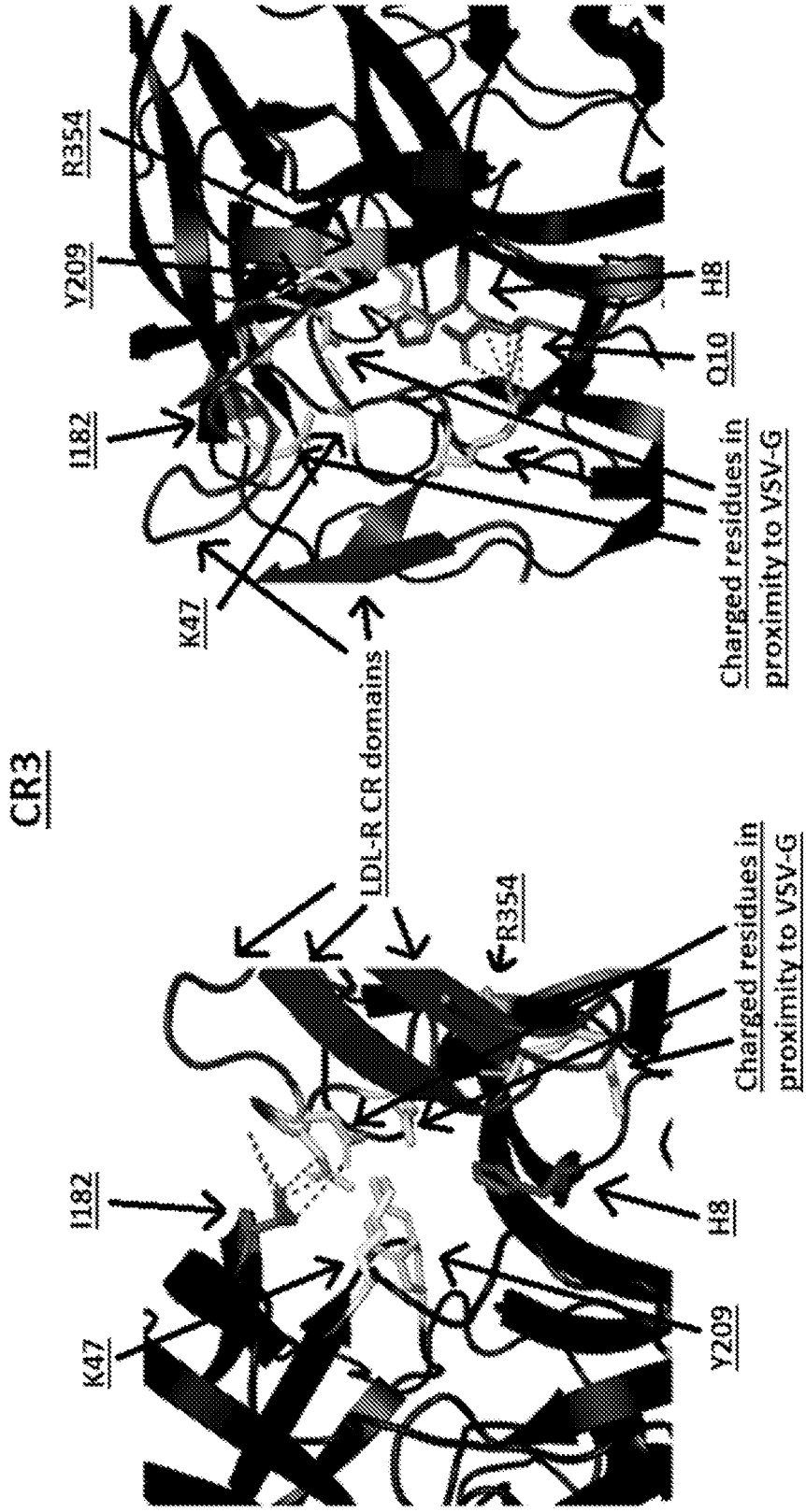

CR3
LDL-R CR domains
K47
I182
Y209
R354
H8
Q10
Charged residues in proximity to VSV-G
K47
I182
Y209
R354
H8
Charged residues in proximity to VSV-G

FIG. 1A

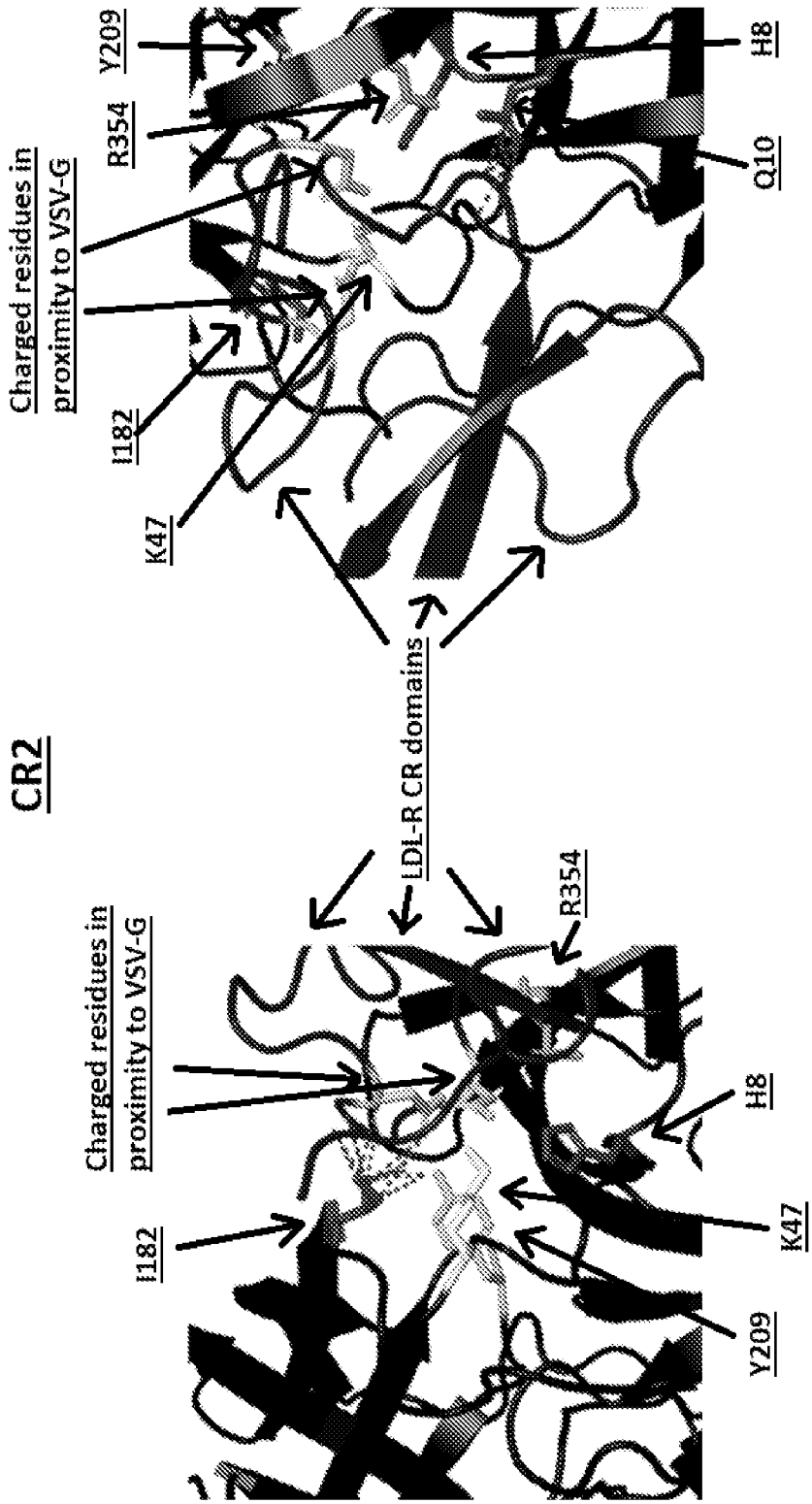

CR2
LDL-R CR domains
Charged residues in proximity to VSV-G
I182
K47
R354
Y209
H8
Q10
Charged residues in proximity to VSV-G
I182
K47
R354
Y209
H8

FIG. 1B

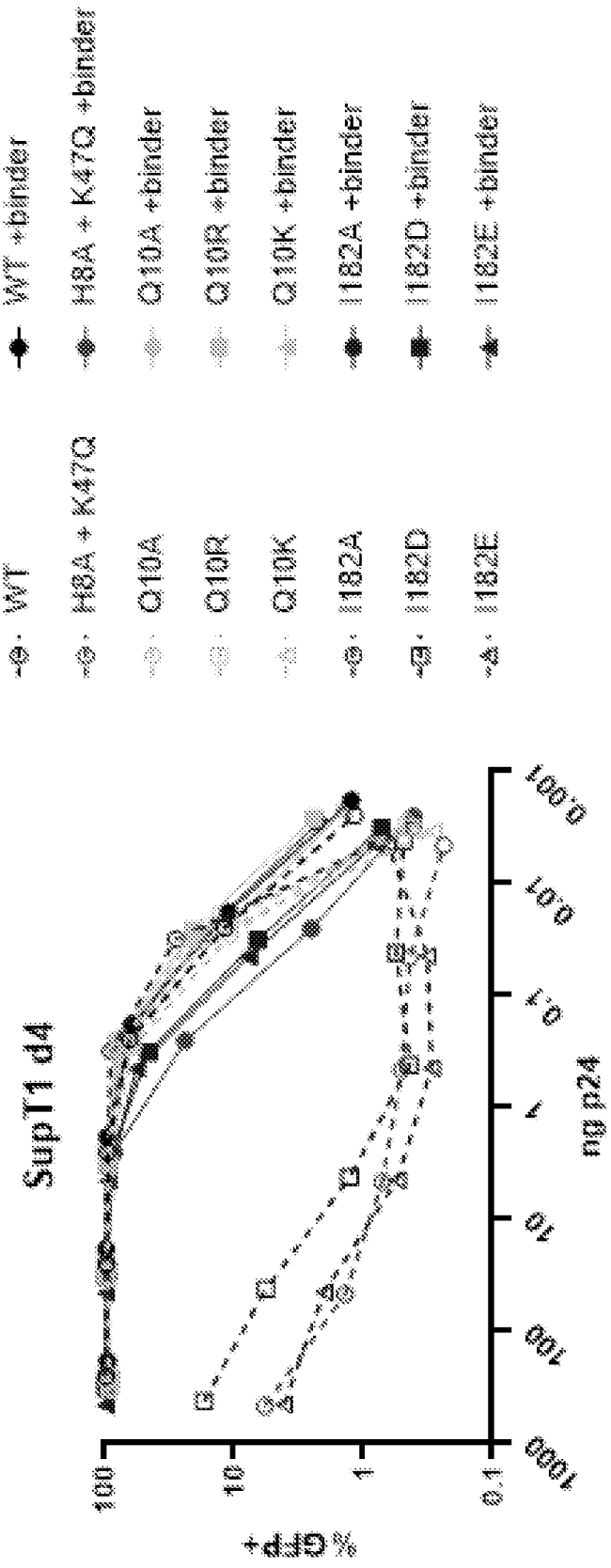

WT
H8A + K47Q
Q10A
Q10R
Q10K
I182A
I182D
I182E
WT +binder
H8A + K47Q +binder
Q10A +binder
Q10R +binder
Q10K +binder
I182A +binder
I182D +binder
I182E +binder
SupT1 d4
% GFP+
ng p24
100
10
1
0.1
1000
100
10
1
0.1
0.01

FIG. 2A

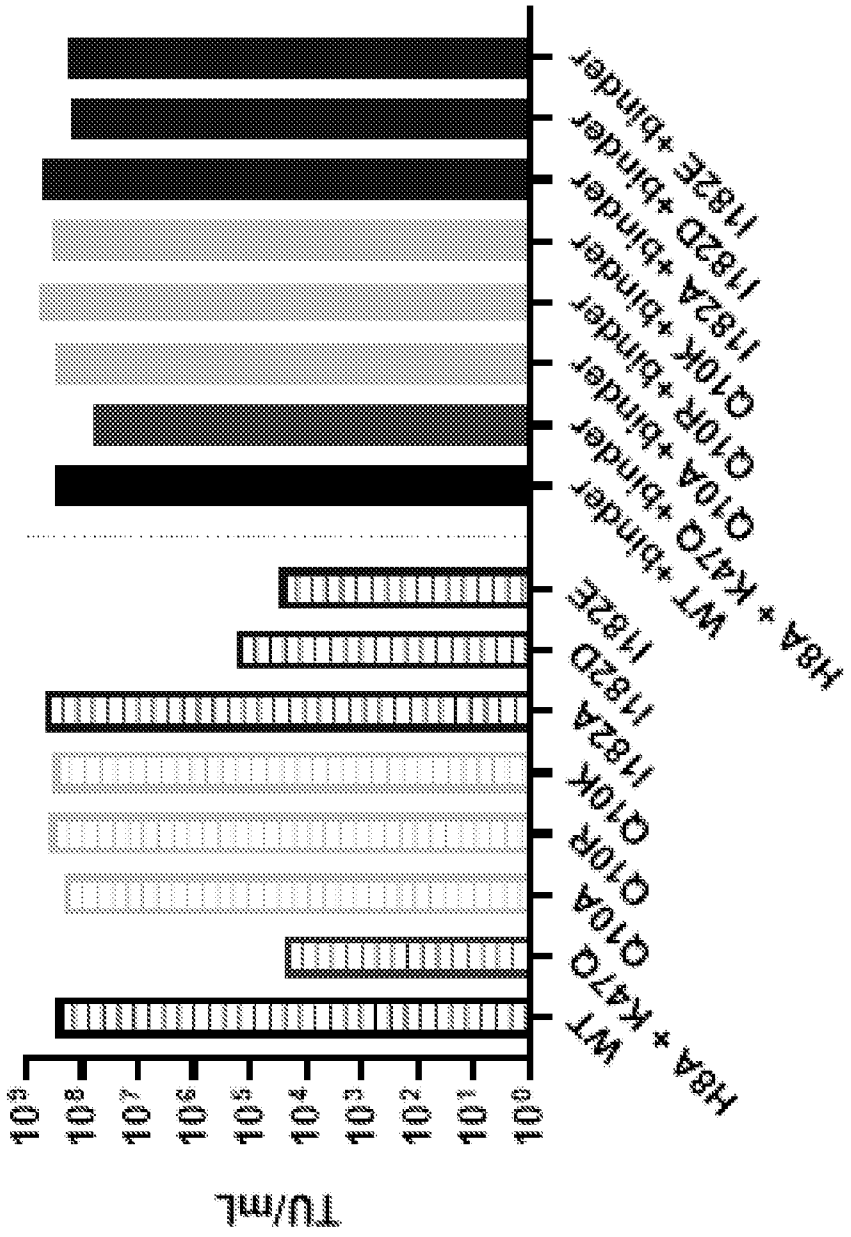

TU/mL
10^0
10^1
10^2
10^3
10^4
10^5
10^6
10^7
10^8
10^9
H8A + K47Q
WT
Q10A
Q10R
Q10K
I18A
I18D
I18E
WT +binder
H8A + K47Q +binder
Q10A +binder
Q10R +binder
Q10K +binder
I18A +binder
I18D +binder
I18E +binder

FIG. 2B

```
SEQ_ID_NO_2     KFTIVFPHENQKGNWKNVPSNYHYCPSSSDLNWHNDLIGTALQVKMPKSEHKAIQADGWMCH  60
SEQ_ID_NO_11    KIEIVFPQHTPGIWKNVPHEYNYCPTSADKNSHGTQTGIPVELTWPKGLFTHQVDGFMCH  60
SEQ_ID_NO_13    KFTIVFPHHQKGMWKNTPSTYHYCPSSSDQNWHNDLIGVSLHVNIPKSEKAIQADGWMCH  60
SEQ_ID_NO_15    KITISFPQSLKGIWRPVPKGVNYCPTSADKNLHGDLIDIGIRLRAPNSFKGISAIGWMCH  60
SEQ_ID_NO_17    KFTIVAPQSQKGIWKDVPPNYRYCPSSADQNWHGDLLGVNIRAKMPKVHEKAIKADGWMCH  60
SEQ_ID_NO_19    KFSIVFPQSQKGNWKNVPSSYHYCPSSSDQNWHNDLLGITMKVKMPKTHKAIQADGWMCH  60
SEQ_ID_NO_21    KFTVFPHNQKGNWKNVPANYQYCPSSSDLNWHHNGLIGTSLQVKMPKSHKAIQADGWMCH  60
                **:*.**:.*:*:*.**.*****:*:*.*.*.  :.  **  .*.**:***

SEQ_ID_NO_2     ASKWVTTCDFRWYGPKYITHSIRSFTPSVPQCKESIEQTKQGTWLNPGFPPQSCGYATVI  120
SEQ_ID_NO_11    SAIWMTTCDFRWYGPKYITHSIHNFEPTDVQCLEAIKAYKDGVSFNPGFPPQSCGYGTVP  120
SEQ_ID_NO_13    AAKWVTTCDFRWYGPKYITHSIHSMSPTLEQCKTSIEQTKQGVWINPGFPPQSCGYATVP  120
SEQ_ID_NO_15    AARWITTCDFRWYGPKYITHSIHSFRPSNDQCKEAIRLTNEGNWINPGFPPQSCGYASVP  120
SEQ_ID_NO_17    AAKWVTTCDYRWYGPQYITHSIHSFIPTKAQCTESIKQTKDGVWINPGFPPKNCGYASVS  120
SEQ_ID_NO_19    AAKWITTCDFRWYGPKYITHSIHSIQPTSEQCKESIKQTKQGTWMSPGFPPQNCGYATVL  120
SEQ_ID_NO_21    AAKWVTTCDFRWYGPKYVTHSIKSWIPPVDQCKESIAQTKQGTWLNPGFPPQSCGYASVP  120
                :: *.:*****:*****:*****:.*  *:  **  :*  ::*  :.*******:*.***.:*::
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FIG. 3

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SEQ_ID_NO_2     DATAVIVQVTPHHVLVDEYTGEWVDSQFINGKCSNYICPTVHNSTTWHSDYKVKGLCDSN  180
SEQ_ID_NO_11    DATAHIVTVTPHSVKVDEYTGEWIDSHFIGGRCKGQICETVHNSTKWFTSSDGESVCSQL  180
SEQ_ID_NO_13    DAEVVVQATPHHVLVIEYTGEWIDSQLVGGKCSNEVCQTVHNSTVWHADYKITGLCESN  180
SEQ_ID_NO_15    DSTSVVVTVTPKQVLVDEYSGSWIDSQFPGGSCTSPICDTVHNSTLWHADHTLDSICPQE  180
SEQ_ID_NO_17    DAESLIVQATAHSVMIDEYSGIWLDSQFPTGRCTGSTCETIHNSTLWYADYQVTGLCDSA  180
SEQ_ID_NO_19    DSVAVVVQATPHHVLVIEYTGEWIDSQFPNGKCETEECETVHNSTVWYSDYKVTGLCDAI  180
SEQ_ID_NO_21    DATAVIVKATPHQVLVIDEYTGEWVDSQFPTGKCNKDICPTVHNSTTWHSDYKVTGLCDAN  180
                **: .** .* * * :****:*.*:* :: * *  * *:***** * .:. .:*.

SEQ_ID_NO_2     LISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGGKACKMQYCKHWGVRLPSGVWFEMA  240
SEQ_ID_NO_11    FTLVGSTFESDSEELTTSMGLPETGIRSNYFPYVSTEGICKMPFCRKPGYKLKNDLWFCIT  240
SEQ_ID_NO_13    LASVDITFFSEDGQNTSLGKPNTGFRSNHFAYESGFKACRMQYCTQWGIRLPSGVWFELV  240
SEQ_ID_NO_15    FVAMTAVLFTESGKFELFGKPNSGIRSNYFPYESLKTWTCQMDFCKRKGFKLPSGVWFEIE  240
SEQ_ID_NO_17    LVSTEVTFYSEDGLMTSIGRQNTGYRSNYFPYEKGAAACRMKYCTHGIRLPSGVWFEMV  240
SEQ_ID_NO_19    LVDIELTFFSEDGKESIGKPNTGYRSNYIAYEKGDKVCKMNYCKHAGVRLPSGVWFEFV  240
SEQ_ID_NO_21    LISMDITFFSEDGKLTSLGKEGTGFRSNYFAYEWGDKACRMQYCKHWGVRLPSGVWFEMA  240
                :  .:::::.  .:*  :* **:**:* *  .  *:* :* * * :*  .:.:**::
```

FIG. 3 (Continued)

```
SEQ_ID_NO_2     DKDLFA-----AARFPECPEGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAGLP  296
SEQ_ID_NO_11    DPDLDKTVRDLPHIKDCDLSSSIVTPGEHATDISLISDVERILDYALCQNTWSKIEAGEP  300
SEQ_ID_NO_13    DKDLFQ------AAKLPECPRGSSISAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAKLP  296
SEQ_ID_NO_15    DAEKSHKAQVELKIKRCPHGAVISAPNQNAADINLIMDVERILDYSLCQATWSKIQNKEA  300
SEQ_ID_NO_17    DKELLE------SVQMPECPAGLTISAPTQTSVDVSLILDVERMLDYSLCQETWSKVHSGLP  296
SEQ_ID_NO_19    DQDVYA-----AAKLPECPVGATISAPTQTSVDVSLILDVERILDYSLCQETWSKIRSKQP  296
SEQ_ID_NO_21    DKDIYN-----DAKFPDCPEGSSIAAPSQTSVDVSLIQDVERILDYSLCQETWSKIRAHLP  296
                *  :        ::  *   .  *  :* : :.*:.** *****:***:**** *****:.

SEQ_ID_NO_2     ISPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRVDIAAPILSRMVGMISGTTTEREL  356
SEQ_ID_NO_11    ITPVDLGYLGPKNPGAGPVFTIINGSLHYFMSRYLRVDLAEDGPVIFRMEGKVAGTRIVRQL  360
SEQ_ID_NO_13    VSPVDLSYLAPKNPGSGPAFTIINGTLKYFETRYIRVDISNPTIPHMVGTMSGTTTERFL  356
SEQ_ID_NO_15    LTPIDISYLGPKNPGPGPAFTIINGTLHYFNTRYIRVDIAGPVTKEITGPVSGTSTSRVL  360
SEQ_ID_NO_17    ISPVDLGYIAPKNPGAGPAFTIVNGTLKYFDTRYLRIDIEGPVLKKMTGKVSGTPTKREL  356
SEQ_ID_NO_19    VSPVDLSYLAPKNPGTGPAFTIINGTLKYFETRYIRIDIDNPIISKMVGKISGSQTERFL  356
SEQ_ID_NO_21    ISPVDLSYLSPKNPGTGPAFTIINGTLKYFETRYIRVDIAGPIIPQMRGVISGTTTERFL  356
                ::*****:.*:.*****  **.*****:**:*** ::*:*:::::  *:  .:  * :::*:  * *
```

FIG. 3 (Continued)

```
SEQ_ID_NO_2     WDDWAPYEDVEIGPNGVLRTSSGYKFPLYMIGHGMLDSDLHLSSKAQVFEHPHIQDAASQ  416
SEQ_ID_NO_11    WDQWFPFGEVEIGPNGVLKTKQGYKFPLHIIGTGEVDNDIKMERIVKHWEHPHIEAAQTF  420
SEQ_ID_NO_13    WNDWYPYEDVEIGPNGVLKTPTGFKFPLYMIGHGMLDSDLHKSSQAQVFEHPHAKDAASQ  416
SEQ_ID_NO_15    WDQWFPYGENSIGPNGLLKTASGYKYPLFMVGTGVLDADIHKLGEATVIEHPHAKEAQKV  420
SEQ_ID_NO_17    WTEWFPYDDVEIGPNGVLKTPEGYKFPLYMIGHGLLDSDLQKTSQAEVFHHPQIAEAVQK  416
SEQ_ID_NO_19    WTEWFPYEGVEIGPNGILKTPTGYKFPLFMIGHGMLDSDLHKTSQAEVFEHPHLAEAPKQ  416
SEQ_ID_NO_21    WTDWYPYEDVEIGPNGVLKTATGYKFPLYMIGHGMLDSDLHISSKAQVFEHPHIQDAASQ  416
                * :* *:   .*****:*:*  *:*:**.::* * :* *::    .   .**:   *

SEQ_ID_NO_2     LP---DDESLFFGDTGLSKNPIELVEGWFSSWKSSIASFFFIIGLIIGLFLVLRVGIHLC  473
SEQ_ID_NO_11    LKKDDTEEVLYYGDTGVSKNPVELVEGWFSGWRSSIMGVLAVIIGFVILIFLIRLIGVLS  480
SEQ_ID_NO_13    LP---DDETLFFGDTGLSKNPVELVEGWFSSWKSTLASFFLIIGLGVALIFIIRIIVAIR  473
SEQ_ID_NO_15    VD---DSEVIFFGDTGVSKNPVEVVEGWFSGWRSSLMSIFGIILLIVCLVLIVRILIALK  477
SEQ_ID_NO_17    LP---DDETLFFGDTGISKNPVEVIEGWFSNWRSSVMAIVFAILLLVITVLMVRLCVAFR  473
SEQ_ID_NO_19    LP---EEETLFFGDTGISKNPVELIEGWFSSWKSTVVTFFFAIGVFILLYVVARIVIAVR  473
SEQ_ID_NO_21    LP---DDETLFFGDTGLSKNPIELVEGWFSGWKSTIASFFFIIGLVIGLYLVLRIGIALC  473
                :     .* ::::****;****:*:;*****.*:*::  ..  *   :   .: *:   .

SEQ_ID_NO_2     IKLKHTK-KRQIYTDIEMNRLGK-- 495
SEQ_ID_NO_11    -SLFRQKRRPIYKSDVEMAHFR--- 501
SEQ_ID_NO_13    YKYKG-RKTQKIYNDVEMSRLGNK- 496
SEQ_ID_NO_15    YCCVRHKKRTIYKEDLEMGRIFRRA 502
SEQ_ID_NO_17    H--FCCQKRHKIYNDLEMNQLRR-- 494
SEQ_ID_NO_19    YRYQGSN-NKRIYNDIEMSRFRK-- 495
SEQ_ID_NO_21    IKCRVQEKRPKIYTDVEMNRLDR-- 496
                      .       *:** ::
```

FIG. 3 (Continued)

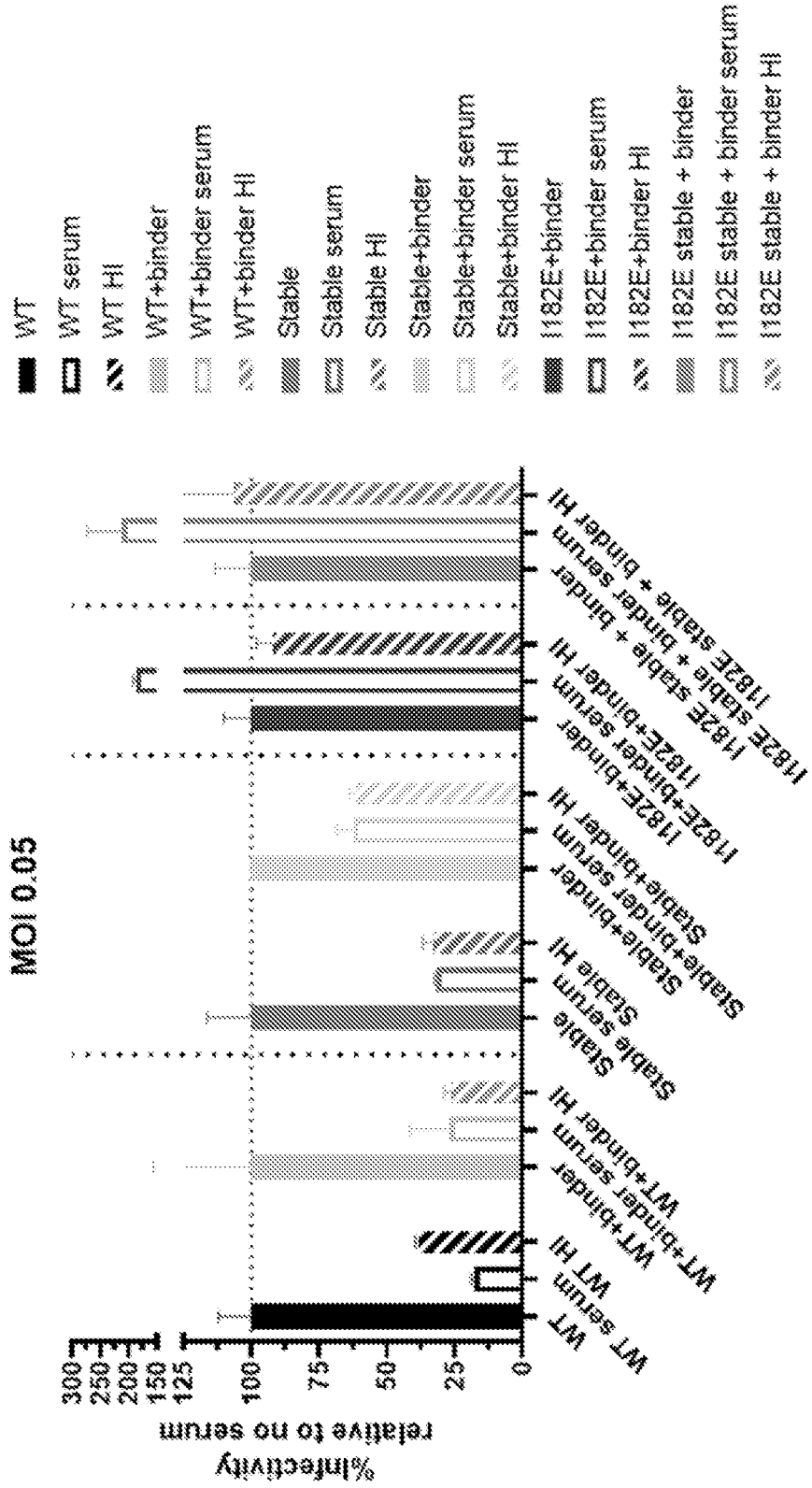

WT
WT serum
WT HI
WT+binder
WT+binder serum
WT+binder HI
Stable
Stable serum
Stable HI
Stable+binder
Stable+binder serum
Stable+binder HI
I182E+binder
I182E+binder serum
I182E+binder HI
I182E stable + binder
I182E stable + binder serum
I182E stable + binder HI
MOI 0.05
%Infectivity
relative to no serum
300
250
200
150
125
100
75
50
25
0
WT serum
WT HI
WT+binder
WT+binder serum
WT+binder HI
Stable
Stable serum
Stable HI
Stable+binder
Stable+binder serum
Stable+binder HI
I182E+binder
I182E+binder serum
I182E+binder HI
I182E stable + binder
I182E stable + binder serum
I182E stable + binder HI

FIG. 4

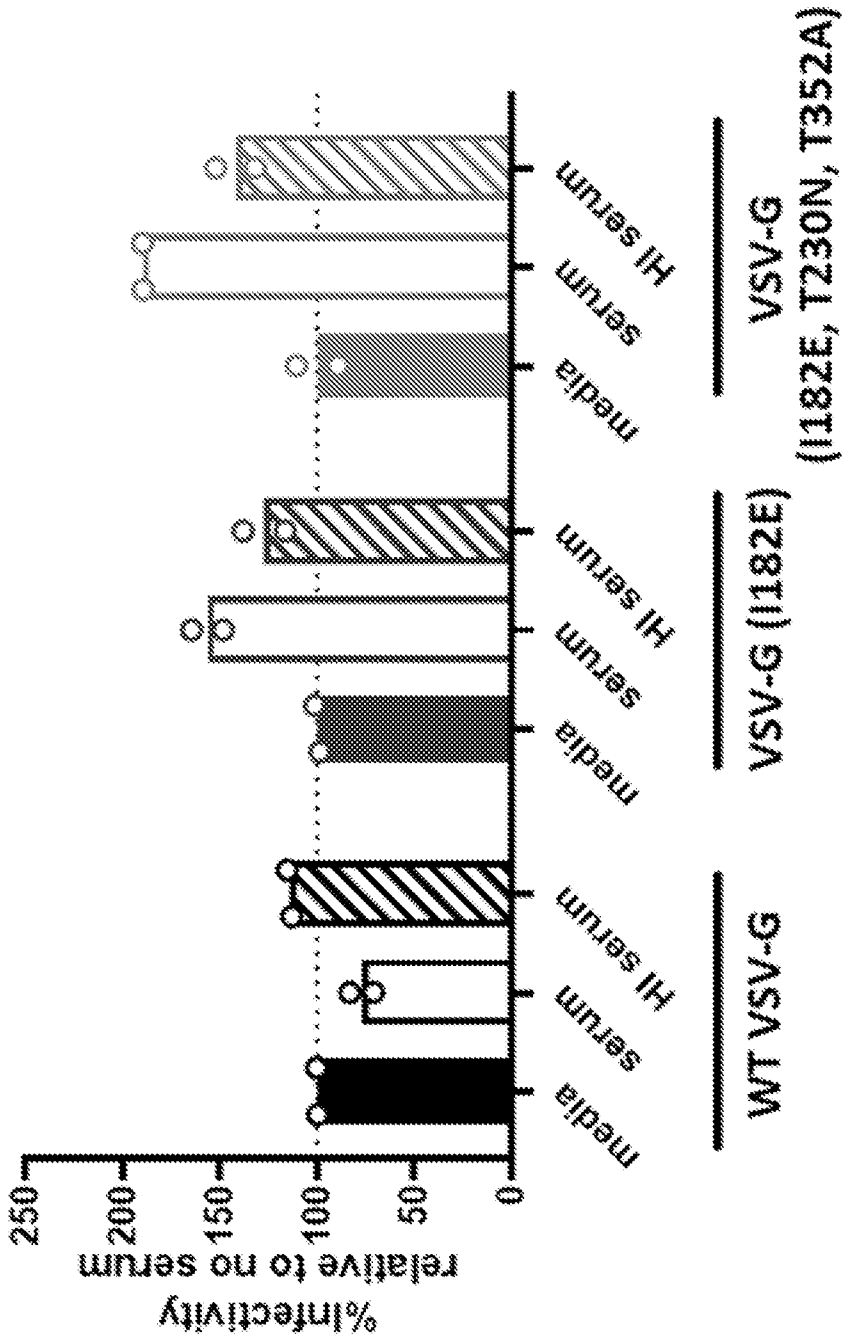

%Infectivity
relative to no serum
250
200
150
100
50
0
media
serum
HI serum
media
serum
HI serum
media
serum
HI serum
WT VSV-G
VSV-G (I182E)
VSV-G
(I182E, T230N, T352A)

FIG. 5

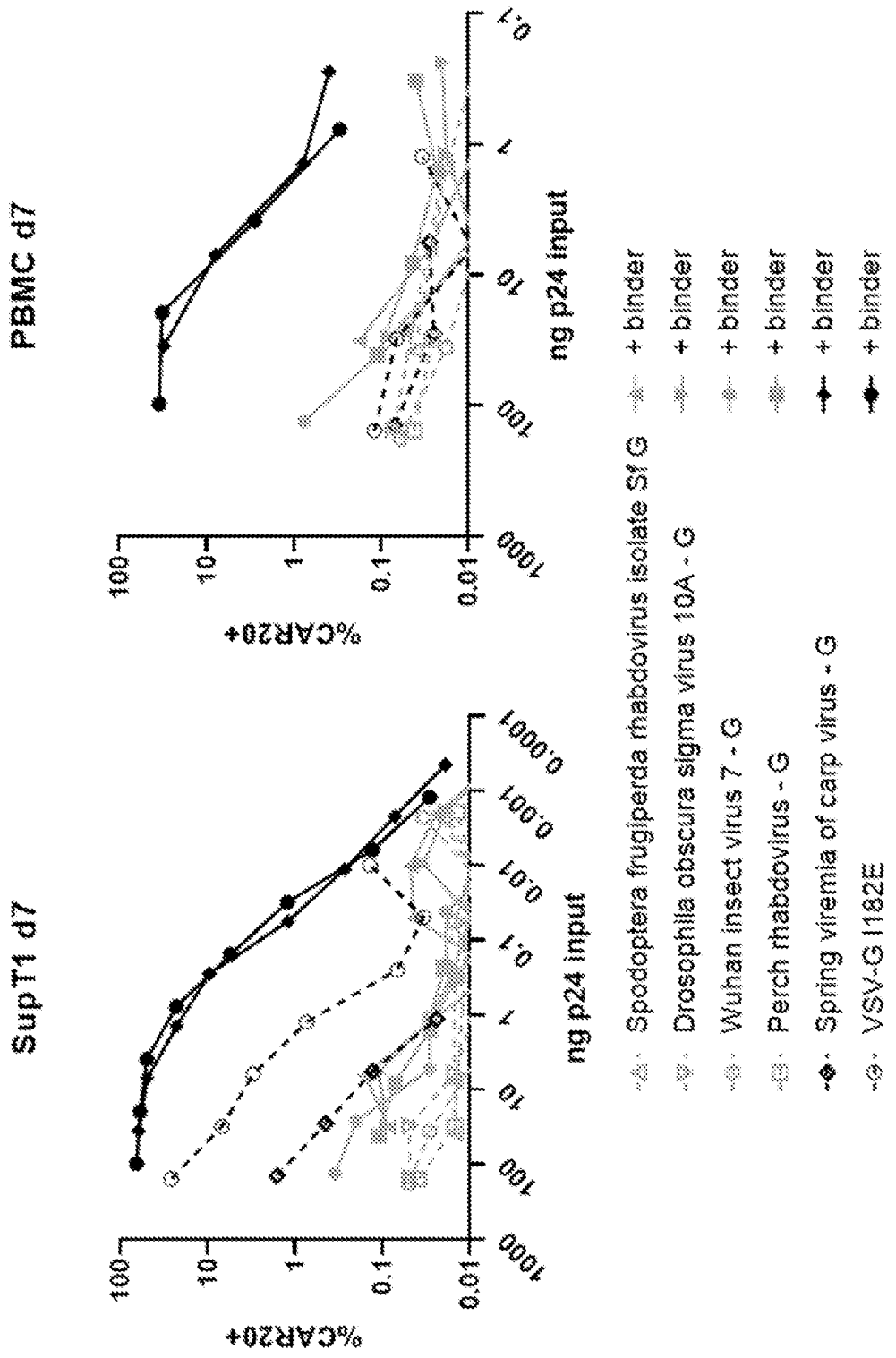

PBMC d7
SupT1 d7
%CAR20+
ng p24 input
100
10
1
0.1
0.01
1000
100
10
1
0.1
0.01
0.001
0.0001
Spodoptera frugiperda rhabdovirus isolate Sf G
Drosophila obscura sigma virus 10A - G
Wuhan insect virus 7 - G
Perch rhabdovirus - G
Spring viremia of carp virus - G
VSV-G I102E
+ binder

FIG. 6

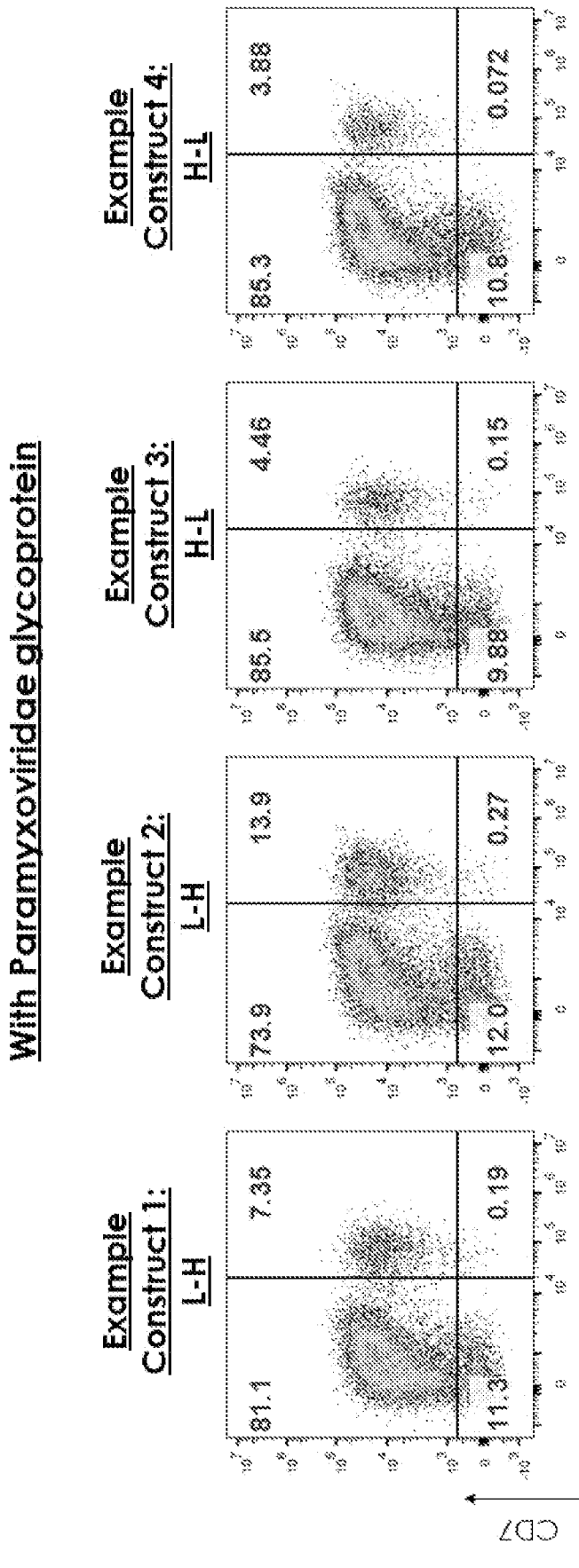


FIG. 7A FIG. 7B FIG. 7C FIG. 7D

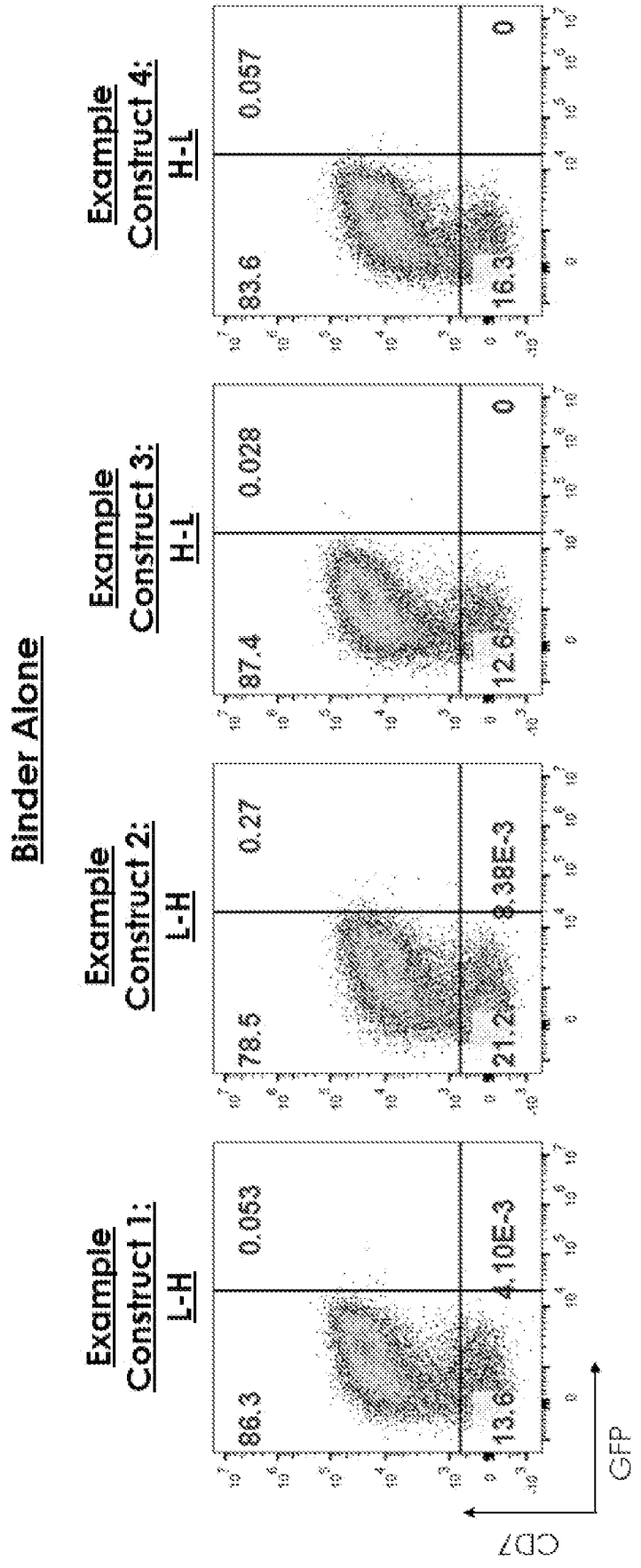


FIG. 7E FIG. 7F FIG. 7G FIG. 7H

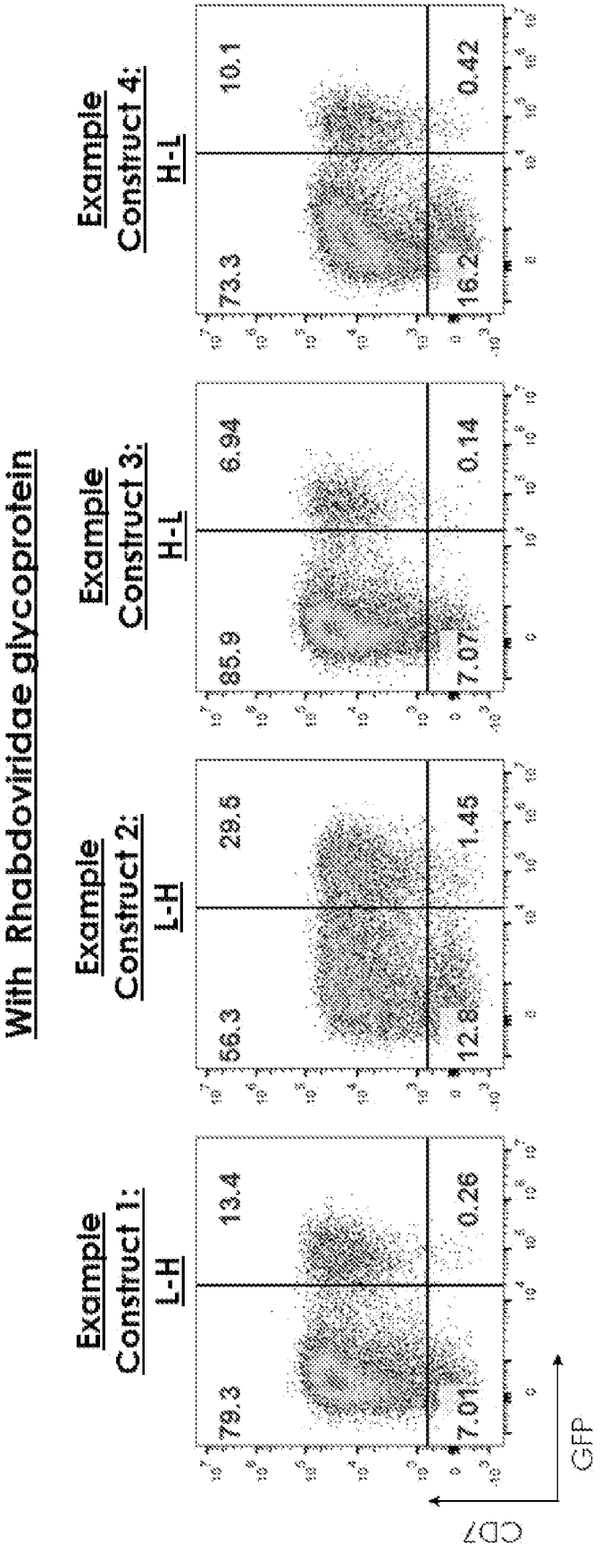


FIG. 7I FIG. 7J FIG. 7K FIG. 7L

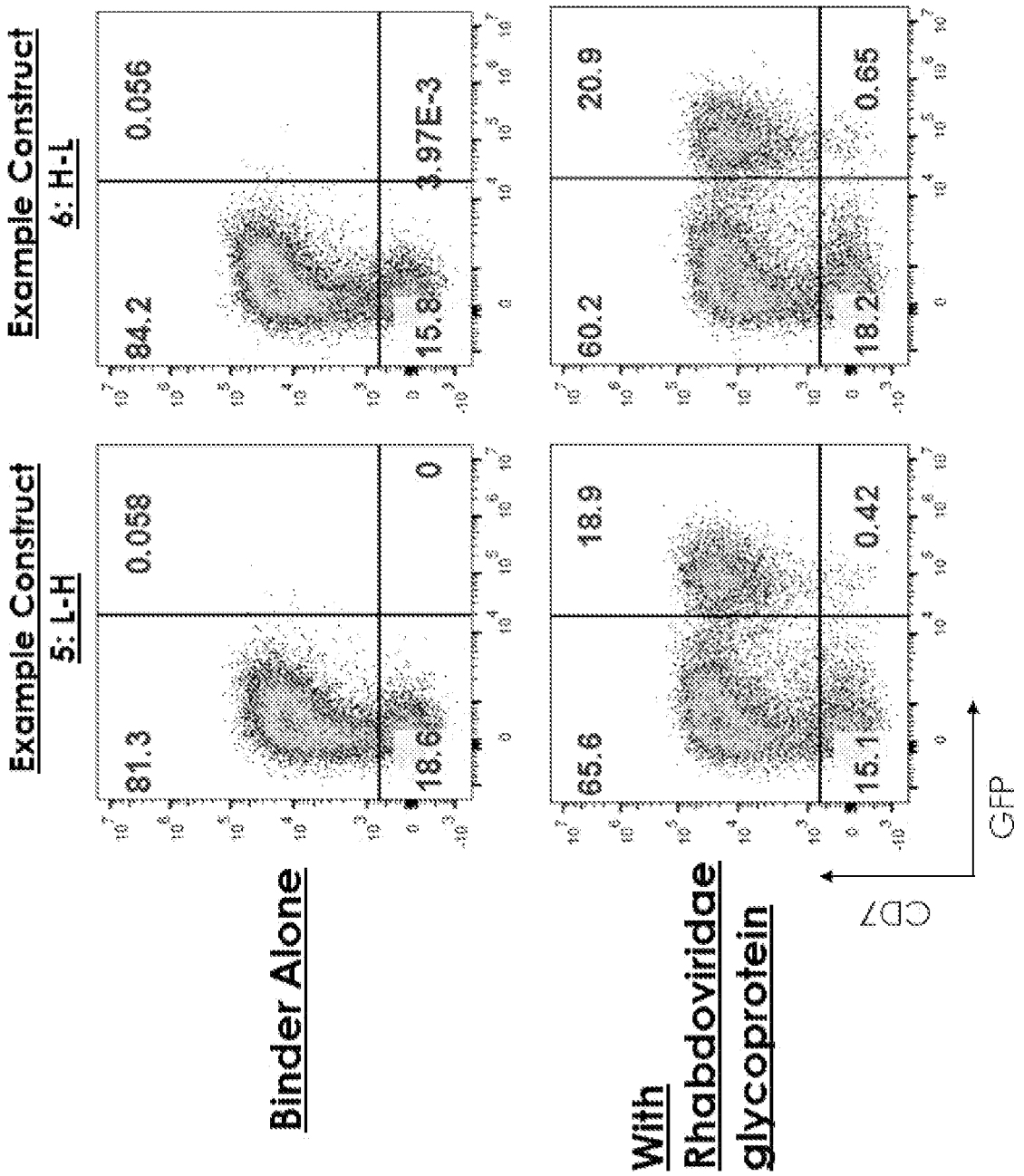

Example Construct
5: L-H
Example Construct
6: H-L
Binder Alone
With
Rhabdoviridae
glycoprotein
81.3
0.058
18.6
0
84.2
0.056
15.8
1.97E-3
65.6
18.9
15.1
0.42
60.2
20.9
18.2
0.65
CD7
GFP

FIG. 7M

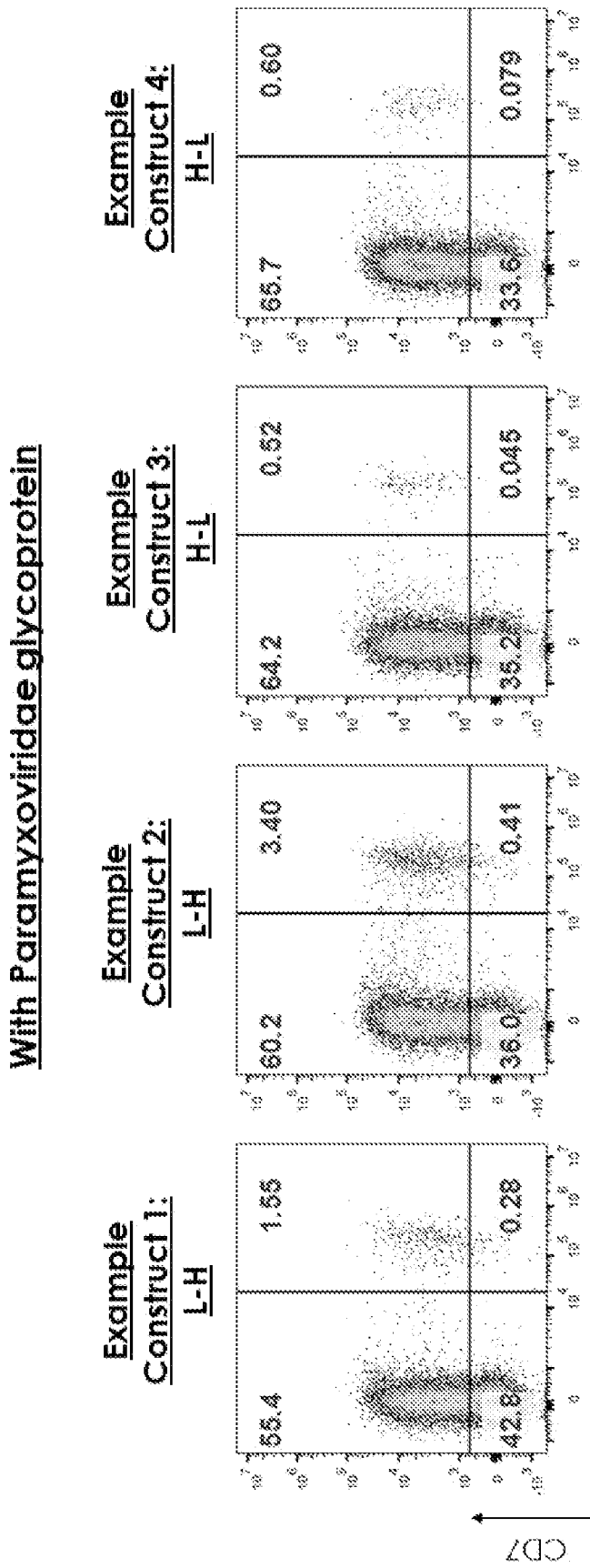


FIG. 8A FIG. 8B FIG. 8C FIG. 8D

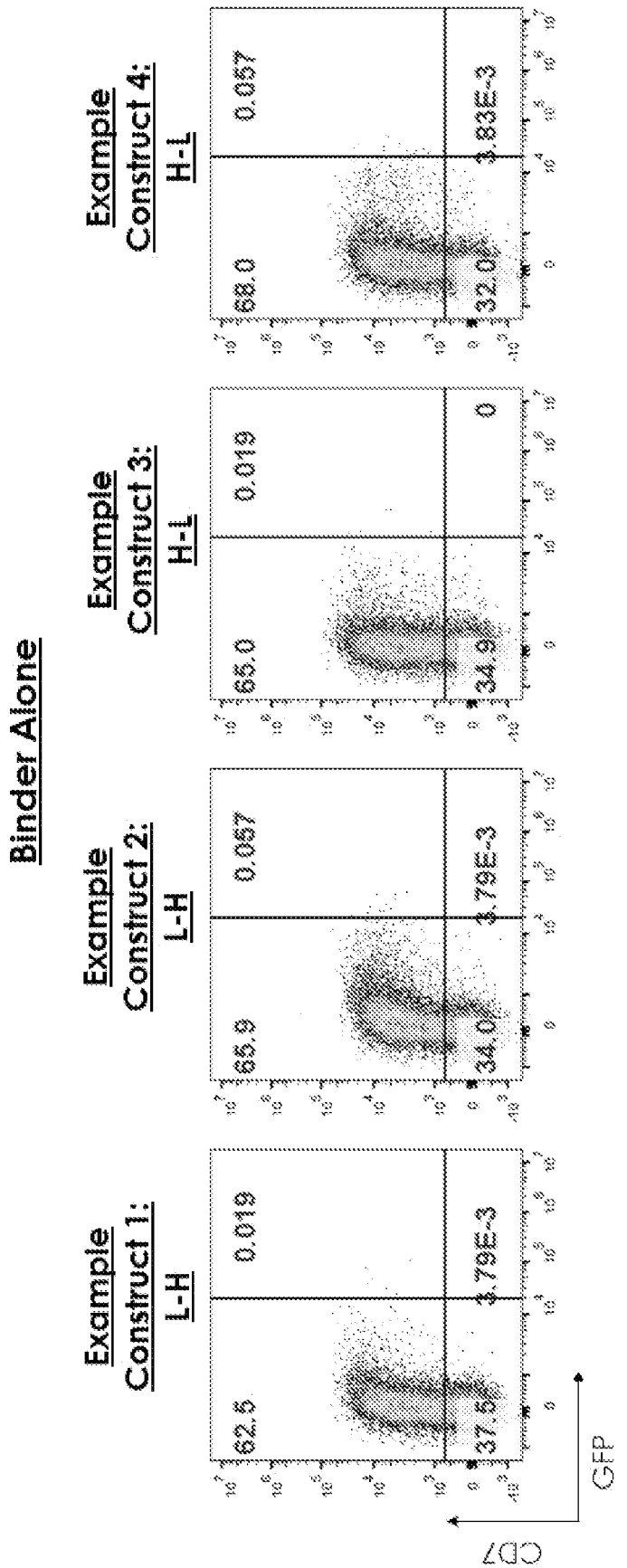


FIG. 8E FIG. 8F FIG. 8G FIG. 8H

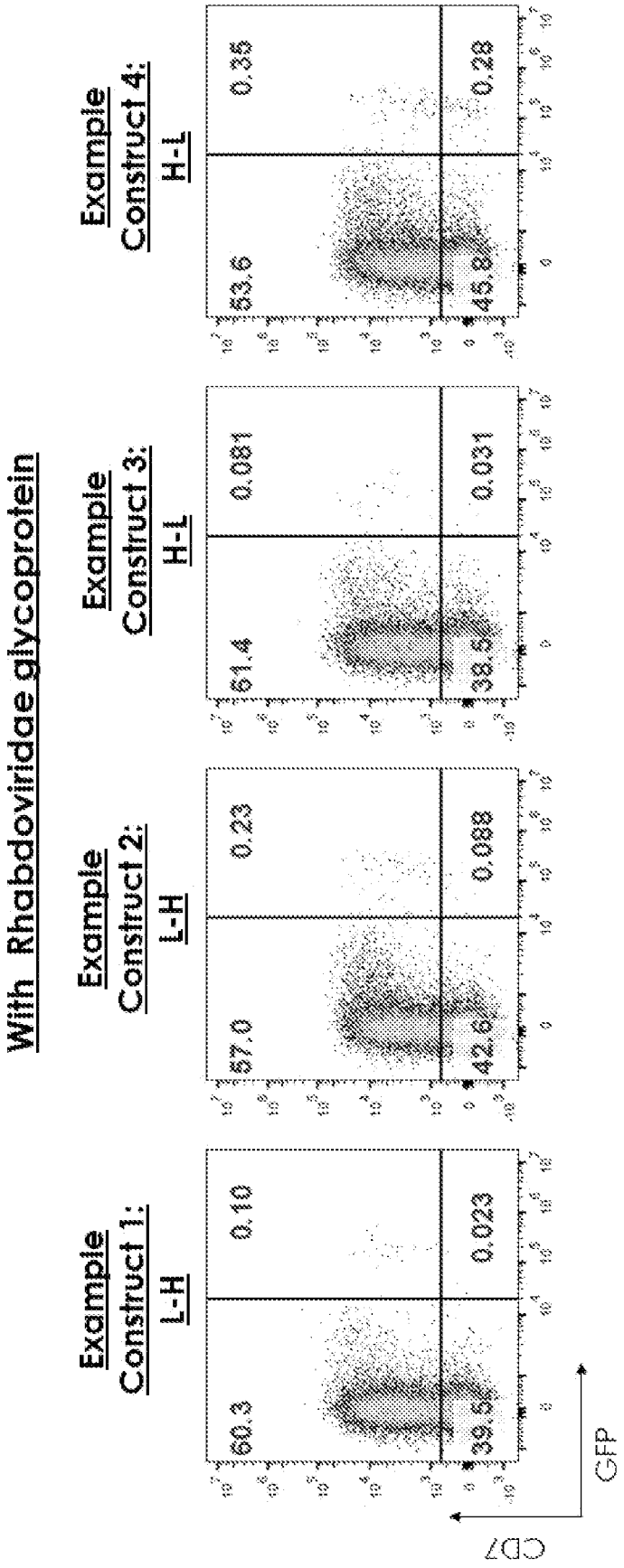


FIG. 8I FIG. 8J FIG. 8K FIG. 8L

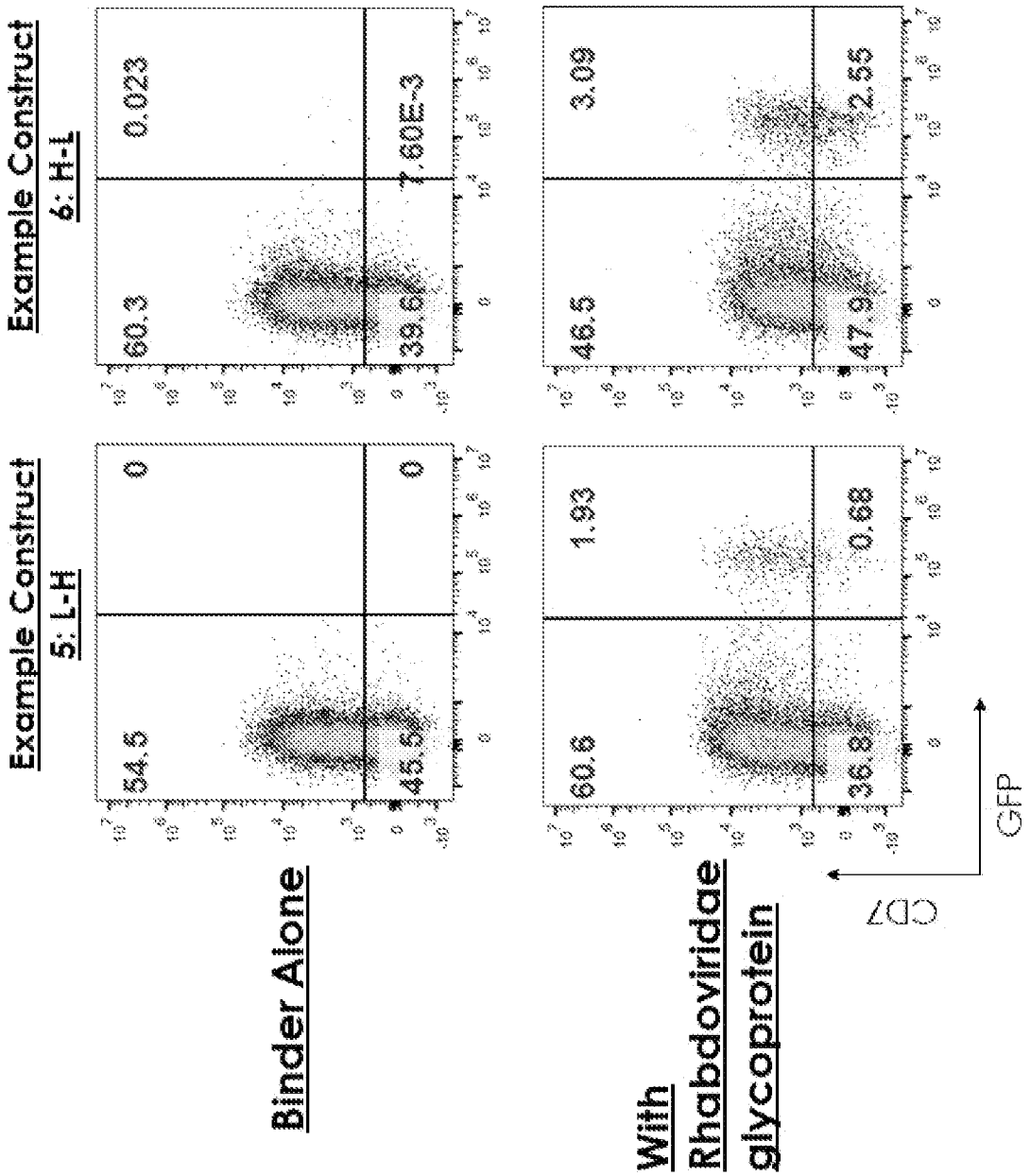

Example Construct
5: L-H
Example Construct
6: H-L
Binder Alone
With
Rhabdoviridae
glycoprotein
54.5
0
45.5
0
60.3
0.023
39.6
7.60E-3
60.6
1.93
36.8
0.68
46.5
3.09
47.9
2.55
CD7
GFP

FIG. 8M

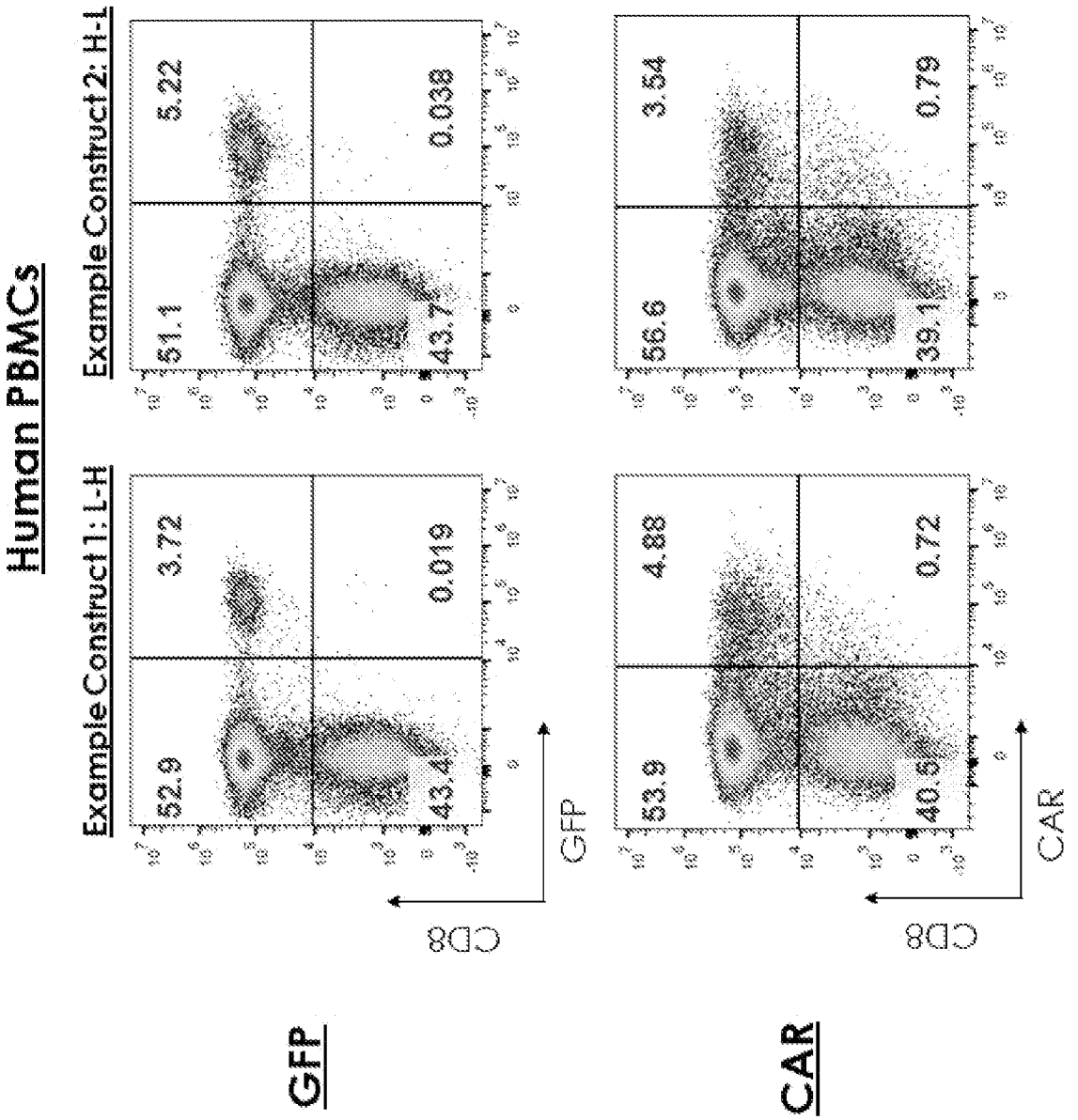

Human PBMCs
Example Construct 1: L-H
Example Construct 2: H-L
GFP
CAR
CD8
GFP
CAR
52.9
3.72
43.4
0.019
51.1
5.22
43.7
0.038
53.9
4.88
40.6
0.72
56.6
3.54
39.1
0.79

FIG. 9A

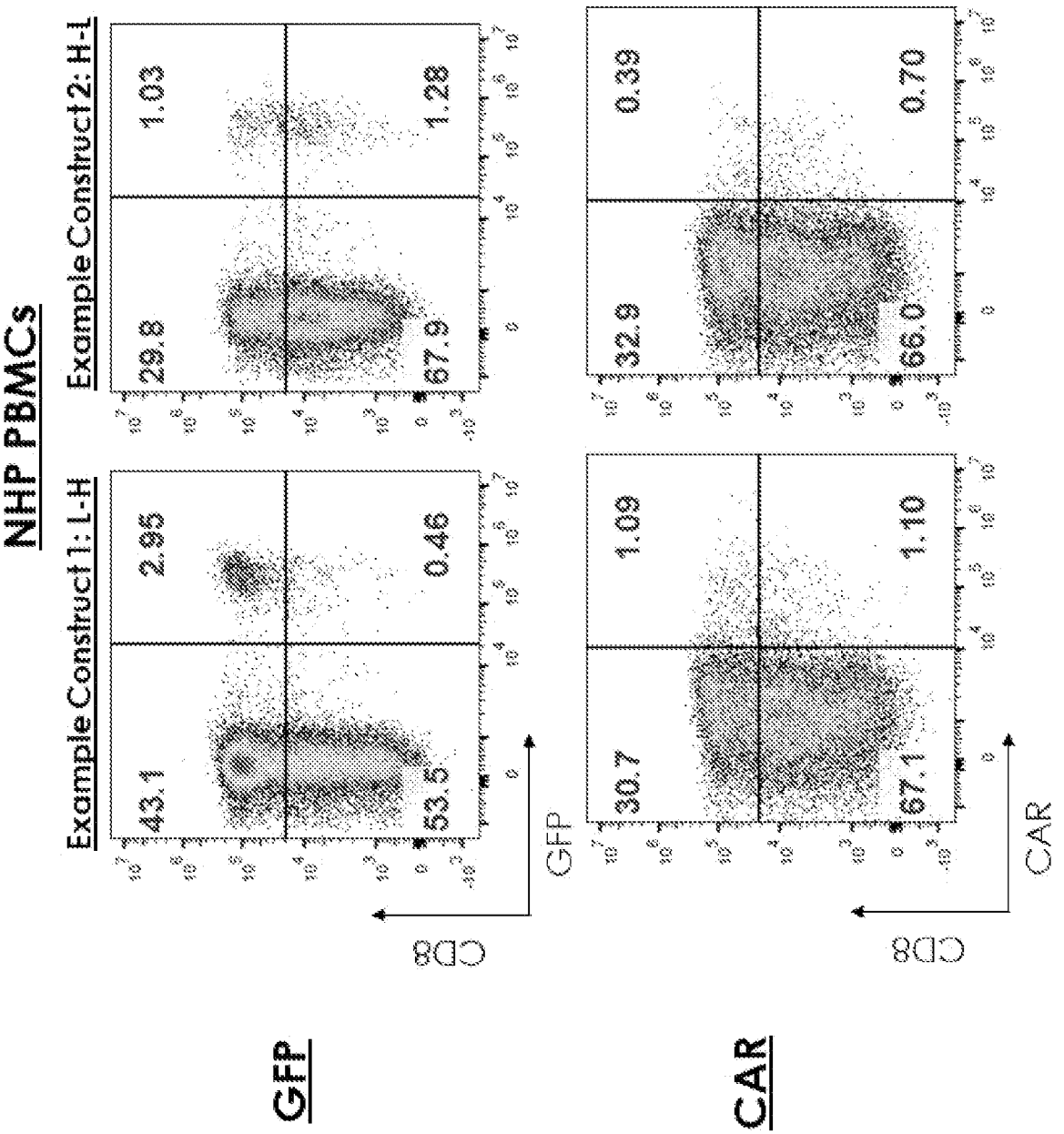

NHP PBMCs
Example Construct 1: L-H
Example Construct 2: H-L
GFP
CAR
CD8
GFP
CAR
43.1
2.95
53.5
0.46
29.8
1.03
67.9
1.28
30.7
1.09
67.1
1.10
32.9
0.39
66.0
0.70

FIG. 9B

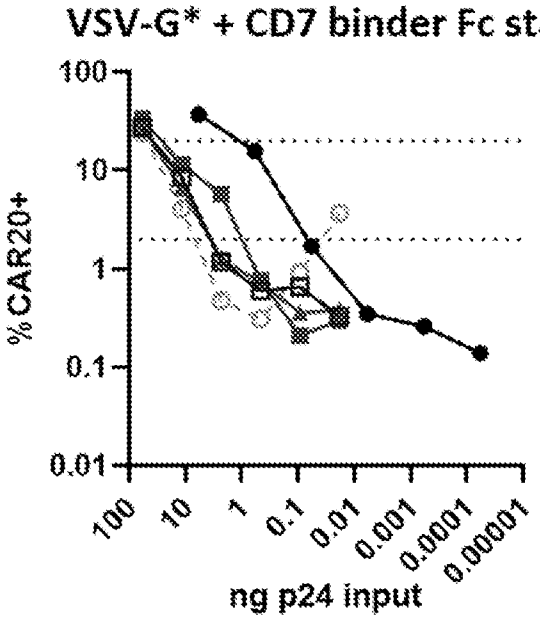


FIG. 10A

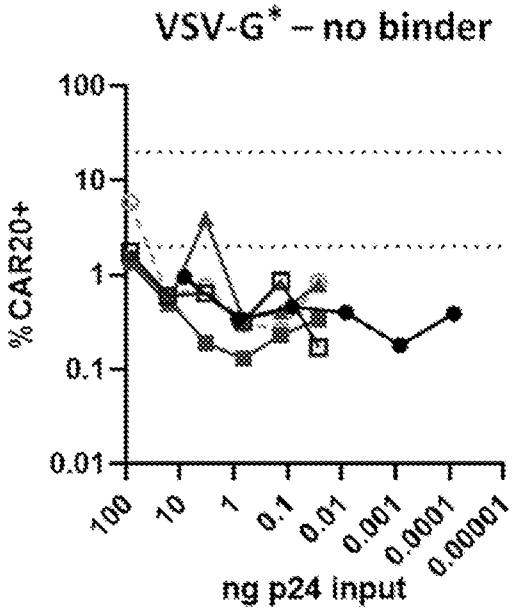
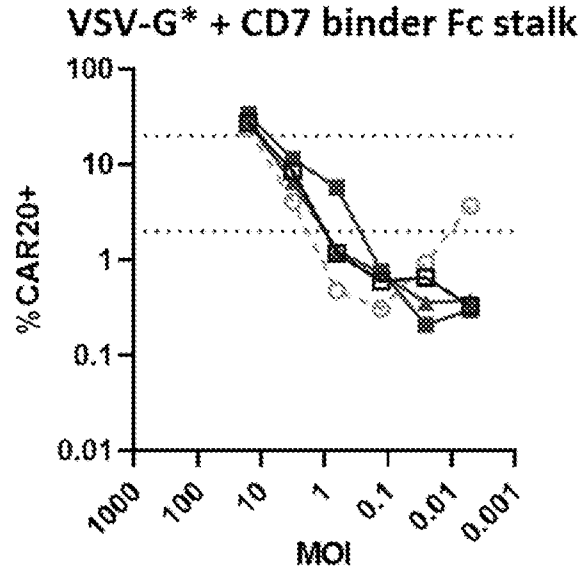


FIG. 10B



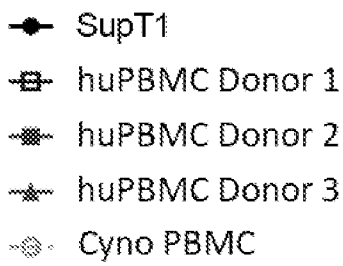


FIG. 10C

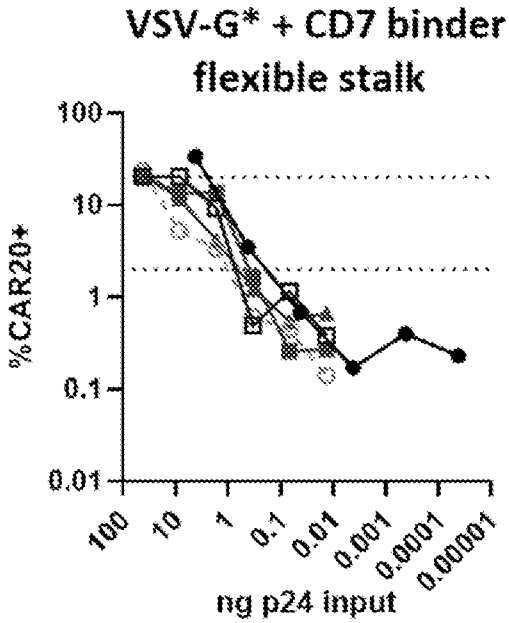


FIG. 11A

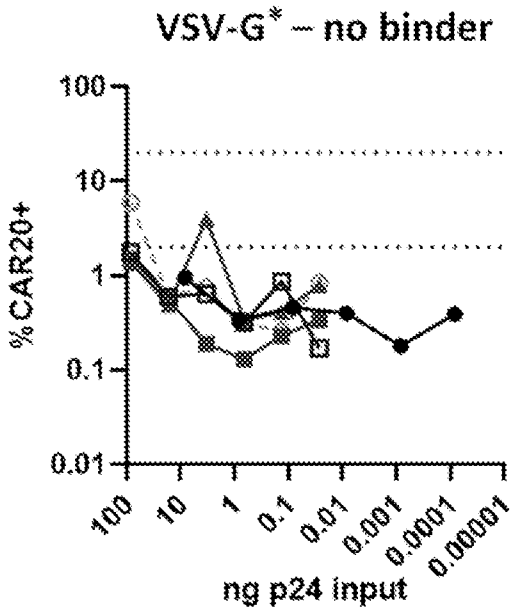
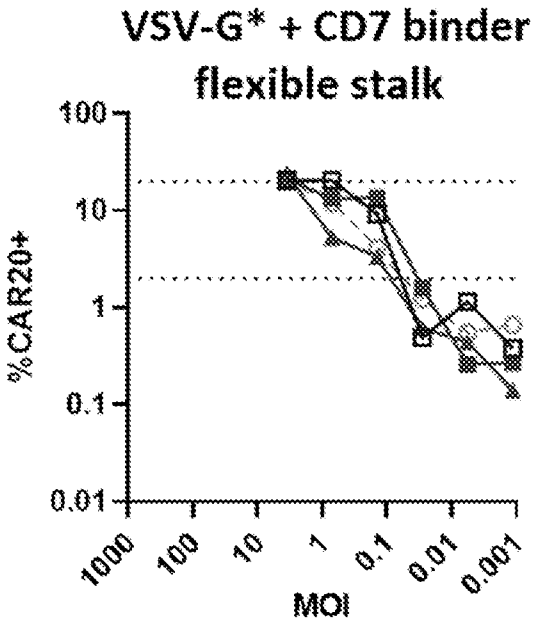


FIG. 11B



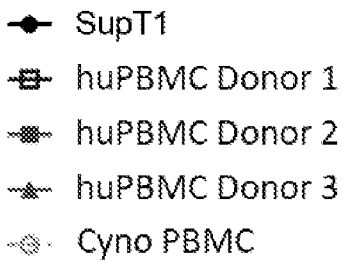


FIG. 11C

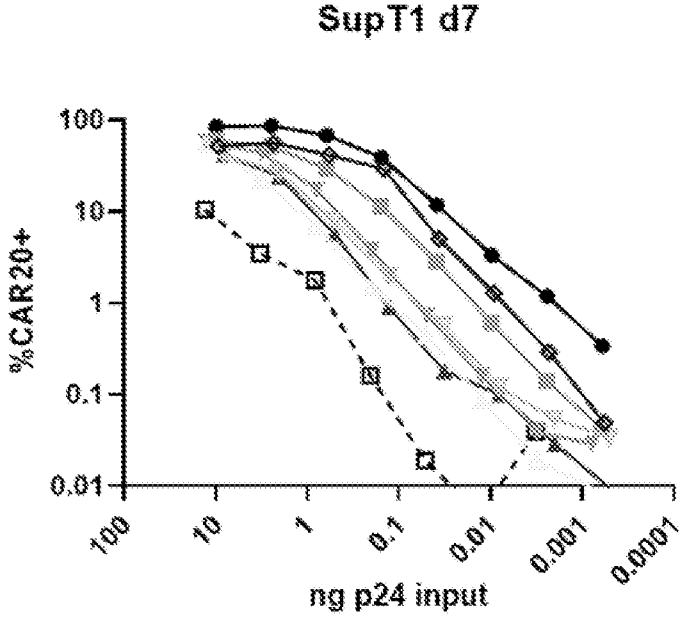


FIG. 12A

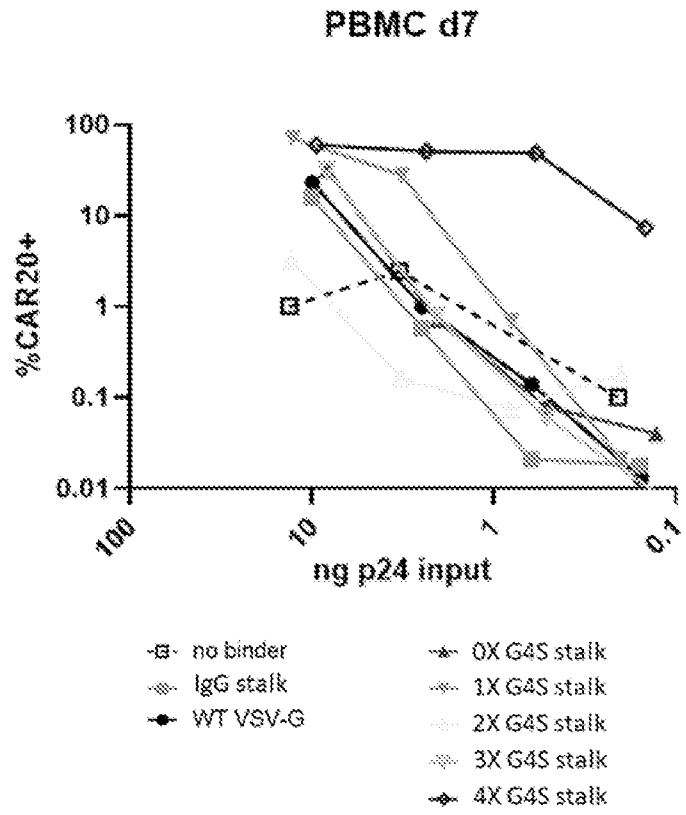


FIG. 12B

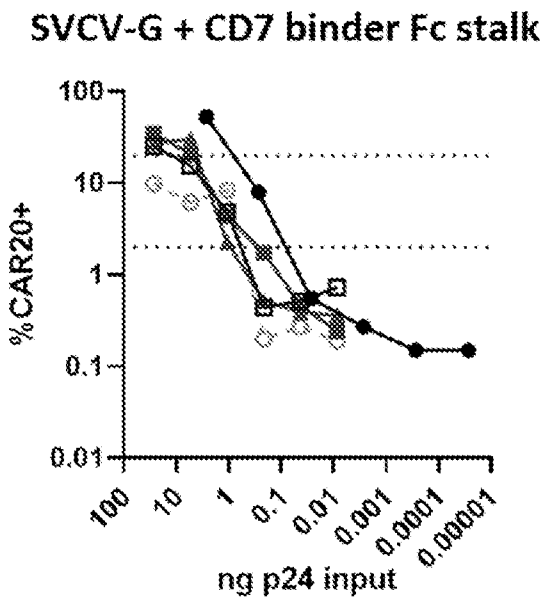


FIG. 13A

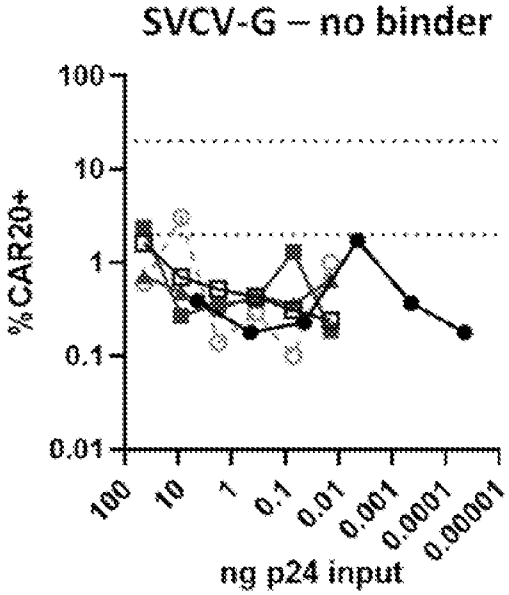


FIG. 13B

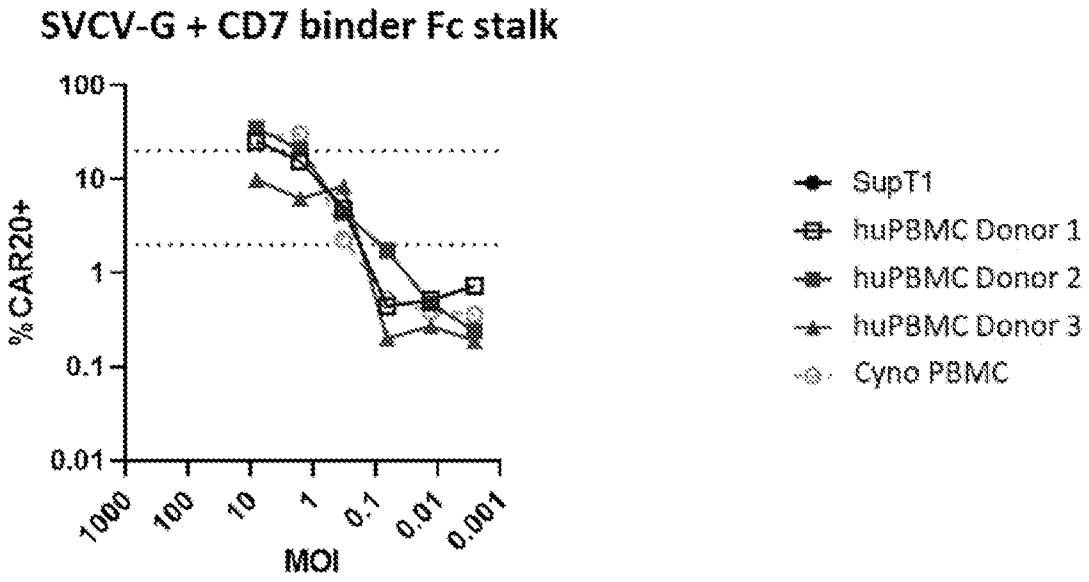


FIG. 13C

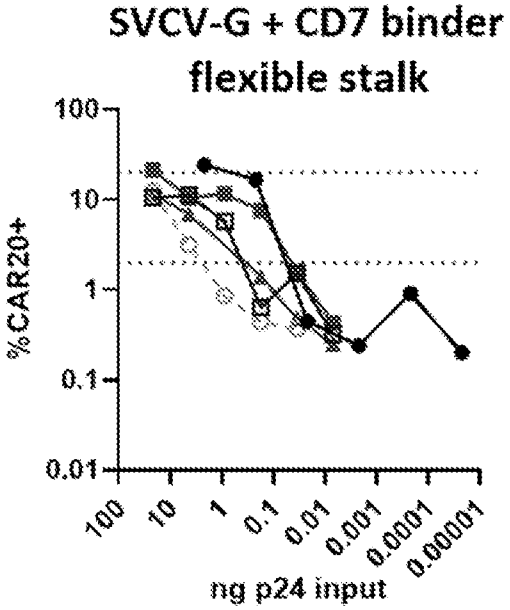


FIG. 14A

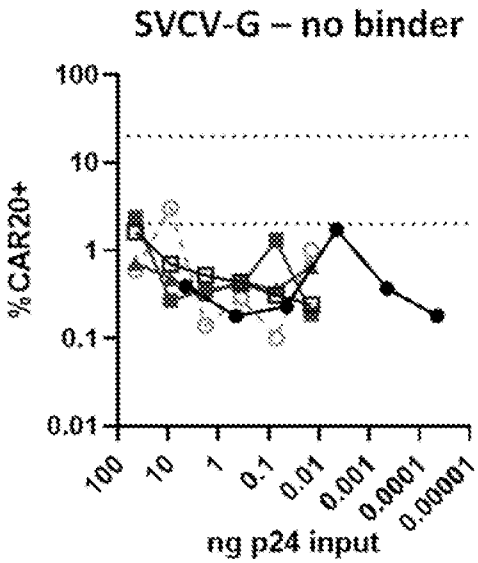


FIG. 14B

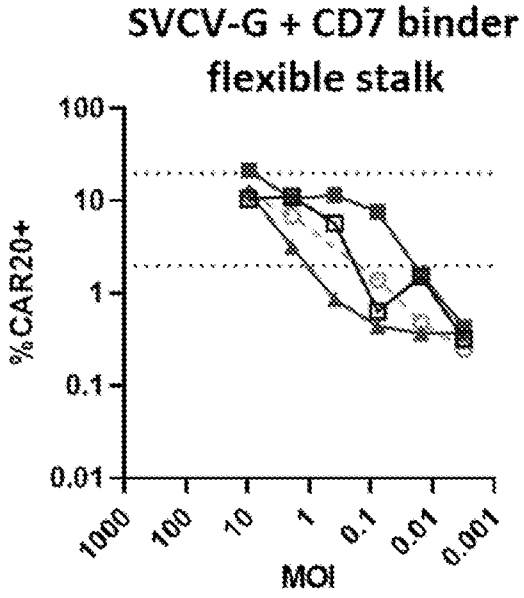
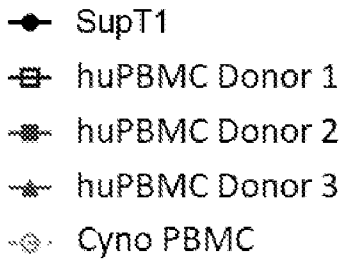


FIG. 14C



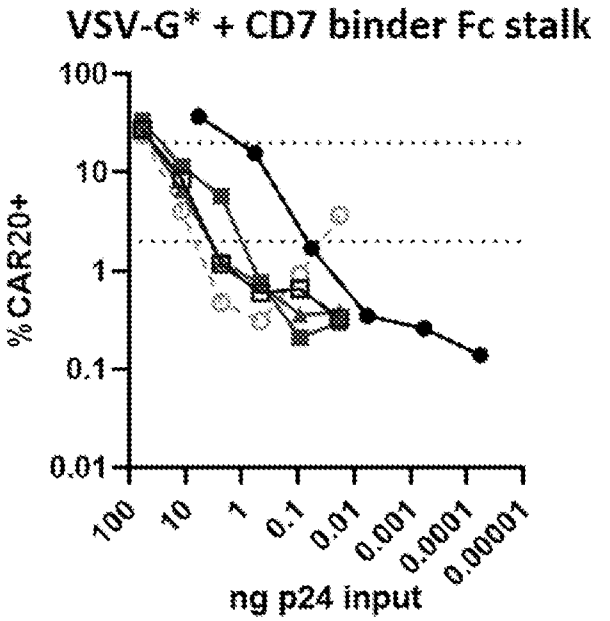


FIG. 15A

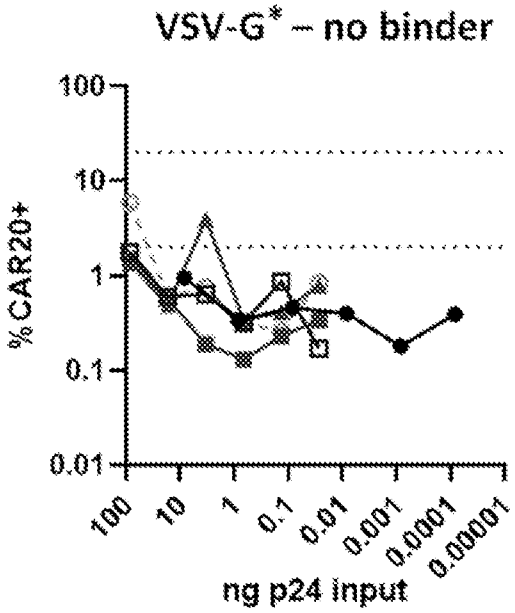


FIG. 15B

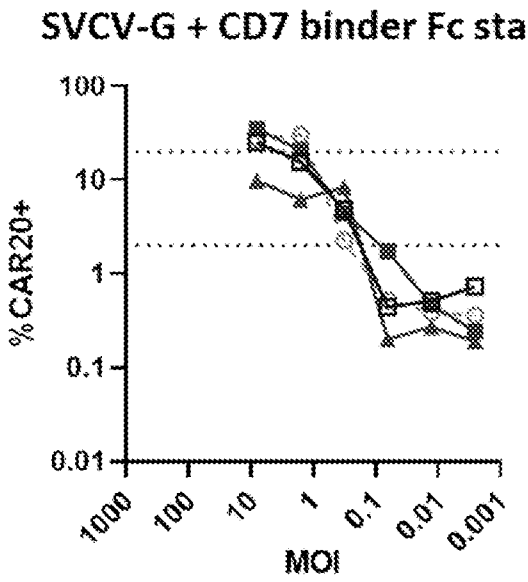


FIG. 15C

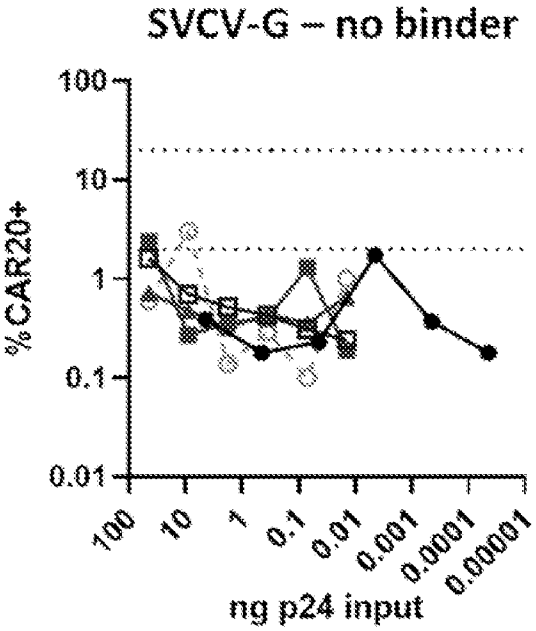
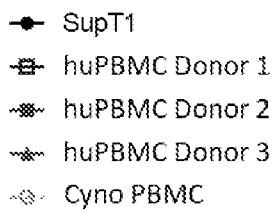


FIG. 15D



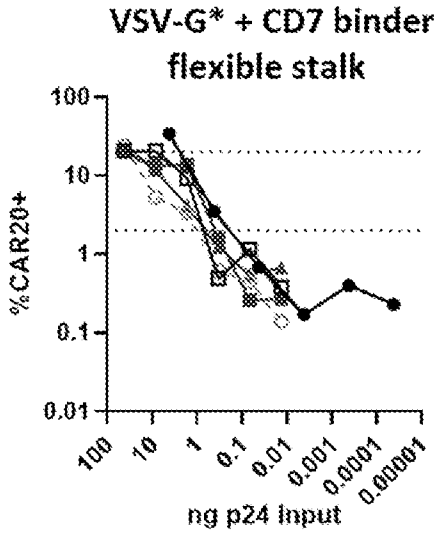


FIG. 16A

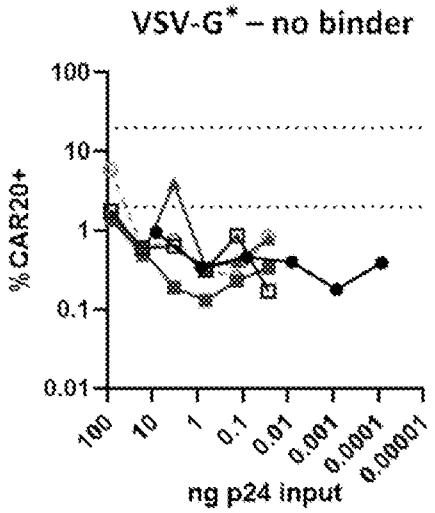


FIG. 16B

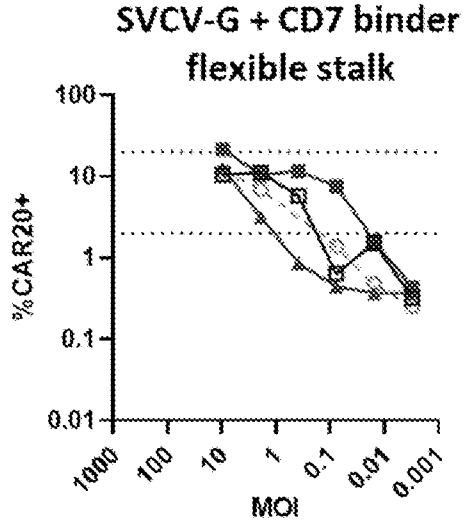


FIG. 16C

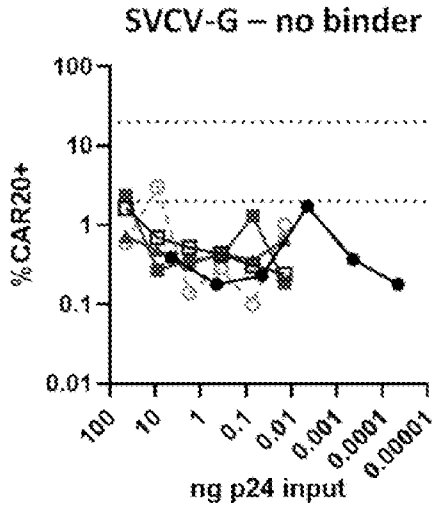
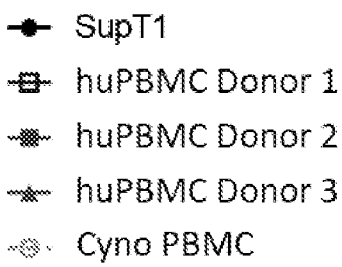


FIG. 16D



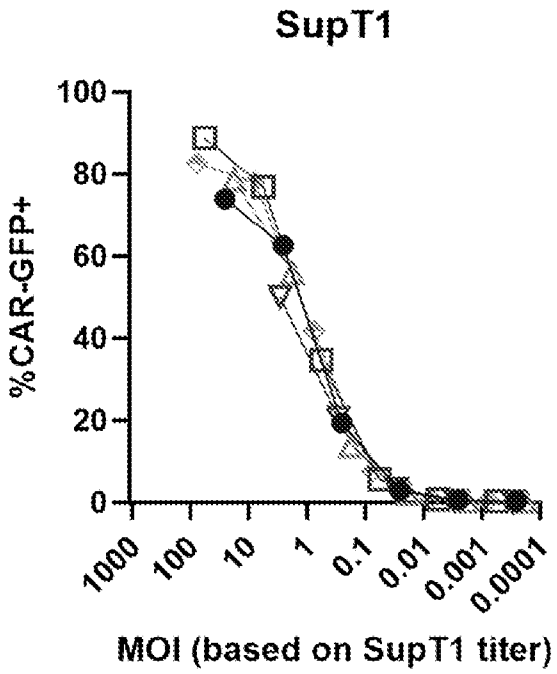


FIG. 17A

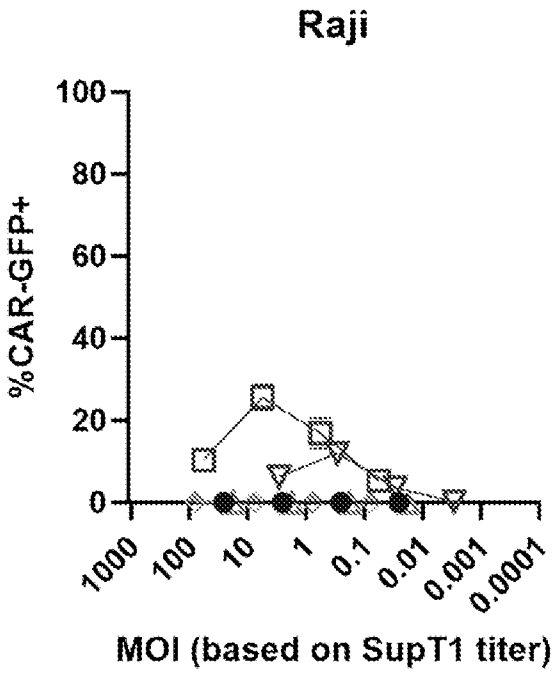


FIG. 17B

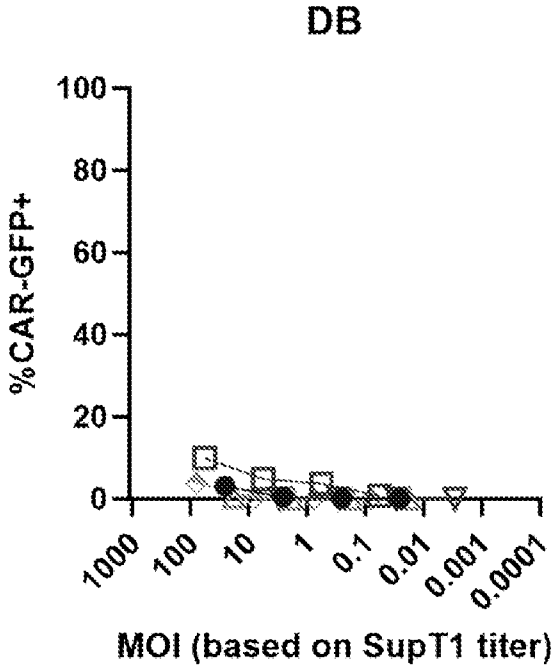
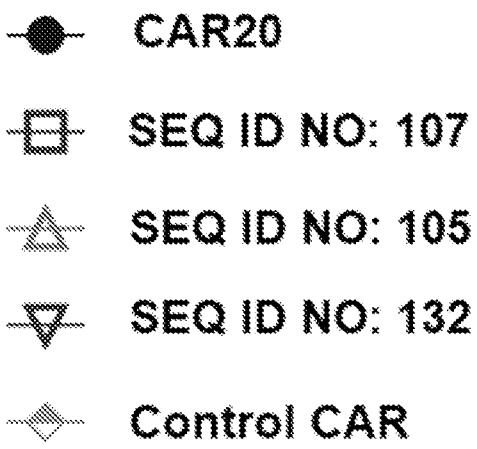


FIG. 17C



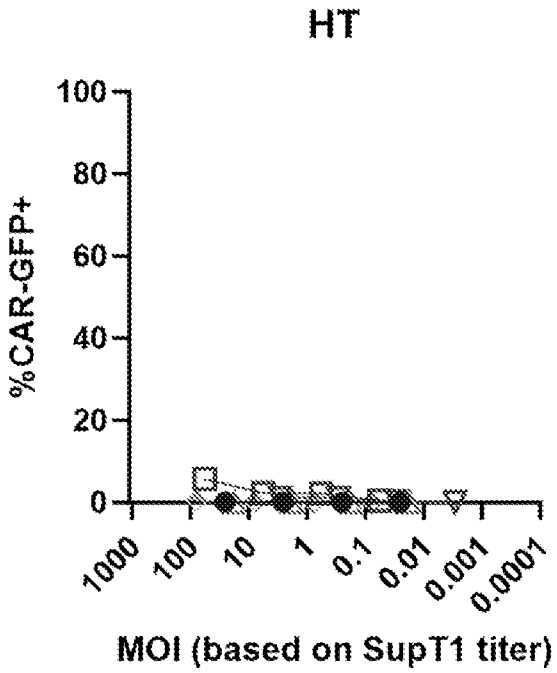


FIG. 17D

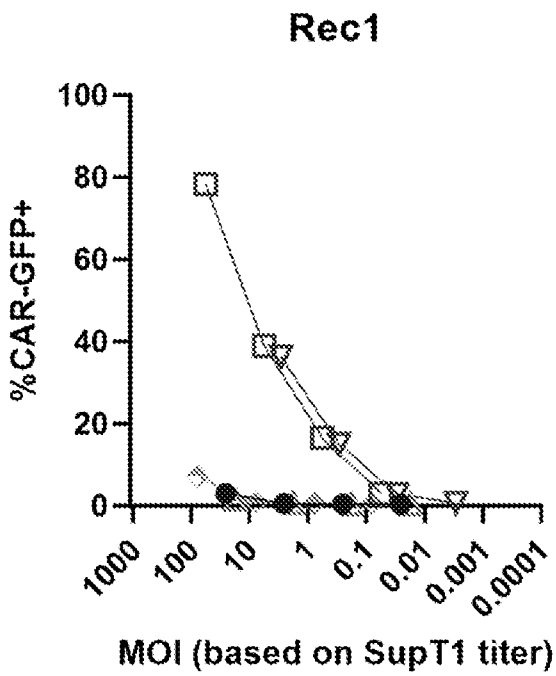
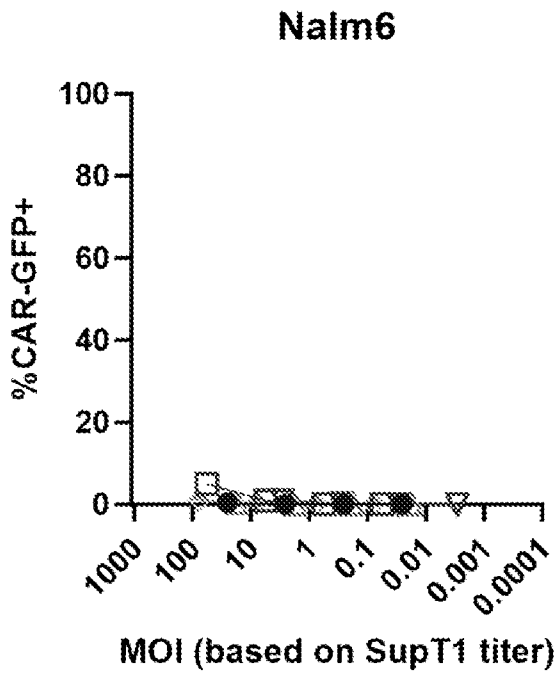


FIG. 17E



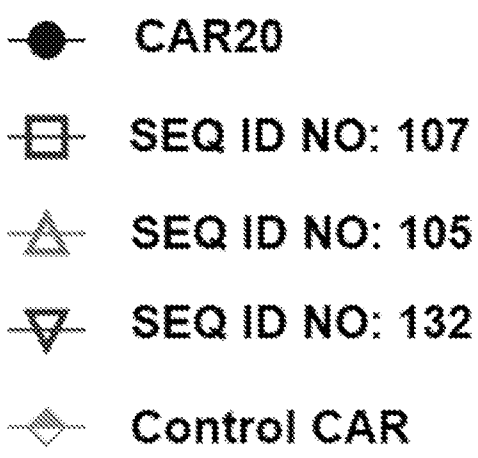


FIG. 17F

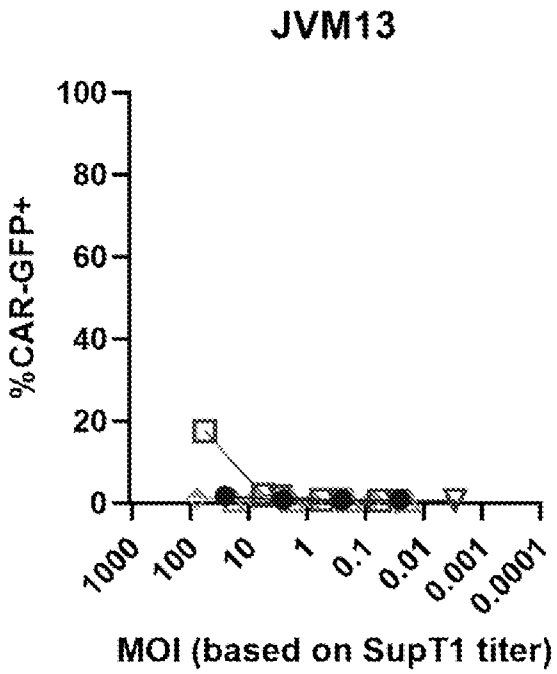


FIG. 17G

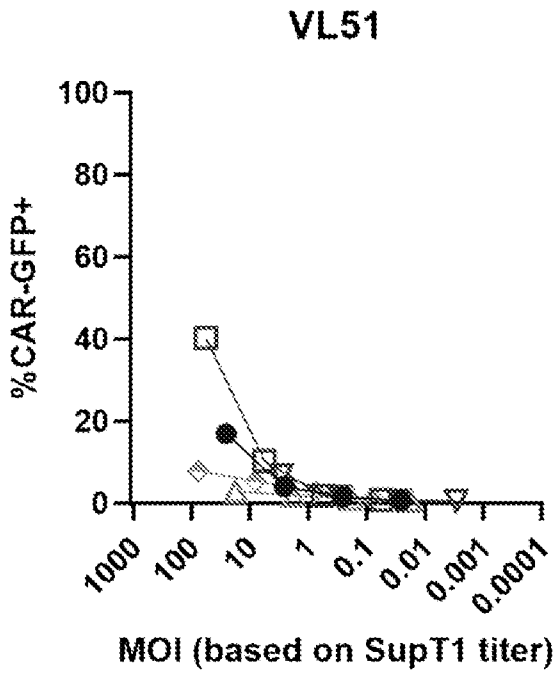
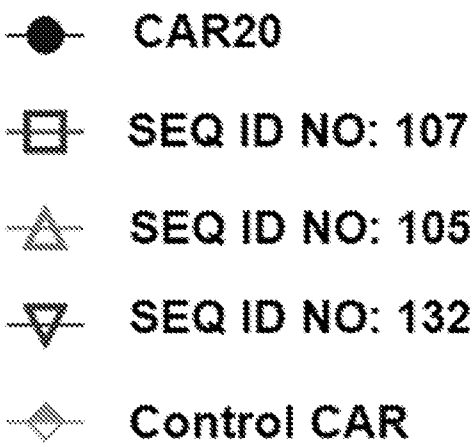


FIG. 17H



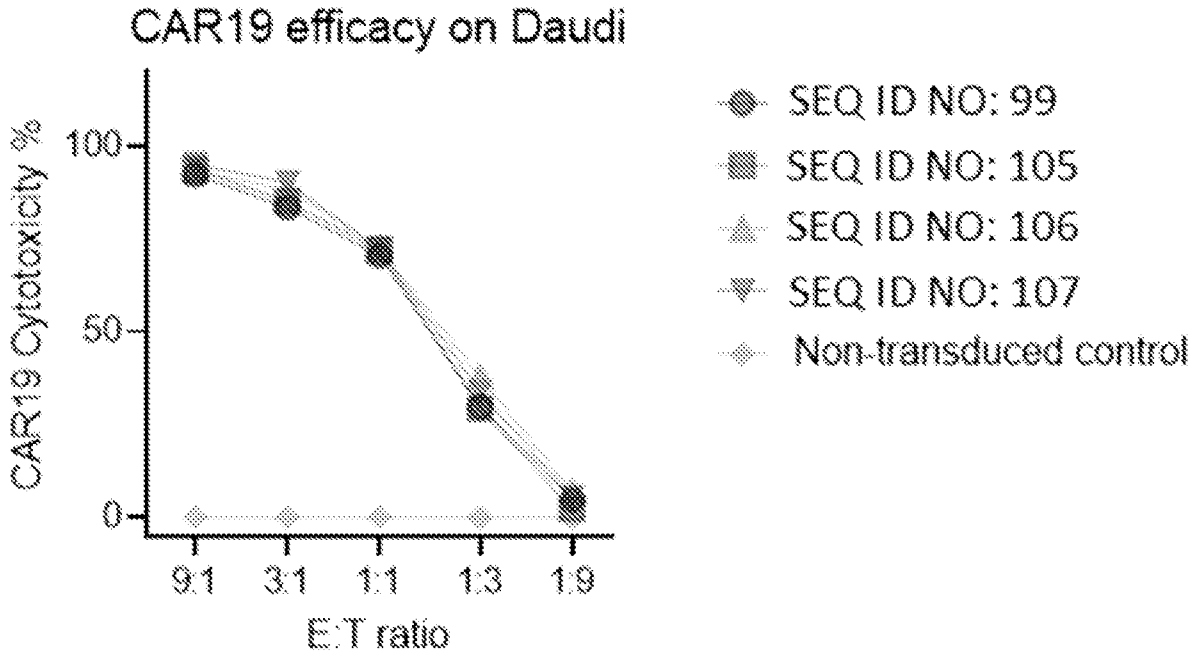


FIG. 18A

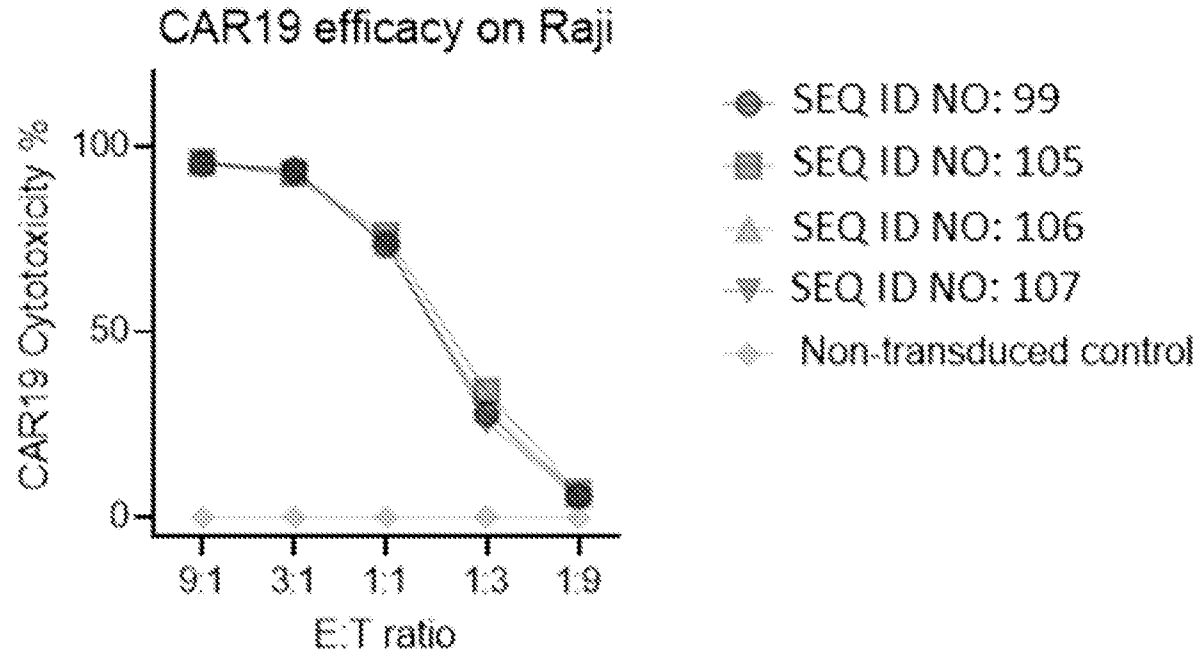


FIG. 18B

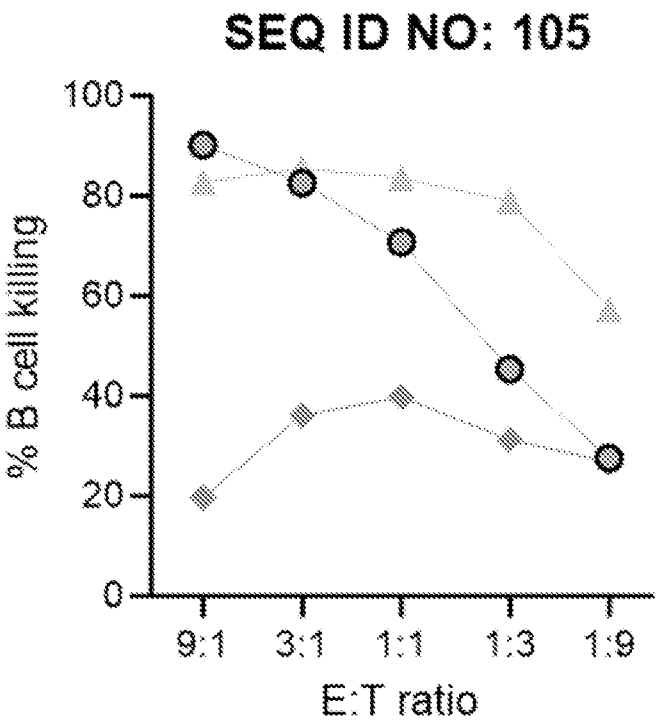


FIG. 19A

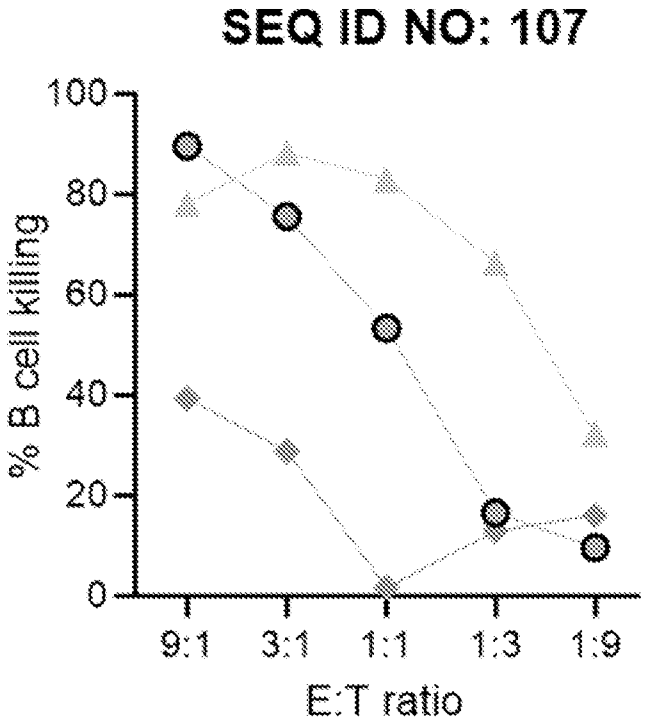


FIG. 19B

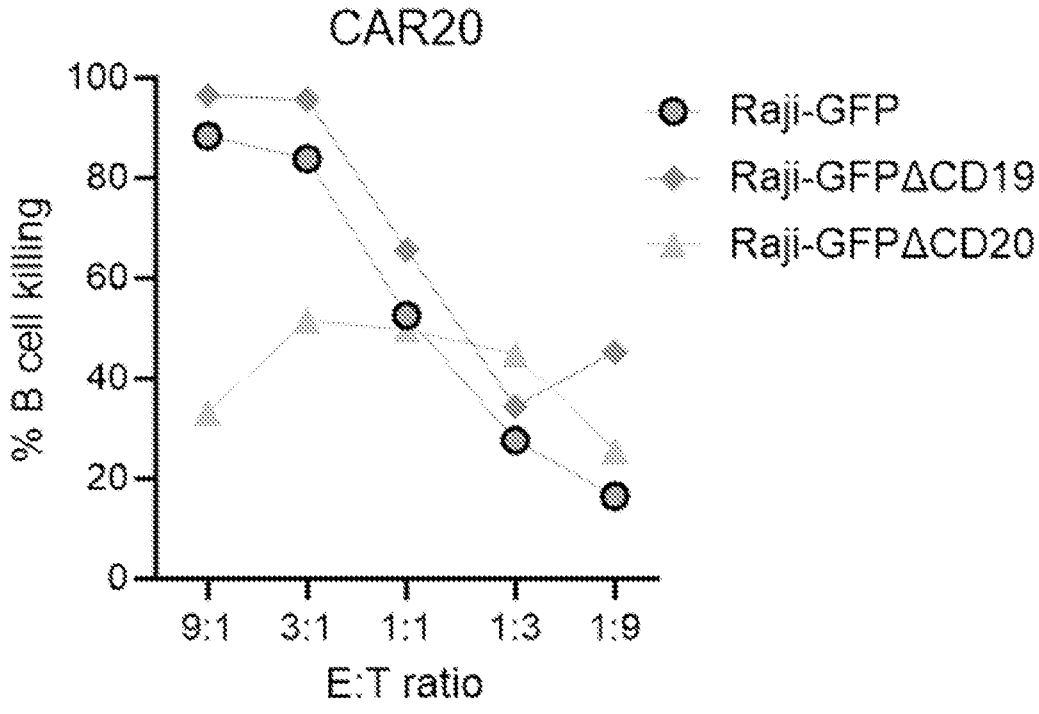


FIG. 19C

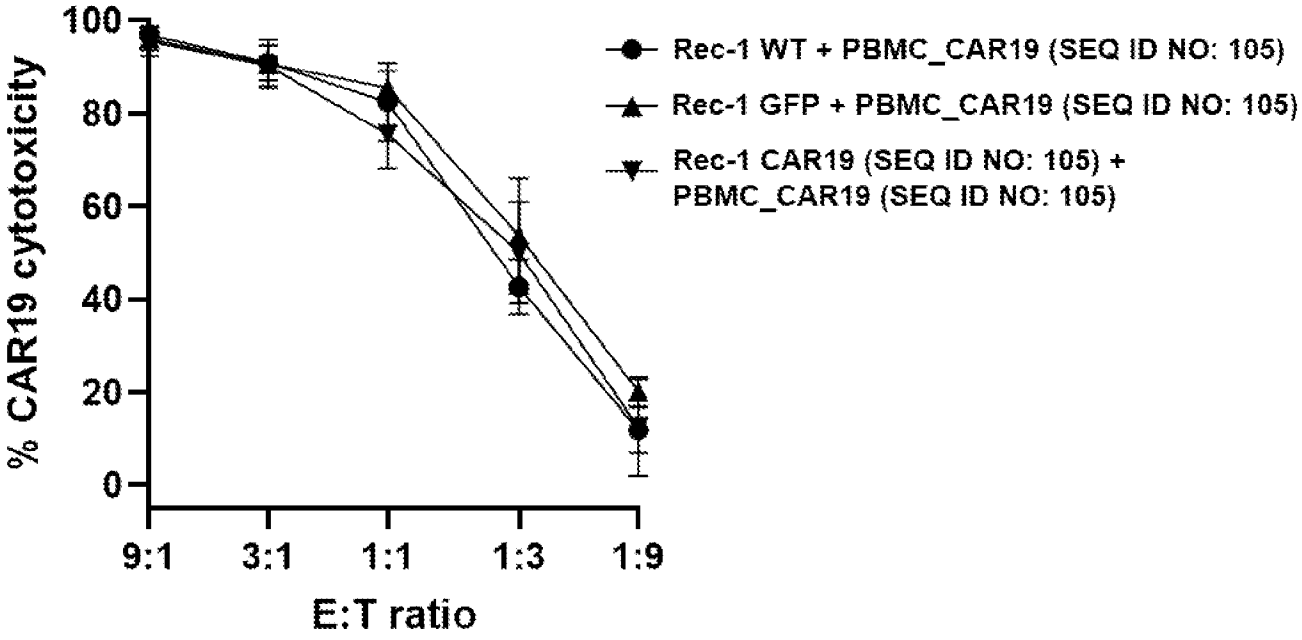


FIG. 20A

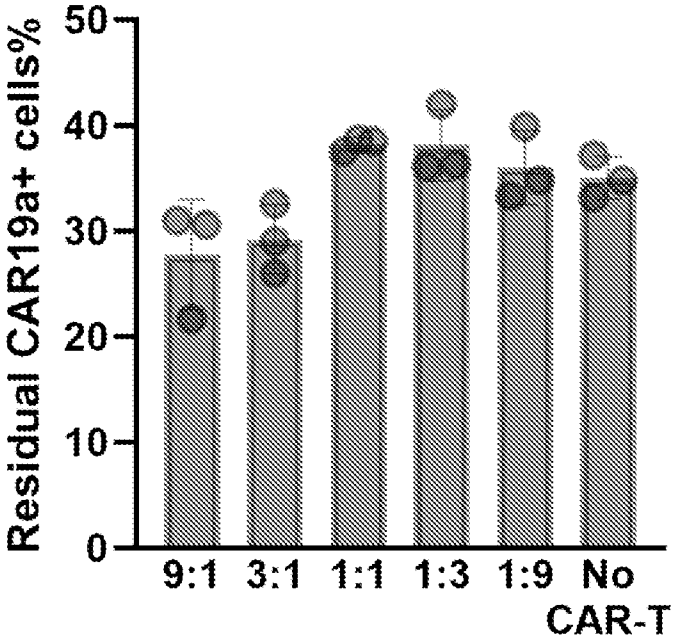


FIG. 20B

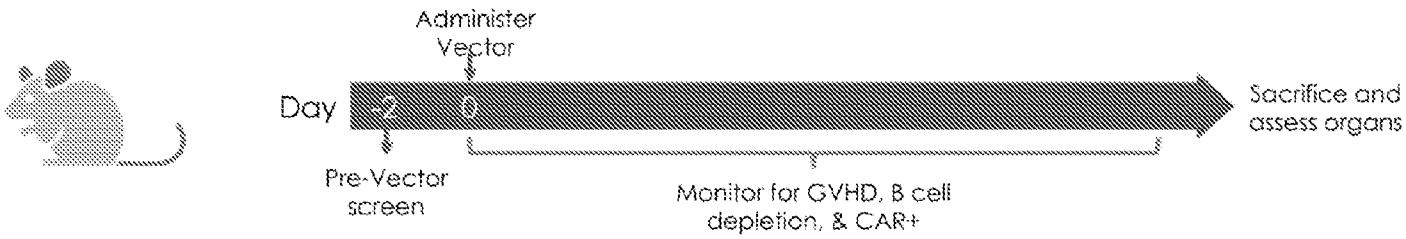


FIG. 21A

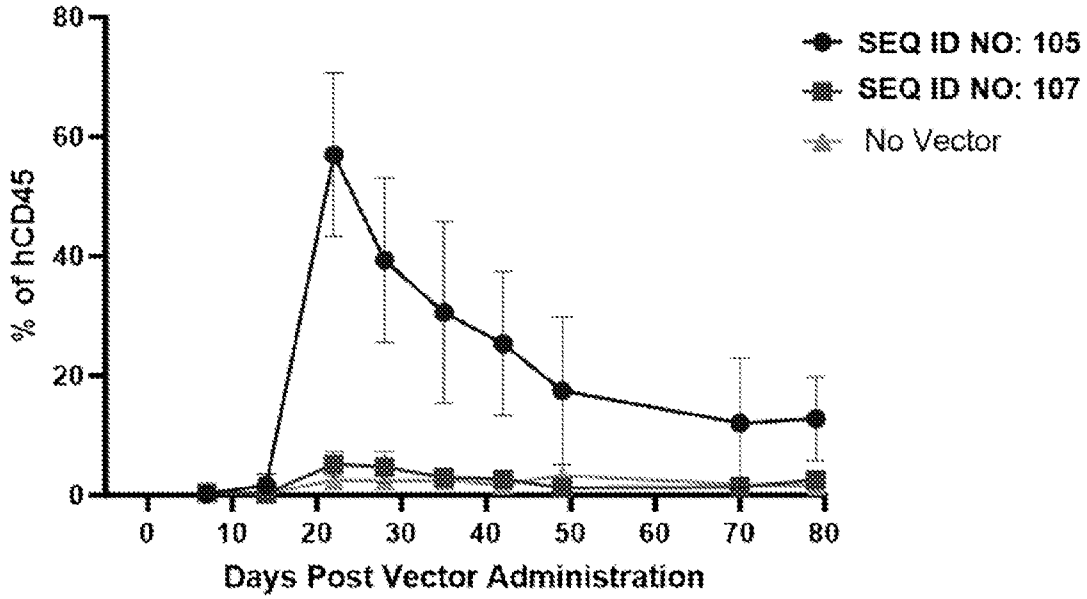


FIG. 21B

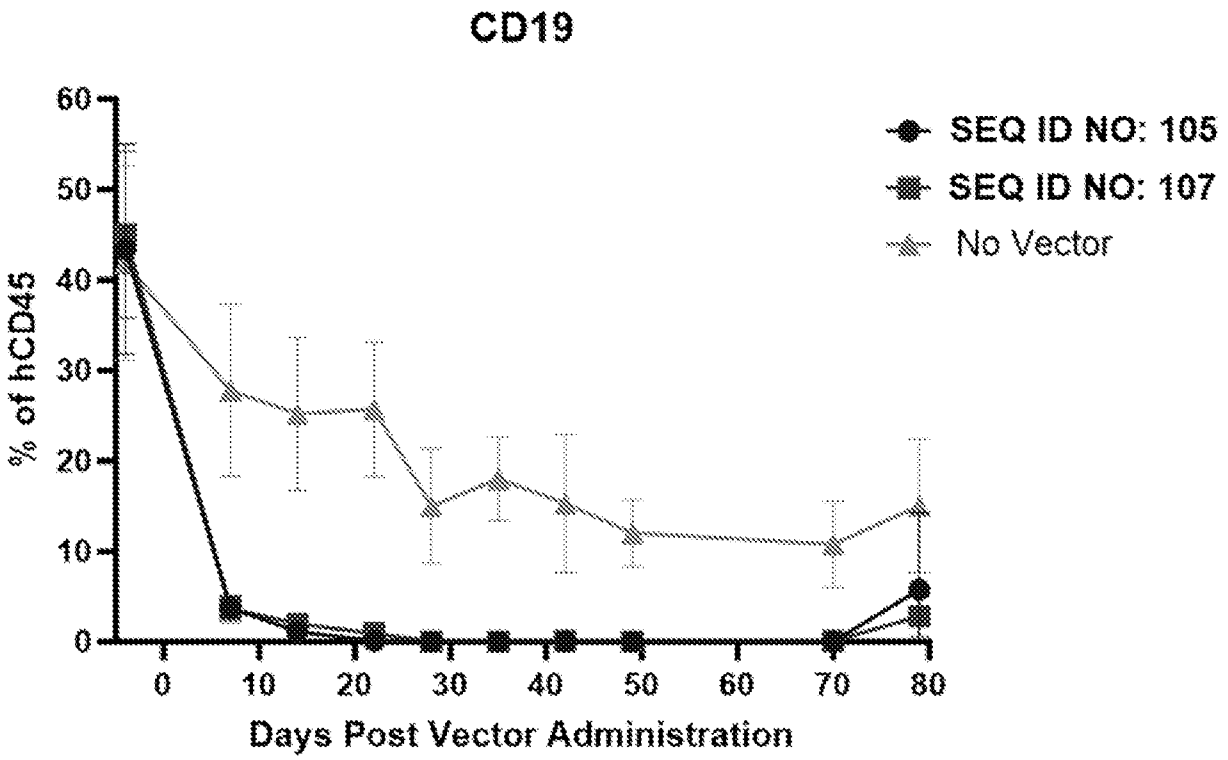


FIG. 22A

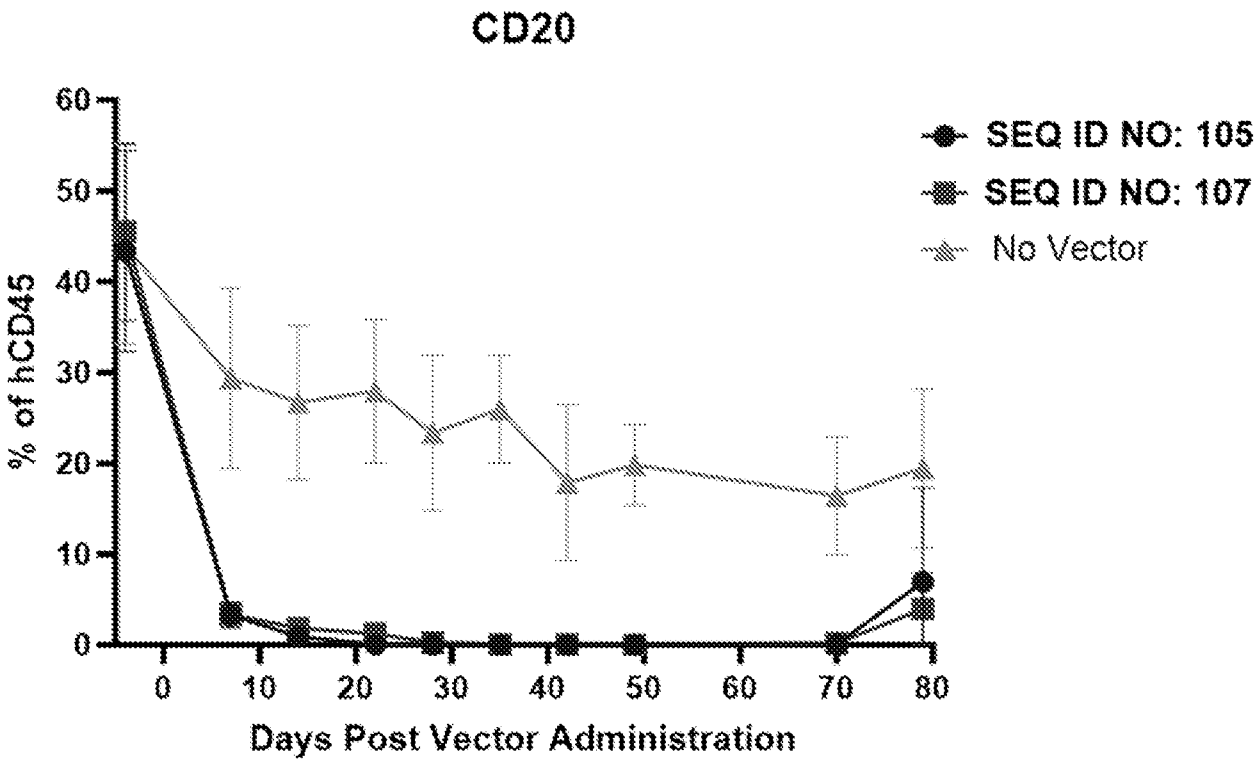


FIG. 22B

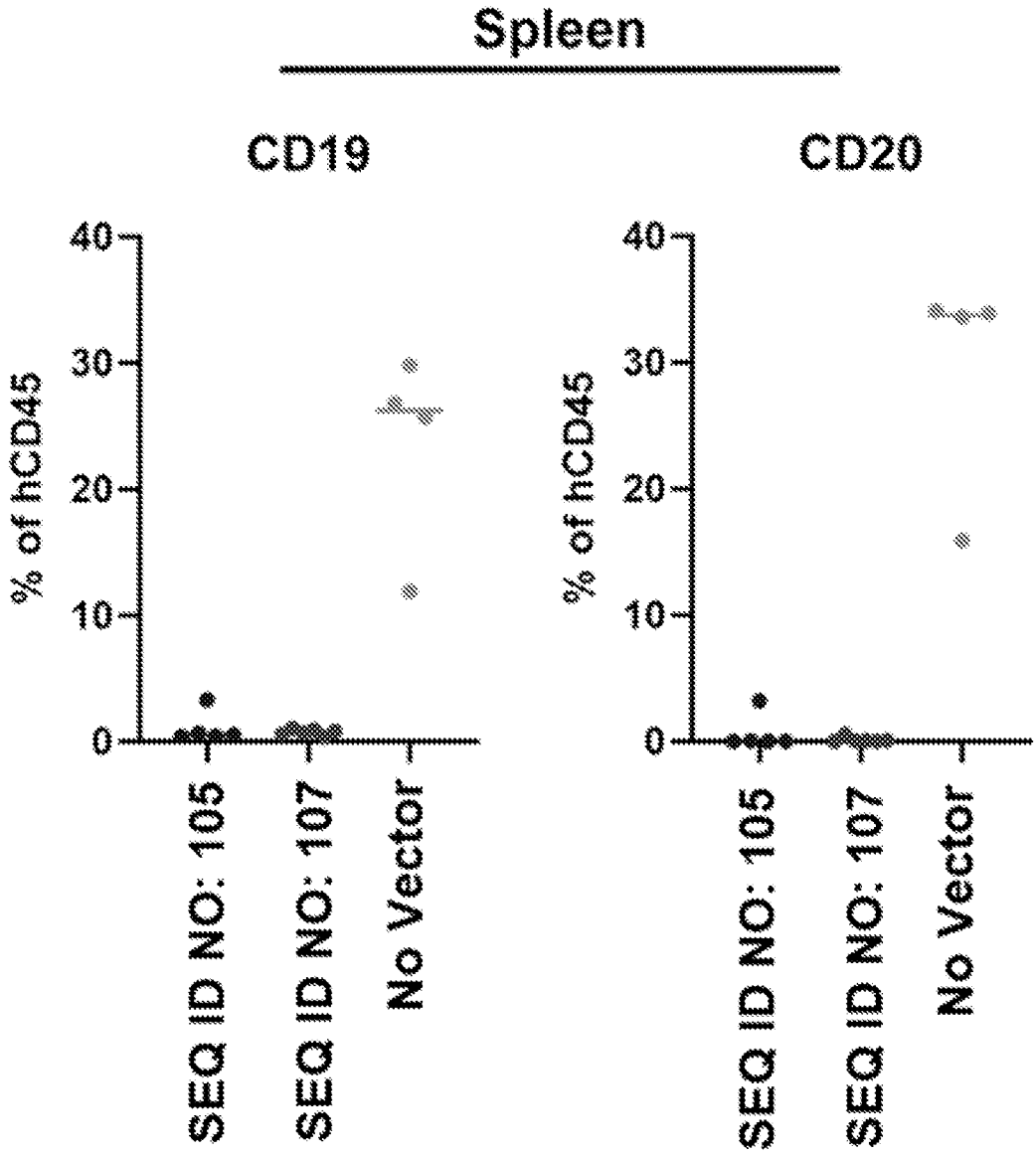

Spleen
CD19
CD20
% of hCD45
40
30
20
10
0
SEQ ID NO: 105
SEQ ID NO: 107
No Vector

FIG. 23A

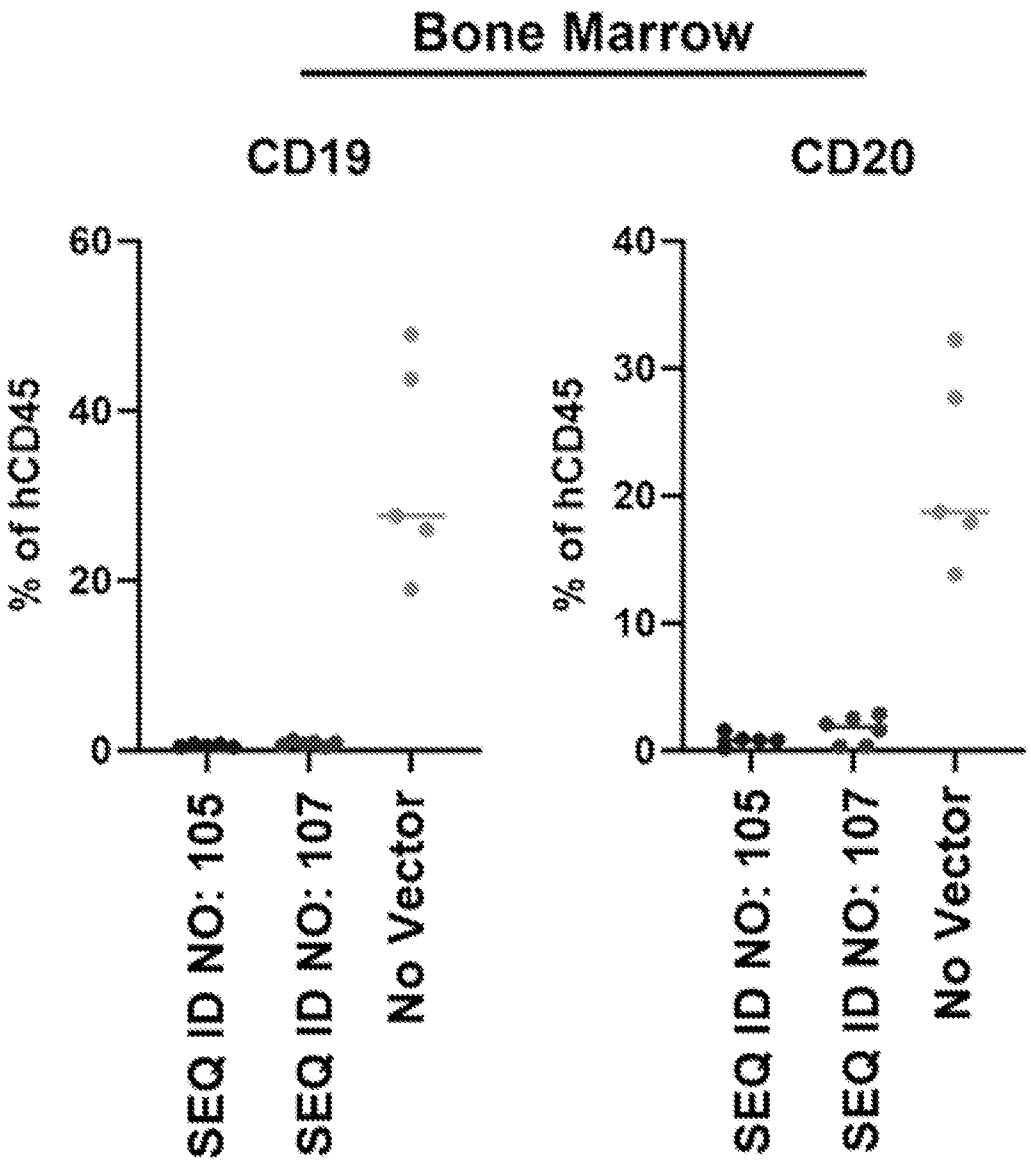

Bone Marrow
CD19
CD20
% of hCD45
60
40
20
0
40
30
20
10
0
SEQ ID NO: 105
SEQ ID NO: 107
No Vector

FIG. 23B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2024/033431

A. CLASSIFICATION OF SUBJECT MATTER

IPC: ***A61K 48/00*** (2024.01); *A61P 35/00* (2024.01); *A61P 37/00* (2024.01); *C07K 14/005* (2024.01); *C07K 14/145* (2024.01); *C07K 14/705* (2024.01); *C07K 16/28* (2024.01); *C12N 15/113* (2024.01); *C12N 15/63* (2024.01); *C12N 15/86* (2024.01); *C12N 7/01* (2024.01); *A61K 31/711* (2024.01); *A61K 38/16* (2024.01)

CPC: ***A61K 48/005;*** *A61K 2239/48; C07K 2319/03; C07K 2319/30; C12N 2740/15041; A61K 39/4611; A61K 39/4631; A61P 35/00; C07K 14/005; C07K 14/145; C12N 15/86; C12N 2740/16043; C12N 2740/16045; C12N 2760/20022; C12N 2760/20222; A61K 39/464424*

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2018/0028677 A1 (CHILDREN'S MEDICAL CENTER CORPORATION) 01 February 2018 (01.02.2018) entire document	1, 41, 42
A	US 2022/0306698 A1 (EXUMA BIOTECH CORP.) 29 September 2022 (29.09.2022) entire document	1, 41, 42
A	US 2022/0243223 A1 (JUNO THERAPEUTICS GMBH) 04 August 2022 (04.08.2022) entire document	1, 41, 42
A	US 2020/0054559 A1 (MASSACHUSETTS INSTITUTE OF TECHNOLOGY et al.) 20 February 2020 (20.02.2020) entire document	1, 41, 42

☑ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"D" document cited by the applicant in the international application
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
25 September 2024 (25.09.2024)	**04 November 2024 (04.11.2024)**

Name and mailing address of the ISA/US	Authorized officer
COMMISSIONER FOR PATENTS **MAIL STOP PCT, ATTN: ISA/US** **P.O. Box 1450** **Alexandria, VA 22313-1450 UNITED STATES OF AMERICA**	**TAINA MATOS**
Facsimile No. **571-273-8300**	Telephone No. **571-272-4300**

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2024/033431

Box No. I **Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)**

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
   a. ☑ forming part of the international application as filed.
   b. ☐ furnished subsequent to the international filing date for the purposes of international search (Rule 13*ter*.1(a)),
      ☐ accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.

2. ☐ With regard to any nucleotide and/or amino acid sequence disclosed in the international application, this report has been established to the extent that a meaningful search could be carried out without a WIPO Standard ST.26 compliant sequence listing.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2024/033431

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☑ Claims Nos.: **19, 29-34, 39, 40, 43-49**
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees need to be paid.

Group I+: claims 1-18, 20-28, 35-38, 41, 42, and 50 are drawn to viral particles, and nucleic acids encoding the same.

The first invention of Group I+ is restricted to a viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having the formula T-S1, wherein T is a target binding domain and S1 is a stalk portion, where the heterologous viral glycoprotein is selected to be SEQ ID NO:22. The first named invention has been selected based on the guidance set forth in section 10.54 of the PCT International Search and Preliminary Examination Guidelines. Specifically, the first named invention was selected based on the VSV-G polypeptide sequences listed in instant claim 42. It is believed that claims 1, 41, and 42 read on this first named invention and thus these claims will be searched without fee to the extent that they read on SEQ ID NO:22.

Applicant is invited to elect additional heterologous viral glycoproteins, targeting moieties, heterologous molecules of interest, and their respective, corresponding, SEQ ID NOs to be searched in a specific combination by paying additional fee for each set of election. An exemplary election would be to a viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having the formula T-S1, wherein T is a target binding domain and S1 is a stalk portion, where the heterologous viral glycoprotein is selected to be SEQ ID NO:23. Additional heterologous viral glycoproteins, targeting moieties, heterologous molecules of interest, and their respective, corresponding, SEQ ID NOs will be searched upon the payment of additional fees. Applicants must specify the claims that read on any additional elected inventions. Applicants must further indicate, if applicable, the claims which read on the first named invention if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/ examined.

The inventions listed in Groups I+ do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2024/033431

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☑ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: **1, 41, 42**

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

The Groups I+ formulas do not share a significant structural element responsible for abrogating LDL receptor binding, requiring the selection of alternative heterologous viral glycoproteins where "the VSV-G polypeptide comprises a sequence of SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24 or SEQ ID NO: 25."

Additionally, even if Groups I+ were considered to share the technical features of a viral particle comprising a heterologous viral glycoprotein and a targeting moiety, wherein the targeting moiety comprises a polypeptide having the formula T-S1, wherein T is a target binding domain and S1 is a stalk portion; a viral particle comprising a heterologous viral glycoprotein, a targeting moiety, and a nucleic acid molecule encoding for a heterologous molecule of interest. However, these shared technical features do not represent a contribution over the prior art.

Specifically, US 2022/0306698 A1 to Exuma Biotech Corp. discloses a viral particle (the viral particles are copseudotyped with envelope glycoproteins from 2 or more heterologous viruses, Para. [0354]) comprising a heterologous viral glycoprotein and a targeting moiety (the viral particles are copseudotyped with envelope glycoproteins from 2 or more heterologous viruses, Para. [0354]; CARs of the invention include at least one antigen-specific targeting region (ASTR), a transmembrane domain (TM), and an intracellular activating domain (IAD) and can include a stalk, Para. [0031]; a "binding polypeptide" that includes one or more polypeptides, typically glycoproteins, that identify and bind the target host cell, and one or more "fusogenic polypeptides" that mediate fusion of the retroviral and target host cell membranes, Para. [0058]), wherein the targeting moiety comprises a polypeptide having the formula T-S1, wherein T is a target binding domain and S1 is a stalk portion (the viral particles are copseudotyped with envelope glycoproteins from 2 or more heterologous viruses, Para. [0354]; CARs of the invention include at least one antigen-specific targeting region (ASTR), a transmembrane domain (TM), and an intracellular activating domain (IAD) and can include a stalk, Para. [0031]; a "binding polypeptide" that includes one or more polypeptides, typically glycoproteins, that identify and bind the target host cell, and one or more "fusogenic polypeptides" that mediate fusion of the retroviral and target host cell membranes, Para. [0058]); a viral particle comprising a heterologous viral glycoprotein, a targeting moiety (the viral particles are copseudotyped with envelope glycoproteins from 2 or more heterologous viruses, Para. [0354]; CARs of the invention include at least one antigen-specific targeting region (ASTR), a transmembrane domain (TM), and an intracellular activating domain (IAD) and can include a stalk, Para. [0031]; a "binding polypeptide" that includes one or more polypeptides, typically glycoproteins, that identify and bind the target host cell, and one or more "fusogenic polypeptides" that mediate fusion of the retroviral and target host cell membranes, Para. [0058]), and a nucleic acid molecule encoding for a heterologous molecule of interest (a plasmid on which a gene(s) or other coding sequence of interest is encoded, Para. [0065]).

The inventions listed in Groups I+ therefore lack unity under Rule 13 because they do not share a same or corresponding special technical features.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2024/033431

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2021/045836 A1 (REGENERON PHARMACEUTICALS INC.) 11 March 2021 (11.03.2021) entire document	1, 41, 42