

particles, including virus-like particles and viral vectors, for targeting desired cells are needed. The provided disclosure addresses this need.

Summary

[0005] Provided herein is a targeted lipid particle which includes (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) single domain antibody (sdAb) variable domain, wherein the sdAb variable domain is attached to the C-terminus of the G protein or the biologically active portion thereof, wherein the F protein molecule or the biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer. In some embodimentexamples, the single domain antibody is attached to the G protein via a linker. In some embodimentexamples, the linker is a peptide linker.

[0005a] In one aspect, the present disclosure refers to a targeted lipid particle, comprising: (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) single domain antibody (sdAb) variable domain, wherein the sdAb variable domain is attached to the C-terminus of the G protein or the biologically active portion thereof and/or wherein the sdAb is attached to the G protein or the biologically active portion thereof via a peptide linker, wherein the sdAb binds to a cell surface molecule of a target cell, wherein the F protein molecule or the biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer.

[0006] Provided herein is a targeted lipid particle which includes (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or biologically active portion thereof attached to a single domain antibody (sdAb) variable domain via a peptide linker, wherein the single domain antibody binds to a cell surface molecule of a target cell, wherein the F protein molecule or biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer. In some embodimentexamples, N-terminus of the F protein molecule or biologically active portion thereof is exposed on the outside of lipid bilayer. In some embodimentexamples, the C-terminus of the G protein is exposed on the outside of the lipid bilayer.

[0007] In some embodimentexamples, the single domain antibody binds a cell surface molecule present on a target cell. In some embodimentexamples, the cell surface molecule is a protein, glycan, lipid or low molecular weight molecule. In some of any embodimentexamples, the single domain antibody binds an antigen or portion thereof present on a target cell. In some embodimentexamples, the antigen is the cell surface molecule or a portion of the cell surface molecule that contains an epitope recognized by the single domain antibody. In some of any embodimentexamples, the target cell is selected from the group consisting of tumor-infiltrating lymphocytes, T cells, neoplastic or tumor cells, virus-infected cells, stem cells, central nervous system (CNS) cells, hematopoietic stem cells (HSCs), liver cells or fully differentiated cells. In some

embodimentexamples, the target cell is selected from the group consisting of a CD3+ T cell, a CD4+ T cell, a CD8+ T cell, a hepatocyte, a haematopoietic stem cell, a CD34+ haematopoietic stem cell, a CD105+ haematopoietic stem cell, a CD117+ haematopoietic stem cell, a CD105+ endothelial cell, a B cell, a CD20+ B cell, a CD19+ B cell, a cancer cell, a CD133+ cancer cell, an EpCAM+ cancer cell, a CD19+ cancer cell, a Her2/Neu+ cancer cell, a GluA2+ neuron, a GluA4+ neuron, a NKG2D+ natural killer cell, a SLC1A3+ astrocyte, a SLC7A10+ adipocyte, or a CD30+ lung epithelial cell. In some of any **embodimentexamples**, the target cell is a hepatocyte. In some of any **embodimentexamples**, the cell surface molecule or antigen is selected from the group consisting of ASGR1, ASGR2 and TM4SF5.

[0008] In some of any **embodimentexamples**, the target cell is a T cell. In some of any **embodimentexamples**, the cell surface molecule or antigen is CD8 or CD4.

[0009] In some of any **embodimentexamples**, the cell surface molecule or antigen is LDL-R.

[0010] Provided herein are targeted lipid particles comprising (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5, optionally human ASGR1, human ASGR2 and human ASGR2,

wherein the F protein molecule or the biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer.

[0010a] In one aspect, the present disclosure refers to a targeted lipid particle, comprising: (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, TM4SF5, CD8, CD4, and low density lipoprotein receptor (LDL-R), wherein the F protein molecule or the biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer.

[0011] Provided herein are targeted lipid particles comprising (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds a cell surface molecule selected from the group consisting of CD8 and CD4, , optionally human CD8 or human CD4, wherein the F protein molecule or the biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer.

[0012] Provided herein are targeted lipid particles comprising (a) a lipid bilayer enclosing a lumen, (b) a henipavirus F protein molecule or biologically active portion thereof; and (c) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds a cell surface molecule that is low density lipoprotein receptor (LDL-R), optionally human LDL-R, wherein the F protein molecule or the biologically active portion thereof and the targeted envelope protein are embedded in the lipid bilayer.

[0013] In some of any [embodimentexamples](#), the lipid particle is a lentiviral vector. In some of any [embodimentexamples](#), the binding domain is attached to the G protein via a linker. In some of any [embodimentexamples](#), the linker is a peptide linker.

[0014] Provided herein is a lentiviral vector, comprising a binding domain that targets a cell surface molecule selected from the group consisting of ASGR1, ASGR2 and TM4SF5, optionally human ASGR1, human ASGR2 and human TM4SF5, wherein the lentiviral vector is pseudotyped with a retargeted viral fusion protein, said retargeted viral fusion protein comprising: (a) a henipavirus F protein molecule or biologically active portion thereof; and (b) a targeted envelope protein comprising the binding domain attached to a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof.

[0015] Provided herein is a lentiviral vector, comprising a binding domain that targets a cell surface molecule selected from the group consisting of CD8 and CD4, optionally human CD8 and human CD4, wherein the lentiviral vector is pseudotyped with a retargeted viral fusion protein, said retargeted viral fusion protein comprising: (a) a henipavirus F protein molecule or biologically active portion thereof; and (b) a targeted envelope protein comprising the binding domain attached to a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof.

[0016] Provided herein is a lentiviral vector, comprising a binding domain that targets low density lipoprotein receptor (LDL-R), optionally wherein the LDL-R is human LDL-R, wherein the lentiviral vector is pseudotyped with a retargeted viral fusion protein comprising (a) a henipavirus F protein molecule or biologically active portion thereof; and (b) a targeted envelope protein comprising the binding domain attached to a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof.

[0017] In some of any **embodimentexamples**, the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof.

[0018] Provided herein is a lentiviral vector, comprising (a) a henipavirus F protein molecule or biologically active portion thereof; and (b) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds CD4; and (c) a cargo comprising nucleic acid encoding a chimeric antigen receptor (CAR), wherein the CAR comprises (i) an extracellular antigen binding domain that binds an extracellular antigen (e.g., CD19 or BCMA) and (ii) an intracellular signaling region a CD3zeta signaling domain and, optionally a 4-1BB or CD28 co-stimulatory signaling domain. In some **embodimentexamples**, the extracellular antigen binding domain of the CAR is an scFv.

[0018a] In one aspect, the present disclosure refers to a lentiviral vector, comprising: (a) a henipavirus F protein molecule or biologically active portion thereof; and (b) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds CD4; and (c) a cargo comprising nucleic acid encoding a chimeric antigen receptor (CAR), wherein the CAR comprises (i) an extracellular antigen binding domain that binds CD19, (ii) a transmembrane domain and (iii) an intracellular signaling region comprising a CD3zeta signaling domain.

[0019] In some of any **embodimentexamples**, the lentiviral vector is capable of delivering the nucleic acid encoding the CAR to T cells. In some **embodimentexamples** the T cells are in vivo in a subject.

[0020] Provided herein is a lentiviral vector, comprising:(a) a henipavirus F protein molecule or biologically active portion thereof; and(b) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds ASGR1; wherein the lentiviral vector is capable of targeting to hepatocytes. In some of any **embodimentexamples**, the lentiviral vector further comprises an exogenous agent for delivery to hepatocytes.

[0020a] In one aspect, the present disclosure refers to a lentiviral vector, comprising: (a) a henipavirus F protein molecule or biologically active portion thereof; and (b) a targeted envelope protein comprising (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain, wherein the binding domain is attached to the C-terminus of the G protein or the biologically active portion thereof, and wherein the binding domain binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2 and TM4SF5.

[0021] In some of any **embodimentexamples**, the lentiviral vector is capable of delivering the exogenous agent to hepatocytes, optionally wherein the hepatocytes are in vivo in a subject.

[0022] In some of any **embodimentexamples**, the binding domain is attached to the G protein via a linker. In some of any **embodimentexamples**, the linker is a peptide linker. In some of any **embodimentexamples**, the binding domain is a single domain antibody. In some of any **embodimentexamples**, the binding domain is a single chain variable fragment (scFv).

[0023] In some of any **embodimentexamples**, the peptide linker comprises up to 65 amino acids in length. In some of any **embodimentexamples**, the peptide linker comprises up to 50 amino acids

in length. In some of any embedimentexamples, the peptide linker comprises from or from about 2 to 65 amino acids, 2 to 60 amino acids, 2 to 56 amino acids, 2 to 52 amino acids, 2 to 48 amino acids, 2 to 44 amino acids, 2 to 40 amino acids, 2 to 36 amino acids, 2 to 32 amino acids, 2 to 28 amino acids, 2 to 24 amino acids, 2 to 20 amino acids, 2 to 18 amino acids, 2 to 14 amino acids, 2 to 12 amino acids, 2 to 10 amino acids, 2 to 8 amino acids, 2 to 6 amino acids, 6 to 65 amino acids, 6 to 60 amino acids, 6 to 56 amino acids, 6 to 52 amino acids, 6 to 48 amino acids, 6 to 44 amino acids, 6 to 40 amino acids, 6 to 36 amino acids, 6 to 32 amino acids, 6 to 28 amino acids, 6 to 24 amino acids, 6 to 20 amino acids, 6 to 18 amino acids, 6 to 14 amino acids, 6 to 12 amino acids, 6 to 10 amino acids, 6 to 8 amino acids, 8 to 65 amino acids, 8 to 60 amino acids, 8 to 56 amino acids, 8 to 52 amino acids, 8 to 48 amino acids, 8 to 44 amino acids, 8 to 40 amino acids, 8 to 36 amino acids, 8 to 32 amino acids, 8 to 28 amino acids, 8 to 24 amino acids, 8 to 20 amino acids, 8 to 18 amino acids, 8 to 14 amino acids, 8 to 12 amino acids, 8 to 10 amino acids, 10 to 65 amino acids, 10 to 60 amino acids, 10 to 56 amino acids, 10 to 52 amino acids, 10 to 48 amino acids, 10 to 44 amino acids, 10 to 40 amino acids, 10 to 36 amino acids, 10 to 32 amino acids, 10 to 28 amino acids, 10 to 24 amino acids, 10 to 20 amino acids, 10 to 18 amino acids, 10 to 14 amino acids, 10 to 12 amino acids, 12 to 65 amino acids, 12 to 60 amino acids, 12 to 56 amino acids, 12 to 52 amino acids, 12 to 48 amino acids, 12 to 44 amino acids, 12 to 40 amino acids, 12 to 36 amino acids, 12 to 32 amino acids, 12 to 28 amino acids, 12 to 24 amino acids, 12 to 20 amino acids, 12 to 18 amino acids, 12 to 14 amino acids, 14 to 65 amino acids, 14 to 60 amino acids, 14 to 56 amino acids, 14 to 52 amino acids, 14 to 48 amino acids, 14 to 44 amino acids, 14 to 40 amino acids, 14 to 36 amino acids, 14 to 32 amino acids, 14 to 28 amino acids, 14 to 24 amino acids, 14 to 20 amino acids, 14 to 18 amino acids, 18 to 65 amino acids, 18 to 60 amino acids, 18 to 56 amino acids, 18 to 52 amino acids, 18 to 48 amino acids, 18 to 44 amino acids, 18 to 40 amino acids, 18 to 36 amino acids, 18 to 32 amino acids, 18 to 28 amino acids, 18 to 24 amino acids, 18 to 20 amino acids, 20 to 65 amino acids, 20 to 60 amino acids, 20 to 56 amino acids, 20 to 52 amino acids, 20 to 48 amino acids, 20 to 44 amino acids, 20 to 40 amino acids, 20 to 36 amino acids, 20 to 32 amino acids, 20 to 28 amino acids, 20 to 26 amino acids, 20 to 24 amino acids, 24 to 65 amino acids, 24 to 60 amino acids, 24 to 56 amino acids, 24 to 52 amino acids, 24 to 48 amino acids, 24 to 44 amino acids, 24 to 40 amino acids, 24 to 36 amino acids, 24 to 32 amino acids, 24 to 30 amino acids, 24 to 28 amino acids, 28 to 65 amino acids, 28 to 60 amino acids, 28 to 56 amino acids, 28 to 52 amino acids, 28 to 48 amino acids, 28 to 44 amino acids, 28 to 40 amino acids, 28 to 36 amino acids, 28 to 34 amino acids,

28 to 32 amino acids, 32 to 65 amino acids, 32 to 60 amino acids, 32 to 56 amino acids, 32 to 52 amino acids, 32 to 48 amino acids, 32 to 44 amino acids, 32 to 40 amino acids, 32 to 38 amino acids, 32 to 36 amino acids, 36 to 65 amino acids, 36 to 60 amino acids, 36 to 56 amino acids, 36 to 52 amino acids, 36 to 48 amino acids, 36 to 44 amino acids, 36 to 40 amino acids, 40 to 65 amino acids, 40 to 60 amino acids, 40 to 56 amino acids, 40 to 52 amino acids, 40 to 48 amino acids, 40 to 44 amino acids, 44 to 65 amino acids, 44 to 60 amino acids, 44 to 56 amino acids, 44 to 52 amino acids, 44 to 48 amino acids, 48 to 65 amino acids, 48 to 60 amino acids, 48 to 56 amino acids, 48 to 52 amino acids, 50 to 65 amino acids, 50 to 60 amino acids, 50 to 56 amino acids, 50 to 52 amino acids, 54 to 65 amino acids, 54 to 60 amino acids, 54 to 56 amino acids, 58 to 65 amino acids, 58 to 60 amino acids, or 60 to 65 amino acids. In some of any [embodimentexamples](#), peptide linker comprises a polypeptide that is 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64 or 65 amino acids in length. In some of any [embodimentexamples](#), wherein the peptide linker is a flexible linker that comprises GS, GGS, GGGGS (SEQ ID NO:43), GGGGGS (SEQ ID NO:41) or combinations thereof. In some of any [embodimentexamples](#), the peptide linker comprises (GGS)_n, wherein n is 1 to 10. In some of any [embodimentexamples](#), the peptide linker comprises (GGGGS)_n (SEQ ID NO: 42), wherein n is 1 to 10. In some of any [embodimentexample](#), the peptide linker comprises (GGGGGS)_n (SEQ ID NO:27), wherein n is 1 to 6.

[0024] In some of any [embodimentexamples](#), the G protein or the biologically active portion thereof is a wild-type Nipah virus G (NiV-G) protein or a Hendra virus G protein. In some of any [embodimentexamples](#), the G protein or the biologically active portion thereof is a wild-type NiV-G protein or a functionally active variant or biologically active portion thereof. In some of any [embodimentexamples](#), the mutant NiV-G protein or functionally active variant or biologically active portion thereof comprises an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44.

[0025] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that is truncated and lacks up to 40 contiguous amino acid residues at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44).

[0026] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that is truncated at the N-terminus of wild-type NiV-G and has the sequence set forth in any of SEQ ID NOS: 10-15, 35-40 or 45-50 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NOS: 10-15, 35-40 or 45-50.

[0027] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that has a 5 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 10 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:10. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 35 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:35. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 45 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about

82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:45.

[0028] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that has a 10 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 36 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:36. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 11 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:11. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 46 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:46.

[0029] In some of any embodimentexamples, the NiV-G protein or the biologically active portion has a 15 amino acid truncation at or near the N-terminus of the wild-type NiV-G

protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 12 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:12. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 37 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:37. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 47 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:47.

[0030] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that has a 20 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 13 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or

about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:13. In some of any **embodimentexamples**, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 38 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:38. In some of any **embodimentexamples**, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 48 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:48.

[0031] In some of any **embodimentexamples**, the NiV-G protein is a biologically active portion has a 25 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any **embodimentexamples**, the NiV-G protein has the amino acid sequence set forth in SEQ ID NO: 14 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:14. In some of any **embodimentexamples**, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 39 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or

about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:39. In some of any [embodimentexamples](#), the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 49 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:49.

[0032] In some of any [embodimentexamples](#), the NiV-G protein is a biologically active portion has a 30 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any [embodimentexamples](#), the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 15 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:15. In some of any [embodimentexamples](#), the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 40 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:40.

[0033] In some of any [embodimentexamples](#), the NiV-G protein is a biologically active portion that has a 34 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any [embodimentexamples](#), the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 22 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at

least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:22. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 53 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:53.

[0034] In some of any embodimentexamples, the G-protein, the biologically active portion thereof is a functionally active variant that is a mutant NiV-G protein that exhibits reduced binding to Ephrin B2 or Ephrin B3.

[0035] In some of any embodimentexamples, the mutant NiV-G protein includes one or more amino acid substitutions corresponding to amino acid substitutions selected from the group consisting of E501A, W504A, Q530A and E533A with reference to numbering set forth in SEQ ID NO:28. In some of any embodimentexamples, the mutant NiV-G protein includes the amino acid substitutions E501A, W504A, Q530A and E533A with reference to numbering set forth in SEQ ID NO:28.

[0036] In some of any embodimentexamples, the mutant NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 16 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:16. In some of any embodimentexamples, the mutant NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 51 or an amino acid sequence having at least at or

about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:51.

[0037] In some of any [embodimentexamples](#), the F protein or the biologically active portion thereof is a wild-type Nipah virus F (NiV-F) protein or a Hendra virus F protein or is a functionally active variant or biologically active portion thereof. In some of any [embodimentexamples](#), the F protein or the biologically active portion thereof is a wild-type NiV-F protein or a functionally active variant or a biologically active portion thereof. In some of any [embodimentexamples](#), the NiV-F-protein or the functionally active variant or biologically active portion thereof comprises the amino acid sequences set forth in SEQ ID NO: 2, or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 2.

[0038] In some of any [embodimentexamples](#), the NiV-F protein is a biologically active portion thereof that has a 20 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO:2).

[0039] In some of any [embodimentexamples](#), the NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:5 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 5.

[0040] In some of any [embodimentexamples](#), the NiV-F protein is a biologically active portion thereof that includes i) a 20 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO:2); and ii) a point mutation on an N-linked glycosylation site.

[0041] In some of any [embodimentexamples](#), the NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:7 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 7.

[0042] In some of any [embodimentexamples](#), the NiV-F protein is a biologically active portion thereof that has a 22 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO:2).

[0043] In some of any [embodimentexamples](#), NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:8 or an amino acid sequence that is encoded by a sequence of nucleotides encoding a sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 8.

[0044] In some of any [embodimentexamples](#), the NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:23 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 23. In some of any [embodimentexamples](#), the F-protein or the biologically active portion thereof comprises an F1 subunit or a fusogenic portion thereof.

[0045] In some of any [embodimentexamples](#), the F protein comprises the sequence set forth in SEQ ID NO:23 and the G protein comprises the sequence set forth in SEQ ID NO:16.

[0046] In some of any [embodimentexamples](#), the F protein consists or consists essentially of the sequence set forth in SEQ ID NO:23 and/or the G protein consists or consists essentially of the sequence set forth in SEQ ID NO:16.

[0047] In some of any [embodimentexamples](#), the F1 subunit is a proteolytically cleaved portion of the F0 precursor. In some of any [embodimentexamples](#), the F1 subunit comprises the sequence set forth in SEQ ID NO: 4, or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at least at or about 84%, at least at or about 85%, at least at or about 86%, at least at or about 87%, at least at or about 88%, at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:4.

[0048] In some of any [embodimentexample](#), the lipid bilayer is derived from a membrane of a host cell used for producing a retrovirus or retrovirus-like particle. In some of any [embodimentexamples](#), the host cell is selected from the group consisting of CHO cells, BHK cells, MDCK cells, C3H 10T1/2 cells, FLY cells, Psi-2 cells, BOSC 23 cells, PA317 cells, WEHI cells, COS cells, BSC 1 cells, BSC 40 cells, BMT 10 cells, VERO cells, W138 cells, MRC5 cells, A549 cells, HT1080 cells, 293 cells, 293T cells, B-50 cells, 3T3 cells, NIH3T3 cells, HepG2 cells, Saos-2 cells, Huh7 cells, HeLa cells, W163 cells, 211 cells, and 211A cells. In some of any [embodimentexamples](#), the host cell comprises 293T cells. In some of any [embodimentexamples](#), the lipid bilayer is or comprises a viral envelope. In some of any [embodimentexamples](#), the retrovirus-like particle is replication defective.

[0049] In some of any [embodimentexamples](#), the targeted lipid particle comprises one or more viral components other than the F protein molecule and the G protein. In some of any [embodimentexamples](#), the one or more viral components are from a retrovirus. In some of any [embodimentexamples](#), the retrovirus is a lentivirus. In some of any [embodimentexamples](#), the one or more viral components comprise a viral packaging protein selected from one or more of Gag, Pol, Rev and Tat. In some of any [embodimentexamples](#), the one or more viral components comprises one or more of (e.g., all of) the following nucleic acid sequences: 5' LTR (e.g., comprising U5 and lacking a functional U3 domain), Psi packaging element (Psi), Central polypurine tract (cPPT)/central termination

sequence (CTS) (e.g. DNA flap), Poly A tail sequence, a posttranscriptional regulatory element (e.g. WPRE), a Rev response element (RRE), and 3' LTR (e.g., comprising U5 and lacking a functional U3).

[0050] In some of any [embodimentexamples](#), the targeted lipid particle is a lentiviral vector.

[0051] In some of any [embodimentexamples](#), the targeted lipid particle or the lentiviral vector is replication defective.

[0052] In some of any [embodimentexamples](#), the targeted lipid particle or the lentiviral vector further comprises an exogenous agent. In some of any [embodimentexamples](#), the targeted lipid particle further comprises an exogenous agent. In some [embodimentexamples](#), the lentiviral vector further comprises an exogenous agent.

[0053] In some of any [embodimentexamples](#), the exogenous agent is present in the lumen. In some of any [embodimentexamples](#), the exogenous agent is a protein or a nucleic acid. In some [embodimentexamples](#), the nucleic acid is a DNA or RNA.

[0054] In some of any [embodimentexamples](#), the exogenous agent is a nucleic acid encoding a cargo for delivery to the target cell. In some of any [embodimentexamples](#), the exogenous agent encodes a therapeutic agent or a diagnostic agent.

[0055] In some of any [embodimentexamples](#), the exogenous agent encodes a membrane protein. In some [embodimentexamples](#), the membrane protein is an antigen receptor for targeting cells expressed by or associated with a disease or condition. In some [embodimentexamples](#), the membrane protein is a chimeric antigen receptor (CAR). In some [embodimentexamples](#), the CAR comprises (i) an extracellular antigen binding domain that binds an extracellular antigen (e.g., CD19 or BCMA), optionally wherein the extracellular antigen binding domain is an scFv, (ii) a transmembrane domain and (iii) an intracellular signaling region comprising a CD3zeta signaling domain and, optionally a co-stimulatory signaling domain, e.g., a 4-1BB or CD28 co-stimulatory signaling domain. In some [embodimentexamples](#), the target cell is a T cell. In some [embodimentexamples](#), the cell surface molecule on the target cell is CD4 or CD8. In some [embodimentexamples](#), the binding domain is an scFv that binds CD4 (e.g. human CD4). In some [embodimentexamples](#), the binding domain is a single domain antibody that binds CD4 (e.g. human CD4). In some [embodimentexamples](#), the binding domain is an scFv that binds CD8 (e.g. human CD8). In some [embodimentexamples](#), the binding domain is a single domain antibody that binds CD8 (e.g. human CD8).

[0056] In some of any [embodimentexamples](#), the exogenous agent is a nucleic acid comprising a payload gene for correcting a genetic deficiency, optionally a genetic deficiency in the target cell. In some [embodimentexamples](#), the genetic deficiency is associated with a liver cell or a hepatocyte. In some [embodimentexamples](#), the target cell is a hepatocyte. In some [embodimentexample](#), the cell surface molecule is a molecule selected from the group consisting of ASGR1, ASGR2 and TM4SF5. In some [embodimentexamples](#), the binding domain is an scFv that binds ASGR1 (e.g. human ASGR1). In some [embodimentexamples](#), the binding domain is a single domain antibody that binds ASGR1 (e.g. human ASGR1). In some [embodimentexamples](#), the binding domain is an scFv that binds ASGR2 (e.g. human ASGR2). In some [embodimentexamples](#), the binding domain is a single domain antibody that binds ASGR2 (e.g. human ASGR2). In some [embodimentexample](#), the binding domain is a scFv that binds TM4SF5 (e.g. human TM4SF5). In some [embodimentexamples](#), the binding domain is a single domain antibody that binds TM4SF5 (e.g. human TM4SF5).

[0057] In some of any [embodimentexamples](#), the single domain antibody binds a cell surface molecule present on a target cell. In some of any [embodimentexamples](#), the cell surface molecule is a protein, glycan, lipid or low molecular weight molecule. In some of any [embodimentexamples](#), the target cell is selected from the group consisting of tumor-infiltrating lymphocytes, T cells, neoplastic or tumor cells, virus-infected cells, stem cells, central nervous system (CNS) cells, hematopoietic stem cells (HSCs), liver cells or fully differentiated cells. In some of any [embodimentexamples](#), the target cell is selected from the group consisting of a CD3+ T cell, a CD4+ T cell, a CD8+ T cell, a hepatocyte, a haematopoietic stem cell, a CD34+ haematopoietic stem cell, a CD105+ haematopoietic stem cell, a CD117+ haematopoietic stem cell, a CD105+ endothelial cell, a B cell, a CD20+ B cell, a CD19+ B cell, a cancer cell, a CD133+ cancer cell, an EpCAM+ cancer cell, a CD19+ cancer cell, a Her2/Neu+ cancer cell, a GluA2+ neuron, a GluA4+ neuron, a NKG2D+ natural killer cell, a SLC1A3+ astrocyte, a SLC7A10+ adipocyte, or a CD30+ lung epithelial cell.

[0058] In some of any [embodimentexamples](#), the single domain antibody binds an antigen or portion thereof present on a target cell. In some of any [embodimentexamples](#), the cell surface molecule or antigen is selected from the group consisting of ASGR1, ASGR2 and TM4SF5. In some [embodimentexample](#), the antigen or portion thereof is human ASGR1. In some [embodimentexamples](#), the antigen or portion thereof is human ASGR2. In some [embodimentexamples](#), the antigen or portion thereof is human TM4SF5.

[0059] Provided herein is a polynucleotide comprising a nucleic acid sequence encoding (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain that binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5. In some [embodimentexamples](#), the cell surface molecule is human ASGR1. In some [embodimentexample](#), the cell surface molecule is human ASGR2. In some [embodimentexamples](#), the cell surface molecule is human TM4SF5. In some of any [embodimentexamples](#), the cell surface molecule or antigen is CD8 or CD4.

[0059a] In one aspect, the present disclosure refers to a polynucleotide comprising a nucleic acid sequence encoding: (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a single domain antibody (sdAb) variable domain, wherein the sdAb variable domain is attached to the C-terminus of the G protein or the biologically active portion thereof; or (ii) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain that binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, TM4SF5, CD4, CD8, and low density lipoprotein receptor (LDL-R).

[0060] Provided herein is a nucleic acid sequence encoding (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain that binds a cell surface molecule selected from the group consisting of CD4 and CD8. In some [embodimentexamples](#), the cell surface molecule is human CD4. In some [embodimentexamples](#), the cell surface molecule is human CD8. In some [embodimentexamples](#), the cell surface molecule or antigen is low density lipoprotein receptor (LDL-R). In some [embodimentexamples](#), the cell surface molecule or antigen is human LDL-R.

[0061] Provided herein is a polynucleotide comprising a nucleic acid sequence encoding (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a binding domain that binds low density lipoprotein receptor (LDL-R). In some [embodimentexamples](#), the binding domain binds human LDL-R. In some of any [embodimentexamples](#), the binding domain is a single domain antibody (sdAb). In some of any [embodimentexamples](#), the binding domain is a single chain variable fragment (scFv).

[0062] Provided herein is a polynucleotide comprising a nucleic acid sequence encoding (i) a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and (ii) a single domain antibody (sdAb) variable domain, wherein the sdAb variable domain is attached to the C-terminus of the G protein or the biologically active portion thereof. In some of any [embodimentexamples](#), the polynucleotide further comprises (iii) a nucleic acid sequence encoding a henipavirus F protein molecule or a biologically active portion thereof.

[0063] In some [embodimentexamples](#), the nucleic acid sequence is a first nucleic acid sequence and the polynucleotide further comprise a second nucleic acid sequence encoding a henipavirus F protein molecule or a biologically active portion thereof. In some [embodimentexamples](#), the polynucleotide comprise an IRES or a sequence encoding a linking peptide between the first and second nucleic acid sequence. In some [embodimentexamples](#), the

linking peptide is a self-cleaving peptide or a peptide that causes ribosome skipping, optionally a T2A peptide.

[0064] In some of any [embodimentexamples](#), the polynucleotide includes at least one promoter that is operatively linked to control expression of the nucleic acid. In some of any [embodimentexamples](#), the promoter is operatively linked to control expression of the first nucleic acid sequence and the second nucleic acid sequence. In some of any [embodimentexamples](#), the promoter is a constitutive promoter. In some of any [embodimentexamples](#), the promoter is an inducible promoter.

[0065] In some of any [embodimentexamples](#), the sdAb variable domain is attached to the G protein via an encoded peptide linker. In some [embodimentexamples](#), the binding domain is attached to the G protein via an encoded peptide linker. In some of any [embodimentexamples](#), the encoded peptide linker comprises up to 25 amino acids in length. In some of any [embodimentexamples](#), the encoded peptide linker comprises up to 65 amino acids in length. In some of any [embodimentexamples](#), the encoded peptide linker comprises from or from about 2 to 65 amino acids, 2 to 60 amino acids, 2 to 56 amino acids, 2 to 52 amino acids, 2 to 48 amino acids, 2 to 44 amino acids, 2 to 40 amino acids, 2 to 36 amino acids, 2 to 32 amino acids, 2 to 28 amino acids, 2 to 24 amino acids, 2 to 20 amino acids, 2 to 18 amino acids, 2 to 14 amino acids, 2 to 12 amino acids, 2 to 10 amino acids, 2 to 8 amino acids, 2 to 6 amino acids, 6 to 65 amino acids, 6 to 60 amino acids, 6 to 56 amino acids, 6 to 52 amino acids, 6 to 48 amino acids, 6 to 44 amino acids, 6 to 40 amino acids, 6 to 36 amino acids, 6 to 32 amino acids, 6 to 28 amino acids, 6 to 24 amino acids, 6 to 20 amino acids, 6 to 18 amino acids, 6 to 14 amino acids, 6 to 12 amino acids, 6 to 10 amino acids, 6 to 8 amino acids, 8 to 65 amino acids, 8 to 60 amino acids, 8 to 56 amino acids, 8 to 52 amino acids, 8 to 48 amino acids, 8 to 44 amino acids, 8 to 40 amino acids, 8 to 36 amino acids, 8 to 32 amino acids, 8 to 28 amino acids, 8 to 24 amino acids, 8 to 20 amino acids, 8 to 18 amino acids, 8 to 14 amino acids, 8 to 12 amino acids, 8 to 10 amino acids, 10 to 65 amino acids, 10 to 60 amino acids, 10 to 56 amino acids, 10 to 52 amino acids, 10 to 48 amino acids, 10 to 44 amino acids, 10 to 40 amino acids, 10 to 36 amino acids, 10 to 32 amino acids, 10 to 28 amino acids, 10 to 24 amino acids, 10 to 20 amino acids, 10 to 18 amino acids, 10 to 14 amino acids, 10 to 12 amino acids, 12 to 65 amino acids, 12 to 60 amino acids, 12 to 56 amino acids, 12 to 52 amino acids, 12 to 48 amino acids, 12 to 44 amino acids, 12 to 40 amino acids, 12 to 36 amino acids, 12 to 32 amino acids, 12 to 28 amino acids, 12 to 24 amino acids, 12 to 20 amino acids, 12 to 18 amino acids, 12 to 14 amino acids, 14 to 65 amino acids, 14 to 60 amino acids, 14 to 56 amino acids, 14 to 52 amino acids, 14 to 48 amino acids, 14 to 44 amino acids,

14 to 40 amino acids, 14 to 36 amino acids, 14 to 32 amino acids, 14 to 28 amino acids, 14 to 24 amino acids, 14 to 20 amino acids, 14 to 18 amino acids, 18 to 65 amino acids, 18 to 60 amino acids, 18 to 56 amino acids, 18 to 52 amino acids, 18 to 48 amino acids, 18 to 44 amino acids, 18 to 40 amino acids, 18 to 36 amino acids, 18 to 32 amino acids, 18 to 28 amino acids, 18 to 24 amino acids, 18 to 20 amino acids, 20 to 65 amino acids, 20 to 60 amino acids, 20 to 56 amino acids, 20 to 52 amino acids, 20 to 48 amino acids, 20 to 44 amino acids, 20 to 40 amino acids, 20 to 36 amino acids, 20 to 32 amino acids, 20 to 28 amino acids, 20 to 26 amino acids, 20 to 24 amino acids, 24 to 65 amino acids, 24 to 60 amino acids, 24 to 56 amino acids, 24 to 52 amino acids, 24 to 48 amino acids, 24 to 44 amino acids, 24 to 40 amino acids, 24 to 36 amino acids, 24 to 32 amino acids, 24 to 30 amino acids, 24 to 28 amino acids, 28 to 65 amino acids, 28 to 60 amino acids, 28 to 56 amino acids, 28 to 52 amino acids, 28 to 48 amino acids, 28 to 44 amino acids, 28 to 40 amino acids, 28 to 36 amino acids, 28 to 34 amino acids, 28 to 32 amino acids, 32 to 65 amino acids, 32 to 60 amino acids, 32 to 56 amino acids, 32 to 52 amino acids, 32 to 48 amino acids, 32 to 44 amino acids, 32 to 40 amino acids, 32 to 38 amino acids, 32 to 36 amino acids, 36 to 65 amino acids, 36 to 60 amino acids, 36 to 56 amino acids, 36 to 52 amino acids, 36 to 48 amino acids, 36 to 44 amino acids, 36 to 40 amino acids, 40 to 65 amino acids, 40 to 60 amino acids, 40 to 56 amino acids, 40 to 52 amino acids, 40 to 48 amino acids, 40 to 44 amino acids, 44 to 65 amino acids, 44 to 60 amino acids, 44 to 56 amino acids, 44 to 52 amino acids, 44 to 48 amino acids, 48 to 65 amino acids, 48 to 60 amino acids, 48 to 56 amino acids, 48 to 52 amino acids, 50 to 65 amino acids, 50 to 60 amino acids, 50 to 56 amino acids, 50 to 52 amino acids, 54 to 65 amino acids, 54 to 60 amino acids, 54 to 56 amino acids, 58 to 65 amino acids, 58 to 60 amino acids, or 60 to 65 amino acids.

[0066] In some of any [embodimentexamples](#), the encoded peptide linker comprises a polypeptide that is 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64 or 65 amino acids in length. In some of any [embodimentexamples](#), the encoded peptide linker comprises GS, GGS, GGGGS (SEQ ID NO:43), GGGGGS (SEQ ID NO:41) and combinations thereof. In some of any [embodimentexamples](#), the encoded peptide linker comprises (GGS)_n, wherein n is 1 to 10. In some of any [embodimentexamples](#), the encoded peptide linker comprises (GGGGS)_n (SEQ ID NO:42), wherein n is 1 to 10. In some of any [embodimentexample](#), the encoded peptide linker comprises (GGGGGS)_n (SEQ ID NO:27), wherein n is 1 to 4. . In some of any [embodimentexamples](#), the sequence encoding the G protein is a wild-type

Nipah virus G (NiV-G) protein or a Hendra virus G protein or is a functionally active variant or a biologically active portion thereof. In some [embodimentexamples](#), the variant is a variant thereof that exhibits reduced binding for the native binding partner. In some of any [embodimentexamples](#), the nucleic acid sequence encoding the G protein is a wild-type Nipah virus G (NiV-G) protein or a Hendra virus G protein or is a variant thereof that exhibits reduced binding for the native binding partner. In some [embodimentexamples](#), the encoded G protein is a wild-type NiV-G protein or a functionally active variant or a biologically active portion thereof. In some of any [embodimentexamples](#), the nucleic acid sequence encoding the G protein is a wild-type NiV-G protein. In some of any [embodimentexamples](#), the nucleic acid sequence encoding the G-protein is a mutant NiV-G protein that exhibits reduced binding to Ephrin B2 or Ephrin B3.

[0067] In some of any [embodimentexample](#), the NiV-G protein or functionally active variant or biologically active portion thereof comprises the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO: 28 or SEQ ID NO: 44 or comprises an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44. In some of any [embodimentexamples](#), the NiV-G protein is a biologically active portion that is truncated and lacks up to 40 contiguous amino acid residues at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9,SEQ ID NO:28 or SEQ ID NO:44). In some of any [embodimentexamples](#), the NiV-G protein is a biologically active portion that is truncated at the N-terminus of wild-type NiV-G and comprises the sequence set forth in any of SEQ ID NOS: 10-15, 35-40 or 45-50 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NOS: 10-15, 35-40 or 45-50.

[0068] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that comprises a 5 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 10 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:10. In some of any embodimentexamples, NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 35 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:35. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 45 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:45.

[0069] In some of any embodimentexamples, NiV-G protein is a biologically active portion that comprises a 10 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the mutant NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 11 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or

about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:11. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 36 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:36. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 46 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:46.

[0070] In some of any embodimentexamples, the is a biologically active portion that NiV-G protein comprises a 15 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 12 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:12. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 37

or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:37. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 47 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:47.

[0071] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that comprises a 20 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 13 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:13. In some of any embodimentexamples, NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 38 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:38. In some of any

embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 48 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:48.

[0072] In some of any **embodimentexamples**, the NiV-G protein is a biologically active portion that comprises a 25 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any **embodimentexamples**, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 14 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:14. In some of any **embodimentexamples**, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 39 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:39. In some of any **embodimentexamples**, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 49 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or

about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:49.

[0073] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that comprises a 30 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44). In some of any

embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 15 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:15. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 40 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:40. In some of any embodimentexamples, the NiV-G protein or the biologically active portion comprises the amino acid sequence set forth in SEQ ID NO: 50 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 50.

[0074] In some of any embodimentexamples, the NiV-G protein is a biologically active portion that has a 34 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO:9,SEQ ID NO:28 or SEQ ID NO:44).In some of any embodimentexample, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in

SEQ ID NO: 22 or an amino acid sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:22. In some of any embodimentexamples, the NiV-G protein or the biologically active portion has the amino acid sequence set forth in SEQ ID NO: 53 or an amino acid sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:53.

[0075] In some of any embodimentexamples, the G-protein is a mutant NiV-G protein that exhibits reduced binding to Ephrin B2 or Ephrin B3. In some of any embodimentexample, the mutant NiV-G protein comprises: one or more amino acid substitutions corresponding to amino acid substitutions selected from the group consisting of E501A, W504A, Q530A and E533A with reference to numbering set forth in SEQ ID NO:28. In some of any embodimentexamples, the mutant NiV-G protein comprises amino acid substitutions E501A, W504A, Q530A and E533A with reference to numbering set forth in SEQ ID NO:28.

[0076] In some of any embodimentexamples, the mutant NiV-G protein comprises: i) a truncation at or near the N-terminus; and ii) point mutations selected from the group consisting of E501A, W504A, Q530A and E533A. In some of any embodimentexamples, the mutant NiV-G protein comprises the amino acid sequence set forth in SEQ ID NO: 16 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:16. In some of any embodimentexamples, the mutant NiV-G protein comprises the amino acid sequence set forth in

SEQ ID NO: 51 or an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:51.

[0077] In some of any embodimentexamples, the F protein or the biologically active portion thereof is a wild-type Nipah virus F (NiV-F) protein or a Hendra virus F protein or is a functionally active variant or biologically active portion thereof. In some of any embodimentexamples, the F protein or the biologically active portion thereof is a wild-type NiV-F protein or a functionally active variant or a biologically active portion thereof. In some of any embodimentexamples, the NiV-F-protein or the functionally active variant or biologically active portion thereof comprises the amino acid sequence set forth in SEQ ID NO: 2, or an amino acid sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 2.

[0078] In some of any embodimentexamples, the NiV-F protein is a biologically active portion thereof that has a 20 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO:2). In some of any embodimentexamples, the NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:5 or an amino acid sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 5. In some of any embodimentexamples, the NiV-F protein is a biologically active portion thereof that comprises i) a 20 amino acid truncation at or near the

C-terminus of the wild-type NiV-F protein (SEQ ID NO:2); and ii) a point mutation on an N-linked glycosylation site.

[0079] In some of any [embodimentexamples](#), the NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:7 or an amino acid sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 7.

[0080] In some of any [embodimentexamples](#), the NiV-F protein is a biologically active portion thereof that has a 22 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO:2). In some of any [embodimentexamples](#), the NiV-F protein or the biologically active portion has the sequence set forth in SEQ ID NO:8 or an amino acid sequence that is encoded by a sequence of nucleotides encoding a sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 8.

[0081] In some of any [embodimentexamples](#), the NiV-F protein has the sequence set forth in SEQ ID NO:23 or an amino acid sequence having at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO: 23. In some of any [embodimentexamples](#), the F protein comprises the sequence set forth in SEQ ID NO:23 and the G protein comprises the sequence set forth in SEQ ID NO:16. In some of any [embodimentexamples](#), the F protein consists or consists essentially of the sequence set forth in SEQ

ID NO:23 and the G protein consists or consists essentially of the sequence set forth in SEQ ID NO:16.

[0082] Provided herein is a vector, comprising the polynucleotide of any of the embodimentexamples described herein. In some of any embodimentexamples, the vector is a mammalian vector, viral vector or artificial chromosome, optionally wherein the artificial chromosome is a bacterial artificial chromosome (BAC).

[0082a] In one aspect, the present disclosure refers to a vector, comprising the polynucleotide disclosed herein.

[0083] Provided herein is a plasmid, comprising the polynucleotide of any of the embodimentexamples described herein. In some of any embodimentexamples, the plasmid further comprises one or more nucleic acids encoding proteins for lentivirus production.

[0083a] In one aspect, the present disclosure refers to a plasmid, comprising the polynucleotide disclosed herein.

[0084] Provided herein is a cell comprising the polynucleotide of any of embodimentexamples described herein or the vector of any of the embodimentexamples described herein, or the plasmid of any of the embodimentexamples described herein.

[0084a] In one aspect, the present disclosure refers to a cell comprising the polynucleotide disclosed herein, or the vector disclosed herein, or the plasmid disclosed herein.

[0085] Provided herein is a method of making a targeted lipid particle comprising a henipavirus F protein molecule or biologically active portion thereof and a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody (sdAb) variable domain, the method comprising a) providing a cell that comprises a nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and a nucleic acid encoding a targeted envelope protein, the targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody (sdAb) variable domain; b) culturing the cell under conditions that allow for production of a targeted lipid particle, and c) separating, enriching, or purifying the targeted lipid particle from the cell, thereby making the targeted lipid particle.

[0085a] In one aspect, the present disclosure refers to a method of making a targeted lipid particle comprising a henipavirus F protein molecule or biologically active portion thereof and a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody (sdAb) variable domain, the method comprising: a) providing a cell that comprises a nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and a nucleic acid encoding a targeted envelope protein, the targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody (sdAb) variable domain; b) culturing the cell under conditions that allow for production of a targeted lipid particle, and c) separating, enriching, or purifying the targeted lipid particle from the cell, thereby making the targeted lipid particle.

[0086] Provided herein is a method of making a pseudotyped lentiviral vector, the method comprising a) providing a producer cell that comprises a lentiviral viral nucleic acid(s), a nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof, and a nucleic acid encoding a targeted envelope protein, said targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody; b) culturing the cell under conditions that allow for production of the lentiviral vector, and c) separating, enriching, or purifying the lentiviral vector from the cell, thereby making the pseudotyped lentiviral vector.

[0086a] In one aspect, the present disclosure refers to a method of making a pseudotyped lentiviral vector, the method comprising: a) providing a producer cell that comprises a lentiviral viral nucleic acid(s), a nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof, and a nucleic acid encoding a targeted envelope protein, said targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody; b) culturing the cell under conditions that allow for production of the lentiviral vector, and c) separating, enriching, or purifying the lentiviral vector from the cell, thereby making the pseudotyped lentiviral vector.

[0087] In some of any embodimentexamples, the single domain antibody binds a cell surface molecule present on a target cell. In some of any embodimentexamples, the cell surface molecule is a protein, glycan, lipid or low molecular weight molecule. In some of any embodimentexamples, the target cell is selected from the group consisting of tumor-infiltrating lymphocytes, T cells, neoplastic or tumor cells, virus-infected cells, stem cells, central nervous system (CNS) cells, hematopoietic stem cells (HSCs), liver cells or fully differentiated cells. In some of any embodimentexamples, the target cell is selected from the group consisting of a CD3+ T cell, a CD4+ T cell, a CD8+ T cell, a hepatocyte, a haematopoietic stem cell, a CD34+ haematopoietic stem cell, a CD105+ haematopoietic stem cell, a CD117+ haematopoietic stem cell, a CD105+ endothelial cell, a B cell, a CD20+ B cell, a CD19+ B cell, a cancer cell, a CD133+ cancer cell, an EpCAM+ cancer cell, a CD19+ cancer cell, a Her2/Neu+ cancer cell, a GluA2+ neuron, a GluA4+ neuron, a NKG2D+ natural killer cell, a SLC1A3+ astrocyte, a SLC7A10+ adipocyte, or a CD30+ lung epithelial cell. In some of any embodimentexamples, the single domain antibody binds an antigen or portion thereof present on a target cell.

[0088] Provided herein is a method of making a targeted lipid particle comprising a henipavirus F protein molecule or biologically active portion thereof and a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a binding domain, the method comprising a) providing a cell that comprises a nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and a nucleic acid encoding a targeted envelope protein, the targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and binding domain, wherein the binding domain (i) binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5, optionally human ASGR1, human ASGR2 and human ASGR2; (ii) binds a cell surface

molecule selected from the group consisting of CD4 or CD8, optionally human CD4 or human CD8; or (iii) binds a cell surface molecule that is low density lipoprotein receptor (LDL-R), optionally human LDL-R; b) culturing the cell under conditions that allow for production of a targeted lipid particle, and c) separating, enriching, or purifying the targeted lipid particle from the cell, thereby making the targeted lipid particle.

[0088a] In one aspect, the present disclosure refers to a method of making a targeted lipid particle comprising a henipavirus F protein molecule or biologically active portion thereof and a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a binding domain, the method comprising: a) providing a cell that comprises a nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and a nucleic acid encoding a targeted envelope protein, the targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and binding domain, wherein the binding domain: (i) binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5; (ii) binds a cell surface molecule selected from the group consisting of CD4 or CD8; or (iii) binds a cell surface molecule that is low density lipoprotein receptor (LDL-R); b) culturing the cell under conditions that allow for production of a targeted lipid particle, and c) separating, enriching, or purifying the targeted lipid particle from the cell, thereby making the targeted lipid particle, wherein the targeted lipid particle is a pseudotyped lentiviral vector.

[0088b] In one aspect, the present disclosure refers to a method of making a targeted lipid particle comprising a henipavirus F protein molecule or biologically active portion thereof and a targeted envelope protein, comprising: a) providing a cell that comprises the polynucleotide disclosed herein, or the vector disclosed herein, or the plasmid disclosed herein; b) culturing the cell under conditions that allow for production of a targeted lipid particle, and c) separating, enriching, or purifying the targeted lipid particle from the cell, thereby making the targeted lipid particle.

[0089] Provided herein is a method of making a pseudotyped lentiviral vector, the method comprising a) providing a producer cell that comprises a lentiviral viral nucleic acid(s), a

nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof, and a nucleic acid encoding a targeted envelope protein, said targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and binding domain, wherein the binding domain: (i) binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5, optionally human ASGR1, human ASGR2 and human ASGR2; (ii) binds a cell surface molecule selected from the group consisting of CD4 or CD8, optionally human CD4 or human CD8; or (iii) binds a cell surface molecule that is low density lipoprotein receptor (LDL-R), optionally human LDL-R; b) culturing the producer cell under conditions that allow for production of a lentiviral vector, and c) separating, enriching, or purifying the lentiviral vector from the cell, thereby making the pseudotyped lentiviral vector.

[0089a] In one aspect, the present disclosure refers to a method of making a pseudotyped lentiviral vector, comprising: a) providing a producer cell that comprises a lentiviral viral nucleic acid(s), and the polynucleotide disclosed herein, or the vector disclosed herein, or the plasmid disclosed herein; b) culturing the cell under conditions that allow for production of the lentiviral vector, and c) separating, enriching, or purifying the lentiviral vector from the cell, thereby making the pseudotyped lentiviral vector.

[0090] In some of any [embodimentexamples](#), the binding domain is a single domain antibody. In some of any [embodimentexamples](#), the binding domain is a single chain variable fragment (scFv). In some of any [embodimentexamples](#), the cell surface molecule is selected from the group consisting of ASGR1, ASGR2 and TM4SF5. In some of any [embodimentexamples](#), the cell surface molecule is CD8 or CD4, In some of any [embodimentexamples](#), the cell surface molecule is LDL-R.

[0091] Provided herein is a method of making a targeted lipid particle comprising a henipavirus F protein molecule or biologically active portion thereof and a targeted envelope protein comprising a) providing a cell that comprises the polynucleotide of any of the [embodimentexamples](#) provided herein the vector of any of the [embodimentexamples](#) described herein, or the plasmid of any of the [embodimentexamples](#) described herein; b) culturing the cell under conditions that allow for production of a targeted lipid particle, and c) separating, enriching, or purifying the targeted lipid particle from the cell, thereby making the targeted lipid particle.

[0092] Provided herein is a method of making a pseudotyped lentiviral vector, comprising: a) providing a producer cell that comprises a lentiviral viral nucleic acid(s), and the polynucleotide of any of the [embodimentexamples](#) listed herein or the vector of any of the [embodimentexamples](#) listed herein b) culturing the cell under conditions that allow for production of the lentiviral vector, and c) separating, enriching, or purifying the lentiviral vector from the cell, thereby making the pseudotyped lentiviral vector. In some of any [embodimentexamples](#), prior to step (b) the method further comprises providing the cell a polynucleotide encoding a henipavirus F protein molecule or biologically active portion thereof.

[0093] In some of any [embodimentexamples](#), the cell is a mammalian cell.

[0094] In some of any [embodimentexamples](#), the cell is a producer cell comprising viral nucleic acid. In some of any [embodimentexamples](#), the viral nucleic acid is a retroviral nucleic acid or lentiviral nucleic acid and the targeted lipid particle is a viral particle or a viral-like particle. In some of any [embodimentexamples](#), the viral particle or a viral-like particle is a retroviral particle or a retroviral-like particle. In some [embodimentexamples](#), the viral particle or a viral-like particle is a lentiviral particle or lentiviral-like particle.

[0095] In some of any [embodimentexamples](#), the viral nucleic acid(s) lacks one or more genes involved in viral replication. In some of any [embodimentexamples](#), the viral nucleic acid comprises a nucleic acid encoding a viral packaging protein selected from one or more of Gag, Pol, Rev and Tat. In some of any [embodimentexamples](#), the viral nucleic acid comprises: one or more of (e.g., all of) the following nucleic acid sequences: 5' LTR (e.g., comprising U5 and lacking a functional U3 domain), Psi packaging element (Psi), Central polypurine tract (cPPT)/central termination sequence (CTS) (e.g. DNA flap), Poly A tail sequence, a posttranscriptional regulatory element (e.g. WPRE), a Rev response element (RRE), and 3' LTR (e.g., comprising U5 and lacking a functional U3).

[0096] Provided herein is a producer cell comprising the polynucleotide of any of the [embodimentexamples](#) listed herein or the vector of any of the [embodimentexamples](#) listed herein, or the plasmid of any of the [embodimentexamples](#) described herein.

[\[0096a\] In one aspect, the present disclosure refers to a producer cell comprising the polynucleotide disclosed herein, or the vector disclosed herein, or the plasmid disclosed herein.](#)

[0097] In some of any [embodimentexamples](#), the producer cell further comprises a nucleic acid encoding a henipavirus F protein or a biologically active portion thereof.

[0098] In some of any [embodimentexample](#), the cell further comprises a viral nucleic acid. In some of any [embodimentexamples](#), the viral nucleic acid is a lentiviral nucleic acid. Provided herein is a producer cell comprising (i) a viral nucleic acid(s) and (ii) nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and (iii) a nucleic acid encoding a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a single domain antibody (sdAb) variable domain, optionally wherein the viral nucleic acid(s) are lentiviral nucleic acids. In some of any [embodimentexamples](#) the single domain antibody binds a cell surface molecule present on a target cell. In some of any [embodimentexamples](#) the cell surface molecule is a protein, glycan, lipid or low molecular weight molecule.

[\[0098a\] In one aspect, the present disclosure refers to a producer cell comprising \(i\) a viral nucleic acid\(s\) and \(ii\) nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and \(iii\) a nucleic acid encoding a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G \(G protein\) or a biologically active portion thereof and a single domain antibody \(sdAb\) variable domain.](#)

[0099] In some of any [embodimentexamples](#) the target cell is selected from the group consisting of tumor-infiltrating lymphocytes, T cells, neoplastic or tumor cells, virus-infected cells, stem

cells, central nervous system (CNS) cells, hematopoietic stem cells (HSCs), liver cells or fully differentiated cells. In some of any [embodimentexamples](#) the target cell is selected from the group consisting of a CD3+ T cell, a CD4+ T cell, a CD8+ T cell, a hepatocyte, a haematopoietic stem cell, a CD34+ haematopoietic stem cell, a CD105+ haematopoietic stem cell, a CD117+ haematopoietic stem cell, a CD105+ endothelial cell, a B cell, a CD20+ B cell, a CD19+ B cell, a cancer cell, a CD133+ cancer cell, an EpCAM+ cancer cell, a CD19+ cancer cell, a Her2/Neu+ cancer cell, a GluA2+ neuron, a GluA4+ neuron, a NKG2D+ natural killer cell, a SLC1A3+ astrocyte, a SLC7A10+ adipocyte, or a CD30+ lung epithelial cell. In some of any [embodimentexamples](#) the single domain antibody binds an antigen or portion thereof present on a target cell.

[0100] Provided herein is a producer cell comprising (i) a viral nucleic acid(s) and (ii) nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and (iii) a nucleic acid encoding a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and binding domain, wherein the binding domain (i) binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5, optionally human ASGR1, human ASGR2 and human ASGR2; (ii) binds a cell surface molecule selected from the group consisting of CD4 or CD8, optionally human CD4 or human CD8; or (iii) binds a cell surface molecule that is low density lipoprotein receptor (LDL-R), optionally human LDL-R. In some of any [embodimentexamples](#) the viral nucleic acid(s) are lentiviral nucleic acid.

[0100a] In one aspect, the present disclosure refers to a producer cell comprising (i) a viral nucleic acid(s) and (ii) nucleic acid encoding a henipavirus F protein molecule or biologically active portion thereof and (iii) a nucleic acid encoding a targeted envelope protein comprising a henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof and a binding domain, wherein the binding domain: (i) binds a cell surface molecule selected from the group consisting of ASGR1, ASGR2, and TM4SF5; (ii) binds a cell surface molecule selected from the group consisting of CD4 or CD8; or (iii) binds a cell surface molecule that is low density lipoprotein receptor (LDL-R).

[0101] In some of any [embodimentexamples](#) the cell surface molecule or antigen is selected from the group consisting of ASGR1, ASGR2 and TM4SF5. In some of any [embodimentexamples](#), the cell surface molecule or antigen is CD8 or CD4. In some of any [embodimentexamples](#), the cell surface molecule or antigen is LDL-R.

[0102] In some of any [embodimentexamples](#), the viral nucleic acid(s) lacks one or more genes involved in viral replication. In some of any [embodimentexamples](#), the viral nucleic acid comprises a nucleic acid encoding a viral packaging protein selected from one or more of Gag, Pol, Rev and Tat.

[0103] In some of any [embodimentexamples](#), the viral nucleic acid comprises one or more of (e.g., all of) the following nucleic acid sequences: 5' LTR (e.g., comprising U5 and lacking a functional U3 domain), Psi packaging element (Psi), Central polypurine tract (cPPT)/central termination sequence (CTS) (e.g. DNA flap), Poly A tail sequence, a posttranscriptional

regulatory element (e.g. WPRE), a Rev response element (RRE), and 3' LTR (e.g., comprising U5 and lacking a functional U3).

[0104] In some of any [embodimentexamples](#), the henipavirus F protein molecule or biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 2; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:2. In some of any [embodimentexamples](#), the henipavirus F protein molecule or biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 5; (ii) an amino acid sequence having at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:5.

[0105] In some of any [embodimentexamples](#), the henipavirus F protein molecule or biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 7; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:7. In some of any [embodimentexamples](#), the henipavirus F protein molecule or biologically active portion thereof comprises (i) a sequence encoding by a nucleotide sequence encoding the sequence set forth in SEQ ID NO: 8; (ii) a amino acid sequence encoded by a nucleotide sequence encoding a sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:8.

[0106] In some of any embodimentexamples, the henipavirus F protein molecule or biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 23; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:23.

[0107] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:9, SEQ ID NO:28 or SEQ ID NO:44.

[0108] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 10; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:10.

[0109] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 35; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or

about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:35.

[0110] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 45; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:45.

[0111] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 11; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:11.

[0112] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 36; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:36.

[0113] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ

ID NO: 46; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:46.

[0114] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 12; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:12.

[0115] In some of any embodimentexample, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 37; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:37.

[0116] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 47; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at

or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:47.

[0117] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 13; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:13.

[0118] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 38; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:38.

[0119] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 48; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:48.

[0120] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 14; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%,

at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:14.

[0121] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 39; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:39.

[0122] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 49; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:49.

[0123] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 15; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at

or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:15.

[0124] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 40; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:40.

[0125] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises: (i) the sequence set forth in SEQ ID NO: 50; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:50.

[0126] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 16; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%, at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:16.

[0127] In some of any embodimentexamples, the henipavirus envelope attachment glycoprotein G (G protein) or a biologically active portion thereof comprises (i) the sequence set forth in SEQ ID NO: 51; (ii) an amino acid sequence having at least at or about 80%, at least at or about 81%,

at least at or about 82%, at least at or about 83%, at or about 84%, at least at or about 85%, at least at or about 86%, or at least at or about 87%, at least at or about 88%, or at least at or about 89%, at least at or about 90%, at least at or about 91%, at least at or about 92%, at least at or about 93%, at least at or about 94%, at least at or about 95%, at least at or about 96%, at least at or about 97%, at least at or about 98%, or at least at or about 99% sequence identity to SEQ ID NO:51.

[0128] In some ~~aspects~~ of the provided ~~embodiment~~examples, the targeted lipid particle has greater expression of the targeted envelope protein compared to a reference lipid particle that has incorporated into a similar lipid bilayer the same envelope protein but that is fused to an alternative targeting moiety, optionally wherein the alternative targeting moiety is a single chain variable fragment (scFv). In some of any ~~embodiment~~examples, the expression is increased by at or greater than 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 200%, 300%, 400%, 500% or more. In some ~~embodiment~~examples, the expression is increased by at or greater than 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold or more, preferably at or about or greater than 10-fold or more. In some of any ~~embodiment~~examples, the titer in target cells following transduction is at or greater than 1×10^6 transduction units (TU)/mL, at or greater than 2×10^6 TU/mL, at or greater than 3×10^6 TU/mL, at or greater than 4×10^6 TU/mL, at or greater than 5×10^6 TU/mL, at or greater than 6×10^6 TU/mL, at or greater than 7×10^6 TU/mL, at or greater than 8×10^6 TU/mL, at or greater than 9×10^6 TU/mL, or at or greater than 1×10^7 TU/mL. Also provided herein is a composition wherein among the population of lipid particles, greater than at or about 50%, greater than at or about 55%, greater than at or about 60%, greater than at or about 65%, greater than at or about 70%, or greater than at or about 75% are surface positive for the targeted envelope protein. In some of any ~~embodiment~~examples, the targeted envelope protein is present on the surface of the targeted lipid particle at a density of at least about (0.001, 0.002, 0.005, 0.01, 0.02, 0.05, 0.1, 0.2 or 0.5) targeted envelope proteins/nm².

[0129] Provided herein is a viral vector particle or viral-like particle produced from the producer cell of any of the ~~embodiment~~examples provided herein.

[0129a] In one aspect, the present disclosure refers to a targeted lipid particle or pseudotyped lentiviral vector produced by the method disclosed herein or from the producer cell disclosed herein.

[0130] Provided herein is a composition comprising a plurality of targeted lipid particles of any of the ~~embodiment~~examples provided herein. In some ~~embodiment~~examples, the composition further includes a pharmaceutically acceptable carrier. In some of any ~~embodiment~~examples, the targeted lipid particles comprise an average diameter of less than 1 μ m. In some of any ~~embodiment~~examples, the

composition further includes a targeted envelope protein present on the surface of the targeted lipid particles at an average density of at least about (0.001, 0.002, 0.005, 0.01, 0.02, 0.05, 0.1, 0.2 or 0.5) targeted envelope proteins/nm².

[0130a] In one aspect, the present disclosure refers to a composition comprising a plurality of targeted lipid particles disclosed herein or a plurality of lentiviral vectors disclosed herein.

[0131] Provided herein is a producer cell containing greater membrane (e.g., plasma membrane) expression of the targeted envelope protein compared to a reference producer cell that has incorporated into its membrane (e.g. plasma membrane) the same envelope protein but that is fused to an alternative targeting moiety, optionally wherein the alternative targeting moiety is a single chain variable fragment (scFv). In some [embodimentexamples](#), the expression is increased by at or greater than 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 200%, 300%, 400%, 500% or more. In some [embodimentexamples](#), the expression is increased by at or greater than 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold or more, preferably at or about or greater than 10-fold or more. In some [embodimentexamples](#), the producer cell has the expression of the targeted envelope protein on a membrane (e.g., plasma membrane) of the producer cell is at least 20 proteins (e.g., at least 50, 100, 200, 500, 1000, 2000, 5000, or 10,000 proteins) per square micron. In some of any [embodimentexamples](#), the targeted envelope protein comprises at least 0.1% (e.g., at least 0.2%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, or 10%) of the total membrane (e.g., plasma membrane) proteins of the producer cell (e.g., by total protein weight).

[0132] Provided herein is a method of transducing a cell comprising transducing a cell with any of the viral vectors described herein or with any of the compositions described herein. In some of any [embodimentexamples](#), the targeted envelope protein of the lentiviral vector or targeted lipid particle targets CD4 and the cell is a CD4⁺ cell. In some of any [embodimentexamples](#), the targeted envelope protein of the lentiviral vector targets CD8 and the cell is a CD8⁺ cell. In some of any [embodimentexamples](#), the targeted envelope protein of the lentiviral vector targets ASGR1, ASGR2 or TM4SF5 and the cell is a hepatocyte.

[0132a] In one aspect, the present disclosure refers to a method of transducing a cell comprising transducing a cell with a lentiviral vector disclosed herein or a composition comprising a lentiviral vector or plurality of lentiviral vectors disclosed herein.

[0133] Provided herein is a method of delivering an exogenous agent to a subject (e.g., a human subject), the method comprising administering to the subject the targeted lipid particle of any of the [embodimentexamples](#) provided herein or the composition of any of the [embodimentexamples](#) provided herein, wherein the targeted lipid particle or lentiviral vector comprise the exogenous agent.

[0133a] In one aspect, the present disclosure refers to use of the targeted lipid particle or lentiviral vector disclosed herein, in the manufacture of a medicament for delivering an exogenous agent to a subject, wherein the targeted lipid particle or lentiviral vector comprises the exogenous agent.

[0134] Provided herein is a method of delivering an exogenous agent to a subject (e.g., a human subject), the method comprising administering to the subject any of the compositions

described herein, wherein targeted lipid particle or lentiviral vectors of the plurality comprise the exogenous agent.

[0134a] In one aspect, the present disclosure refers to use of the composition disclosed herein, in the manufacture of a medicament for delivering an exogenous agent to a subject, wherein the targeted lipid particles or lentiviral vectors of the plurality comprise the exogenous agent.

[0135] Provided herein is a method of delivering a chimeric antigen receptor (CAR) to a cell, comprising contacting a cell with any of the lentiviral vectors described herein or a targeted lipid particle of any of the embodiment examples described herein, wherein the lentiviral vector or targeted lipid particle comprise nucleic acid encoding the CAR.

[0135a] In one aspect, the present disclosure refers to a method of delivering a chimeric antigen receptor (CAR) to a cell, comprising contacting a cell with the lentiviral vector disclosed herein or a targeted lipid particle disclosed herein, wherein the lentiviral vector or targeted lipid particle comprises a nucleic acid encoding the CAR.

[0136] Provided herein is a method of delivering a chimeric antigen receptor (CAR) to a cell, comprising contacting a cell with any of the compositions described herein, wherein lentiviral vectors or targeted lipid particles of the plurality comprise nucleic acid encoding the CAR.

[0136a] In one aspect, the present disclosure refers to a method of delivering a chimeric antigen receptor (CAR) to a cell, comprising contacting a cell with the composition disclosed herein, wherein the lentiviral vectors or the targeted lipid particles of the plurality comprise a nucleic acid encoding the CAR.

[0137] Provided herein is a method of delivering an exogenous agent to a hepatocyte, comprising contacting a cell with any of the lentiviral vectors described herein, or a targeted lipid particle or lentiviral vector of any of the embodiment examples described herein.

[0137a] In one aspect, the present disclosure refers to a method of delivering an exogenous agent to a hepatocyte, comprising contacting a cell with the lentiviral vector disclosed herein or a targeted lipid particle or lentiviral vector disclosed herein, wherein the exogenous agent is a nucleic acid comprising a payload gene for correcting a genetic deficiency.

[0137b] In one aspect, the present disclosure refers to a targeted lipid particle disclosed herein, or a lentiviral vector disclosed herein, for use in delivering an exogenous agent to a subject, wherein the targeted lipid particle or lentiviral vector comprises the exogenous agent.

[0138] Provided herein is a method of delivering an exogenous agent to a hepatocyte, comprising contacting a cell with any of the compositions described herein, wherein lentiviral vectors or targeted lipid particles of the plurality comprise an exogenous agent for delivery to the hepatocyte. In some of any embodimentexamples, the contacting transduces the cell with lentiviral vector or the targeted lipid particle.

[0138a] In one aspect, the present disclosure refers to a method of delivering an exogenous agent to a hepatocyte, comprising contacting a cell with the composition disclosed herein, wherein the lentiviral vectors or the targeted lipid particles of the plurality comprise an exogenous agent for delivery to the hepatocyte.

[0139] Provided herein is a method of treating a disease or disorder in a subject (e.g., a human subject), the method comprising administering to the subject the targeted lipid particle of any of the embodimentexamples provided herein or the composition of any of the embodimentexamples provided herein.

[0139a] In one aspect, the present disclosure refers to use of a targeted lipid particle disclosed herein, or the lentiviral vector disclosed herein, or the composition disclosed herein, in the manufacture of a medicament for treating a disease or disorder in a subject.

[0139b] In one aspect, the present disclosure refers to a targeted lipid particle disclosed herein, or a lentiviral vector disclosed herein, for use in treating a disease or disorder in a subject.

[0140] Provided herein is a method of fusing a mammalian cell to a targeted lipid particle, the method comprising administering to the subject the targeted lipid particle of any of the embodimentexamples provided herein or the composition of any of the embodimentexamples provided herein. In some of any embodimentexamples, the fusing of the mammalian cell to the targeted lipid particle delivers an exogenous agent to a subject (e.g., a human subject). In some of any embodimentexamples, the fusing of the mammalian cell to the targeted lipid particle treats a disease or disorder in a subject (e.g., a human subject). In some of any embodimentexample, the targeted envelope protein of the lentiviral vector or targeted lipid particle targets CD4 and the cell is a CD4+ cell. In some of any embodimentexamples, the targeted envelope protein of the lentiviral vector targets CD8

and the cell is a CD8⁺ cell. In some of any [embodimentexamples](#), the targeted envelope protein of the lentiviral vector targets ASGR1, ASGR2 or TM4SF5 and the cell is a hepatocyte.

[0140a] In one aspect, the present disclosure refers to use of a targeted lipid particle disclosed herein, the lentiviral vector disclosed herein, or the composition disclosed herein, in the manufacture of a medicament for fusing a mammalian cell to a targeted lipid particle in a subject.

[0140b] In one aspect, the present disclosure refers to a targeted lipid particle disclosed herein, or a lentiviral vector disclosed herein, for use in fusing a mammalian cell to a targeted lipid particle in a subject.

[0140c] In one aspect, the present disclosure refers to a composition disclosed herein, for use in delivering an exogenous agent to a subject, wherein the targeted lipid particles or lentiviral vectors of the plurality comprise the exogenous agent.

[0141] In some of any [embodimentexample](#), the targeted lipid particle has greater expression of the targeted envelope protein compared to a reference lipid particle that has incorporated into a similar lipid bilayer the same envelope protein but that is fused to an alternative targeting moiety. In some [embodimentexamples](#), the alternative targeting moiety is a single chain variable fragment (scFv). In some of any [embodimentexamples](#), the expression is increased by at or greater than 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 200%, 300%, 400%, 500% or more. In some of any [embodimentexamples](#), the expression is increased by at or greater than 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold or more, preferably at or about or greater than 10-fold or more.

[0142] In some of any [embodimentexample](#), the titer in target cells following transduction is at or greater than 1×10^6 transduction units (TU)/mL, at or greater than 2×10^6 TU/mL, at or greater than 3×10^6 TU/mL, at or greater than 4×10^6 TU/mL, at or greater than 5×10^6 TU/mL, at or greater than 6×10^6 TU/mL, at or greater than 7×10^6 TU/mL, at or greater than 8×10^6 TU/mL, at or greater than 9×10^6 TU/mL, or at or greater than 1×10^7 TU/mL.

[0143] In some of any [embodimentexample](#), among the population of lipid particles or lentiviral vectors in the composition, greater than at or about 50%, greater than at or about 55%, greater than at or about 60%, greater than at or about 65%, greater than at or about 70%, or greater than at or about 75% are surface positive for the targeted envelope protein. In some of any [embodimentexamples](#), the targeted envelope protein is present on the surface of the targeted lipid particle at a density of at least about (0.001, 0.002, 0.005, 0.01, 0.02, 0.05, 0.1, 0.2 or 0.5) targeted envelope proteins/nm².

[0144] Provided herein is a composition comprising a plurality of the targeted lipid particles of any of the [embodimentexamples](#) described herein or a plurality of lentiviral vectors of any of the [embodimentexamples](#) described herein, wherein the targeted envelope protein is present on the surface of the targeted lipid particles at an average density of at least about (0.001, 0.002, 0.005, 0.01, 0.02, 0.05, 0.1, 0.2 or 0.5) targeted envelope proteins/nm².

[0145] In some of any [embodimentexamples](#), the producer cell has greater membrane (e.g., plasma membrane) expression of the targeted envelope protein compared to a reference producer cell that has incorporated into its membrane (e.g. plasma membrane) the same envelope protein but that is fused to an alternative targeting moiety, optionally wherein the alternative targeting

moiety is a single chain variable fragment (scFv). In some of any **embodimentexamples**, the expression is increased by at or greater than 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 200%, 300%, 400%, 500% or more. In some of any **embodimentexamples**, the expression is increased by at or greater than 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold or more, preferably at or about or greater than 10-fold or more. In some of any **embodimentexamples**, the producer cell has the expression of the targeted envelope protein on a membrane (e.g., plasma membrane) of the producer cell is at least 20 proteins (e.g., at least 50, 100, 200, 500, 1000, 2000, 5000, or 10,000 proteins) per square micron. In some of any **embodimentexamples**, the targeted envelope protein comprises at least 0.1% (e.g., at least 0.2%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, or 10%) of the total membrane (e.g., plasma membrane) proteins of the producer cell (e.g., by total protein weight).

Detailed Description

[0146] Provided herein are targeted lipid particles containing a lipid bilayer enclosing a lumen or cavity and a targeted envelope protein containing (1) a henipavirus envelope attachment glycoprotein G (G protein) or biologically active portion thereof and (2) a binding domain, such as a single domain antibody (sdAb) variable domain, in which the targeted envelope protein is embedded in the lipid bilayer of the lipid particles. In particular embodiments, the binding domain, such as a single domain antibody, is an antibody with the ability to bind, such as specifically bind, to a desired target molecule. Exemplary binding domains are described in Section II.A.2. In some embodiments, the targeted lipid particles also contains a henipavirus fusion (F) protein molecule or a biologically active portion thereof embedded in the lipid bilayer. In particular embodiments, the lipid particles can be a virus-like particle, a virus, or a viral vector, such as a lentiviral vector.

[0147] In some embodiments, one or both of the G protein and the F protein is from a Hendra (HeV) or a Nipah (NiV) virus, or is a biologically active portion thereof or is a variant or mutant thereof. In particular embodiments, both the G protein and the F protein is from a Hendra (HeV) or a Nipah (NiV) virus. In some embodiments, the fusion and attachment glycoproteins mediate cellular entry of Nipah virus.

[0148] The F protein, such as NiV-F, is a class I fusion protein that has structural and functional features in common with fusion proteins of many families (e.g., HIV-1 gp41 or influenza virus hemagglutinin [HA]), such as an ectodomain with a hydrophobic fusion peptide