## CROSS REFERENCE TO RELATED APPLICATIONS

**[0001]** This application claims priority to U.S. Patent Application No. 13/436,472, filed March 30, 2012, now U.S. Patent No. 8,323,662, issued December 4, 2012; and U.S. Provisional Patent Application Nos. 61/666,103, filed June 29, 2012; 61/732,756, filed December 3, 2012; and 61/789,575, filed March 15, 2013, all of which are incorporated herein by reference in their entirety.

## INCORPORATION BY REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

**[0002]** Incorporated by reference in its entirety is a computer-readable amino acid/nucleotide sequence listing submitted concurrently herewith and identified as follows: One 246,173 byte ASCII (Text) file named "46417A_SeqListing.txt" created on March 29, 2013.

## FIELD OF THE INVENTION

**[0003]** The disclosure relates to materials and methods useful for generating improved pseudotyped lentiviral vector particles.

## BACKGROUND

**[0004]** Dendritic cells (DCs) are essential antigen presenting cells for the initiation and control of immune responses. DCs can capture and process antigens, migrate from the periphery to a lymphoid organ, and present the antigens to resting T cells in a major histocompatibility complex (MHC)-restricted fashion. These cells are derived from bone marrow (BM) and display dendritic morphology and high mobility. The discovery of DCs as specialized antigen-presenting cells (APCs) has fueled attempts at DC-based immunization/vaccination strategies that involve targeting DCs for display of specific antigens. Recombinant virus-based vectors have been developed as a mechanism to directly deliver a gene encoding a designated antigen(s) to host cells. Through induction of a desired adaptive immune response, the expressed gene product provides a therapeutic benefit.

**[0005]** Challenges in achieving a safe and effective system include designing a vector that efficiently targets a desired set of host cells, providing a suitable delivery system, and

expressing a desired antigen to elicit an effective immune response so that it can be utilized broadly across a designated human subject population.

**[0006]** The envelope glycoproteins of Sindbis virus and other alphaviruses disclosed herein incorporate into the lipid bilayer of the viral particle membrane. Typically, the viral membrane (envelope) includes multiple copies of trimers of two glycoprotein heterodimers, E1 and E2, which are produced from cleavage of a single precursor protein. The precursor protein comprises, from its N- to C-terminus, the E3, E2, 6K and E1 proteins. The small E3 glycoprotein serves as a signal sequence for translocation of the E2 protein into the membrane, and is cleaved from E2 by furin or some other $Ca^{2+}$-dependent serine proteinase. The 6K protein serves as a signal sequence for translocation of the E1 protein into the membrane and is then cleaved from the precursor protein. WO 2008/011636 and US 2011/0064763 disclose lentiviral packaging systems.

## SUMMARY OF THE INVENTION

**[0007]** The inventors have discovered that lentiviral vector particles that exhibit two characteristics (a) pseudotyped with a highly mannosylated alphavirus glycoprotein and (b) comprising a Vpx protein, have unexpectedly improved transduction efficiency for cells expressing DC-SIGN. These particles infect cells expressing DC-SIGN, particularly dendritic cells, significantly more efficiently than lentiviral vector particles having only one of these two characteristics. In particular instances, highly mannosylated pseudotyped lentiviral vector particles are provided that comprise a Vpx protein and a lentiviral genome comprising a sequence of interest (e.g., a polynucleotide encoding an antigen).

*Methods of generating pseudotyped lentiviral vector particles*

**[0008]** One aspect of the disclosure provides a method of generating a pseudotyped lentiviral vector particle comprising: (a) culturing in a culture medium comprising a mannosidase inhibitor, preferably a mannosidase I inhibitor, and a virus packaging cell comprising: (1) a lentiviral vector genome comprising a polynucleotide encoding an exogenous antigen, (2) a polynucleotide encoding an alphavirus glycoprotein that preferentially binds cells expressing DC-SIGN, and (3) a polynucleotide encoding a SAMHD1 inhibitor; and (b) isolating a pseudotyped lentiviral vector particle that preferentially binds cells expressing DC-SIGN.

**[0009]** Another aspect of the disclosure provides a method of generating a pseudotyped lentiviral vector particle comprising: (a) culturing in a culture medium comprising

kifunensine a virus packaging cell comprising: (1) a lentiviral vector genome comprising a polynucleotide encoding an exogenous antigen, (2) a polynucleotide encoding a Sindbis E2 glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, and (3) a polynucleotide encoding a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity; and (b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN. In some embodiments, the E2 glycoprotein is 90% identical to SEQ ID NO: 30 [SIN-Var1]. In some embodiments, (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein. In some embodiments, the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

**[0010]** In some or any of the embodiments described herein, the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx (SEQ ID NO: 44).

**[0011]** In some or any of the embodiments described herein, the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

**[0012]** In some or any of the embodiments described herein, the Vpr protein comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0013]** In some or any of the embodiments described herein, the antigen is a tumor-specific antigen or a virus-specific antigen. In some or any of the embodiments described herein, the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, e.g., MAGE-A3 and MAGE-A1, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, e.g., TRP2, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, merkel cell virus T-antigen oncoproteins and alpha-fetoprotein. In some or any of the embodiments described herein, the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a

coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a polyoma virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

**[0014]** In some or any of the embodiments described herein, the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen. In some or any of the embodiments described herein, the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens. In some or any of the embodiments described herein, the self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57. In some or any of the embodiments described herein, the first antigen is MAGE-A3 and the second antigen is NY-ESO-1.

**[0015]** In some or any of the embodiments described herein, the kifunensine is present in the culture medium at a concentration of about 0.01 μg/ml to about 1 mg/ml. In some or any of the embodiments described herein, the kifunensine is present in the culture medium at a concentration of about 0.1 μg/ml to about 1 μg/ml. In some or any of the embodiments described herein, the kifunensine is present in the culture medium at a concentration of about 0.25 μg/ml to about 2 μg/ml.

**[0016]** In some or any of the embodiments described herein, the virus packaging cell further comprises: (i) a polynucleotide comprising gag and pol genes; and (ii) a polynucleotide encoding a rev protein. In some or any of the embodiments described herein, the gag and pol genes are human codon optimized and comprise a non-optimized window around position 1228 to 1509 of SEQ ID NO: 54. In some or any of the embodiments described herein, the polynucleotide comprising gag and pol genes lacks a functional rev responsive element (RRE). In some or any of the embodiments described herein, the polynucleotide comprising gag and pol genes lacks a functional RRE because the RRE has been deleted. In some or any of the embodiments described herein, the pol gene encodes an inactive integrase enzyme. In some or any of the embodiments described herein, the integrase enzyme has a D64V mutation.

**[0017]** In some or any of the embodiments described herein, the polynucleotide encoding the Vpx protein or Vpr protein is on the same or different plasmid as the polynucleotide encoding the rev protein, or the polynucleotide comprising the gag and pol genes.

**[0018]** In some or any of the embodiments described herein, the lentiviral vector genome is derived from HIV-1.

**[0019]** In some or any of the embodiments described herein, the lentiviral vector genome has an inactivated 3' long terminal repeat (LTR) or a self-inactivating 3' long terminal repeat (LTR). In some or any of the embodiments described herein, the lentiviral vector genome comprises a U3 element lacking at least one of an enhancer sequence, a TATA box, an Sp1 site, an NK-kappa B site, or a polypurine tract (PPT).

**[0020]** In some or any of the embodiments described herein, the lentiviral vector genome comprises the nucleotide sequence of any one of SEQ ID NOs: 21 [SIN vector], 22 [703 vector], or 23 [704 vector].

**[0021]** In some or any of the embodiments described herein, the lentiviral vector genome further comprises a nucleotide sequence encoding a dendritic cell maturation/stimulatory factor. In some or any of the embodiments described herein, the dendritic cell maturation/stimulatory factor is selected from the group consisting of GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand, and drug-inducible CD40.

**[0022]** In some or any of the embodiments described herein, the nucleotide sequence encoding an antigen is operably linked to a promoter selected from the group consisting of the human Ubiquitin-C promoter (UbiC), the cytomegalovirus immediate early promoter (CMV), the Rous sarcoma virus promoter (RSV), and the tetracycline-responsive promoter. In some or any of the embodiments described herein, the promoter is an intron-deficient promoter. In some or any of the embodiments described herein, the intron-deficient promoter is a UbiC

**[0023]** Related aspects of the disclosure provide a lentiviral vector particle produced by any of the methods recited above.

*Compositions comprising pseudotyped lentiviral vector particles*

**[0024]** Another aspect of the disclosure provides a composition comprising pseudotyped lentiviral vector particles comprising (a) a SAMHD1 inhibitor, (b) an exogenous

polynucleotide encoding an antigen, and (c) an envelope glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, wherein at least 60%, or at least 70%, or at least 80%, preferably at least 90% of N-linked glycans in said composition comprise a $Man_5$ through $Man_9$ structure, preferably $Man_9$.

**[0025]** Another aspect of the disclosure provides a composition comprising pseudotyped lentiviral vector particles comprising (a) a Vpx protein, (b) an exogenous polynucleotide encoding an antigen, and (c) an envelope glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, wherein at least 80% of N-linked glycans in said composition comprise a $Man_9$ structure.

**[0026]** In some or any of the embodiments described herein, the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx protein (SEQ ID NO: 44).

**[0027]** In some or any of the embodiments described herein, the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

**[0028]** In some or any of the embodiments described herein, the Vpr protein comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0029]** In some or any of the embodiments described herein, the pseudotyped lentiviral vector particle infects dendritic cells expressing DC-SIGN with an *in vitro* transduction efficiency of at least 1%, or at least 5%, or at least 10%, or at least 20%. See, e.g., the procedure of Example 8.

**[0030]** In some or any of the embodiments described herein, the glycoprotein is a Sindbis virus E2 glycoprotein. In some or any of the embodiments described herein, the E2 glycoprotein has at least 90% identity to SEQ ID NO: 30 [SIN-Var1]. In some or any of the embodiments described herein, (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein.

**[0031]** In some or any of the embodiments described herein, the antigen is a tumor-specific antigen or a virus-specific antigen. In some or any of the embodiments described herein, the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, e.g., MAGE-A3 and MAGE-A1, MART-1/Melan-A, BAGE, RAGE, gp100, gp75,

mda-7, tyrosinase, tyrosinase-related protein, e.g., TRP2, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, merkel cell virus T-antigen oncoproteins and alpha-fetoprotein. In some or any of the embodiments described herein, the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

**[0032]** In some or any of the embodiments described herein, the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen. In some or any of the embodiments described herein, the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens. In some or any of the embodiments described herein, the self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57. In some or any of the embodiments described herein, the first antigen is NY-ESO-1 and the second antigen is MAGE-A3.

**[0033]** In some or any of the embodiments described herein, the lentiviral vector genome is derived from HIV-1.

**[0034]** In some or any of the embodiments described herein, the lentiviral vector genome has an inactivated 3' long terminal repeat (LTR) or a self-inactivating 3' long terminal repeat (LTR). In some aspects, the lentiviral vector genome comprises a U3 element lacking at least one of an enhancer sequence, a TATA box, an Sp1 site, an NK-kappa B site, or a polypurine tract (PPT).

**[0035]** In some or any of the embodiments described herein, the lentiviral vector genome comprises the nucleotide sequence of any one of SEQ ID NOs: 21 [SIN vector], 22 [703 vector], or 23 [704 vector].

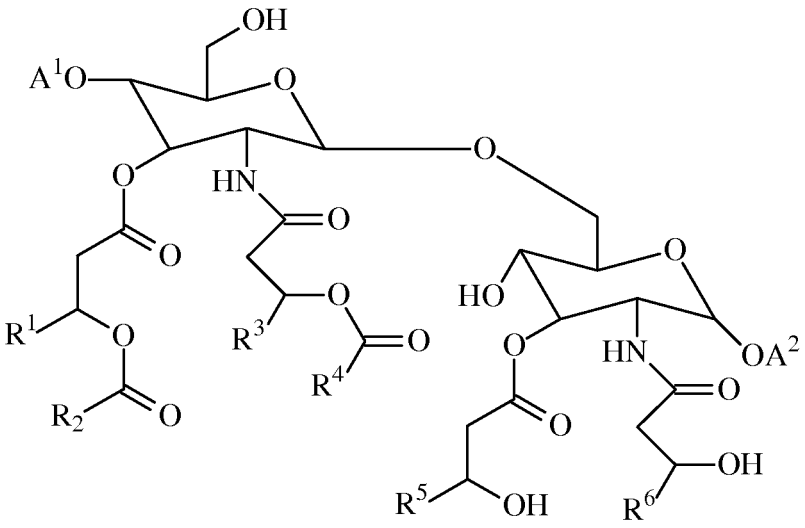
**[0036]** In some or any of the embodiments described herein, the lentiviral vector genome further comprises a nucleotide sequence encoding a dendritic cell maturation/stimulatory factor. In some or any of the embodiments described herein, the dendritic cell maturation/stimulatory factor is selected from the group consisting of GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand, and drug-inducible CD40.

**[0037]** In some or any of the embodiments described herein, the nucleotide sequence encoding an antigen is operably linked to a promoter selected from the group consisting of the human Ubiquitin-C promoter (UbiC), the cytomegalovirus immediate early promoter (CMV), the Rous sarcoma virus promoter (RSV), and the tetracycline-responsive promoter. In some or any of the embodiments described herein, the promoter is an intron-deficient promoter. In some or any of the embodiments described herein, the intron-deficient promoter is a human Ubiquitin-C (UbiC) promoter.

**[0038]** In some or any of the embodiments described herein, the pseudotyped lentiviral vector particles have an IU of at least $10^5$/mL.

**[0039]** In some or any of the embodiments described herein, the composition further comprises an immunostimulating agent.

**[0040]** In some or any of the embodiments described herein, the composition further comprises an adjuvant. For example, as disclosed herein, adjuvants include alum, or 3 De-O-acylated monophosphoryl lipid A (MPL). Classes of adjuvants disclosed herein include (a) aluminum salts, (b) oil-in-water emulsion formulations, optionally with or without other specific immunostimulating agents such as muramyl peptides or other bacterial cell wall components, (c) saponin adjuvants, including ISCOMs (immunostimulating complexes) and ISCOMATRIX; (d) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (e) cytokines; and (f) adjuvants of formula (I).



[0041]

(I)

wherein the moieties A1 and A2 are independently selected from the group of hydrogen, phosphate, and phosphate salts. Sodium and potassium are exemplary counterions for the phosphate salts. The moieties $R^1$, $R^2$, $R^3$, $R^4$, $R^5$, and $R^6$ are independently selected from the group of hydrocarbyl having 3 to 23 carbons, represented by $C_3$-$C_{23}$. For added clarity it will be explained that when a moiety is "independently selected from" a specified group having multiple members, it should be understood that the member chosen for the first moiety does not in any way impact or limit the choice of the member selected for the second moiety. The carbon atoms to which $R^1$, $R^3$, $R^5$ and $R^6$ are joined are asymmetric, and thus may exist in either the R or S stereochemistry. In one embodiment all of those carbon atoms are in the R stereochemistry, while in another embodiment all of those carbon atoms are in the S stereochemistry.

**[0042]** In various embodiments of the disclosure, the adjuvant has the chemical structure of formula (I) but the moieties A1, A2, R1, R2, R3, R4, R5, and R6 are selected from subsets of the options previously provided for these moieties, where these subsets are identified below by E1, E2, etc.

E1: $A_1$ is phosphate or phosphate salt and $A_2$ is hydrogen.

E2: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_3$-$C_{21}$ alkyl; and $R^2$ and $R^4$ are $C_5$-$C_{23}$ hydrocarbyl.

E3: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_5$-$C_{17}$ alkyl; and $R^2$ and $R^4$ are $C_7$-$C_{19}$ hydrocarbyl.

E4: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_7$-$C_{15}$ alkyl; and $R^2$ and $R^4$ are $C_9$-$C_{17}$ hydrocarbyl.

E5: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_9$-$C_{13}$ alkyl; and $R^2$ and $R^4$ are $C_{11}$-$C_{15}$ hydrocarbyl.

E6: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_9$-$C_{15}$ alkyl; and $R^2$ and $R^4$ are $C_{11}$-$C_{17}$ hydrocarbyl.

E7: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_7$-$C_{13}$ alkyl; and $R^2$ and $R^4$ are $C_9$-$C_{15}$ hydrocarbyl.

E8: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_{11}$-$C_{20}$ alkyl; and $R^2$ and $R^4$ are $C_{12}$-$C_{20}$ hydrocarbyl.

E9: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_{11}$ alkyl; and $R^2$ and $R^4$ are $C_{13}$ hydrocarbyl.

E10: $R^1$, $R^3$, $R^5$ and $R^6$ are undecyl and $R^2$ and $R^4$ are tridecyl.

**[0043]** In certain options, each of E2 through E10 is combined with embodiment E1, and/or the hydrocarbyl groups of E2 through E9 are alkyl groups, preferably straight chain alkyl groups. A preferred adjuvant is E1 in combination with E10, where (i) $A_1$ is phosphate or phosphate salt and $A_2$ is hydrogen and (ii) $R^1$, $R^3$, $R^5$ and $R^6$ are undecyl and $R^2$ and $R^4$ are tridecyl.

**[0044]** In some or any of the embodiments described herein, the envelope glycoproteins also bind cells expressing mouse SIGNR1.

**[0045]** In some or any of the embodiments described herein, the pseudotyped lentiviral vector particles also more efficiently transduce cells expressing mouse SIGNR1 compared to cells not expressing mouse SIGNR1.

**[0046]** Other features and advantages of the present disclosure will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the disclosure, are given by way of illustration only, because various changes and modifications within the spirit and scope of the disclosure will become apparent to those skilled in the art from this detailed description.

## BRIEF DESCRIPTION OF THE DRAWINGS

**[0047]** **Figures 1A** and **1B** illustrate the ability of pseudotyped lentiviral vector particles produced in the presence of various mannosidase inhibitors (e.g., kifunensine, DMNJ, and swainsonine) to infect HT1080 cells stably expressing the DC-SIGN receptor (1A) or lacking DC-SIGN (1B). Efficiency of infection was assessed by determining GFP expression from the lentiviral vector. The y-axis is the percentage of GFP positive cells.

**[0048]** **Figures 2A** and **2B** illustrate the ability of pseudotyped lentiviral vector particles produced in the presence of 400 μg/ml DMNJ or various concentrations of kifunensine to infect HT1080 cells stably expressing the DC-SIGN receptor (2A) or lacking DC-SIGN (2B). Efficiency of infection was assessed as in Figure 1.

**[0049]** **Figure 3A** is a diagram illustrating the substrate specificity for the PNGaseF and EndoH. PNGaseF is a general endoglycosidase that will cleave all N-linked glycosylation

regardless of glycosylation profile. EndoH is a specialized endoglycosidase that will only cleave high-mannose N-linked glycosylation. EndoH cleaves only hi-mannose N-linked glycosylation (i.e., EndoH will target 2 of 4 sites on SINVar1 in the absence of kifunensine, and 4 of 4 sites on SINVar1 in the presence of kifunensine). **Figure 3B** illustrates the results of an experiment to determine the glycosylation status of the glycoproteins on pseudotyped lentiviral vector particles produced in the presence of kifunensine or DMNJ using gel shifts by running on an SDS-PAGE gel and immunoblotting with antibody against the Sindbis viral envelope.

**[0050]** **Figure 4A** illustrates the ability of pseudotyped lentiviral vector particles produced in the presence of 400 μg/ml DMNJ or various concentrations of kifunensine to infect HT1080 cells stably expressing the DC-SIGN receptor. Efficiency of infection was assessed as in Figure 1. **Figure 4B** illustrates the results of an experiment to determine the glycosylation status of the E2 glycoprotein on pseudotyped lentiviral vector particles produced in Figure 4A.

**[0051]** **Figure 5A** is a Western blot (anti-HA) of HA-tagged SIVmacVpx expressed in 293T cells. was cloned into a mammalian expression vector driven by a CMV promoter (construct named pENV-SIVmacVpx). **Figure 5B** is a Western blot (anti-HA) of viral protein extracts from viral particles comprising HA-tagged SIVmacVpx. 100ng of p24 was loaded per well onto a gel for immunoblotting with anti-HA antibody. Anti-p24 antibody was used as a loading control.

**[0052]** **Figure 6** is a scatter plot of transduction events measured by gating on dendritic cells that were positive for CD11c and assessing the percentage of cells positive for GFP (x-axis; as a result of infection by the VSV-G pseudotyped, integration-defective lentivirus with or without Vpx) with DC-SIGN on the y-axis.

**[0053]** **Figure 7** is a scatter plot of transduction events measured by gating on dendritic cells that were positive for CD11c and assessing the percentage of cells positive for GFP (x-axis; as a result of infection by the VSV-G pseudotyped, integration-competent lentivirus with or without Vpx) with DC-SIGN on the y-axis.

**[0054]** **Figure 8** is a scatter plot of transduction events measured by gating on dendritic cells infected with SINvar1-pseudotyped, integration-defective lentivirus with or without Vpx and produced in the presence of absence of kifunensine. The y-axis measures cells that were

positive for CD11c or DC-SIGN and the x-axis measures the percentage of cells positive for GFP.

**[0055]** **Figure 9A** is a Western blot of Sindbis virus glycoproteins prepared according to Example 1 with no treatment (lanes 1-3), 400 μg/ml of DMNJ (lanes 4-6), or 1 μg/ml of kifunensine (lanes 7-9). The particles were not treated with endoglycosidase (lanes 1, 4, 7), incubated with EndoH for 1 hour (lanes 2, 5, 8), or incubated with PNGaseF for 1 hour (lanes 3, 6, 9). Samples were then analyzed using a gel-shift assay and immunoblotting with antibody against the Sindbis virus envelope. **Figure 9B** (no mannosidase inhibitor) is an intensity profile of each band from lanes 1-3 and its location on the lane. **Figure 9C** (DMNJ treated) is an intensity profile of each band from lanes 4-6 and its location on the lane. **Figure 9D** (kifunensine treated) is an intensity profile of each band from lanes 7-9 and its location on the lane.

**[0056]** For **Figure 10A**, 293T huDC-SIGN cells were transduced with vectors packaged with the Wild Type (WT) or defective integrase (D64V) and a vector genome containing the extended 3'PPT (703) or 3'PPT deletion (704). At 48 hours post-transduction, nested Alu-PCR analysis was performed on genomic DNA extracted from the transduced cells. Error bars indicate standard error of the mean from transductions performed in triplicate. **Figures 10B** and **10C** demonstrate the integration rate of WT/703 and D64V/704 vectors encoding GFP-T2A-NeoR using two independent methods. For **Figure 10B**, HT1080 huDC-SIGN cells were transduced with serial dilutions of the indicated vectors. Transduced cells were grown under G418 selection and neomycin resistant colonies, representing individual integration events, were counted. Integration Events were calculated as described in Example 10. For **Figure 10C**, HT1080 huDC-SIGN cells were transduced with the indicated vectors. Flow cytometry was performed at multiple time points post-transduction to determine the percentage of GFP-expressing cells. Error bars indicate standard error of the mean from flow cytometry triplicates.

**[0057]** **Figure 11**: Human PBMCs were treated with GM-CSF and IL-4 for 3 days, then incubated with 20 ng p24 of ID-VP02 encoding GFP. At the time of vector addition, the culture consisted primarily of DCs, B-cells, and T-cells. Three days after transduction, cells were analyzed for surface markers and categorized as either DCs ($CD11c^{pos}$) 6%, B-cells ($CD11c^{neg}$, $CD19^{pos}$) 10%, or T-cells ($CD11c^{neg}$, $CD3\varepsilon^{pos}$) 80%. Transduction events were measured by assessing percent of cells positive for GFP within each population of cells. Numbers in plots are the percentage of cells within the $GFP^{+}$ gate.

**[0058]** **Figure 12**: A portion of the vector genome (top) is represented containing long terminal repeats (LTR) at each end. The splice donor (SD) and splice acceptor (SA) sites flank the psi packaging signal (Ψ), the partial *gag* sequence and the Rev-responsive element (RRE). Components between the antigen promoter (Promoter) and the 3' LTR are not highlighted and therefore forward slash marks (//) are used. A portion of the WT *gag/pol* (middle) is represented showing the *gag* (black box) and *pol* (grey box) genes followed by the RRE. The two components that are homologous between the WT *gag/pol* and the vector genome (the RRE and the first 354 bp of *gag*) are represented in brackets (not drawn to scale). The hypothesized region of recombination between the vector genome and the WT *gag/pol* are shown with connecting lines. A portion of the RI *gag/pol* (bottom) is represented showing the codon-optimized *gag* and *pol* genes (white boxes to distinguish from wild-type). The non-codon-optimized frameshift between the *gag* and *pol* genes is represented in its native codon sequence (overlapping black and grey boxes). Primers used for the psi-gag recombination assay are shown with their approximate locations on the constructs. First round PCR primers are represented with closed arrows and are the pairs 709 and 710 (to detect the psi-gag recombinant) or 709 and 378 (to detect integrated vector genome). The expected amplicon for integrated vector with primer pairs 709 and 378 is 1697 bp. The nested PCR primers are represented with open arrows and are the pairs 863 and 835 (to detect psi-gag recombinant with the WT *gag/pol*) or 863 and 864 (to detect psi-gag recombination with the RI *gag/pol*). The expected amplicon with either of the psi-gag recombinant primer pairs is 937 bp.

**[0059]** **Figure 13**: 293T cells were transfected with either WT *gag/pol* or RI *gag/pol* plasmids in the presence of either Rev plasmid (+) or empty backbone plasmid (-). Twenty-four hours later cells were lysed and analyzed for expression of Gag proteins using anti-p24 antibody. Unprocessed Gag protein (p55) and p24 are indicated with arrows. Lysate from untransfected cells was included as a control. Equal loading of wells was confirmed with anti-actin antibody.

**[0060]** **Figure 14A:** GFP-encoding vector was produced with two plasmid amounts (6 μg or 3 μg) of either WT *gag/pol* or RI *gag/pol*. Resulting p24 levels in vector supernatant is shown in the table. **Figure 14B:** 293T cells were transduced with 2-fold dilutions of vectors produced in 14A and analyzed for GFP expression after 2 days. GFU/mL were calculated and plotted on the y-axis. The μg amount of *gag/pol* plasmid used to make vector (6 μg or 3

μg) are plotted on the x-axis. WT *gag/pol* and RI *gag/pol* are shown in black or white columns respectively.

**[0061]** **Figure 15:** C57BL/6 mice were immunized with the indicated doses ($2 \times 10^7$, $1 \times 10^8$, or $5 \times 10^8$ TU) of LV encoding full-length OVA or HBSS vehicle alone. LVs were either integration-competent (INT+) or integration-deficient (INT-) and generated with either WT- or RI *gag/pol*, as indicated. At day 12 post immunization, the percentage of $OVA_{257}$-specific splenic CD8 T cells was measured by ICS for IFN-γ after *ex vivo* peptide restimulation.

**[0062]** **Figure 16:** C57BL/6 mice (5 per group) were immunized with $5 \times 10^8$ TU of Integration-deficient (INT-) LV generated with either WT or RI *gag/pol* encoding a polyepitope antigen (LV1b) that contains the H-$2^b$-restricted $OVA_{257}$ CD8 T cell epitope and then challenged on day 28 post-immunization with $1 \times 10^7$ $TCID_{50}$ wild type WR-strain vaccine virus (VV-WT), WR-strain recombinant OVA vaccine virus (rVV-OVA), or left unchallenged. On day 33 (day 5 post-challenge) viral load in the ovaries of each animal were measured by $TCID_{50}$ assay.

**[0063]** **Figure 17A:** 293T cells were transduced with either WT *gag/pol* or RI *gag/pol* vectors. Two days later, genomic DNA was isolated and analyzed for integrated proviral DNA by PCR using primer pair 709 and 378 that binds within the vector genome as schematized in Figure 12. PCR products were visualized on a 1% agarose gel. The amplicon size of the vector genome is indicated with an arrow. No template control was included in the PCR and gel. **Figure 17B:** Genomic DNA from Figure 17A was analyzed for proviral psi-gag recombinants with first round PCR followed by nested PCR. The first round PCR used primer pairs 709 and 710 that bind in the vector genome and the frameshift within *gag/pol* respectively. 1 μl of the first round PCR product was used as template either undiluted (1:1), or with 1:100, or 1:1000 dilutions in a nested PCR. Primer pairs for nested PCR were either 863 and 835, or 863 and 864. The former pair (863, 835) binds in the vector genome and the WT *gag/pol* respectively. The latter pair (863, 864) binds in the vector genome and the RI *gag/pol*. All primers and their binding sites are schematized in Figure 12. Template only controls were included. Resulting nested PCR products were visualized on a 1% agarose gel. The amplicon size of the psi-gag recombinant is shown with an arrow. **Figure 17C:** The band from the nested PCR for WT *gag/pol* (the bright band below 1 kb) was cloned into a TOPO-TA vector and sequenced. Sequence of the WT *gag/pol* psi-gag recombinant band is shown with regions marked for aligning with the vector genome, partial

gag or WT *gag/pol*. Double slashes (//) and dots indicate sequences not shown for simplicity. Numbers on sequence indicate nucleotide position on the amplicon. Base pairs 1-414 of the psi-gag recombinant aligns with the vector genome, while bp 120-937 aligns with the WT *gag/pol*. For reference, the partial *gag* sequence is bp 76-439 of the recombinant. **Figure 17D:** The band from nested PCR for the RI *gag/pol* (faint band between 1 kb and 3 kb) was cloned into a TOPO-TA vector and sequenced. Sequence of the RI *gag/pol* recombinant band is shown with regions marked for aligning with the vector genome or the RI *gag/pol*. Dots indicate sequences not shown for simplicity. Numbers on sequence indicate nucleotide position on the amplicon. Base pairs 1-1253 of the RI recombinant aligns with the vector genome, while bp 1254-1329 aligns with the RI *gag/pol*. For reference, the partial *gag* sequence is bp 76-439 of the recombinant. Full sequence and alignment are shown in (Supplementary Figure S1B).

**[0064]** **Figure 18**: HT1080 cells and HT1080 cells stably expressing (**A**) human DC-SIGN (HT1080 huDC-SIGN), (**B**) mouse SIGNR1 (HT1080 mSIGNR1), (**C**) mouse SIGNR3 (HT1080 mSIGNR3), or (**D**) mouse SIGNR5 (HT1080 mSIGNR5), were incubated with concentrated (1,000-fold) integration-deficient VSV-G pseudotyped vector encoding GFP, or ID-VP02 pseudotyped vectors encoding GFP that were produced either in the absence or presence of kifunensine (kifu).

**[0065]** **Figure 19A:** The expression of SIGNR1 and SIGNR5 on spleen and lymph cells was analyzed on live, single cell events. Control staining pattern lacking SIGNR1 or SIGNR5-specific antibodies is shown. **Figure 19B:** Live, single cell events from spleen and lymph node were subdivided into B cells (B220+ TCRβ-, labeled R4), T cells ($TCR\beta^+$, $B220^-$, labeled R5), and DCs ($B220^-$ $TCR\beta^-$ $MHC\text{-}II^+$ $CD11c^{hi}$, labeled R7) and subsequently analyzed for expression of SIGNR5 and SIGNR1. For all subsets, frequencies of positive events were $\leq 0.00$ in negative control stains lacking SIGNR1- and SIGNR5-specific antibodies.

**[0066]** **Figure 20:** The phenotype of GFP-expressing cells in the draining lymph node after subcutaneous injection with GFP-encoding ID-VP02 was analyzed by flow cytometry. Female BALB/c mice (15 per group) were injected subcutaneously in the footpad with $3 \times 10^{10}$ genomes of ID-VP02 encoding GFP, control ID-VP02 encoding a non-fluorescent protein, or left untreated. Four days later, the popliteal and cervical lymph nodes were separately pooled from 5 mice (3 pools per treatment group) and analyzed for the presence of GFP-expressing cells. (**A**) Live, singlet events from the popliteal (draining) or cervical (non-

draining) lymph nodes were analyzed for GFP expression. Popliteal lymph node cells from naïve or negative control ID-VP02 served as negative controls. (**B**) Frequency of CD11c and MHC-II on $GFP^+$ events from the popliteal lymph nodes of mice injected with GFP-encoding ID-VP02 are shown as black dots overlayed on total B220- TCRβ- events, shown in gray, as a reference. (**C**) Expression of SIGNR1 on $GFP^+$ $CD11c^+$ $MHC\text{-}II^+$ events, shown with (left panel) and without (right panel) inclusion of SIGNR1-specific antibody. Gate statistics are the mean value of three biological replicates. Values in panel (**A**) are number of positive events per $1 \times 10^6$ cells, whereas all other gate values are percentages.

**[0067] Figure 21:** C57BL/6 mice (3 per group) received a single subcutaneous injection of $3 \times 10^{10}$ genomes of ID-VP02 at the base of the tail. Biodistribution, as determined by the presence of reverse-transcribed vector DNA, of ID-VP02 in the indicated tissues was evaluated by quantitative PCR at 1, 4, 8, 21, or 42 days post-injection. Inguinal and cervical lymph nodes are indicated as draining and non-draining, respectively. Input DNA was normalized to 200 ng. The limit of quantitation (LOQ) of 10 copies per reaction was defined by the lowest copy number on the standard curve. Samples that did not amplify within 40 qPCR cycles were designated as not detected (ND).

**[0068] Figure 22:** (**A**) C57BL/6 mice were immunized with indicated doses (vector genomes) of ID-VP02 encoding full-length OVA or HBSS vehicle alone. At day 12 post immunization, the percentage of $OVA_{257}$-specific splenic CD8 T cells was measured by ICS. (**B**) The kinetics of the primary and secondary CD8 T cell response to ID-VP02 encoding OVA was determined by immunizing mice (5 per group) with $1 \times 10^{10}$ genomes of ID-VP02 in a prime-boost regimen with a 35 day interval and analyzing splenic CD8 T cell responses at the indicated timepoints. Immunizations were staggered such that all groups were analyzed by ICS on the same day. (**C**) Representative intracellular IFN-γ, TNF-α, and IL-2, and surface CD107a staining on viable CD8 T cells after peptide restimulation. (**D**) Frequency of CD8 T cells expressing combinations of IFN-γ, TNF-α, IL-2, and CD107a around the peak and post contraction of the primary and secondary responses. Negligible numbers of CD8 T cells that were IFN-γ negative expressed any other effector molecule. (**E**) The effector/memory phenotype of $CD44^{hi}$ $H\text{-}2K^b\text{-}OVA_{257}$ $pentamer^+$ CD8 T cells was assessed by staining with CD127 and KLRG1 at the indicated timepoints.

**[0069] Figure 23:** (**A**) Experimental schedule: C57BL/6 mice (5 per group) were immunized with $5 \times 10^{10}$, $1 \times 10^{10}$, or $2 \times 10^9$ vector genomes of ID-VP02 encoding a polyepitope antigen (LV1b) that contains the $H\text{-}2^b$-restricted $OVA_{257}$ and LCMV $GP_{33}$ CD8 T

cell epitopes and then challenged on day 35 post-immunization with $1 \times 10^7$ TCID50 wild-type WR-strain vaccine virus (VV-WT), WR-strain recombinant OVA vaccine virus (rVV-OVA), or left unchallenged. On day 40 (day 5 post-challenge) splenic CD8 T cell responses and viral load in the ovaries were measured. (**B**) $OVA_{257}$- and LCMV $GP_{33}$-specific CD8 T cell responses were measured by staining for intracellular IFN-γ and TNF-α after *ex vivo* peptide restimulation. Representative dot plots of the CD8 T cell cytokine profile is shown. (**C**) Frequency of $OVA_{257}$-specific IFN-γ+ CD8 T cells for each animal. (**D**) Viral load (measured by $TCID_{50}$ assay) within the ovaries of each animal.

**[0070]** **Figure 24:** (**A**) BALB/c mice (5 per group) were immunized with indicated doses, in vector genomes, of ID-VP02 encoding AH1A5, a heteroclitic mutant of the endogenous CT26 tumor rejection epitope AH1, linked to OVA (OVA-AH1A5) or HBSS vehicle alone. At day 12 post immunization, the percentage of AH1A5- or AH1-specific splenic CD8 T cells was measured by ICS. (**B**) Twelve days after immunization, a 1:1:1 mixture of dye-labeled target cells each pulsed with AH1, AH1A5, or a control peptide were transferred intravenously into immunized and naive mice (3 per group). The following day, spleens were harvested and the relative recovery of each population was compared between naïve and immunized mice to calculate specific killing. (**C**) BALB/c mice (10 per group) were immunized with $4 \times 10^9$ vector genomes of ID-VP02 encoding OVA-AH1A5. Four weeks later, mice were injected subcutaneously with $8x10^4$ CT26 tumor cells on the right flank and mice were euthanized when tumors exceeded 100 $mm^2$. (**D**) Therapeutic immunization: BALB/c mice (10 per group) were injected subcutaneously with $8 \times 10^4$ CT26 tumor cells. Four days later, mice were either immunized with $4x10^9$ vector genomes of ID-VP02 encoding OVA-AH1A5 or left untreated and mice were euthanized when tumors exceeded 100 $mm^2$.

## DETAILED DESCRIPTION

**[0071]** This disclosure relates to methods and materials useful for generating pseudotyped lentiviral vector particles that efficiently bind to and productively infect cells expressing DC-SIGN (e.g., dendritic cells). The methods and materials in this disclosure relate to the unexpected discovery that the combination of a Vpx protein in a lentiviral vector particle with highly mannosylated (e.g., by culturing the virus packaging cells in the presence of kifunensine) alphavirus glycoproteins (e.g., Sindbis virus glycoproteins) in the envelope results in lentiviral vector particles that infect non-dividing cells expressing DC-SIGN (e.g., dendritic cells)significantly more efficiently than lentiviral vector particles that either lack a

Vpx protein or highly mannosylated glycoproteins in the envelope. One advantageous aspect of the disclosure is that lentiviral vector particles pseudotyped with a Sindbis virus E2 glycoprotein and produced in the presence of kifunensine infect dendritic cells significantly more efficiently if the particles also comprise a Vpx protein in the virion, thus allowing for delivery and expression of a sequence of interest (e.g., a polynucleotide encoding an antigen) to a dendritic cell.

## Definitions

**[0072]** The term "functional fragment" when used in reference to a polypeptide means a polypeptide that is truncated, i.e., missing one or more amino acids from the N-terminus or C-terminus, and that retains the desired activity. When used in reference to a Vpx protein, "functional fragment" means a fragment that retains the ability to inhibit the activity of SAMHD1. The term may analogously be applied to polynucleotides that are truncated.

**[0073]** The term "variant" when used in reference to a polypeptide means a polypeptide that has one or more substitutions, deletions or insertions relative to a parent polypeptide. In some contexts, the variant is one that retains the desired activity. When used in reference to a Vpx protein, "functional variant" means a variant that retains the ability to inhibit the activity of SAMHD1. The term may analogously be applied to polynucleotides that have one or more substitutions, deletions or insertions relative to a parent polynucleotide.

**[0074]** As used herein, the term "conservative amino acid substitution" is the replacement of one amino acid with another amino acid having similar properties, e.g. size, charge, hydrophobicity, hydrophilicity, and/or aromaticity, and includes exchanges as indicated below:

| Original | Exemplary |
|---|---|
| Ala (A) | val; leu; ile |
| Arg (R) | lys; gln; asn |
| Asn (N) | gln; his; asp, lys; gln |
| Asp (D) | glu; asn |
| Cys (C) | ser; ala |
| Gln (Q) | asn; glu |
| Glu (E) | asp; gln |
| Gly (G) | ala |
| His (H) | asn; gln; lys; arg |
| Ile (I) | leu; val; met; ala; |

| | |
|---|---|
| | phe; norleucine |
| Leu (L) | norleucine; ile; val; |
| | met; ala; phe |
| Lys (K) | arg; gln; asn |
| Met (M) | leu; phe; ile |
| Phe (F) | leu; val; ile; ala; tyr |
| Pro (P) | ala |
| Ser (S) | thr |
| Thr (T) | ser |
| Trp (W) | tyr; phe |
| Tyr (Y) | trp; phe; thr; ser |
| Val (V) | ile; leu; met; phe; |
| | ala; norleucine |

**[0075]** Amino acid residues which share common side-chain properties are often grouped as follows.

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

**[0076]** As used herein, the terms "integration deficient" and "integration defective" are used interchangeably. An integration deficient viral vector is one that is at least 10-fold (preferably, at least 20-fold, at least 30-fold, at least 40-fold, at least 50-fold, at least 60-fold, at least 70-fold, at least 80-fold, at least 90-fold, at least 100-fold, at least 150-fold, at least 200-fold, at least 250-fold, at least 300-fold, at least 350-fold, at least 400-fold, at least 450-fold, at least 500-fold, at least 550-fold, at least 600-fold, at least 650-fold, at least 700-fold, at least 750-fold, at least 800-fold, at least 850-fold, at least 900-fold, at least 950-fold, or at least 1000-fold) less efficient at integrating than an integration-competent viral vector. For example, integration-deficient may mean at least about 20-fold to about 100-fold less

efficient at integrating than a viral vector which has not been modified to be integration defective. Integration can be measured by any method known in the art, e.g., by PCR detection of integration events near an Alu element.

**[0077]** A "pseudotyped" lentivirus is a lentiviral particle having one or more envelope glycoproteins that are encoded by a virus that is distinct from the lentiviral genome. The envelope glycoprotein may be modified, mutated or engineered as described herein.

**[0078]** As used herein, the term "exogenous antigen" refers to an antigen that has been genetically engineered to be expressed in the lentiviral vectors disclosed herein. Accordingly, the term explicitly includes antigens derived from HIV that have been genetically engineered to be expressed in the lentiviral vectors disclosed herein.

**[0079]** As used herein, a Sindbis E2 glycoprotein that "preferentially binds dendritic cells expressing DC-SIGN" is a glycoprotein that binds dendritic cells expressing DC-SIGN more efficiently than cells that do not express DC-SIGN.

**[0080]** The Sindbis virus envelope protein contains four N-linked glycans—two on the E2 protein and two on the E1 protein. Two N-glycans of the virus produced in mammalian cells in the absence of a mannosidase I inhibitor have a high-mannose structure (one E2 N-linked glycan and one E1 N-linked glycan), while the remaining two have a complex structure. The two complex structure N-glycans are exposed on the surface of the envelope protein, while the two high-mannose structure N-glycans are buried within the center of the trimer of the envelope proteins. See Morizono et al., *J Virol*, 84:14, 6923-34 (2010), incorporated by reference. Accordingly, typically 50% of the N-linked glycans on a viral particle with a Sindbis virus glycoprotein produced in mammalian cells would have the high-mannose structure. A "highly mannosylated" viral particle is a particle wherein at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 99%, or 100% of N-linked glycans on the viral envelope glycoproteins comprise at least a $Man_5$ structure, preferably $Man_9$, measured by, for example, mass spectrometry (see Crispin et al., JBC 2009).

## SAMHD1 Inhibitors

### *Vpx and Vpr*

**[0081]** In some or any embodiments, the SAMHD1 inhibitor is a Vpx protein or a Vpr protein. Vpx is encoded by viruses of the HIV-2, SIV sooty mangabey (SIVsm), SIV red capped mangabey (SIVrcm), and SIV macaque (SIVmac), among others. Vpx of HIV-2 and SIV is a 112-amino-acid (aa), 18-kDa protein and is packaged in the virion in significant

quantities through its interaction with the p6 region of the $p55^{gag}$ precursor. Vpx was recently shown to inhibit the activity of a restriction factor expressed in human dendritic and myeloid cells, SAMHD1. Laguette et al., *Nature*, 474, 654–657 (2011). SAMHD1 was identified as the restriction factor that renders human dendritic and myeloid cells largely refractory to HIV-1 infection.

**[0082]** Vpx from SIV and HIV-2 are 83% identical at the amino acid level. See Goujon et al., *J Virol*, 82:24, 12335-12345 (2008). Accordingly, it may be assumed that residues that differ between SIV and HIV-2 are not important for Vpx function. Moreover, mutational analysis of Vpx from SIV and HIV-2 has been carried out by others and can be used as a guide in generating Vpx variants for use in the materials and methods of this disclosure. See Goujon et al. Asn26Ala, Ser52Ala, and Ser63Ala/Ser65Ala mutants do not affect Vpx function. Deletion of the proline-rich C-terminal 11 residue, Ser13Ala, Lys84Ala/Lys85Ala, Thr17Ala, Thr28Ala, Gly86Ala/Cys87Ala, Ser13Ala/Thr17Ala/Thr28Ala, His39Ala, and Tyr66Ala/Tyr68Ala/Tyr71Ala, Trp49Ala/Trp53Ala/Trp56Ala, and Lys68Ala/Lys77Ala mutations abolish Vpx activity.

**[0083]** In some or any embodiments, the lentiviral vector particles described herein comprise a Vpx protein or a variant thereof. In some or any embodiments, the variant retains the ability to inhibit SAMHD1. In some or any embodiments, the variant comprises an amino acid sequence at least 75%, 80%, 85%, 90% or 95% identical to SEQ ID NO: 45 (SIVsm Vpx). In some or any embodiments, the variant comprises an amino acid sequence at least 75%, 80%, 85%, 90% or 95% identical to SEQ ID NO: 46 (SIVrcm Vpx). In some or any embodiments, the variant comprises an amino acid sequence at least 75%, 80%, 85%, 90% or 95% identical to SEQ ID NO: 44 (SIVmac Vpx). In some or any embodiments, the variant comprises an amino acid sequence at least 75%, 80%, 85%, 90% or 95% identical to SEQ ID NO: 47 (HIV-2).

**[0084]** The anti-SAMHD1 activity of Vpx has been localized to the N-terminal 86 residues of Vpx. Gramberg et al., *J Virol*, 84:3, 1387-1396. Accordingly, in some or any embodiments, the functional fragment comprises the SAMHD1 inhibitory region of Vpx, i.e., amino acid residues 1 through 86 of SEQ ID NO: 44.

**[0085]** While Vpx is only present in some lentiviruses, all primate lentiviruses encode a gene closely related to Vpx called Vpr. Vpr is known to cause cell-cycle arrest. Recently, however, Vpr proteins isolated from SIVdeb and SIVmus were shown to inhibit human SAMHD1. Lim et al., *Cell Host & Microbe*, 11, 194-204 (2012). Accordingly, in some or

any embodiments, the lentiviral vector particles described herein comprise a SAMHD1-inhibiting Vpr protein or a variant thereof that retains the ability to inhibit SAMHD1. In some or any embodiments, the variant comprises an amino acid sequence at least 75%, 80%, 85%, 90% or 95% identical to SEQ ID NO: 48 (SIVdeb Vpr). In some or any embodiments, the variant comprises an amino acid sequence at least 75%, 80%, 85%, 90% or 95% identical to SEQ ID NO: 49 (SIVmus Vpr).

**[0086]** Information from sequence alignments of Vpx proteins can be used to generate functional variants and functional fragment variants of Vpx, as defined above. Techniques for deleting and mutating amino acids are well known in the art. *See* Ausubel, F.M. *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, (1998), including all supplements through 2011. Generally, to construct functional variants, either non-conservative or conservative substitutions or deletions can be introduced at the positions that differ between viruses encoding a Vpx protein, as these positions tend to be permit non-conservative substitutions while retaining function. For positions with amino acid residues conserved across viruses, the residue is either retained or conservative substitutions are introduced. Vpx, Vpr and variants thereof are tested for the ability to inhibit the activity of SAMHD1 according to the methods disclosed herein or known in the art. See Lim et al., *Cell Host & Microbe*, 11, 194-204 (2012) and Lahouassa et al., *Nature Immunol*, 13:3, 223-229 (2012), incorporated by reference in their entirety.

**[0087]** Despite previous reports indicating that packaging of SIVmac Vpx into HIV-1 virions required modification of the p6 region of the Gag protein to resemble the SIVmac p6 (Sunseri et al., *J Virol*, 86:6 (2012)), the inventors have unexpectedly discovered that SIVmac Vpx is efficiently packaged into the HIV-1-based pseudotyped lentiviral vectors disclosed herein without the need for modifying p6 or fusing Vpx to HIV-1 Vpr. Accordingly, in some or any embodiments, the Vpx protein is not fused to a Vpr protein. Similarly, in some or any embodiments, the gag protein in the packaging cell is not modified from its native sequence.

**[0088]** In some or any embodiments, the Vpx protein is fused to HIV-1 Vpr protein.

**[0089]** Typically, the Vpx protein is packaged in the viral particle. However, in some or any embodiments, a gene encoding a Vpx protein is included on the lentiviral genome and is expressed when the viral particle infects a target cell.

## Viral Vector Envelope

**[0090]** Arthropod-borne viruses (Arboviruses) are viruses that are transmitted to a host, such as humans, horses, or birds by an infected arthropod vector such as a mosquito. Arboviruses are further divided into sub-families of viruses including alphaviruses and flaviviruses, which have a single-stranded RNA genome of positive polarity and a glycoprotein-containing envelope. For example, dengue fever virus, yellow fever virus and West Nile virus belong to the flavivirus family, and Sindbis virus, Semliki Forest virus and Venezuelan Equine Encephalitis virus, are members of the alphavirus family (Wang et al. *J. Virol.* 66, 4992 (1992)). The envelope of Sindbis virus includes two transmembrane glycoproteins (Mukhopadhyay et al. *Nature Rev. Microbio.* 3, 13 (2005)): E1, believed to be responsible for fusion, and E2, believed to be responsible for cell binding. Sindbis virus envelope glycoproteins are known to pseudotype other retroviruses, including oncoretroviruses and lentiviruses.

**[0091]** The envelope of Sindbis virus and other alphaviruses incorporates into the lipid bilayer of the viral particle membrane, and typically includes multiple copies of two glycoproteins, E1 and E2. Each glycoprotein has membrane-spanning regions; E2 has an about 33 residue cytoplasmic domain whereas the cytoplasmic tail of E1 is very short (about 2 residues). Both E1 and E2 have palmitic acids attached in or near the membrane-spanning regions. E2 is initially synthesized as a precursor protein that is cleaved by furin or other Ca2+-dependent serine proteinase into E2 and a small glycoprotein called E3. Located between sequences encoding E2 and E1 is a sequence encoding a protein called 6K. E3 and 6K are signal sequences which serve to translocate the E2 and E1 glycoproteins, respectively, into the membrane. In the Sindbis virus genome, the coding region for Sindbis envelope proteins includes sequence encoding E3, E2, 6K, and E1. As used herein, the "envelope" of an arbovirus virus includes at least E2, and may also include E1, 6K and E3. An exemplary sequence of envelope glycoproteins of Sindbis virus, strain HR, is presented as SEQ ID No. 17 (E3, E2, 6K, and E1 polyprotein). Sequences of envelope glycoproteins for other arboviruses can be found in e.g., GenBank. For example, sequence encoding Dengue virus glycoproteins can be found in Accession GQ252677 (among others in GenBank) and in the virus variation database at NCBI (GenBank accessions and virus variation database are incorporated by reference for envelope glycoprotein sequences) and sequence encoding Venezuelan equine encephalitis virus envelope glycoproteins in Accession NP 040824 (incorporated by reference for sequences of envelope glycoproteins).

**[0092]** It is understood that references to a "residue number of the E2 glycoprotein" (such as residue 160, 70, 76 or 159) are defined by reference to the amino acid sequence of the protein of SEQ ID NO: 18, which is the E2 glycoprotein of Sindbis strain HR (i.e., "Sindbis HR reference strain"). For example, if a variant of Sindbis E2 glycoprotein has been produced in which residue 70 has been deleted from SEQ ID NO: 18, then "residue 160" will refer to actual residue 159 of such a variant. Analogous positions in other alphaviruses can be determined through alignments that maximize homology.

**[0093]** The use of the terms "attachment," "binding," "targeting" and the like are used interchangeably and are not meant to indicate a mechanism of the interaction between Sindbis virus envelope glycoprotein and a cellular component. DC-SIGN (Dendritic Cell Specific ICAM-3 (Intracellular Adhesion Molecules 3)-Grabbing Nonintegrin; also known as CD209) is a C-type lectin-like receptor capable of rapid binding and endocytosis of materials (Geijtenbeek, T. B., et al. Annu. Rev. Immunol. 22: 33-54, 2004). E2 appears to target virus to dendritic cells through DC-SIGN. As shown herein, cells expressing DC-SIGN are transduced by viral vector particles pseudotyped with Sindbis virus E2 better (at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold better) than isogenic cells that don't express DC-SIGN. The mechanism of how E2 glycoprotein facilitates viral infection appears to involve DC-SIGN, possibly through direct binding to DC-SIGN or causing a change in conformation or some other mechanism. Regardless of the actual mechanism, the targeting by E2 is preferential for cells expressing DC-SIGN, namely dendritic cells.

**[0094]** Sindbis virus also binds to cells via heparan sulfate (Klimstra et al., *J Virol* 72: 7357, 1998; Burmes and Griffin, *J Virol* 72: 7349, 1998). Because heparan sulfate and other cell surface glycosaminoglycans are found on the surface of most cell types, it is desirable to reduce interaction between heparan sulfate and Sindbis envelope glycoproteins. This can be accomplished by diminishing the binding of Sindbis virus envelope to heparan sulfate or increasing the binding, e.g., increasing avidity, of Sindbis virus envelope to dendritic cells or both. As a result, nonspecific binding to other molecules, which may be expressed by other cell types and which may occur even if the envelope is specific for DC-SIGN, is reduced, and the improved specificity may serve to avoid undesired side effects, such as side effects that may reduce the desired immune response, or side effects associated with off-target transduction of other cell types. Alternatively or in addition to the advantages of relatively specific transduction of cells expressing DC-SIGN, viral particles pseudotyped with Sindbis

virus envelope E2 glycoprotein may offer other advantages over viral particles pseudo-typed with glycoproteins such as VSVG. Examples of such advantages include reduced complement-mediated lysis and/or reduced neuronal cell targeting, both of which are believed to associate with administration of VSV-G pseudo-typed viral particles.

**[0095]** In various embodiments, the lentiviral vector particles disclosed herein specifically bind to cells expressing DC-SIGN and have reduced or abrogated binding to heparan sulfate. That is, a Sindbis virus envelope E2 glycoprotein may be modified to preferentially direct the virus to dendritic cells that express DC-SIGN relative to other cell types. Based on information obtained from structural studies and molecular modeling among other studies, variant sequences of envelope proteins, especially E2 and E1 glycoproteins, are designed and generated such that the glycoproteins maintain their functions as envelope proteins, but have the desired binding specificity, avidity, or level of binding. Candidate variant sequences may be created for each glycoprotein and assayed using the methods described below, or other methods known in the art, to identify envelope glycoproteins with the most desirable characteristics.

**[0096]** Certain variant sequences of Sindbis E2 have at least one amino acid alteration at residue 160 as compared to SEQ ID NO: 1 or SEQ ID NO: 18 (E2 Sindbis HR reference sequence). Residue 160 is deleted or changed to an amino acid other than glutamic acid. An alteration is most commonly a substitution of at least one amino acid, but alternatively can be an addition or deletion of one or more amino acids. Preferably, any additional amino acids are few in number and do not comprise an antigenic epitope (e.g., hemagglutinin tag sequence), which may compromise safety. When there are two or more alterations, they can both be of the same type (e.g., substitution) or differing types (e.g., a substitution and a deletion). Multiple alterations can be scattered or located contiguously in the protein sequence.

**[0097]** In some embodiments, variant sequences comprise at least one amino acid alteration in the region of about residue 50 to about residue 180 of Sindbis virus E2 (SEQ ID NO: 18). Within this region are amino acids that are involved with binding to heparan sulfate. By reducing the net positive charge of E2, electrostatic interaction with heparan sulfate can be reduced, resulting in decreased binding to heparan sulfate. Candidate positively charged amino acids in this region include lysines at residues 63, 70, 76, 84, 97, 104, 129, 131, 133, 139, 148, 149, 159 and arginine at residues 65, 92, 128, 137, 157, 170, 172 (Bear et al., *Virology* 347: 183-190, 2006) of SEQ ID NO: 18. At least several of these

amino acids are directly implicated in E2 binding to heparan sulfate. Net positive charge can be reduced by deletion of lysine or arginine or substitution of lysine or arginine with a neutral or negatively charged amino acid. For example, one or more of these lysines and arginines may be replaced with glutamic or aspartic acid. Certain embodiments have at least one substitution of lysine 70, 76 or 159. In cases where E2 is expressed as a polyprotein with E3, the lysine located adjacent to the natural E3/E2 cleavage site is maintained – that is, the recognition sequence and cleavage site is unaltered. Alternatively, the native endopeptidase cleavage site sequence is replaced with a recognition sequence for a different endopeptidase.

**[0098]** Certain variants of Sindbis virus E2 are also modified in a way that positively impacts binding to dendritic cells. Alteration of the glutamic acid found at residue 160 in the reference HR sequence (SEQ ID NO: 18) can improve binding to dendritic cells (see Gardner et al., *J Virol* 74, 11849, 2000, which is incorporated in its entirety). Alterations, such as a deletion of residue 160 or substitution of residue 160 are found in certain variants. In particular variants, a non-charged amino acid is substituted for Glu, in other variants, a non-acidic amino acid is substituted for Glu. Typically, Glu160 is replaced with one of the small or aliphatic amino acids, including glycine, alanine, valine, leucine or isoleucine.

**[0099]** Other variants comprise two or more (e.g., 3, 4, or 5) amino acid alterations. Typically in these variants one of the alterations is Glu160 and the remaining alteration(s) are changes of one or more of the lysines and arginines in the region spanning residue about 50 to about 180. Certain of the variants comprise an alteration of Glu160 to a non-acidic residue or deletion and one or more alterations of lysine 70, lysine 76, or lysine 159 with a non-basic amino acid. Some specific variants comprise a Glu160 to Gly, Lys 70 to Glu, and Lys 159 to Glu; a Glu 160 to Gly, Lys 70, 76 and 159 to Glu; a deletion of Glu 160 and Lys 70 and 159 to Glu; and a deletion of Glu 160 and Lys 70, 76, and 159 to Glu. In some embodiments, the E2 variant is between 80 and 100% (e.g., 82%, 85%, 87%, 90%, 92%, 95%, 97%, or 99%) identical to any one of SEQ ID NOs: 30 - 43 [SINvar1-14 E2].

**[0100]** In certain cases, E2 protein is first expressed as a polyprotein in fusion with at least E3 or in fusion with a leader sequence. Regardless of whether the leader sequence is E3 or another sequence, E2 in the viral envelope should be free of the E3 or other leader sequence. In other words, E2 is preferably not an E3/E2 fusion protein. In certain embodiments, E2 is expressed as part of E3-E2-6K-E1 polyprotein. In these embodiments, the polyprotein is between 80 and 100% (e.g., 82%, 85%, 87%, 90%, 92%, 95%, 97%, or 99%) identical to any one of SEQ ID NOs: 3 - 16 [SINvar1-14 polyprotein]. Sindbis virus naturally expresses E2

as part of a polyprotein and the junction regions for E3/E2, E2/6K, and 6K/E1 have sequences recognized and cleaved by endopeptidases. Normally, the E3/E2 junction is cleaved by furin or a furin-like serine endopeptidase between residues 65 and 66. Furin has specificity for paired arginine residues that are separated by two amino acids. To maintain E3/E2 cleavage by furin, residues 62-66 (RSKRS; SEQ ID NO: 26) should maintain the two arginine residues with two amino acid separation and the serine residue. Alternatively, a different cleavage sequence can be used in place of the E3/E2 furin cleavage sequence or any of the other cleavage sequences. Recognition and cleavage sites can be incorporated for endopeptidases, including, without limitation, aspartic endopeptidases (e.g., cathepsin D, chymosin, HIV protease), cysteine endopeptidases (bromelains, papain, calpain), metalloendopeptidases, (e.g., collagenase, thermolysin), serine endopeptidases (e.g., chymotrypsin, factor IXa, factor X, thrombin, trypsin), streptokinases. The recognition and cleavage site sequences for these enzymes are well known.

**[0101]** Amino acids in Sindbis virus E2, other than those already mentioned, may also be altered. Generally, a variant E2 sequence will have at least 80% sequence amino acid identity to the reference E2 sequence, or it may have at least 82%, at least 85%, at least 87%, at least 90%, at least 92%, at least 95%, or at least 98% sequence identity. In some embodiments, a variant E2 sequence has at least 80% sequence amino acid identity to SEQ ID NO: 30 [SINvar1], or it may have at least 82%, at least 85%, at least 87%, at least 90%, at least 92%, at least 95%, or at least 98% sequence identity. In some embodiments, a variant E2 sequence has at least 80% sequence amino acid identity to SEQ ID NO: 31 [SINvar2], or it may have at least 82%, at least 85%, at least 87%, at least 90%, at least 92%, at least 95%, or at least 98% sequence identity. In some embodiments, a variant E2 sequence has at least 80% sequence amino acid identity to SEQ ID NO: 32 [SINvar3], or it may have at least 82%, at least 85%, at least 87%, at least 90%, at least 92%, at least 95%, or at least 98% sequence identity.

**[0102]** The variant glycoprotein should exhibit biological function, such as the ability to facilitate infection of dendritic cells by a viral particle having an envelope comprising E2. Experiments have identified regions of envelope glycoproteins that appear to have an important role in various aspects of viral assembly, attachment to cell surface, and infection. When making variants, the following information can be used as guidelines. The cytoplasmic tail of E2 – approximately residues 408 to 415 – is important for virus assembly (West et al. J Virol 80: 4458-4468, 2006; incorporated in its entirety). Other regions are

involved in forming secondary structure (approximately residues 33-53); and involved in transport and protein stability (approximately residues 86-119) (Navaratmarajah et al., J Virol 363: 124-147, 2007; incorporated in its entirety). The variant may retain hydrophobic character of a region that spans the membrane, approximately residues 370-380. The variant may retain one or both N-linked glycosylation sites residues NIT (residues 196-198) and NFT (residues 318-320) and may retain one or more of the sites that are palmitoylated (C-396, C416 and C417) (Strauss and Strauss Microbiol Rev 58, 491-562, 1994; pp. 499-509 incorporated). On the other hand, many regions of E2 may be altered without deleterious event. For example, insertions of transposons at many different locations in E2 still resulted in viable virus (Navaratmarajah, ibid).

**[0103]** In certain embodiments, a tag peptide may be incorporated into E3, 6K, or E1 proteins. For some purposes, a tag may be incorporated into E2, but a tag is not desirable for use in a product for administration to human patients. A tag peptide, which is a short sequence (e.g., 5-30 amino acids), can be used to facilitate detection of envelope expression and its presence in viral particles. For detection purposes, a tag sequence will typically be detectable by antibodies or chemicals. Another use for a tag is to facilitate purification of viral particles. A substrate containing a binding partner for the tag can be used to absorb virus. Elution of the virus can be accomplished by treatment with a moiety that displaces the tag from the binding partner or when the tag sequence is in linkage with a cleavable sequence, treatment with the appropriate endopeptidase will conveniently allow release of virus. (See, for example, Qiagen catalog, Factor Xa Protease System). Removal of the tag peptide is generally desirable for safety purposes of the virus particles use in animal subjects. If the tag is not removed, an immune response to the tag may occur.

**[0104]** Suitable tags include, without limitation, FLAG (DYKDDDDK) (SEQ ID NO: 28) (U.S. Patent No. 4,703,004, incorporated in its entirety), for which antibodies are commercially available, chitin binding protein, maltose binding protein, glutathione-S-transferase, poly(His) (U.S. Patent No. 4,569,794, incorporated in its entirety), thioredoxiin, HA (hemagglutinin)-tag, among others. Poly(His) can be adsorbed onto affinity media containing bound metal ions, e.g., nickel or cobalt, and eluted with a low pH medium.

**[0105]** The viral particles may be evaluated to determine the specificity of the envelope glycoprotein incorporated into the virus that targets dendritic cells. For example, a mixed population of bone marrow cells can be obtained from a subject and cultured *in vitro*. Alternatively, isogenic cells lines that express or don't express DC-SIGN can be obtained and

used. The recombinant virus can be administered to the mixed population of bone marrow cells or isogenic cell lines, and expression of a reporter gene incorporated into the virus can be assayed in the cultured cells. Certain embodiments may employ a limiting dilution analysis, in which the mixed population of cells is split into separate parts, which are then separately incubated with decreasing amounts of virus (*e.g.,* 2-fold, 5-fold, 10-fold less virus in each part). In some embodiments, at least about 50%, more preferably at least about 60%, 70%, 80% or 90%, still more preferably at least about 95% of infected cells in the mixed cell population are dendritic cells that express DC-SIGN. In certain embodiments, the ratio of infected dendritic cells to infected non-dendritic cells (or non DC-SIGN expressing cells) is at least about 2:1, at least about 3:1, at least about 4:1, at least about 5:1, at least about 6:1, at least about 7:1, at least about 8:1, at least about 9:1, at least about 10:1, at least about 20:1, at least about 30:1, at least about 40:1, at least about 50:1, at least about 100:1, at least about 200:1, at least about 500:1, at least about 1000:1, at least about 5000:1, at least about 10,000:1, or more. For limiting dilution, greater selectivity is typically seen at higher dilutions (i.e., lower amounts) of input virus.

**[0106]** Activity of pseudotyped viral particles can be determined by any of a variety of techniques. For example, a preferred method to measure infectivity efficiency (IU, infectious units) is by administering viral particles to cells and measuring expression of a product encoded in the vector genome. Any product that can be assayed may be used. One convenient type of product is a fluorescent protein, such as green fluorescent protein (GFP). Other products that can be used include proteins expressed on a cell surface (e.g., detection by antibody binding), enzymes, and the like. If the product is an antigen and cells are dendritic cells, infectivity / activity can be assessed by determining an immune response. Furthermore, it is possible to ascertain side effects in a mammal. The ability to specifically target dendritic cells can also be tested directly, for example, in cell culture as described below.

**[0107]** Viral particles can also be prepared and tested for their selectivity and/or their ability to facilitate penetration of the target cell membrane. Viral particles that have an envelope with unmodified glycoproteins can be used as controls for comparison. Briefly, cells expressing a receptor for an envelope glycoprotein are infected by the virus using a standard infection assay. After a specified time, for example 48 hours post-infection, cells can be collected and the percentage of cells infected by the virus can be determined by flow cytometry, for example. Selectivity can be scored by calculating the percentage of cells

infected by virus. Similarly, the effect of a variant envelope glycoprotein on viral titer can be quantified by dividing the percentage of cells infected by virus comprising a variant envelope by the percentage of cells infected by virus comprising the corresponding wild type (unmodified) envelope glycoprotein. A particularly suitable variant will have the best combination of selectivity and infectious titer. Once a variant is selected, viral concentration assays may be performed to confirm that these viruses can be concentrated without compromising activity. Viral supernatants are collected and concentrated by ultracentrifugation. The titers of viruses can be determined by limited dilution of viral stock solution and infection of cells expressing the receptor for the envelope glycoprotein, measuring the expression of a product expressed by the viruses as described above.

**[0108]** The entry of a lentiviral vector particle into a target cell is another type of evaluation of activity. BlaM-Vpr (beta-lactamase Vpr) fusion protein has been utilized to evaluate HIV-1 viral penetration; a fusion of BlaM and a Sindbis virus envelope glycoprotein, such as E1 or an E2/E1 fusion protein can be used to assess the efficacy of an envelope protein in facilitating fusion and penetration into a target cell. Viral particles may be prepared, for example, by transient transfection of packaging cells with one or more vectors comprising the viral elements, BlaM-Vpr, and the variant envelope of interest (and an affinity molecule if appropriate). The resulting viruses can be used to infect cells expressing a molecule the targeting molecule (or affinity molecule) specifically binds in the absence or presence of the free inhibitor of binding (such as an antibody). Cells can then be washed with $CO_2$-independent medium and loaded with CCF2 dye (Aurora Bioscience). After incubation at room temperature to allow completion of the cleavage reaction, the cells can be fixed by paraformaldehyde and analyzed by flow cytometry and microscopy. The presence of blue cells indicates the penetration of viruses into the cytoplasm; fewer blue cells would be expected when blocking antibody is added (Cavrois et al. *Nat Biotechnol* 20: 1151-1154, 2002; incorporated in its entirety).

**[0109]** To investigate whether penetration is dependent upon a low pH, and to identify envelope glycoproteins with the desired pH dependence, $NH_4Cl$ or other compound that alters pH can be added at the infection step ($NH_4Cl$ will neutralize the acidic compartments of endosomes). In the case of $NH_4Cl$, the disappearance of blue cells will indicate that penetration of viruses is low pH-dependent. In addition, to confirm that the activity is pH-dependent, lysosomotropic agents, such as ammonium chloride, chloroquine, concanamycin, bafilomycin Al, monensin, nigericin, etc., may be added into the incubation buffer. These

agents elevate the pH within the endosomal compartments (e.g., Drose and Altendorf, *J. Exp. Biol.* 200, 1-8, 1997). The inhibitory effect of these agents will reveal the role of pH for viral fusion and entry. The different entry kinetics between viruses displaying different fusogenic molecules may be compared and the most suitable selected for a particular application.

**[0110]** PCR-based entry assays can be utilized to monitor reverse transcription and measure kinetics of viral DNA synthesis as an indication of the kinetics of viral entry. For example, viral particles comprising a particular envelope protein molecule are incubated with target cells, such as 293T cells, DCs, or any other cells that have been engineered to express, or which naturally express, the appropriate binding partner (receptor) for the envelope protein molecule. Either immediately, or after a time increment (to allow infection to occur), unbound viruses are removed and aliquots of the cells are analyzed for viral nucleic acids. DNA is extracted from these aliquots and subjected to amplification analysis, generally in a semi-quantitative assay, primed with LTR-specific primers. The appearance of LTR-specific DNA products indicates the success of viral entry.

## Lentiviral Vector Genome

**[0111]** The viral vector particle comprises a genome, which comprises at least one sequence (e.g., 1, 2, 3, 4, or 5) of interest. Other sequences may be included, such as sequences that allow the genome to be packaged into the virus particle and sequences that promote expression of the sequence(s) of interest following transduction of the target cell. The genome can be derived from any of a large number of suitable, available lentiviral genome based vectors, including those identified for human gene therapy applications, such as those described by Pfeifer and Verma (*Annu. Rev. Genomics Hum. Genet.* 2:177-211, 2001; which is incorporated herein by reference in its entirety). For the sake of simplicity, the genome is also referred to as "viral vector genome" or "vector genome."

*Backbone*

**[0112]** Suitable lentiviral vector genomes include those based on Human Immunodeficiency Virus (HIV-1), HIV-2, feline immunodeficiency virus (FIV), equine infectious anemia virus, Simian Immunodeficiency Virus (SIV) and maedi/visna virus. A desirable characteristic of lentiviruses is that they are able to infect both dividing and non-dividing cells, it is not necessary for target cells to be dividing (or to stimulate the target cells to divide). Generally, the genome and envelope glycoproteins will be based on different viruses, such that the resulting viral vector particle is pseudotyped. Safety features of the

vector genome are desirably incorporated. Safety features include self-inactivating LTR and a non-integrating genome.

**[0113]** In some exemplary embodiments, the viral vector genome comprises sequences from a lentivirus genome, such as the HIV-1 genome or the SIV genome. The viral genome construct may comprise sequences from the 5' and 3' LTRs of a lentivirus, and in particular may comprise the R and U5 sequences from the 5' LTR of a lentivirus and an inactivated or self-inactivating 3' LTR from a lentivirus. The LTR sequences may be LTR sequences from any lentivirus from any species. For example, they may be LTR sequences from HIV, SIV, FIV or BIV. Typically, the LTR sequences are HIV LTR sequences.

**[0114]** The vector genome may comprise an inactivated or self-inactivating 3' LTR (Zufferey et al. *J Virol* 72: 9873, 1998; Miyoshi et al., *J Virol* 72:8150, 1998; US2010/0323403, all incorporated in their entirety). A self-inactivating vector generally has a deletion of the enhancer and promoter sequences from the 3' long terminal repeat (LTR), which is copied over into the 5' LTR during vector integration. In one instance, the U3 element of the 3' LTR contains a deletion of its enhancer sequence, the polypurine tract (PPT), the TATA box, Sp1 and NF-kappa B sites. As a result of the self-inactivating 3' LTR, the provirus that is generated following entry and reverse transcription will comprise an inactivated 5' LTR. The rationale is to improve safety by reducing the risk of mobilization of the vector genome and the influence of the LTR on nearby cellular promoters. The self-inactivating 3' LTR may be constructed by any method known in the art. In various embodiments, the pseudotyped lentiviral vector comprises a lentiviral vector genome comprising the sequence of SEQ ID NO: 23. This vector comprises a deletion of the 3' PPT and TATA box. Thus, the vector is self-inactivating such that (a) transcription of the full-length vector genome from reversed transcribed dsDNA vectors in the infected target cell is prevented, (b) the risk of insertional activation that can occur when a 3'LTR can function as a promoter after integration is minimized, and (c) the extended U3 deletion can be complemented by additional, redundant safety mechanisms (e.g., mutation of integrase).

**[0115]** Optionally, the U3 sequence from the lentiviral 5' LTR may be replaced with a promoter sequence in the viral construct, such as a heterologous promoter sequence. This can increase the titer of virus recovered from the packaging cell line. An enhancer sequence may also be included. Any enhancer/promoter combination that increases expression of the viral RNA genome in the packaging cell line may be used. In one example, the CMV

enhancer/promoter sequence is used (US Patent No. 5,385,839 and US Patent No. 5,168,062, each of which is incorporated in its entirety).

**[0116]** In certain embodiments, the risk of insertional mutagenesis is minimized by constructing the lentiviral vector genome to be integration defective. A variety of approaches can be pursued to produce a non-integrating vector genome. These approaches entail engineering a mutation(s) into the integrase enzyme component of the *pol* gene, such that it encodes a protein with an inactive integrase. The vector genome itself can be modified to prevent integration by, for example, mutating or deleting one or both attachment sites, or making the 3' LTR-proximal polypurine tract (PPT) non-functional through deletion or modification. In addition, non-genetic approaches are available; these include pharmacological agents that inhibit one or more functions of integrase. The approaches are not mutually exclusive, that is, more than one of them can be used at a time. For example, both the integrase and attachment sites can be non-functional, or the integrase and PPT site can be non-functional, or the attachment sites and PPT site can be non-functional, or all of them can be non-functional.

**[0117]** As stated above, one approach is to make and use a non-functional integrase. Integrase is involved in cleavage of viral double-stranded blunt-ended DNA and joining the ends to 5'-phosphates in the two strands of a chromosomal target site. Integrase has three functional domains: N-terminal domain, which contains a zinc-binding motif (HHCC), the central domain core, which contains the catalytic core and a conserved DD35E motif (D64, D116, E152 in HIV-1), and a C-terminal domain, which has DNA binding properties. Point mutations introduced into integrase are sufficient to disrupt normal function. Many integrase mutations have been constructed and characterized (see, Philpott and Thrasher, *Human Gene Therapy* 18:483, 2007; Apolonia, Thesis submitted to University College London, April 2009, pp, 82-97; Engelman et al. *J Virol* 69: 2729, 1995; Nightingale et al. Mol Therapy, 13: 1121, 2006; all of which are incorporated in their entirety). The sequence encoding the integrase protein can be deleted or mutated to render the protein inactive, preferably without significantly impairing reverse transcriptase activity or nuclear targeting, thereby only preventing integration of the provirus into the target cell genome. Acceptable mutations can reduce integrase catalysis, strand transfer, binding to *att* sites, binding to host chromosomal DNA, and other functions. For example, a single aspartic acid to asparagine substitution at residue 35 of HIV or SIV integrase completely abolishes viral DNA integration. Deletions of integrase will generally be confined to the C-terminal domain. Deletion of coding sequence

for residues 235-288 result in a useful non-functional integrase (Engelman et al. J Virol 69:2729, 1995). As further examples, mutations can be generated, for example, Asp64 (residue numbers are given for HIV-1, corresponding residue numbers for integrase from other lentiviruses or retroviruses can be readily determined by one of ordinary skill) (e.g., D64E, D64V), Asp116 (e.g., D116N), Asn120 (e.g., N120K), Glu152, Gln148 (e.g., Q148A), Lys156, Lys159, Trp235 (e.g.W235E), Lys264 (e.g., K264R), Lys266 (e.g., K266R), Lys273 (e.g., K273R). Other mutations can be constructed and tested for integration, transgene expression, and any other desirable parameter. Assays for these functions are well known. Mutations can be generated by any of a variety of techniques, including site-directed mutagenesis and chemical synthesis of nucleic acid sequence. One mutation may be made or more than one of these mutations can be present in integrase. For example, an integrase may have mutations at two amino acids, three amino acids, four amino acids, and so on.

**[0118]** Alternatively or in combination with the use of integrase mutant(s), the attachment sites (*att*) in U3 and U5 can also be mutated. Integrase binds to these sites and the 3'-terminal dinucleotide is cleaved at both ends of the vector genome. A CA dinucleotide is located at the recessed 3' end; the CA is required for processing, mutation of the nucleotides blocks integration into the host chromosome. The A of the CA dinucleotide is the most critical nucleotide for integration, and mutations at both ends of the genome will give the best results (Brown et al *J Virol* 73:9011 (1999). In one exemplification, the CA at each end is changed to TG. In other exemplifications, the CA at each end is changed to TG at one end and GT at the other end. In other exemplifications, the CA at each end is deleted; in other exemplifications, the A of the CA is deleted at each end.

**[0119]** Integration can also be inhibited by mutation or deletion of polypurine tract (PPT) (WO 2009/076524; incorporated in its entirety), located proximally to the 3' LTR. The PPT is a polypurine sequence of about 15 nucelotides that can serve as a primer binding site for plus-strand DNA synthesis. In this case, mutations or deletions of PPT targets the reverse transcription process. Without wishing to be held to a mechanism, by mutating or deleting PPT, production of linear DNA is radically reduced and essentially only 1-LTR DNA circles are produced. Integration requires a linear double-stranded DNA vector genome, and integration is essentially eliminated without it. As stated above, a PPT can be made non-functional by mutation or by deletion. Typically, the entire about 15 nt PPT is deleted, although in some embodiments, shorter deletions of 14 nt, 13, nt, 12 nt, 11 nt, 10 nt, 9 nt, 8 nt, 7 nt, 6 nt, 5 nt, 4 nt, 3 nt and 2 nt may be made. When mutations are made, typically

multiple mutations are made, especially in the 5' half of the PPT (McWilliams et al., *J Virol* 77:11150, 2003), although single and double mutations in the first four bases still reduce transcription. Mutations made at the 3' end of PPT generally have a more dramatic effect (Powell and Levin *J Virol* 70:5288, 1996).

**[0120]** These different approaches to make a vector genome non-integrating can be used individually or in combination. Using more than one approach may be used to build a fail-safe vector through redundant mechanisms. Thus, PPT mutations or deletions can be combined with *att* site mutations or deletions or with Integrase mutations or PPT mutations or deletions can be combined with both *att* site mutations or deletions and Integrase mutations. Similarly, *att* site mutations or deletions and Integrase mutations may be combined with each other or with PPT mutations or deletions.

**[0121]** An additional approach to enhancing the safety of the pseudotyped lentiviral particles involves modifying the plasmid comprising the gag/pol genes to remove sites of potential recombination with the lentiviral vector. This approach can be used individually or in combination with any of the approaches described herein. For example, the gag and pol genes can be mammalian or human "codon optimized", i.e., at least 50%, 60%, 70%, 75%, 80%, 85%, 90% of 95% of the codons of the gag and/or pol genes are replaced with codons that encode the same amino acid but that are preferred by mammalian cells, e.g., human cells, thus improving or optimizing expression in the mammalian, e.g. human, cells. To codon optimize the gag and pol genes, a polynucleotide is generated that alters "wild-type" codons to codons more frequently utilized in the human genome. In HIV, however, certain portions of the genome should retain substantially the original codons (e.g., at least 75%, 80%, 85%, 90%, 95% or 100% of the original codons) in order to permit frameshifting that is required to synthesize Gag and Pol starting from the same initiation codon of its mRNA. Translation of Gag-Pol requires a shift of the reading frame in the 5′ direction (−1 shift) at the p7/p1 junction, around codon 432 of the mRNA. Translation of Gag-Pol then proceeds in this new reading frame until a stop codon is reached about 3,000 nucleotides later. Ribosomal −1 frameshifting is a very controlled event requiring both a specific consensus slippery sequence and a downstream secondary RNA structure which causes the ribosome to pause. Thus, according to the present disclosure, the nucleic acid encoding gag and pol contains a "non-optimized window": a region starting at around position 1228 (or starting around position 1218-1298, or 1218-1238, or 1228-1238, or 1218-1228, or 1228-1298, or 1238-1248, or 1248-1258, or 1258-1268, or 1268-1278, or 1278-1288, or 1288-1298) of SEQ ID NO: 54

(the gag-pol open reading frame) and ending at position 1509 (or ending around position 1373-1558, or 1373-1509, or 1373-1500, or 1373-1470, or 1373-1440, or 1373-1410, or 1373-1401, or 1373-1392, or 1373-1383, or 1401-1509, or 1440-1509, or 1499-1519, or 1499-1509, or 1509-1519) of SEQ ID NO: 54 that is not substantially changed from the wild-type gag-pol sequence. In other words, the non-optimized window retains substantially the original codons (e.g., at least 90%, 95% , or 100% of the original codons). It is understood that the non-optimized window corresponding to nucleotides 1228-1509 of SEQ ID NO: 54 may have a different actual nucleotide numbering when SEQ ID NO: 54 is mutated or is part of a larger nucleotide sequence; for example, if a plasmid contains 100 nucleotides 5' to SEQ ID NO: 54, then the non-optimized window will correspond to nucleotides 1328-1609 in the plasmid. In some embodiments, the region from nucleotides 1229 to 1298 retains substantially the original codons, and/or the region from nucleotides 1510-1558 is codon optimized. In some embodiments, the codon optimized polynucleotide encoding Gag and Pol comprises SEQ ID NO: 54. In some embodiments, the plasmid encoding the codon optimized gag-pol polynucleotide comprises the sequence of SEQ ID NO: 55.

**[0122]** In some or any embodiments, the plasmid encoding the human codon optimized gag and pol genes (and comprising the non-optimized window described above) also lacks a Rev responsive element (RRE). Deletion of the RRE removes yet another region of homology and potential recombination between the gag/pol plasmid and the lentiviral vector plasmid. In combination, such an approach eliminates or minimizes regions of homology between the gag/pol plasmid and the lentiviral vector, thus minimizing the chances for recombination between these plasmids that could result in a replication-competent virus. It is understood that the RRE may still be present in the packaging cell and process, but is present on a different plasmid.

*Regulatory elements*

**[0123]** As discussed herein, the viral vector genome comprises a sequence of interest that is desirable to express in target cells. Typically, the sequence of interest is located between the 5' LTR and 3' LTR sequences. Further, the sequence of interest is preferably in a functional relationship with other genetic elements, for example transcription regulatory sequences including promoters or enhancers, to regulate expression of the sequence of interest in a particular manner. In certain instances, the useful transcriptional regulatory sequences are those that are highly regulated with respect to activity, both temporally and spatially. Expression control elements that may be used for regulating the expression of the

components are known in the art and include, but are not limited to, inducible promoters, constitutive promoters, secretion signals, enhancers and other regulatory elements.

**[0124]** The sequence of interest and any other expressible sequence is typically in a functional relationship with internal promoter/enhancer regulatory sequences. An "internal" promoter/enhancer is one that is located between the 5' LTR and the 3' LTR sequences in the viral vector construct and is operably linked to the sequence of interest. The internal promoter/enhancer may be any promoter, enhancer or promoter/enhancer combination known to increase expression of a gene with which it is in a functional relationship. A "functional relationship" and "operably linked" mean, without limitation, that the sequence is in the correct location and orientation with respect to the promoter and/or enhancer that the sequence of interest will be expressed when the promoter and/or enhancer is contacted with the appropriate molecules.

**[0125]** The choice of an internal promoter/enhancer is based on the desired expression pattern of the sequence of interest and the specific properties of known promoters/enhancers. Thus, the internal promoter may be constitutively active. Non-limiting examples of constitutive promoters that may be used include the promoter for ubiquitin (US Patent No. 5,510,474; WO 98/32869, each of which is incorporated herein by reference in its entirety), CMV (Thomsen et al., *PNAS* 81:659, 1984; US Patent No. 5,168,062, each of which is incorporated herein by reference in its entirety), beta-actin (Gunning et al. 1989 *Proc. Natl. Acad. Sci. USA* 84:4831-4835, which is incorporated herein by reference in its entirety) and pgk (see, for example, Adra et al. 1987 *Gene* 60:65-74; Singer-Sam et al. 1984 Gene 32:409-417; and Dobson et al. 1982 *Nucleic Acids Res.* 10:2635-2637, each of the foregoing which is incorporated herein by reference in its entirety). In some embodiments, the promoter used to control expression of the antigens encoded by the pseudotyped lentiviral vector genome is an intron-deficient promoter. In some embodiments, the human Ubiquitin-C (UbiC) promoter is used to control expression of the antigens encoded by the pseudotyped lentiviral vector genome. In various embodiments, the UbiC promoter has been modified to remove introns, i.e., the promoter is intron deficient. The full-length UbiC promoter is 1250 nucleotides. The intron begins at 412 and goes all the way to the end (412-1250). This region can be deleted for the purpose of minimizing heterogeneous viral genomic transcripts. The HIV viral genome has a native intron within it. Thus, a lentivirus comprising a UbiC promoter would have a total of 2 introns in the lentivirus genome. The UbiC intron can exist in both spliced

and unspliced forms. Deletion of the UbiC intron eliminates the possibility of heterogenous viral transcripts and ensures homogeneity in the delivered pseudotyped lentiviral particles.

**[0126]** Alternatively, the promoter may be a tissue specific promoter. In some preferred embodiments, the promoter is a target cell-specific promoter. For example, the promoter can be from any product expressed by dendritic cells, including CD11c, CD103, TLRs, DC-SIGN, BDCA-3, DEC-205, DCIR2, mannose receptor, Dectin-1, Clec9A, MHC classII. In addition, promoters may be selected to allow for inducible expression of the sequence of interest. A number of systems for inducible expression are known in the art, including the tetracycline responsive system, the lac operator-repressor system, as well as promoters responsive to a variety of environmental or physiological changes, including heat shock, metal ions, such as metallothionein promoter, interferons, hypoxia, steroids, such as progesterone or glucocorticoid receptor promoter, radiation, such as VEGF promoter. A combination of promoters may also be used to obtain the desired expression of the gene of interest. The artisan of ordinary skill will be able to select a promoter based on the desired expression pattern of the gene in the organism or the target cell of interest.

**[0127]** The viral genome may comprise at least one RNA Polymerase II or III responsive promoter. This promoter can be operably linked to the sequence of interest and can also be linked to a termination sequence. In addition, more than one RNA Polymerase II or III promoters may be incorporated. RNA polymerase II and III promoters are well known to one of skill in the art. A suitable range of RNA polymerase III promoters can be found, for example, in Paule and White, Nucleic Acids Research., Vol. 28, pp 1283-1298 (2000), which is incorporated herein by reference in its entirety. RNA polymerase II or III promoters also include any synthetic or engineered DNA fragment that can direct RNA polymerase II or III to transcribe downstream RNA coding sequences. Further, the RNA polymerase II or III (Pol II or III) promoter or promoters used as part of the viral vector genome can be inducible. Any suitable inducible Pol II or III promoter can be used with the methods of the disclosure. Particularly suited Pol II or III promoters include the tetracycline responsive promoters provided in Ohkawa and Taira, Human Gene Therapy, Vol. 11, pp 577-585 (2000) and in Meissner et al. Nucleic Acids Research, Vol. 29, pp 1672-1682 (2001), each of which is incorporated herein by reference in its entirety.

**[0128]** An internal enhancer may also be present in the viral construct to increase expression of the gene of interest. For example, the CMV enhancer (Boshart et al. *Cell*, 41:521, 1985; which is incorporated herein by reference in its entirety) may be used. Many

enhancers in viral genomes, such as HIV, CMV, and in mammalian genomes have been identified and characterized (see GenBank). An enhancer can be used in combination with a heterologous promoter. One of ordinary skill in the art will be able to select the appropriate enhancer based on the desired expression pattern.

**[0129]** A viral vector genome will usually contain a promoter that is recognized by the target cell and that is operably linked to the sequence of interest, viral components, and other sequences discussed herein. A promoter is an expression control element formed by a nucleic acid sequence that permits binding of RNA polymerase and transcription to occur. Promoters may be inducible, constitutive, temporally active or tissue specific. The activity of inducible promoters is induced by the presence or absence of biotic or abiotic factors. Inducible promoters can be a useful tool in genetic engineering because the expression of genes to which they are operably linked can be turned on or off at certain stages of development of an organism, its manufacture, or in a particular tissue. Inducible promoters can be grouped as chemically-regulated promoters, and physically-regulated promoters. Typical chemically-regulated promoters include, not are not limited to, alcohol-regulated promoters (e.g., alcohol dehydrogenase I (alcA) gene promoter), tetracycline-regulated promoters (e.g., tetracycline-responsive promoter), steroid-regulated promoter (e.g., rat glucocorticoid receptor (GR)-based promoter, human estrogen receptor (ER)-based promoter, moth ecdysone receptor-based promoter, and the promoters based on the steroid/retinoid/thyroid receptor superfamily), metal-regulated promoters (e.g., metallothionein gene-based promoters), and pathogenesis-related promoters (e.g., *Arabidopsis* and maize pathogen-related (PR) protein-based promoters). Typical physically-regulated promoters include, but are not limited to, temperature-regulated promoters (e.g., heat shock promoters), and light-regulated promoters (e.g., soybean SSU promoter).

**[0130]** One of skill in the art will be able to select an appropriate promoter based on the specific circumstances. Many different promoters are well known in the art, as are methods for operably linking the promoter to the gene to be expressed. Both native promoter sequences and many heterologous promoters may be used to direct expression in the packaging cell and target cell. Heterologous promoters are preferred, however, as they generally permit greater transcription and higher yields of the desired protein as compared to the native promoter.

**[0131]** The promoter may be obtained, for example, from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus, bovine papilloma virus, avian sarcoma virus,

cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40). The promoter may also be, for example, a heterologous mammalian promoter, e.g., the actin promoter or an immunoglobulin promoter, a heat-shock promoter, or the promoter normally associated with the native sequence, provided such promoters are compatible with the target cell. In one embodiment, the promoter is the naturally occurring viral promoter in a viral expression system. In some embodiments, the promoter is a dendritic cell-specific promoter. The dendritic cell-specific promoter can be, for example, CD11c promoter.

**[0132]** Transcription may be increased by inserting an enhancer sequence into the vector(s). Enhancers are typically cis-acting elements of DNA, usually about 10 to 300 bp in length, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, alpha-fetoprotein, and insulin) and from eukaryotic cell viruses. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the antigen-specific polynucleotide sequence, but is preferably located at a site 5' from the promoter.

**[0133]** Expression vectors may also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. These sequences are often found in the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs and are well known in the art.

**[0134]** The viral vector genome may also contain additional genetic elements. The types of elements that may be included in the construct are not limited in any way and may be chosen to achieve a particular result. For example, a signal that facilitates nuclear entry of the viral genome in the target cell may be included. An example of such a signal is the HIV-1 flap signal. Further, elements may be included that facilitate the characterization of the provirus integration site in the target cell. For example, a tRNA amber suppressor sequence may be included in the construct. An insulator sequence from e.g., chicken β-globin may also be included in the viral genome construct. This element reduces the chance of silencing an integrated provirus in the target cell due to methylation and heterochromatinization effects. In addition, the insulator may shield the internal enhancer, promoter and exogenous gene from positive or negative positional effects from surrounding DNA at the integration site on the chromosome. In addition, the vector genome may contain one or more genetic elements designed to enhance expression of the gene of interest. For example, a woodchuck

hepatitis virus responsive element (WRE) may be placed into the construct (Zufferey et al. 1999. *J. Virol.* 74:3668-3681; Deglon et al. 2000. *Hum. Gene Ther.* 11:179-190, each of which is incorporated herein by reference in its entirety).

**[0135]** The viral vector genome is typically constructed in a plasmid form that may be transfected into a packaging or producer cell line. The plasmid generally comprises sequences useful for replication of the plasmid in bacteria. Such plasmids are well known in the art. In addition, vectors that include a prokaryotic origin of replication may also include a gene whose expression confers a detectable or selectable marker such as a drug resistance. Typical bacterial drug resistance products are those that confer resistance to ampicillin or tetracycline.

**[0136]** Plasmids containing one or more of the components described herein are readily constructed using standard techniques well known in the art. For analysis to confirm correct sequences in plasmids constructed, the plasmid may be replicated in *E. coli,* purified, and analyzed by restriction endonuclease digestion or its DNA sequence determined by conventional methods.

**[0137]** Vectors constructed for transient expression in mammalian cells may also be used. Transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of a the polypeptide encoded by the antigen-specific polynucleotide in the expression vector. See Sambrook et al., supra, pp. 16.17-16.22. Other vectors and methods suitable for adaptation to the expression of polypeptides are well known in the art and are readily adapted to the specific circumstances.

**[0138]** Using the teachings provided herein, one of skill in the art will recognize that the efficacy of a particular expression system can be tested by transfecting packaging cells with a vector comprising a gene encoding a reporter protein and measuring the expression using a suitable technique, for example, measuring fluorescence from a green fluorescent protein conjugate. Suitable reporter genes are well known in the art.

*Types of Sequences of interest*

**[0139]** The sequence of interest is not limited in any way and includes any nucleic acid that one of ordinary skill desires to have integrated, transcribed, and expressed in the target cell. The product can be a protein or a nucleic acid. The sequence of interest can encode a protein or a nucleic acid molecule, including siRNA, microRNA, a self-complementary

double stranded RNA in which the complementary region is greater than about 20 ribonucleotides in length, or an RNA that is complementary to a message RNA, where binding of said complementary (anti-sense) RNA to the message RNA blocks its ability to be translated into protein. In some instances, the sequence of interest can encode an antigen against which an immune response is desired. In particular, tumor antigens and infectious diseases antigens from agents such as HIV, HSV, HCV, HPV, malaria, or tuberculosis are desirable. Moreover, multiple sequences of interest may be included in a single vector.

**[0140]** In certain cases, the sequence of interest can be a gene encoding a small inhibiting RNA (siRNA) or a microRNA (miRNA) of interest that down-regulates expression of a molecule. For example, the gene encoding an siRNA or a microRNA can be used to down-regulate expression of negative regulators in a cell, including those that inhibit activation or maturation of dendritic cells. siRNAs and microRNAs are well known in the art (Fire et al., *Nature* 391:806, 1998; see also "The RNA Interference Resource" of Applied Biosystems, Trang et al., *Oncogene Suppl* 2:S52, 2008; Taganov, K., et al. 2007. *Immunity* 26:133-137; Dahlberg, J. E. and E. Lund. 2007. *Sci. STKE* 387:pe25; Tiemann and Rossi, *EMBO Mol Med* 1: 142, 2009). Alternatively, the sequence of interest can encode a self-complementary double stranded RNA in which the complementary region is greater than about 20 ribonucleotides in length, or an anti-sense RNA that is greater than about 20 ribonucleotides in length. Those of ordinary skill in the art will appreciate that siRNA, miRNA, dsRNA and anti-sense RNA molecules can be expressed from an RNA polymerase III promoter, or, alternatively, can be a component of a non-coding RNA that is transcribed from an RNA polymerase II promoter.

**[0141]** In addition, the sequence of interest may encode more than one product. In some configurations, the sequence to be delivered can comprise multiple genes encoding at least one protein, at least one siRNA, at least one microRNA, at least one dsRNA or at least one anti-sense RNA molecule or any combinations thereof. For example, the sequence to be delivered can include one or more genes that encode one or more antigens against which an immune response is desired. The one or more antigens can be associated with a single disease or disorder, or they can be associated with multiple diseases and/or disorders. In some instances, a gene encoding an immune regulatory protein can be included along with a gene encoding an antigen against which an immune response is desired, and the combination can elicit and regulate the immune response to the desired direction and magnitude. In other instances, a sequence encoding an siRNA, microRNA, dsRNA or anti-sense RNA molecule

can be constructed with a gene encoding an antigen against which an immune response is desired, and the combination can regulate the scope of the immune response. The products may be produced as an initial fusion product in which the encoding sequence is in functional relationship with one promoter. Alternatively, the products may be separately encoded and each encoding sequence in functional relationship with a promoter. The promoters may be the same or different.

**[0142]** In certain configurations, vectors contain polynucleotide sequences that encode dendritic cell maturation / stimulatory factors. Exemplary stimulatory molecules include GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand (CD40L), drug-inducible CD40 (iCD40), and the like. These polynucleotides are typically under the control of one or more regulatory elements that direct the expression of the coding sequences in dendritic cells. Maturation of dendritic cells contributes to successful vaccination (Banchereau, J and Palucka, A. K. Nat. Rev. Immunol. 5:296-306 (2005); Schuler, G. et al. Curr. Opin. Immunol. 15:138-147 (2003); Figdor, C. G. et al. Nat. Med. 10:475-480 (2004)). Maturation can transform DCs from cells actively involved in antigen capture into cells specialized for T cell priming. For example, engagement of CD40 by CD40L on CD4-helper T cells is a critical signal for DC maturation, resulting in potent activation of CD8 T cells. Such stimulatory molecules are also referred to as maturation factors or maturation stimulatory factors. Immune checkpoints represent significant barriers to activation of functional cellular immunity in cancer, and antagonistic antibodies specific for inhibitory ligands on T cells including CTLA4 and programmed death-1 (PD-1) are examples of targeted agents being evaluated in the clinics. A significant tolerance mechanism in chronic infections and cancer is the functional exhaustion of Ag-specific T cells that express high levels of PD-1. As the potency of therapeutic immunization has been shown to be significantly enhanced by combination with immune checkpoint control, as a non-limiting example, it can be appreciated by those of ordinary skill in the art that an alternative approach to inhibiting immune checkpoint is to inhibit the expression of programmed death (PD) ligands one and two (PD-L1/L2). One way to accomplish inhibition is by the expression of RNA molecules such as those described herein, which repress the expression of PD-L1/L2 in the DCs transduced with the lentivirus vector encoding one or more of the RNA molecules. Maturation of DCs or expression of particular elements such as immune checkpoints, for example PD-1 ligands, can be characterized by flow cytometry

analysis of up-regulation of surface marker such as MHC II, and profile of expressed chemokines and cytokines.

**[0143]** A sequence encoding a detectable product, usually a protein, can be included to allow for identification of cells that are expressing the desired product. For example, a fluorescent marker protein, such as green fluorescent protein (GFP), is incorporated into the construct along with a sequence of interest (e.g., encoding an antigen). In other cases, the protein may be detectable by an antibody or the protein may be an enzyme that acts on a substrate to yield a detectable product, or a product that allows selection of a transfected or transduced target cell, for example confers drug resistance, such as hygromycin resistance. Typical selection genes encode proteins that confer resistance to antibiotics or other toxins suitable for use in eukaryotic cells, e.g., neomycin, methotrexate, blasticidine, among others known in the art, or complement auxotrophic deficiencies, or supply critical nutrients withheld from the media. The selectable marker can optionally be present on a separate plasmid and introduced by co-transfection.

**[0144]** One or more multicistronic expression units may be utilized that include two or more of the elements (e.g., sequence(s) of interest, the envelope molecule, DC maturation factors) necessary for production of the desired virus in packaging cells. The use of multicistronic vectors reduces the total number of nucleic acid molecules required and thus avoids the possible difficulties associated with coordinating expression from multiple vector genomes. In a multicistronic vector the various elements to be expressed are operably linked to one or more promoters (and other expression control elements as necessary). In some configurations, a multicistronic vector comprises a sequence of interest, a sequence encoding a reporter product, and viral elements. The sequence of interest typically encodes an antigen and, optionally, a DC maturation factor. At times, the multicistronic vector comprises a gene encoding an antigen, a gene encoding a DC maturation factor and viral elements.

**[0145]** The disclosed pseudotyped lentiviral vectors can be engineered to express more than one, e.g., two, three, or four, antigens at a time. Several methods are known in the art for simultaneously expressing more than one gene from a single vector. For example, the vectors can comprise multiple promoters fused to the genes' open reading frames (ORFs), insertion of splicing signals between genes, fusion of genes whose expressions are driven by a single promoter, insertion of proteolytic cleavage sites between genes, insertion of internal ribosomal entry sites (IRESs) between genes, insertion of bi-directional promoters between genes, and/or "self-cleaving" 2A peptides. Each component to be expressed in a

multicistronic expression vector may be separated, for example, by an internal ribosome entry site (IRES) element or a viral 2A element, to allow for separate expression of the various proteins from the same promoter. IRES elements and 2A elements are known in the art (U.S. Pat. No. 4,937,190; de Felipe et al. 2004. *Traffic* 5: 616-626, each of which is incorporated herein by reference in its entirety). In one embodiment, oligonucleotides encoding furin cleavage site sequences (RAKR) (Fang et al. 2005. Nat. Biotech 23: 584-590, which is incorporated herein by reference in its entirety) linked with 2A-like sequences from foot-and-mouth diseases virus (FMDV; F2A), porcine teschovirus-1 (P2A), equine rhinitis A virus (ERAV; E2A), and thosea asigna virus (TaV; T2A) (Szymczak et al. 2004. *Nat. Biotechnol.* 22: 589-594, which is incorporated herein by reference in its entirety) are used to separate genetic elements in a multicistronic vector. The 2A peptide consensus sequence is D(V/I)EXNPGP (SEQ ID NO: 56). In some embodiments, the lentiviral vector comprises a polynucleotide encoding T2A (SEQ ID NO: 57). In some embodiments, the 2A peptide is encoded by the polynucleotide of SEQ ID NO: 52. The efficacy of a particular multicistronic vector can readily be tested by detecting expression of each of the genes using standard protocols.

**[0146]** Expression of two or more antigens can also be accomplished using Internal Ribosome Entry Sites (IRES). IRES enable eukaryotic ribosomes to enter and scan an mRNA at a position other than the 5' $m^7$ G-cap structure. If positioned internally, e.g., 3' of a first coding region (or cistron), an IRES will enable translation of a second coding region within the same transcript. The second coding region is identified by the first ATG encountered after the IRES. Exemplary IRES elements include viral IRES such as the picornavirus IRES and the cardiovirus IRES (see, e.g., U.S. Pat. No. 4,937,190) and non-viral IRES elements found in 5' UTRs (e.g., those elements of transcripts encoding immunoglobulin heavy chain binding protein (BiP) (Macejak et al., *Nature*, 35390-4, 1991); Drosophila Antennapedia (Oh et al., *Genes Dev.* 6:1643-53, 1992) and Ultrabithorax (Ye et al., *Mol. Cell Biol.*, 17:1714-21, 1997); fibroblast growth factor 2 (Vagner et al., *Mol. Cell Biol.*, 15:35-44, 1995); initiation factor eIF4G (Gan et al., *J. Biol. Chem.* 273:5006-12, 1998); proto-oncogene c-myc (Nanbru et al., *J. Biol. Chem.*, 272:32061-6, 1995; Stoneley, *Oncogene*, 16:423-8, 1998); and vascular endothelial growth factor (VEGF) (Stein et al., *Mol. Cell Biol.*, 18:3112-9, 1998).

**[0147]** Expression of two or more antigens can also be accomplished using bidirectional promoters, i.e., a promoter region or two back-to-back cloned promoters whose reading

directions point away from each other, and from which two open reading frames flanking the promoter region are transcribed. Examples of such promoters include the PDGF-A, neurotropic JC virus, BRCA1, transcobalamin II, and dipeptidylpeptidase IV promoters.

**[0148]** In a specific exemplification, the viral vector genome comprises: a cytomegalovirus (CMV) enhancer/promoter sequence; the R and U5 sequences from the HIV 5' LTR; a packaging sequence (ψ); the HIV-1 flap signal; an internal enhancer; an internal promoter; a gene of interest; the woodchuck hepatitis virus responsive element; a tRNA amber suppressor sequence; a U3 element with a deletion of its enhancer sequence; the chicken β-globin insulator; and the R and U5 sequences of the 3' HIV LTR. In some exemplifications, the vector genome comprises an intact lentiviral 5' LTR and a self-inactivating 3' LTR (Iwakuma et al. Virology 15:120, 1999, incorporated by reference in its entirety).

**[0149]** Construction of the vector genome can be accomplished using any suitable genetic engineering techniques known in the art, including, without limitation, the standard techniques of restriction endonuclease digestion, ligation, transformation, plasmid purification, and DNA sequencing, for example as described in Sambrook et al. (1989. Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, N.Y.), Coffin et al. (Retroviruses. Cold Spring Harbor Laboratory Press, N.Y. (1997)) and "RNA Viruses: A Practical Approach" (Alan J. Cann, Ed., Oxford University Press, (2000), each of the foregoing which is incorporated herein by reference in its entirety.

**[0150]** In some embodiments, the sequence of interest encodes at least one antigen. Any antigen that is associated with a disease or disorder can be delivered to dendritic cells using the viral particles as described herein. An antigen that is associated with the disease or disorder is identified for preparation of a viral particle that targets dendritic cells. Antigens associated with many diseases and disorders are well known in the art. An antigen may be previously known to be associated with the disease or disorder, or may be identified by any method known in the art. For example, an antigen to a type of cancer from which a patient is suffering may be known, such as a tumor-associated antigen or may be identified from the tumor itself by any of a variety of methods known in the art.

**[0151]** Tumor-associated antigens are known for a variety of cancers including, for example, renal cell carcinoma, prostate cancer, melanoma, and breast cancer. In some breast cancers, for example, the Her-2 receptor is overexpressed on the surface of cancerous cells. Exemplary tumor antigens include, but are not limited to, MAGE, e.g., MAGE-A3 and

MAGE-A1, BAGE, RAGE, and NY-ESO-1, which are unmutated antigens expressed in the immune-privileged areas of the testes and in a variety of tumor cells; lineage-specific tumor antigens such as the melanocyte-melanoma lineage antigens, MART-1/Melan-A, gp100, gp75, mda-7, tyrosinase and tyrosinase-related protein, e.g., TRP2; renal cell carcinoma – 5T4, SM22-alpha, carbonic anhydrases I and IX (also known as G250), hypoxia-inducible factors (e.g., HIF-1alpha and HIF-2alpha), VEGF or prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, and six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, which are antigens expressed in normal and neoplastic cells derived from the same tissue; epitope proteins/peptides derived from genes mutated in tumor cells or genes transcribed at different levels in tumor compared to normal cells, such as telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated or wild-type p53, cytochrome P450 1B1, and abnormally expressed intron sequences such as N-acetylglucosaminyltransferase-V; clonal rearrangements of immunoglobulin genes generating unique idiotypes in myeloma and B-cell lymphomas; epitope proteins/peptides derived from oncoviral processes, such as human papilloma virus proteins E6 and E7; nonmutated oncofetal proteins with a tumor-selective expression, such as carcinoembryonic antigen and alpha-fetoprotein. A number of tumor associated antigens have been reviewed (see, for example, "Tumor-Antigens Recognized By T-Lymphocytes," Boon T, Cerottini J C, Vandeneynde B, Vanderbruggen P, Vanpel A, Annual Review Of Immunology 12: 337-365, 1994; "A listing of human tumor antigens recognized by T cells," Renkvist N, Castelli C, Robbins P F, Parmiani G. Cancer Immunology Immunotherapy 50: (1) 3-15 MAR 2001, each of which is incorporated herein by reference in its entirety.)

**[0152]** In some or any embodiments described herein, the pseudotyped lentiviral vector comprises a polynucleotide encoding MAGE-A3 (SEQ ID NO: 58). In some embodiments, MAGE-A3 is encoded by the polynucleotide of SEQ ID NO: 50. In some embodiments, MAGE-A3 is encoded by the polynucleotide of at least 40, 50, 60, 70, 80, 90, 95, 99 percent identity to SEQ ID NO: 50. In some embodiments, the pseudotyped lentiviral vector comprises a polynucleotide encoding a fragment of MAGE-A3 of at least 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, or 310 amino acids of SEQ ID NO: 58. In some embodiments, the polynucleotide encodes a variant of MAGE-A3 that is at least 40, 50, 60, 70, 80, 90, 95, 99 percent identity to SEQ ID NO: 58. In some embodiments, the pseudotyped lentiviral vector

comprises a polynucleotide encoding NY-ESO-1 (SEQ ID NO: 59). In some embodiments, NY-ESO-1 is encoded by the polynucleotide of SEQ ID NO: 51. In some embodiments, MAGE-A3 is encoded by the polynucleotide of at least 40, 50, 60, 70, 80, 90, 95, 99 percent identity to SEQ ID NO: 51. In some embodiments, the pseudotyped lentiviral vector comprises a polynucleotide encoding a fragment of NY-ESO-1 of at least 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, or 170 amino acids of SEQ ID NO: 59. In some embodiments, the polynucleotide encodes a variant of NY-ESO-1 that is at least 40, 50, 60, 70, 80, 90, 95, 99 percent identity to SEQ ID NO: 59. In some embodiments, the pseudotyped lentiviral vector comprises a polynucleotide encoding MAGE-A3 (SEQ ID NO: 58) and a polynucleotide encoding NY-ESO-1 (SEQ ID NO: 59). In some or any embodiments, NY-ESO-1 and MAGE-A3 are expressed from the same transcript as a fusion protein that comprises NY-ESO-1 and MAGE-A3 and a self-cleaving A2 peptide between the two antigens, e.g., SEQ ID NO: 56 or 57. The antigens may be in any order (e.g., NY-ESO-1 first and MAGE-A3 second, or MAGE-A3 first and NY-ESO-1 second).

**[0153]** The antigen can also be an antigen associated with an infectious disease, such as, for example, HIV/AIDS. The antigen can be, for example, gp120 (Klimstra, W. B., et al. 2003. *J Virol* 77:12022-12032; Bernard, K. A., et al. 2000. *Virology* 276:93-103; Byrnes, A. P., et al. 1998. J Virol 72: 7349-7356, each of which is incorporated herein by reference in its entirety). Other exemplary antigens include, but are not limited to: gag, pol, env, tat, nef and rev (Lieberman, J. et al. 1997. *AIDS Res Hum Retroviruses* 13(5): 383-392; Menendez-Arias, L. et al. 1998. *Viral Immunol* 11(4): 167-181, each of which is incorporated herein by reference in its entirety).

**[0154]** Examples of viral antigens include, but are not limited to, adenovirus polypeptides, alphavirus polypeptides, calicivirus polypeptides, e.g., a calicivirus capsid antigen, coronavirus polypeptides, distemper virus polypeptides, Ebola virus polypeptides, enterovirus polypeptides, flavivirus polypeptides, hepatitis virus (AE) polypeptides, e.g., a hepatitis B core or surface antigen, or a hepatitis C virus E1 or E2 glycoproteins, core, or non-structural proteins, herpesvirus polypeptides, e.g., a herpes simplex virus or varicella zoster virus glycoprotein, immunodeficiency virus polypeptides, e.g., the human immunodeficiency virus envelope or protease, infectious peritonitis virus polypeptides, influenza virus polypeptides, e.g., an influenza A hemagglutinin, neuraminidase, or nucleoprotein, leukemia virus polypeptides, Marburg virus polypeptides, orthomyxovirus polypeptides, papilloma virus polypeptides, parainfluenza virus polypeptides, e.g., the hemagglutinin/neuraminidase,

paramyxovirus polypeptides, parvovirus polypeptides, pestivirus polypeptides, picorna virus polypeptides, e.g., a poliovirus capsid polypeptide, pox virus polypeptides, e.g., a vaccinia virus polypeptide, rabies virus polypeptides, e.g., a rabies virus glycoprotein G, reovirus polypeptides, retrovirus polypeptides, and rotavirus polypeptides.

**[0155]** Examples of bacterial antigens include, but are not limited to, Actinomyces polypeptides, Bacillus polypeptides, Bacteroides polypeptides, Bordetella polypeptides, Bartonella polypeptides, Borrelia polypeptides, e.g., B. burgdorferi OspA, Brucella polypeptides, Campylobacter polypeptides, Capnocytophaga polypeptides, Chlamydia polypeptides, Clostridium polypeptides, Corynebacterium polypeptides, Coxiella polypeptides, Dermatophilus polypeptides, Enterococcus polypeptides, Ehrlichia polypeptides, Escherichia polypeptides, Francisella polypeptides, Fusobacterium polypeptides, Haemobartonella polypeptides, Haemophilus polypeptides, e.g., H. influenzae type b outer membrane protein, Helicobacter polypeptides, Klebsiella polypeptides, L-form bacteria polypeptides, Leptospira polypeptides, Listeria polypeptides, Mycobacteria polypeptides, Mycoplasma polypeptides, Neisseria polypeptides, Neorickettsia polypeptides, Nocardia polypeptides, Pasteurella polypeptides, Peptococcus polypeptides, Peptostreptococcus polypeptides, Pneumococcus polypeptides, Proteus polypeptides, Pseudomonas polypeptides, Rickettsia polypeptides, Rochalimaea polypeptides, Salmonella polypeptides, Shigella polypeptides, Staphylococcus polypeptides, Streptococcus polypeptides, e.g., S. pyogenes M proteins, Treponema polypeptides, and Yersinia polypeptides, e.g., Y. pestis F1 and V antigens.

**[0156]** Examples of fungal antigens include, but are not limited to, Absidia polypeptides, Acremonium polypeptides, Alternaria polypeptides, Aspergillus polypeptides, Basidiobolus polypeptides, Bipolaris polypeptides, Blastomyces polypeptides, Candida polypeptides, Coccidioides polypeptides, Conidiobolus polypeptides, Cryptococcus polypeptides, Curvalaria polypeptides, Epidermophyton polypeptides, Exophiala polypeptides, Geotrichum polypeptides, Histoplasma polypeptides, Madurella polypeptides, Malassezia polypeptides, Microsporum polypeptides, Moniliella polypeptides, Mortierella polypeptides, Mucor polypeptides, Paecilomyces polypeptides, Penicillium polypeptides, Phialemonium polypeptides, Phialophora polypeptides, Prototheca polypeptides, Pseudallescheria polypeptides, Pseudomicrodochium polypeptides, Pythium polypeptides, Rhinosporidium polypeptides, Rhizopus polypeptides, Scolecobasidium polypeptides, Sporothrix

polypeptides, Stemphylium polypeptides, Trichophyton polypeptides, Trichosporon polypeptides, and Xylohypha polypeptides.

**[0157]** Examples of protozoan parasite antigens include, but are not limited to, Babesia polypeptides, Balantidium polypeptides, Besnoitia polypeptides, Cryptosporidium polypeptides, Eimeria polypeptides, Encephalitozoon polypeptides, Entamoeba polypeptides, Giardia polypeptides, Hammondia polypeptides, Hepatozoon polypeptides, Isospora polypeptides, Leishmania polypeptides, Microsporidia polypeptides, Neospora polypeptides, Nosema polypeptides, Pentatrichomonas polypeptides, Plasmodium polypeptides, e.g., P. falciparum circumsporozoite (PfCSP), sporozoite surface protein 2 (PfSSP2), carboxyl terminus of liver state antigen 1 (PfLSA1 c-term), and exported protein 1 (PfExp-1), Pneumocystis polypeptides, Sarcocystis polypeptides, Schistosoma polypeptides, Theileria polypeptides, Toxoplasma polypeptides, and Trypanosoma polypeptides.

**[0158]** Examples of helminth parasite antigens include, but are not limited to, Acanthocheilonema polypeptides, Aelurostrongylus polypeptides, Ancylostoma polypeptides, Angiostrongylus polypeptides, Ascaris polypeptides, Brugia polypeptides, Bunostomum polypeptides, Capillaria polypeptides, Chabertia polypeptides, Cooperia polypeptides, Crenosoma polypeptides, Dictyocaulus polypeptides, Dioctophyme polypeptides, Dipetalonema polypeptides, Diphyllobothrium polypeptides, Diplydium polypeptides, Dirofilaria polypeptides, Dracunculus polypeptides, Enterobius polypeptides, Filaroides polypeptides, Haemonchus polypeptides, Lagochilascaris polypeptides, Loa polypeptides, Mansonella polypeptides, Muellerius polypeptides, Nanophyetus polypeptides, Necator polypeptides, Nematodirus polypeptides, Oesophagostomum polypeptides, Onchocerca polypeptides, Opisthorchis polypeptides, Ostertagia polypeptides, Parafilaria polypeptides, Paragonimus polypeptides, Parascaris polypeptides, Physaloptera polypeptides, Protostrongylus polypeptides, Setaria polypeptides, Spirocerca polypeptides Spirometra polypeptides, Stephanofilaria polypeptides, Strongyloides polypeptides, Strongylus polypeptides, Thelazia polypeptides, Toxascaris polypeptides, Toxocara polypeptides, Trichinella polypeptides, Trichostrongylus polypeptides, Trichuris polypeptides, Uncinaria polypeptides, and Wuchereria polypeptides.

**[0159]** Examples of ectoparasite antigens include, but are not limited to, polypeptides (including protective antigens as well as allergens) from fleas; ticks, including hard ticks and soft ticks; flies, such as midges, mosquitoes, sand flies, black flies, horse flies, horn flies, deer

flies, tsetse flies, stable flies, myiasis-causing flies and biting gnats; ants; spiders, lice; mites; and true bugs, such as bed bugs and kissing bugs.

**[0160]** Once an antigen has been identified and selected, a sequence that encodes the desired antigen is identified. Preferably the sequence comprises a cDNA. Following viral infection, the sequence of interest (e.g., one encoding the antigen) is expressed by the target dendritic cells. If contacted *ex vivo*, the target dendritic cells are then transferred back to the patient, for example by injection, where they interact with immune cells that are capable of generating an immune response against the desired antigen. In preferred embodiments, the recombinant virus is injected into the patient where it transduces the targeted dendritic cells *in situ*. The dendritic cells then express the particular antigen associated with a disease or disorder to be treated, and the patient is able to mount an effective immune response against the disease or disorder.

**[0161]** The viral vector genome may contain a polynucleotide sequence encoding more than one antigen, and upon transduction of a target dendritic cell, generates immune responses to the multitude of antigens delivered to the cell. In some embodiments, the antigens are related to a single disease or disorder. In other embodiments, the antigens are related to multiple diseases or disorders. In some embodiments, the viral vector genome contains a polynucleotide sequence encoding MART-1/Melan-A, NY-ESO-1, and MAGE.

**Production of viral particles**

**[0162]** Any of a variety of methods already known in the art may be used to produce infectious viral, e.g., lentiviral, particles whose genome comprises an RNA copy of the viral vector genome. In one method, the viral vector genome is introduced into a packaging cell line that contains all the components necessary to package viral genomic RNA, transcribed from the viral vector genome, into viral particles. Alternatively, the viral vector genome may comprise one or more genes encoding viral components in addition to the one or more sequences of interest. In order to prevent replication of the genome in the target cell, however, endogenous viral genes required for replication will usually be removed and provided separately in the packaging cell line.

**[0163]** In general, the lentiviral vector particles are produced by a cell line that is transfected with one or more plasmid vectors containing the components necessary to generate the particles. These lentiviral vector particles are typically not replication-competent, i.e., they are only capable of a single round of infection. Most often, multiple

plasmid vectors are utilized to separate the various genetic components that generate the lentiviral vector particles, mainly to reduce the chance of recombination events that might otherwise generate replication competent viruses. A single plasmid vector having all of the lentiviral components can be used if desired, however. As one example of a system that employs multiple plasmid vectors, a cell line is transfected with at least one plasmid containing the viral vector genome (i.e., the vector genome plasmid), including the LTRs, the cis-acting packaging sequence, and the sequence(s) of interest, which are often operably linked to a heterologous promoter, at least one plasmid encoding the virus enzymatic and structural components (i.e., the packaging plasmid that encodes components such as, Gag and Pol), and at least one envelope plasmid encoding an Arbovirus envelope glycoprotein. Additional plasmids can be used to enhance retrovirus particle production, e.g., Rev-expression plasmids, as described herein and known in the art. Viral particles bud through the cell membrane and comprise a core that includes a genome containing the sequence of interest and an Arbovirus envelope glycoprotein that targets dendritic cells. When the Arbovirus glycoprotein is Sindbis virus E2 glycoprotein, the glycoprotein is engineered to have reduced binding to heparan sulfate compared to the reference strain HR E2 glycoprotein (SEQ ID NO: 18).

**[0164]** Transfection of packaging cells with plasmid vectors of the present disclosure can be accomplished by well-known methods, and the method to be used is not limited in any way. A number of non-viral delivery systems are known in the art, including for example, electroporation, lipid-based delivery systems including liposomes, delivery of "naked" DNA, and delivery using polycyclodextrin compounds, such as those described in Schatzlein AG. (2001. *Non-Viral Vectors in Cancer Gene Therapy: Principles and Progresses.* Anticancer Drugs, which is incorporated herein by reference in its entirety). Cationic lipid or salt treatment methods are typically employed, see, for example, Graham et al. (1973. *Virol.* 52:456; Wigler et al. (1979. *Proc. Natl. Acad. Sci. USA* 76:1373-76), each of the foregoing which is incorporated herein by reference in its entirety. The calcium phosphate precipitation method is most often used. However, other methods for introducing the vector into cells may also be used, including nuclear microinjection and bacterial protoplast fusion.

**[0165]** The packaging cell line provides the components, including viral regulatory and structural proteins, that are required in trans for the packaging of the viral genomic RNA into lentiviral vector particles. The packaging cell line may be any cell line that is capable of expressing lentiviral proteins and producing functional lentiviral vector particles. Some

suitable packaging cell lines include 293 (ATCC CCL X), 293T, HeLa (ATCC CCL 2), D17 (ATCC CCL 183), MDCK (ATCC CCL 34), BHK (ATCC CCL-10) and Cf2Th (ATCC CRL 1430) cells. The packaging cell line may stably express the necessary viral proteins. Such a packaging cell line is described, for example, in U.S. Pat. No. 6,218,181, which is incorporated herein by reference in its entirety. Alternatively a packaging cell line may be transiently transfected with nucleic acid molecules encoding one or more necessary viral proteins along with the viral vector genome. The resulting viral particles are collected and used to infect a target cell. The gene(s) encoding envelope glycoprotein(s) is usually cloned into an expression vector, such as pcDNA3 (Invitrogen, CA USA). Eukaryotic cell expression vectors are well known in the art and are available from a number of commercial sources. Packaging cells, such as 293T cells are then co-transfected with the viral vector genome encoding a sequence of interest (typically encoding an antigen), at least one plasmid encoding virus packing components, and a vector for expression of the targeting molecule. The envelope is expressed on the membrane of the packaging cell and incorporated into the viral vector.

**[0166]** Production of virus is measured as described herein and expressed as IU per volume. IU is infectious unit, or alternatively transduction units (TU); IU and TU can be used interchangeably as a quantitative measure of the titer of a viral vector particle preparation. As described herein, virus is produced in which the genome can express a product that is readily measurable. A fluorescent protein, green fluorescent protein, is preferred. The lentiviral vector is typically non-integrating. The virus is then administered to target cells and the number of target cells that express GFP is determined, such as by flow cytometry. The titer is then calculated. The titer is preferably as high as possible, but at least 1 x $10^5$ IU / mL, at least 3 x $10^5$ IU / mL, at least 1 x $10^6$ IU / mL, at least 3 x $10^6$ IU / mL, or at least 1 x $10^7$ IU / mL of cell supernatant (before any concentration). Alternatively, the titer is at least 80%, at least 90%, at least 95%, at least 100% of the titer of the same lentiviral vector pseudotyped in the same cells with VSV-G envelope.

*Production of highly mannosylated viral particles*

**[0167]** The Sindbis virus envelope protein contains four N-linked glycans—two on the E2 protein and two on the E1 protein. Two N-glycans of the virus produced in mammalian cells in the absence of a mannosidase I inhibitor have a high-mannose structure (one E2 N-linked glycan and one E1 N-linked glycan), while the remaining two have a complex structure. The two complex structure N-glycans are exposed on the surface of the envelope protein, while

the two high-mannose structure N-glycans are buried within the center of the trimer of the envelope proteins. Sindbis virus particles with complex N-linked glycans do not bind DC-SIGN as efficiently as particles with less complex, highly mannosylated glycoproteins.

**[0168]** In the present disclosure, the inventors demonstrate that viral particles produced in mammalian cells in the presence of the mannosidase I inhibitor, kifunensine, unexpectedly exhibit significantly increased DC-SIGN-binding as compared to particles produced in the presence of DMNJ.

**[0169]** In some or any embodiments, a virus packaging cell is cultured in the presence of a mannosidase I inhibitor. In some or any embodiments, the mannosidase I inhibitor is kifunensine. In some embodiments, kifunensine is present in the media at a concentration of about 0.01 μg/ml to about 1 mg/ml, about 0.1 μg/ml to about 10 μg/ml, about 0.1 μg/ml to about 9 μg/ml, about 0.1 μg/ml to about 8 μg/ml, about 0.1 μg/ml to about 7 μg/ml, about 0.1 μg/ml to about 6 μg/ml, about 0.1 μg/ml to about 5 μg/ml, about 0.1 μg/ml to about 4 μg/ml, about 0.1 μg/ml to about 3 μg/ml, about 0.1 μg/ml to about 2 μg/ml, about 0.1 μg/ml to about 1 μg/ml, about 0.25 μg/ml to about 10 μg/ml, about 0.25 μg/ml to about 9 μg/ml, about 0.25 μg/ml to about 8 μg/ml, about 0.25 μg/ml to about 7 μg/ml, about 0.25 μg/ml to about 6 μg/ml, about 0.25 μg/ml to about 5 μg/ml, about 0.25 μg/ml to about 4 μg/ml, about 0.25 μg/ml to about 3 μg/ml, about 0.25 μg/ml to about 2 μg/ml, or about 0.25 μg/ml to about 1 μg/ml.

**[0170]** In some or any embodiments wherein a pseudotyped lentiviral vector particle comprises an Sindibis virus E2 glycoprotein and a Vpx protein, the lentiviral particles are produced in the presence of a mannosidase I inhibitor. In some embodiments, the mannosidase inhibitor is deoxymannojirimycin (DMNJ). In preferred embodiments, the mannosidase inhibitor is kifunensine. In some embodiments, DMNJ is present in the media at a concentration of about 1.0 μg/ml to about 1.0 mg/ml, about 1.0 μg/ml to about 900 μg/ml, about 1.0 μg/ml to about 800 μg/ml, about 1.0 μg/ml to about 700 μg/ml, about 1.0 μg/ml to about 600 μg/ml, about 1.0 μg/ml to about 500 μg/ml, about 1.0 μg/ml to about 400 μg/ml, about 1.0 μg/ml to about 300 μg/ml, about 1.0 μg/ml to about 200 μg/ml, about 1.0 μg/ml to about 100 μg/ml, about 50 μg/ml to about 500 μg/ml, about 50 μg/ml to about 400 μg/ml, about 50 μg/ml to about 300 μg/ml, about 50 μg/ml to about 200 μg/ml, about 50 μg/ml to about 100 μg/ml, about 100 μg/ml to about 500 μg/ml, about 100 μg/ml to about

400 μg/ml, about 100 μg/ml to about 300 μg/ml, about 100 μg/ml to about 200 μg/ml, about 200 μg/ml to about 500 μg/ml, or about 200 μg/ml to about 400 μg/ml.

**[0171]** In some or any embodiments, a pseudotyped lentiviral vector particle produced in the presence of a mannosidase I inhibitor (e.g., kifunensine) comprises an envelope glycoprotein (e.g., Sindibis virus E2), wherein at least 60% of N-linked glycans comprise a Mannose$_5$ ($Man_5$), $Man_6$, $Man_7$, $Man_8$, and/or $Man_9$ structure. In some embodiments, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of N-linked glycans comprise a $Man_5$, $Man_6$, $Man_7$, $Man_8$, and/or $Man_{9+}$ structure.

**[0172]** In one scenario, one or more vectors are used to introduce polynucleotide sequences into a packaging cell line for the preparation of a lentiviral vector particle pseudotyped with a Sindbis virus envelope glycoprotein such as E2, as described herein. In some embodiments, the lentiviral vector particle is highly mannosylated. In some embodiments, the lentiviral vector particle also comprises a Vpx protein or variant thereof. In yet other embodiments, the lentiviral vector particle is highly mannosylated and comprises a Vpx protein or variant thereof. The vectors can contain polynucleotide sequences encoding the various components of the virus including the Sindbis virus envelope, a sequence(s) of interest (typically encoding an antigen), and any components necessary for the production of the virus that are not provided by the packaging cell.

**[0173]** The glycosylation profile of a viral envelope protein can be determined by any method known in the art. For example, gel shift assays on viral glycoproteins treated with glycosidases (e.g., EndoH or PNGaseF) or left untreated may be compared. Other methods include cleaving glycans from the viral glycoproteins and separating and identifying the components via HPLC and mass spectrometry methods.

**Delivery of the Virus**

**[0174]** The virus may be delivered to a target cell in any way that allows the virus to contact the target cell, e.g., dendritic cell (DC), in which delivery of a polynucleotide of interest is desired. At times, a suitable amount of virus will be introduced into a human or other animal directly (*in vivo*), e.g., though injection into the body. Suitable animals include, without limitation, horses, dogs, cats, cattle, pigs, sheep, rabbits, chickens or other birds. Viral particles may be injected by a number of routes, such as intravenous, intra-dermal, subcutaneous, intranodal, intra-peritoneal cavity, or mucosal. The virus may be delivered

using a subdermal injection device such the devices disclosed in U.S. Pat. Nos. 7,241,275, 7,115,108, 7,108,679, 7,083,599, 7,083,592, 7,047,070, 6,971,999, 6,808,506, 6,780,171, 6,776,776, 6,689,118, 6,670,349, 6,569,143, 6,494,865, 5,997,501, 5,848,991, 5,328,483, 5,279,552, 4,886,499, all of which are incorporated by reference in their entirety. Other injection locations also are suitable, such as directly into organs comprising target cells. For example, intra-lymph node injection, intra-spleen injection, or intra-bone marrow injection may be used to deliver virus to the lymph node, the spleen and the bone marrow, respectively. Depending on the particular circumstances and nature of the target cells, introduction can be carried out through other means including for example, inhalation, or direct contact with epithelial tissues, for example those in the eye, mouth or skin.

**[0175]** Alternatively, target cells are provided and contacted with the virus *in vitro*, such as in culture plates. The target cells are typically populations of cells comprising dendritic cells obtained from a healthy subject or a subject in need of treatment or in whom it is desired to stimulate an immune response to an antigen. Methods to obtain cells from a subject are well known in the art and includes phlebotomy, surgical excision, and biopsy. Human DCs may also be generated by obtaining CD34α+ human hematopoietic progenitors and using an in vitro culture method as described elsewhere (e.g., Banchereau et al. *Cell* 106, 271-274 (2001) incorporated by reference in its entirety).

**[0176]** The virus may be suspended in media and added to the wells of a culture plate, tube or other container. Media containing the virus may be added prior to the plating of the cells or after the cells have been plated. Cells are typically incubated in an appropriate amount of media to provide viability and to allow for suitable concentrations of virus in the media such that transduction of the host cell occurs. The cells are preferably incubated with the virus for a sufficient amount of time to allow the virus to infect the cells. Preferably the cells are incubated with virus for at least 1 hour, at least 5 hours or at least 10 hours.

**[0177]** In both *in vivo* and *in vitro* delivery, an aliquot of viral particles containing sufficient number to infect the desired target cells may be used. When the target cell is to be cultured, the concentration of the viral particles is generally at least 1 IU/μL, more preferably at least 10 IU/μl, even more preferably at least 300 IU/μL, even more preferably at least $1X10^4$ IU/μL, even more preferably at least $1X10^5$ IU/μL, even more preferably at least $1X10^6$IU/μL, or even more preferably at least $1X10^7$ IU/μL.

**[0178]** Following infection with the virus *in vitro*, target cells can be introduced (or re-introduced) into a human or other animal. The cells can be introduced into the dermis, under the dermis, or into the peripheral blood stream. The cells introduced into an animal are preferably cells derived from that animal, to avoid an adverse immune response. Cells derived from a donor having a similar immune background may also be used. Other cells that also can be used include those designed to avoid an adverse immunologic response.

**[0179]** Target cells may be analyzed for integration, transcription and/or expression of the sequence or gene(s) of interest, the number of copies of the gene integrated, and the location of the integration, for example. Such analysis may be carried out at any time and may be carried out by any method known in the art.

**[0180]** Subjects in which a virus, or virus-infected dendritic cells, are administered can be analyzed for location of infected cells, expression of the virus-delivered polynucleotide or gene of interest, stimulation of an immune response, and monitored for symptoms associated with a disease or disorder by any methods known in the art.

**[0181]** The methods of infecting cells disclosed above do not depend upon individual-specific characteristics of the cells. As a result, they are readily extended to a variety of animal species. In some instances, viral particles are delivered to a human or to human dendritic cells, and in other instances they are delivered to an animal such as a mouse, horse, dog, cat, or mouse or to birds. As discussed herein, the viral vector genome is pseudotyped to confer upon it a broad host range as well as target cell specificity. One of skill in the art would also be aware of appropriate internal promoters and other elements to achieve the desired expression of a sequence of interest in a particular animal species. Thus, one of skill in the art will be able to modify the method of infecting dendritic cells from any species.

**Therapeutic and prophylactic immunizations**

**[0182]** Dendritic cells may be infected with a lentivirus vector particle as described herein for the prevention of, or treatment of, a disease or disorder, particularly those for which activation of an immune response in a patient would be beneficial. Many such diseases are well known. For example, diseases or disorders that are amenable to treatment or prevention by the methods of the present disclosure include, without limitation, cancers, autoimmune diseases, and infections, including viral, bacterial, fungal and parasitic infections. In one method, a disease is treated by viral particles (e.g., highly mannosylated viral particles comprising a Vpx protein) described herein in order to deliver a sequence of interest to

dendritic cells, wherein expression of the sequence of interest produces a disease-specific antigen and leads to stimulation of antigen-specific cellular immune responses and humoral immune responses. Generally, the sequence of interest encodes an antigen against which an immune response is desired, but is not normally expressed in a dendritic cell. The antigen is expressed and presented by the dendritic cell. The viral vector genome may further encode a DC maturation factor.

**[0183]** In a typical usage, viral particles deliver to dendritic cells sequences encoding an antigen against which an immune response is desired. The delivery can be achieved by contacting dendritic cells with the virus *in vitro*, whereupon the infected dendritic cells are provided to a patient. Other times, delivery can be achieved by delivering the virus to a subject for infecting dendritic cells *in vivo*. The dendritic cells then stimulate antigen-specific T cells or B cells in a patient to induce cellular and humoral immune responses to the expressed antigen. In such ways, a patient that is suffering from a disease or disorder is treated by generating immune cells with a desired specificity.

**[0184]** In some of the viruses, DC maturation factors that activate and/or stimulate maturation of the DCs are delivered in conjunction with the sequence of interest. In alternatives, the DCs are activated by delivery of DC maturation factors prior to, simultaneously with, or after delivery of the virus. DC maturation factors may be provided separately from administration of the virus.

**[0185]** As described herein, one or more immune modulation or DC maturation factors can be encoded by one or more sequences that are contained in the viral genome and expressed after the virus infects a dendritic cell. The sequences encoding immune modulation factors can also be provided in a separate vector that is co-transfected with the viral vector encoding one or more antigens in a packaging cell line.

**[0186]** The methods described herein can be used for adoptive immunotherapy in a patient. As described above, an antigen against which an immune response is desired is identified. A polynucleotide encoding the desired antigen is obtained and packaged into a recombinant virus. Target dendritic cells are obtained from the patient and transduced with a recombinant virus containing a polynucleotide that encodes the desired antigen. The dendritic cells are then transferred back into the patient.

**[0187]** The viral particles may be injected *in vivo*, where they infect DCs and deliver a sequence of interest, typically encoding an antigen. The amount of viral particles is at least

$3X10^6$ IU, and can be at least $1X10^7$ IU, at least $3X10^7$IU, at least $1X10^8$ IU, at least $3X10^8$ IU, at least $1X10^9$ IU, or at least $3X10^9$ IU. At selected intervals, DCs from the recipient's lymphoid organs may be used to measure expression, for example, by observing marker expression, such as GFP or luciferase. Nucleic acid monitoring techniques and measurements of reverse transcriptase (RT) activity can also be used to analyze the biodistribution of viral particles. T cells from peripheral blood mononuclear cells, lymph nodes, spleens, or malignant or target pathogen-infected tissue of lentiviral vector particle-treated recipients may be measured from the magnitude and durability of response to antigen stimulation. Tissue cells other than DCs, such as epithelial cells and lymphoid cells, may be analyzed for the specificity of *in vivo* gene delivery.

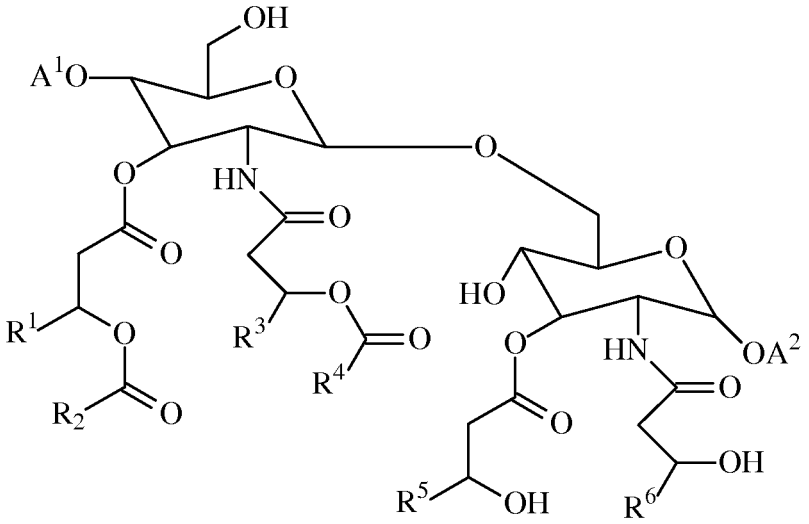
**[0188]** Vaccines often include an adjuvant. The lentiviral vector particles described herein may also be administered along with an adjuvant. The adjuvant may be administered with the recombinant virus particles, before the recombinant virus particles, or after the recombinant virus particles. If administered with the virus particles, desirable adjuvants do not significantly disrupt the integrity of the virus particle, such as disrupting the viral membrane containing the envelope glycoproteins.

**[0189]** A variety of adjuvants can be used in combination with the virus to elicit an immune response to the antigen encoded in the viral vector genome. Preferred adjuvants augment the intrinsic response to an antigen without causing conformational changes in the antigen that affect the qualitative form of the response. Preferred adjuvants include alum, 3 De-O-acylated monophosphoryl lipid A (MPL) (see GB 2220211). QS21 is a triterpene glycoside or saponin isolated from the bark of the Quillaja Saponaria Molina tree found in South America (see Kensil et al., in Vaccine Design: The Subunit and Adjuvant Approach (eds. Powell and Newman, Plenum Press, NY, 1995); U.S. Pat. No. 5,057,540). Other adjuvants are oil in water emulsions (such as squalene or peanut oil), optionally in combination with immune stimulants, such as monophosphoryl lipid A (see Stoute et al., *N. Engl. J. Med.* 336, 86-91 (1997)). Another adjuvant is CpG (*Bioworld Today*, Nov. 15, 1998). Adjuvants can be administered as a component of a therapeutic composition with an active agent or can be administered separately, before, concurrently with, or after administration of the therapeutic agent.

**[0190]** One class of adjuvants is aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate. Such adjuvants can be used with or without other specific immunostimulating agents such as MPL or 3-DMP, QS21, polymeric or monomeric

amino acids such as polyglutamic acid or polylysine. Another class of adjuvants is oil-in-water emulsion formulations. Such adjuvants can be used with or without other specific immunostimulating agents such as muramyl peptides (e.g., N-acetylmuramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'dipalmitoyl-sn- -glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), N-acetylglucsaminyl-N-acetylmuramyl-L-Al-D-isoglu-L-Ala-dipalmitoxy propylamide (DTP-DPP) theramide.TM.), or other bacterial cell wall components. Oil-in-water emulsions include (a) MF59 (WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton Mass.), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi adjuvant system (RAS), (Ribi Immunochem, Hamilton, Mont.) containing 2% squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL+CWS (Detox™). Another class of preferred adjuvants is saponin adjuvants, such as Stimulon.TM. (QS21, Aquila, Worcester, Mass.) or particles generated there from such as ISCOMs (immunostimulating complexes) and ISCOMATRIX. Other adjuvants include Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA). Other adjuvants include cytokines, such as interleukins (IL-1, IL-2, and IL-12), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF).

**[0191]** Another adjuvant that can be used with the compositions herein is identified by chemical formula (I):



(I)

wherein the moieties A1 and A2 are independently selected from the group of hydrogen, phosphate, and phosphate salts. Sodium and potassium are exemplary counterions for the phosphate salts. The moieties $R^1$, $R^2$, $R^3$, $R^4$, $R^5$, and $R^6$ are independently selected from the group of hydrocarbyl having 3 to 23 carbons, represented by $C_3$-$C_{23}$. For added clarity it will be explained that when a moiety is "independently selected from" a specified group having multiple members, it should be understood that the member chosen for the first moiety does not in any way impact or limit the choice of the member selected for the second moiety. The carbon atoms to which $R^1$, $R^3$, $R^5$ and $R^6$ are joined are asymmetric, and thus may exist in either the R or S stereochemistry. In one embodiment all of those carbon atoms are in the R stereochemistry, while in another embodiment all of those carbon atoms are in the S stereochemistry.

**[0192]** "Hydrocarbyl" refers to a chemical moiety formed entirely from hydrogen and carbon, where the arrangement of the carbon atoms may be straight chain or branched, noncyclic or cyclic, and the bonding between adjacent carbon atoms maybe entirely single bonds, i.e., to provide a saturated hydrocarbyl, or there may be double or triple bonds present between any two adjacent carbon atoms, i.e., to provide an unsaturated hydrocarbyl, and the number of carbon atoms in the hydrocarbyl group is between 3 and 24 carbon atoms. The hydrocarbyl may be an alkyl, where representative straight chain alkyls include methyl, ethyl, n-propyl, n-butyl, n-pentyl, n-hexyl, and the like, including undecyl, dodecyl, tridecyl, tetradecyl, pentadecyl, hexadecyl, heptadecyl, octadecyl, etc.; while branched alkyls include isopropyl, sec-butyl, isobutyl, tert-butyl, isopentyl, and the like. Representative saturated cyclic hydrocarbyls include cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, and the like; while unsaturated cyclic hydrocarbyls include cyclopentenyl and cyclohexenyl, and the like.

Unsaturated hydrocarbyls contain at least one double or triple bond between adjacent carbon atoms (referred to as an "alkenyl" or "alkynyl", respectively, if the hydrocarbyl is non-cyclic, and cycloalkeny and cycloalkynyl, respectively, if the hydrocarbyl is at least partially cyclic). Representative straight chain and branched alkenyls include ethylenyl, propylenyl, 1-butenyl, 2-butenyl, isobutylenyl, 1-pentenyl, 2-pentenyl, 3-methyl-1-butenyl, 2-methyl-2-butenyl, 2,3-dimethyl-2-butenyl, and the like; while representative straight chain and branched alkynyls include acetylenyl, propynyl, 1-butynyl, 2-butynyl, 1-pentynyl, 2-pentynyl, 3-methyl-1-butynyl, and the like.

**[0193]** The adjuvant of formula (I) may be obtained by synthetic methods known in the art, for example, the synthetic methodology disclosed in PCT International Publication No. WO 2009/035528, which is incorporated herein by reference, as well as the publications identified in WO 2009/035528, where each of those publications is also incorporated herein by reference. Certain of the adjuvants may also be obtained commercially. A preferred adjuvant is Product No. 699800 as identified in the catalog of Avanti Polar Lipids, Alabaster, AL, see E1 in combination with E10, below.

**[0194]** In various embodiments of the disclosure, the adjuvant has the chemical structure of formula (I) but the moieties A1, A2, R1, R2, R3, R4, R5, and R6 are selected from subsets of the options previously provided for these moieties, where these subsets are identified below by E1, E2, etc.

E1: $A_1$ is phosphate or phosphate salt and $A_2$ is hydrogen.

E2: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_3$-$C_{21}$ alkyl; and $R^2$ and $R^4$ are $C_5$-$C_{23}$ hydrocarbyl.

E3: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_5$-$C_{17}$ alkyl; and $R^2$ and $R^4$ are $C_7$-$C_{19}$ hydrocarbyl.

E4: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_7$-$C_{15}$ alkyl; and $R^2$ and $R^4$ are $C_9$-$C_{17}$ hydrocarbyl.

E5: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_9$-$C_{13}$ alkyl; and $R^2$ and $R^4$ are $C_{11}$-$C_{15}$ hydrocarbyl.

E6: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_9$-$C_{15}$ alkyl; and $R^2$ and $R^4$ are $C_{11}$-$C_{17}$ hydrocarbyl.

E7: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_7$-$C_{13}$ alkyl; and $R^2$ and $R^4$ are $C_9$-$C_{15}$ hydrocarbyl.

E8: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_{11}$-$C_{20}$ alkyl; and $R^2$ and $R^4$ are $C_{12}$-$C_{20}$ hydrocarbyl.

E9: $R^1$, $R^3$, $R^5$ and $R^6$ are $C_{11}$ alkyl; and $R^2$ and $R^4$ are $C_{13}$ hydrocarbyl.

E10: $R^1$, $R^3$, $R^5$ and $R^6$ are undecyl and $R^2$ and $R^4$ are tridecyl.

**[0195]** In certain options, each of E2 through E10 is combined with embodiment E1, and/or the hydrocarbyl groups of E2 through E9 are alkyl groups, preferably straight chain alkyl groups.

**[0196]** The adjuvant of formula (I) may be formulated into a pharmaceutical composition, optionally with a co-adjuvant, each as discussed below. In this regard reference is made to US Patent Publication No. 2008/0131466 which provides formulations, e.g., aqueous formulation (AF) and stable emulsion formulations (SE) for GLA adjuvant, where these formulations may be utilized for any of the adjuvants of formula (I).

**[0197]** An adjuvant can be administered with the virus of the disclosure as a single composition, or can be administered before, concurrent with or after administration of the recombinant virus of the disclosure. Immunogen and adjuvant can be packaged and supplied in the same vial or can be packaged in separate vials and mixed before use. Immunogen and adjuvant are typically packaged with a label indicating the intended therapeutic application. If immunogen and adjuvant are packaged separately, the packaging typically includes instructions for mixing before use. The choice of an adjuvant and/or carrier depends on the stability of the vaccine containing the adjuvant, the route of administration, the dosing schedule, the efficacy of the adjuvant for the species being vaccinated, and, in humans, a pharmaceutically acceptable adjuvant is one that has been approved or is approvable for human administration by pertinent regulatory bodies. For example, Complete Freund's adjuvant is not suitable for human administration. Alum, MPL and QS21 are preferred. Optionally, two or more different adjuvants can be used simultaneously, such as alum with MPL, alum with QS21, MPL with QS21, and alum, QS21 and MPL together. Also, Incomplete Freund's adjuvant can be used (Chang et al., Advanced Drug Delivery Reviews 32, 173-186 (1998)), optionally in combination with any of alum, QS21, and MPL and all combinations thereof.

## Pharmaceutical compositions and kits

**[0198]** Also contemplated herein are pharmaceutical compositions and kits containing a virus provided herein and one or more components. Pharmaceutical compositions can include viral vector particles as provided herein and a pharmaceutical carrier. Kits can include the pharmaceutical compositions and/or combinations provided herein, and one or more components, such as instructions for use, a device for administering a compound to a subject, and a device for administering a compound to a subject.

**[0199]** Provided herein are pharmaceutical compositions containing viral particles as provided herein and a suitable pharmaceutical carrier. Pharmaceutical compositions provided herein can be in various forms, e.g., in solid, liquid, powder, aqueous, or lyophilized form. Examples of suitable pharmaceutical carriers are known in the art. Such carriers and/or

additives can be formulated by conventional methods and can be administered to the subject at a suitable dose. Stabilizing agents such as lipids, nuclease inhibitors, polymers, and chelating agents can preserve the compositions from degradation within the body.

**[0200]** The viral vector particles provided herein can be packaged as kits. Kits can optionally include one or more components such as instructions for use, devices, and additional reagents, and components, such as tubes, containers and syringes for practice of the methods. Exemplary kits can include the viruses provided herein, and can optionally include instructions for use, a device for detecting a virus in a subject, a device for administering the virus to a subject, and a device for administering a compound to a subject.

**[0201]** Kits comprising polynucleotides encoding a gene of interest (typically an antigen) are also contemplated herein. The kit may include at least one plasmid encoding virus packaging components and vector encoding Sindbis virus E2 glycoprotein variant. Some kits will contain at least one plasmid encoding virus packaging components, a vector encoding Sindbis virus E2 glycoprotein variant, and a vector encoding at least one DC maturation factor.

**[0202]** Kits comprising a viral vector encoding a sequence of interest (typically an antigen) and optionally, a polynucleotide sequence encoding a DC maturation factor are also contemplated herein. In some kits, the kit includes at least one plasmid encoding virus packaging components and a vector encoding Sindbis virus E2 glycoprotein variant.

**[0203]** A kit may also contain instructions. Instructions typically include a tangible expression describing the virus and, optionally, other components included in the kit, and methods for administration, including methods for determining the proper state of the subject, the proper dosage amount, and the proper administration method, for administering the virus. Instructions can also include guidance for monitoring the subject over the duration of the treatment time.

**[0204]** Kits provided herein also can include a device for administering a virus to a subject. Any of a variety of devices known in the art for administering medications or vaccines can be included in the kits provided herein. Exemplary devices include, but are not limited to, a hypodermic needle, an intravenous needle, a catheter, a needle-less injection device, an inhaler, and a liquid dispenser, such as an eyedropper. Typically, the device for administering a virus of the kit will be compatible with the virus of the kit; for example, a needle-less injection device such as a high pressure injection device can be included in kits

with viruses not damaged by high pressure injection, but is typically not included in kits with viruses damaged by high pressure injection.

**[0205]** Kits provided herein also can include a device for administering a compound, such as a DC activator or stimulator, to a subject. Any of a variety of devices known in the art for administering medications to a subject can be included in the kits provided herein. Exemplary devices include a hypodermic needle, an intravenous needle, a catheter, a needle-less injection, but are not limited to, a hypodermic needle, an intravenous needle, a catheter, a needle-less injection device, an inhaler, and a liquid dispenser such as an eyedropper. Typically the device for administering the compound of the kit will be compatible with the desired method of administration of the compound.

## Exemplary Embodiments

### Methods of generating pseudotyped lentiviral vector particles

**[0206]** In some embodiments of the disclosure, a method of generating a pseudotyped lentiviral vector particle comprises:

(a) culturing in a culture medium comprising a mannosidase I inhibitor a virus packaging cell comprising:

(1) a lentiviral vector genome comprising a polynucleotide encoding an exogenous antigen,

(2) a polynucleotide encoding an alphavirus glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, and

(3) a polynucleotide encoding a SAMHD1 inhibitor; and

(b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN.

**[0207]** In specific aspects, the mannosidase inhibitor is kifunensine or DMNJ.

**[0208]** In specific aspects, the alphavirus glycoprotein is a Sindbis virus E2 glycoprotein.

**[0209]** In specific aspects, the SAMHD1 inhibitor is a Vpx protein, e.g., a SIVmac Vpx protein, a SIVsm protein, a SIVrcm, or an HIV-2 Vpx protein. In specific aspects, the SAMHD1 inhibitor is an antibody or fragment thereof. In specific aspects, the SAMHD1 inhibitor is a Vpr protein with SAMHD1-inhibiting ability, e.g., a SIVdeb Vpr protein or a SIVmus Vpr protein.

**[0210]** In some embodiments of the disclosure, a method of generating a pseudotyped lentiviral vector particle comprises:

(a) culturing in a culture medium comprising kifunensine a virus packaging cell comprising:

(1) a lentiviral vector genome comprising a polynucleotide encoding an exogenous antigen,

(2) a polynucleotide encoding a Sindbis E2 glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, and

(3) a polynucleotide encoding a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity; and

(b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN.

**[0211]** In specific aspects, the E2 glycoprotein is 90% identical to SEQ ID NO: 30 [SIN-Var1]. In some aspects, (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein. In some aspects, the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

**[0212]** In specific aspects, the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx (SEQ ID NO: 44).

**[0213]** In specific aspects, the Vpx protein comprises an amino acid sequence at least 80% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47). In specific aspects, the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

**[0214]** In specific aspects, the Vpr protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence at least 80% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49). In specific aspects, the Vpr protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an

amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0215]** In specific aspects, the antigen is a tumor-specific antigen or a virus-specific antigen. In some aspects, the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, e.g., MAGE-A3 and MAGE-A1, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, e.g., TRP2, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, merkel cell virus T-antigen oncoproteins, and alpha-fetoprotein. In some aspects, the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

**[0216]** In specific aspects, the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen. In specific aspects, the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens. In some aspects, the self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57. In some aspects, the first antigen is NY-ESO-1 and the second antigen is MAGE-A3.

**[0217]** In specific aspects, the kifunensine is present in the culture medium at a concentration of about 0.1 μg/ml to about 10 μg/ml. In some aspects, the kifunensine is present in the culture medium at a concentration of about 0.25 μg/ml to about 2 μg/ml. In some aspects, the kifunensine is present in the culture medium at a concentration of about 0.01 μg/ml to about 1 mg/ml.

**[0218]** In specific aspects, the virus packaging cell further comprises:

(i) a polynucleotide comprising gag and pol genes; and

(ii) a polynucleotide encoding a rev protein. In some aspects, the polynucleotide encoding the Vpx protein is on the same or different plasmid as the polynucleotide encoding the rev protein, or the polynucleotide comprising the gag and pol genes. In some aspects, the gag and pol genes are human codon optimized and comprise a non-optimized window around position 1228 to 1509 of SEQ ID NO: 54. In some aspects, the polynucleotide comprising gag and pol genes lacks a functional rev responsive element (RRE). In some aspects, the pol gene encodes an inactive integrase enzyme. In some aspects, the integrase enzyme has a D64V mutation.

**[0219]** In specific aspects, the lentiviral vector genome is derived from HIV-1.

**[0220]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is capable of integrating.

**[0221]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is integration defective or integration deficient. For example, the lentiviral vector may integrate at a frequency at least 10-fold (e.g., at least 20-fold, at least 30-fold, at least 40-fold, at least 50-fold, at least 60-fold, at least 70-fold, at least 80-fold, at least 90-fold, at least 100-fold, at least 150-fold, at least 200-fold, at least 250-fold, at least 300-fold, at least 350-fold, at least 400-fold, at least 450-fold, at least 500-fold, at least 550-fold, at least 600-fold, at least 650-fold, at least 700-fold, at least 750-fold, at least 800-fold, at least 850-fold, at least 900-fold, at least 950-fold, or at least 1000-fold) less efficient at integrating than an integration-competent viral vector. In exemplary embodiments, the lentiviral vector may be at least about 20-fold to about 100-fold less efficient at integrating.

**[0222]** In specific aspects, the lentiviral vector genome has an inactivated 3' long terminal repeat (LTR) or a self-inactivating 3' long terminal repeat (LTR). In some aspects, the lentiviral vector genome comprises a U3 element lacking at least one of an enhancer sequence, a TATA box, an Sp1 site, an NK-kappa B site, or a polypurine tract (PPT). In some aspects, the pol gene encodes an inactive integrase enzyme and the lentiviral vector genome lacks a functional polypurine tract (PPT).

**[0223]** In specific aspects, the lentiviral vector genome comprises the nucleotide sequence of any one of SEQ ID NOs: 21 [SIN vector], 22 [703 vector], or 23 [704 vector].

**[0224]** In specific aspects, the lentiviral vector genome further comprises a nucleotide sequence encoding a dendritic cell maturation/stimulatory factor. In some aspects, the dendritic cell maturation/stimulatory factor is selected from the group consisting of GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand, and drug-inducible CD40.

**[0225]** In specific aspects, the nucleotide sequence encoding an antigen is operably linked to a promoter selected from the group consisting of the human Ubiquitin-C promoter (UbiC), the cytomegalovirus immediate early promoter (CMV), the Rous sarcoma virus promoter (RSV), and the tetracycline-responsive promoter. In some aspects, the promoter is an intron-deficient promoter. In some aspects, the intron-deficient promoter is a UbiC.

**[0226]** In specific aspects, a lentiviral vector particle produced by the method of paragraph [0206], [0210], or [0218] is provided.

**[0227]** In specific aspects, a lentiviral vector particle produced by the method of paragraph [0216] is provided.

**Compositions comprising pseudotyped lentiviral vector particles**

**[0228]** In some or any embodiments of the disclosure, there is provided a composition comprising pseudotyped lentiviral vector particles comprising (a) a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity, (b) an exogenous polynucleotide encoding an antigen, and (c) a plurality of envelope glycoproteins that preferentially bind cells expressing DC-SIGN, wherein the composition is more highly mannosylated compared to a control composition of the same pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor. For example, such a highly mannosylated composition is characterized by containing envelope glycoproteins that are more EndoH-sensitive than envelope glycoproteins of a control composition prepared in the absence of a mannosidase inhibitor. As another example, such a highly mannosylated composition is characterized by containing envelope glycoproteins exhibiting an increased amount of EndoH-sensitive glycan as compared to envelope glycoproteins of a control composition prepared in the absence of a mannosidase inhibitor. It is understood that the control composition will contain approximately the same number of pseudotyped lentiviral vector particles comprising envelope glycoproteins having the same amino acid sequence(s). It is also understood that while the disclosure is primarily focused on alphavirus E2 glycoprotein, which is responsible for recognition and binding to dendritic cells, and highly mannosylated versions thereof, the

alphavirus envelope also contains E1 glycoproteins that are susceptible to high mannosylation. Thus, references to envelope glycoproteins and highly mannosylated envelope glycoproteins include references to highly mannosylated alphavirus E2 and/or E1 glycoproteins, specifically highly mannosylated Sindbis E2 and/or E1 glycoproteins. High mannosylation of other types of virus envelopes, specifically retrovirus envelopes, also improves recognition of dendritic cells.

**[0229]** In some embodiments of the disclosure, there is provided a composition comprising pseudotyped lentiviral vector particles comprising (a) a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity, (b) an exogenous polynucleotide encoding an antigen, and (c) a plurality of Sindbis E2 glycoproteins that preferentially bind cells expressing DC-SIGN, wherein the composition is more highly mannosylated compared to a control composition of pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor. A substantial number of E2 glycoproteins in such compositions are more highly mannosylated, e.g. more EndoH-sensitive, than E2 glycoprotein in control compositions prepared in the absence of a mannosidase inhibitor.

**[0230]** EndoH is a specialized endoglycosidase that will only cleave high-mannose N-linked glycosylation (see Figure 3A), e.g., Man5-9 glycans; Man3-4 glycans are resistant to EndoH. In contrast, PNGase F will cleave all types of glycosylation, including low-mannose glycans <Man5. When viral particles are produced in the presence of a mannosidase I inhibitor, such as kifunensine, the glycoproteins in the viral envelope will contain more high-mannose glycans that are susceptible to cleavage by EndoH (i.e., will be more "EndoH-sensitive"). One way of detecting the presence of high-mannose glycans in a composition of viral particles is to determine the molecular weight of the envelope glycoproteins by electrophoresis by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) after EndoH treatment. This "gel shift" assay is illustrated in Example 3. Samples of the viral particles, and control compositions of the same viral particles prepared in the absence of mannosidase inhibitor, can be run on a 10% SDS-PAGE gel and immunoblotted with antibody against the Sindbis glycoproteins. Virus envelope produced in the presence of mannosidase I inhibitors is more EndoH-sensitive and consequently runs faster on the gel (a farther distance) after EndoH treatment, compared to control virus. Thus, the presence of high-mannose glycoprotein can be measured using a gel-shift assay after EndoH treatment.

**[0231]** Control virus may be partially sensitive to EndoH treatment due to the presence of glycosylation sites in the Sindbis glycoproteins that are normally high mannose because they

are internal and not exposed to mannosidase I during production. Thus, when run on 10% SDS-PAGE, control virus may exhibit some shift in molecular weight after EndoH treatment, due to EndoH cleavage of such internal high mannose glycans. This shift, however, may be only about 35% of the shift seen when control virus is treated with PNGase F, which cleaves all of the glycans.

**[0232]** Thus, in specific aspects, the amount of EndoH-sensitive glycan is detected by determining molecular weight of the Sindbis glycoproteins by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) after EndoH treatment. An increased amount of endoH-sensitive glycan in the composition, which indicates that the composition of viral particles is highly mannosylated, is detected when EndoH treatment results in the band corresponding to the envelope (E2 and/or E1) glycoproteins on a 10% SDS-PAGE gel shifting to a lower molecular weight compared to control envelope glycoproteins, as determined by visual inspection.

**[0233]** In some illustrative embodiments, the molecular weight of said envelope glycoproteins after treatment with EndoH has shifted completely, and is substantially the same as the molecular weight of said envelope glycoproteins after treatment with PNGaseF. In other illustrative embodiments, the molecular weight of said envelope glycoproteins after treatment with EndoH has shifted approximately 90% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F. In other illustrative embodiments, the molecular weight of said envelope glycoproteins after treatment with EndoH has shifted approximately 90% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F. In yet other illustrative embodiments, the molecular weight of said envelope glycoproteins has shifted about 40% or more, or preferably about 45% or more, or about 50% or more, or about 55% or more, or about 60% or more, or about 65% or more, or about 70% or more, or about 75% or more, or about 80% or more, or about 85% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F. As noted above, reference to envelope glycoproteins specifically includes reference to Sindbis E2 and/or E1 glycoproteins.

**[0234]** In specific aspects, at least 30%, at least 35%, at least 40% ,at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% of the envelope glycoproteins in said composition, e.g. the

Sindbis E2 and/or E1 glycoproteins in said composition, have an increased amount of EndoH-sensitive glycan as compared to control envelope glycoproteins having the same amino acid sequence(s) in a control composition of pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor.

**[0235]** In some embodiments of the disclosure, a composition comprises pseudotyped lentiviral vector particles comprising (a) a SAMHD1 inhibitor, (b) a lentiviral genome comprising a sequence of interest, and (c) an envelope glycoprotein that preferentially binds cells expressing DC-SIGN, wherein at least 80% of N-linked glycans in said composition comprise a $Man_9$ structure.

**[0236]** In specific aspects, the SAMHD1 inhibitor is a Vpx protein, e.g., a SIVmac Vpx protein, a SIVsm Vpx protein, a SIVrcm Vpx protein, or an HIV-2 Vpx protein. In specific aspects, the SAMHD1 inhibitor is an antibody or fragment thereof. In specific aspects, the SAMHD1 inhibitor is a Vpr protein with SAMHD1-inhibiting ability, e.g., a SIVdeb Vpr protein or a SIVmus Vpr protein.

**[0237]** In specific aspects, the sequence of interest encodes a protein or a nucleic acid molecule, such as a siRNA, microRNA, a self-complementary double stranded RNA in which the complementary region is greater than about 20 ribonucleotides in length, or an RNA that is complementary to a message RNA, where binding of said complementary (anti-sense) RNA to the message RNA blocks its ability to be translated into protein. In some instances, the sequence of interest encodes an antigen against which an immune response is desired. In specific aspects, the sequence of interest encodes a tumor antigen or an infectious disease antigens (e.g., from agents such as HIV, HSV, HCV, HPV, malaria, or tuberculosis). In specific aspects, multiple sequences of interest are included in a single vector.

**[0238]** In some embodiments of the disclosure, a composition comprises pseudotyped lentiviral vector particles comprising (a) a Vpx protein, (b) an exogenous polynucleotide encoding an antigen, and (c) an envelope glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, wherein at least 80% of N-linked glycans in said composition comprise a $Man_9$ structure.

**[0239]** In specific aspects, the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx protein (SEQ ID NO: 44).

**[0240]** In specific aspects, the Vpx protein comprises an amino acid sequence at least 80% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx

(SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47). In specific aspects, the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

**[0241]** In specific aspects, the Vpr protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence at least 80% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49). In specific aspects, the Vpr protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0242]** In specific aspects, the pseudotyped lentiviral vector particle infects dendritic cells expressing DC-SIGN with an *in vitro* transduction efficiency of at least at least 1%, or at least 5%, or at least 10%, or at least 20%.

**[0243]** In specific aspects, the glycoprotein is a Sindbis virus E2 glycoprotein. In some aspects, the E2 glycoprotein has at least 90% identity to SEQ ID NO: 30 [SIN-Var1]. In some aspects, (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein.

**[0244]** In specific aspects, the antigen is a tumor-specific antigen or a virus-specific antigen. In some aspects, the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, MAGE-A3 and MAGE-A1, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, e.g., TRP2, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, merkel cell virus T-antigen oncoproteins, and alpha-fetoprotein. In some aspects, the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a

distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

**[0245]** In specific aspects, the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen. In specific aspects, the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens. In some aspects, the self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57. In some aspects, the first antigen is MAGE-A3 and the second antigen is NY-ESO-1.

**[0246]** In specific aspects, the lentiviral vector genome is derived from HIV-1.

**[0247]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is capable of integrating.

**[0248]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is integration deficient or integration defective.

**[0249]** In specific aspects, the lentiviral vector genome has an inactivated 3' long terminal repeat (LTR) or a self-inactivating 3' long terminal repeat (LTR). In some aspects, the lentiviral vector genome comprises a U3 element lacking at least one of an enhancer sequence, a TATA box, an Sp1 site, an NK-kappa B site, or a polypurine tract (PPT).

**[0250]** In specific aspects, the lentiviral vector genome comprises the nucleotide sequence of any one of SEQ ID NOs: 21 [SIN vector], 22 [703 vector], or 23 [704 vector].

**[0251]** In specific aspects, the lentiviral vector genome further comprises a nucleotide sequence encoding a dendritic cell maturation/stimulatory factor. In some aspects, the dendritic cell maturation/stimulatory factor is selected from the group consisting of GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand, and drug-inducible CD40.

**[0252]** In specific aspects, the nucleotide sequence encoding an antigen is operably linked to a promoter selected from the group consisting of the human Ubiquitin-C promoter (UbiC),

the cytomegalovirus immediate early promoter (CMV), the Rous sarcoma virus promoter (RSV), and the tetracycline-responsive promoter. In some aspects, the promoter has been modified to be intron-deficient.

**[0253]** In some aspects, pseudotyped lentiviral vector particles comprise a Rev protein.

**[0254]** In specific aspects, the pseudotyped lentiviral vector particles have an IU of at least $10^5$/mL.

**[0255]** In specific aspects, the composition further comprises an immunostimulating agent.

**[0256]** In specific aspects, the composition further comprises an adjuvant. For example, as noted above, adjuvants include alum, or 3 De-O-acylated monophosphoryl lipid A (MPL). Classes of adjuvants disclosed herein include (a) aluminum salts, (b) oil-in-water emulsion formulations, optionally with or without other specific immunostimulating agents such as muramyl peptides or other bacterial cell wall components, (c) saponin adjuvants, including ISCOMs (immunostimulating complexes) and ISCOMATRIX; (d) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (e) cytokines; and (f) adjuvants of formula (I). Within formula (I), a preferred adjuvant is Product No. 699800 as identified in the catalog of Avanti Polar Lipids, Alabaster, AL, see E1 in combination with E10, where (i) $A_1$ is phosphate or phosphate salt and $A_2$ is hydrogen and (ii) $R^1$, $R^3$, $R^5$ and $R^6$ are undecyl and $R^2$ and $R^4$ are tridecyl. In specific aspects, the envelope glycoproteins also bind cells expressing mouse SIGNR1.

**[0257]** In specific aspects, the pseudotyped lentiviral vector particles also more efficiently transduce cells expressing mouse SIGNR1 compared to cells not expressing mouse SIGNR1.

**[0258]** In some embodiments of the disclosure, the above-mentioned pseudotyped lentiviral vector particles are for use in a method of treatment or prevention of a disease or disorder in a patient. In specific aspects, the disease or disorder is a cancer, an autoimmune disease, or an infection, for example, a viral infection, a bacterial infection, a fungal infection or a parasitic infection.

**Viral vector particles comprising a Vpx protein**

**[0259]** In some embodiments of the disclosure, there is provided a pseudotyped lentiviral vector particle capable of targeting a cell expressing comprising:

(a) a non-native envelope glycoprotein;

(b) a lentiviral vector genome comprising an exogenous polynucleotide of interest; and

(c) a Vpx protein or other SAMHD1 inhibitor.

**[0260]** In some aspects, pseudotyped lentiviral vector particle further comprises a Rev protein.

**[0261]** In some embodiments of the disclosure, a lentiviral vector packaging system for producing a pseudotyped lentiviral vector particle is provided, comprising:

(i) a first polynucleotide encoding a non-native envelope glycoprotein;

(ii) a second polynucleotide comprising gag and pol genes;

(iii) a third polynucleotide encoding a rev protein;

(iv) a fourth polynucleotide encoding a Vpx protein or other SAMHD1 inhibitor; and

(v) a lentiviral vector genome comprising an exogenous polynucleotide of interest;

wherein two or more polynucleotides are on the same plasmid or on different plasmids. In specific aspects, the polynucleotide of (iv) is on the same plasmid as any one or more of the polynucleotides of (i), (ii), (iii) or (v).

**[0262]** In specific aspects, the packaging cell is selected from the group consisting of 293, 293T, HeLa, D17, MDCK, BHK and Cf2Th cells.

**[0263]** In specific aspects, the Vpx protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence that is at least 80% identical to SEQ ID NO: 44 (SIVmac), optionally an SIVmac Vpx protein (SEQ ID NO: 44), SIVsm Vpx protein (SEQ ID NO: 45), SIVrcm Vpx protein (SEQ ID NO: 46), or an HIV-2 VPX protein (SEQ ID NO: 47). In specific aspects, the Vpx protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence that is at least 90% identical to SEQ ID NO: 44 (SIVmac), optionally an SIVmac Vpx protein (SEQ ID NO: 44), SIVsm Vpx protein (SEQ ID NO: 45), SIVrcm Vpx protein (SEQ ID NO: 46), or an HIV-2 VPX protein (SEQ ID NO: 47).

**[0264]** In specific aspects, the Vpr protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence at least 80% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ

ID NO: 49). In specific aspects, the Vpr protein of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the preceding embodiments comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0265]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or lentiviral vector packaging system of any of the above embodiments is derived from HIV-1 or MLV.

**[0266]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is capable of integrating.

**[0267]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is non-integrating.

**[0268]** In specific aspects, the non-native envelope glycoprotein of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is selected from the group consisting of an alphavirus glycoprotein, including Sindbis E2 glycoprotein, VEE E2 glycoprotein, rhabdovirus or vesiculovirus glycoprotein, including VSV-G glycoprotein, arenavirus glycoprotein, coronavirus glycoprotein, paramyxovirus glycoprotein, flavirvirus glycoprotein, orthomyxovirus glycoprotein, and baculovirus glycoprotein, preferably an alphavirus such as Sindbis virus.

**[0269]** In specific aspects, the non-native envelope glycoprotein of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is a Sindbis virus E2 glycoprotein comprising an amino acid sequence at least 80% identical to SEQ ID NO: 30 [SINVar1].

**[0270]** In specific aspects, the non-native envelope glycoprotein of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments preferentially binds a cell expressing SAMHD1. In some aspects, the cell expressing SAMHD1 is a myeloid cell, optionally a dendritic cell, monocyte or a macrophage.

**[0271]** In specific aspects, the non-native envelope glycoprotein of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments preferentially binds dendritic cells expressing DC-SIGN.

**[0272]** In specific aspects, the polynucleotide of interest encodes (i) an antigen, (ii) a therapeutic polypeptide, or (iii) an inhibitory oligonucleotide. In some aspects, the polynucleotide of interest encodes an siRNA.

**[0273]** In specific aspects, the polynucleotide of interest encodes a viral, bacterial, fungal, protozoal or cancer antigen.

**[0274]** In specific aspects, the envelope glycoproteins also bind cells expressing mouse SIGNR1.

**[0275]** In specific aspects, the pseudotyped lentiviral vector particles also more efficiently transduce cells expressing mouse SIGNR1 compared to cells not expressing mouse SIGNR1.

**[0276]** In some embodiments of the disclosure, there is provided a method of producing a pseudotyped lentiviral vector particle of any of the preceding embodiments comprising culturing the packaging system of any of the preceding embodiments in a culture medium. In some aspects, the culture medium comprises a mannosidase I inhibitor, optionally kifunensine or DMNJ.

**[0277]** In some embodiments of the disclosure, there is provided a composition comprising the pseudotyped lentiviral vector particles of any of the preceding embodiments wherein the vector particles are highly mannosylated.

**[0278]** In some embodiments of the disclosure, there is provided a composition comprising the pseudotyped lentiviral vector particles of any of the preceding embodiments wherein at least 80% of N-linked glycans in said composition comprise a $Man_9$ structure.

**[0279]** In some embodiments of the disclosure, there is provided a method of delivering a lentiviral vector genome to a cell expressing SAMHD1, *in vitro* or *in vivo*, comprising contacting the cell with the vector particle of any of the above embodiments. In some aspects, the cell expressing SAMHD1 is a dendritic cell, a monocyte, or a macrophage.

**[0280]** In some embodiments of the disclosure, there is provided a method of eliciting an immune response or immunizing an individual comprising administering the vector particle of any of the above embodiments to an individual, preferably a vector particle that preferentially binds dendritic cells expressing DC-SIGN.

**[0281]** In some embodiments of the disclosure, the above-mentioned pseudotyped lentiviral vector particles are for use in a method of treatment or prevention of a disease or disorder in a patient. In specific aspects, the disease or disorder is a cancer, an autoimmune

disease, or an infection, for example, a viral infection, a bacterial infection, a fungal infection or a parasitic infection.

**Methods of generating viral vector particles with highly mannosylated envelope glycoproteins**

**[0282]** In some embodiments of the disclosure, there is provided a method of generating a virus vector particle that preferentially binds dendritic cells expressing DC-SIGN comprising: culturing a virus packaging cell comprising viral particle components in a culture medium, said components comprising a polynucleotide encoding an envelope glycoprotein that preferentially binds to dendritic cells expressing DC-SIGN, and wherein the culture medium comprises kifunensine at a concentration of about 0.01 μg/ml to about 1 mg/ml, preferably about 0.1 μg/ml to about 10 μg/ml .

**[0283]** In specific aspects, the kifunensine is present in the culture medium at a concentration of about 0.25 μg/ml to about 2 μg/ml.

**[0284]** In specific aspects, the kifunensine is present in the culture medium at a concentration of about 0.1 μg/ml to about 10 μg/ml, or about 0.25 μg/ml to about 2 μg/ml, or about 0.5 μg/ml to about 5 μg/ml.

**[0285]** In specific aspects, the viral particle components comprise a lentiviral vector genome.

**[0286]** In specific aspects, the viral particle infects cells expressing DC-SIGN with a transduction efficiency at least 5-fold higher than a viral particle produced in a culture medium lacking kifunensine.

**[0287]** In specific aspects, the virus packaging cell comprises:

(i) a first polynucleotide encoding a envelope glycoprotein;

(ii) a second polynucleotide comprising gag and pol genes;

(iii) a third polynucleotide encoding a rev protein; and

(iv) a lentiviral vector genome comprising a fourth polynucleotide encoding an antigen.

**[0288]** In specific aspects, the envelope glycoprotein is a Sindbis virus E2 glycoprotein. In some aspects, the E2 glycoprotein comprises [SINVar1] or a variant thereof having at least 80% amino acid sequence identity thereto. In some aspects, the E2 glycoprotein is 90%

identical to SEQ ID NO: 30 [SIN-Var1]. In some aspects, (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein. In some aspects, the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

**[0289]** In specific aspects, the lentiviral vector genome is derived from HIV-1.

**[0290]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is capable of integrating.

**[0291]** In specific aspects, the lentiviral vector genome of the pseudotyped lentiviral vector particle or packaging system of any of the preceding embodiments is integration deficient or integration defective. In some aspects, the pol gene encodes an inactive integrase enzyme and the lentiviral vector genome lacks a functional polypurine tract (PPT).

**[0292]** In specific aspects, the virus packaging cell further comprises a polynucleotide encoding a Vpx protein that retains SAMHD1-inhibiting activity, optionally comprising an amino acid sequence at least 80% identical to SIVmac Vpx (SEQ ID NO: 44).

**[0293]** In some embodiments of the disclosure, there is provided a composition comprising virus particles displaying an alphavirus E2 glycoprotein, wherein at least 80% of N-linked glycans in said composition comprise a $Man_9$ structure.

**[0294]** In specific aspects, the alphavirus E2 glycoprotein is a Sindbis E2 glycoprotein that binds preferentially to dendritic cells expressing DC-SIGN.

**[0295]** In some embodiments of the disclosure, there is provided a method of delivering a viral vector genome to a cell expressing DC-SIGN comprising administering the virus particle or composition of any of the preceding embodiments.

**Additional Embodiments**

**[0296]** 1. A method of generating a pseudotyped lentiviral vector particle comprising:

(a) culturing in a culture medium comprising kifunensine a virus packaging cell comprising:

(1) a lentiviral vector genome comprising a polynucleotide encoding an exogenous antigen,

(2) a polynucleotide encoding a Sindbis E2 glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, and

(3) a polynucleotide encoding a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity; and

(b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN.

**[0297]** 2. The method of embodiment 1, wherein the E2 glycoprotein is 90% identical to SEQ ID NO: 30 [SIN-Var1].

**[0298]** 3. The method of embodiment 1 or 2, wherein (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein.

**[0299]** 4. The method of embodiment 2, wherein the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

**[0300]** 5. The method of any one of the above embodiments, wherein the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx [SEQ ID NO: 44].

**[0301]** 6. The method of any one of embodiments 1 to 4, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

**[0302]** 7. The method of any one of embodiments 1 to 4, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0303]** 8. The method of any one of the above embodiments, wherein the antigen is a tumor-specific antigen or a virus-specific antigen.

**[0304]** 9. The method of embodiment 8, wherein the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement,

Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, and alpha-fetoprotein.

**[0305]** 10. The method of embodiment 8, wherein the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

**[0306]** 11. The method of any one of the above embodiments, wherein the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen.

**[0307]** 12. The method of embodiment 11 wherein the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens.

**[0308]** 13. The method of embodiment 12, wherein self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57.

**[0309]** 14. The method of any one of embodiments 11 to 13, wherein the first antigen is NY-ESO-1 and the second antigen is MAGE-A3.

**[0310]** 15. The method of embodiment 11, wherein the first and second antigen are expressed from a bi-directional promoter.

**[0311]** 16. The method of any one of the above embodiments, wherein the kifunensine is present in the culture medium at a concentration of about 0.1 μg/ml to about 10 μg/ml.

**[0312]** 17. The method of embodiment 16, wherein the kifunensine is present in the culture medium at a concentration of about 0.25 μg/ml to about 2 μg/ml.

**[0313]** 18. The method of any one of the above embodiments, wherein the virus packaging cell further comprises:

(i) a polynucleotide comprising gag and pol genes; and

(ii) a polynucleotide encoding a rev protein.

**[0314]** 19. The method of embodiment 18, wherein the gag and pol genes are human codon optimized and comprise a non-optimized window around position 1228 to 1509 of SEQ ID NO: 54.

**[0315]** 20. The method of embodiment 18 or 19, wherein the polynucleotide comprising gag and pol genes lacks a functional rev responsive element (RRE).

**[0316]** 21. The method of any one of embodiments 18 to 20, wherein the pol gene encodes an inactive integrase enzyme.

**[0317]** 22. The method of embodiment 21, wherein the integrase enzyme has a D64V mutation.

**[0318]** 23. The method of any one of embodiments 18 to 22, wherein the polynucleotide encoding the Vpx protein is on the same or different plasmid as the polynucleotide encoding the rev protein, or the polynucleotide comprising the gag and pol genes.

**[0319]** 24. The method of any one of the above embodiments, wherein the lentiviral vector genome is derived from HIV-1.

**[0320]** 25. The method of any one of the above embodiments, wherein the lentiviral vector genome has an inactivated 3' long terminal repeat (LTR) or a self-inactivating 3' long terminal repeat (LTR).

**[0321]** 26. The method of embodiment 25, wherein the lentiviral vector genome comprises a U3 element lacking at least one of an enhancer sequence, a TATA box, an Sp1 site, an NK-kappa B site, or a polypurine tract (PPT).

**[0322]** 27. The method of any one of the above embodiments, wherein the lentiviral vector genome comprises the nucleotide sequence of any one of SEQ ID NOs: 21, 22, or 23.

**[0323]** 28. The method of any one of the above embodiments, wherein the lentiviral vector genome further comprises a nucleotide sequence encoding a dendritic cell maturation/stimulatory factor.

**[0324]** 29. The method of embodiment 28, wherein the dendritic cell maturation/stimulatory factor is selected from the group consisting of GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand, and drug-inducible CD40.

**[0325]** 30. The method of any one of the above embodiments, wherein the nucleotide sequence encoding an antigen is operably linked to a promoter selected from the group consisting of the human Ubiquitin-C promoter (UbiC), the cytomegalovirus immediate early promoter (CMV), the Rous sarcoma virus promoter (RSV), and the tetracycline-responsive promoter.

**[0326]** 31. The method of embodiment 30, wherein the promoter is an intron-deficient promoter.

**[0327]** 32. The method of embodiment 31, wherein the intron-deficient promoter is a UbiC promoter.

**[0328]** 33. The lentiviral vector particle produced by the embodiment of claim 1.

**[0329]** 34. The lentiviral vector particle produced by the embodiment of claim 18.

**[0330]** 35. A method of generating a pseudotyped lentiviral vector particle comprising:

(a) culturing in a culture medium comprising kifunensine a virus packaging cell comprising:

(1) a lentiviral vector genome comprising a polynucleotide encoding MAGE-A3 and NY-ESO-1, wherein a polynucleotide encoding a self-cleaving TA2 peptide is positioned between the polynucleotide encoding MAGE-A3 and NY-ESO-1, wherein the lentiviral genome lacks a polypurine tract (PPT), and wherein expression of MAGE-A3 and NY-ESO-1 is controlled by a UbiC promoter lacking an intron,

(2) a polynucleotide encoding a Sindbis E2 glycoprotein that preferentially binds dendritic cells expressing DC-SIGN,

(3) a polynucleotide comprising human codon optimized gag and pol genes, wherein the polynucleotide lacks a functional rev responsive element (RRE) and wherein the pol gene encodes an inactive integrase enzyme,

(4) a polynucleotide encoding a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity; and

(b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN.

**[0331]** 36. A composition comprising pseudotyped lentiviral vector particles comprising (a) a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity, (b) an exogenous polynucleotide encoding an antigen, and (c) a plurality of envelope glycoproteins that

preferentially bind cells expressing DC-SIGN, wherein said composition is more highly mannosylated compared to a control composition of the same pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor.

**[0332]** 37. The composition of embodiment 36, wherein the envelope glycoproteins are alphavirus glycoproteins.

**[0333]** 38. The composition of embodiment 37, wherein the envelope glycoproteins are Sindbis glycoproteins.

**[0334]** 39. The composition of any of embodiments 36-38, wherein high mannosylation is characterized by being more EndoH-sensitive than a control composition prepared in the absence of a mannosidase inhibitor.

**[0335]** 40. The composition of any of embodiments 36-38, wherein EndoH sensitivity is determined by assessing the molecular weight of the envelope glycoproteins by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) after EndoH treatment.

**[0336]** 41. The composition of any one of embodiments 36-38, wherein the molecular weight of the envelope glycoproteins after treatment with EndoH has shifted about 45% or more of the distance between (a) envelope glycoproteins not treated with an endoglycosidase, and (b) envelope glycoproteins treated with PNGase F.

**[0337]** 42. The composition of embodiment 41, wherein the molecular weight of the envelope glycoproteins after treatment with EndoH has shifted approximately 70% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F.

**[0338]** 43. The composition of embodiment 41, wherein the molecular weight of the envelope glycoproteins after treatment with EndoH has shifted approximately 90% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F.

**[0339]** 44. The composition of any one of embodiments 36-43, wherein at least 30% of the envelope glycoproteins in said composition have an increased amount of EndoH-sensitive glycan as compared to control glycoproteins having the same amino acid sequence(s) in a control composition of pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor.

**[0340]** 45. The composition of any one of embodiments 36-44, wherein a majority of the envelope glycoproteins are highly mannosylated.

**[0341]** 46. The composition of any one of embodiments 36-45, wherein the pseudotyped lentiviral vector particles are integration deficient.

**[0342]** 47. The composition of any one of embodiments 36-46, wherein the composition comprises a Sindbis E2 glycoprotein.

**[0343]** 48. The composition of embodiment 47, wherein the E2 glycoprotein is 90% identical to SEQ ID NO: 30 [SIN-Var1].

**[0344]** 49. The composition of embodiment 47 or 48, wherein (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein.

**[0345]** 50. The composition of embodiment 49, wherein the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

**[0346]** 51. The composition of any one of embodiments 36-50, wherein the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx [SEQ ID NO: 44].

**[0347]** 52. The composition of any one of embodiments 36-50, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

**[0348]** 53. The composition of any one of embodiments 36-49, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

**[0349]** 54. The composition of any one of embodiments 36-53, wherein the antigen is a tumor-specific antigen or a virus-specific antigen.

**[0350]** 55. The composition of embodiment 54, wherein the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA),

prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, and alpha-fetoprotein.

**[0351]** 56. The composition of embodiment 54, wherein the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

**[0352]** 57. The composition of any one of embodiments 36-56, wherein the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen.

**[0353]** 58. The composition of embodiment 57 wherein the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens.

**[0354]** 59. The composition of embodiment 58, wherein self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57.

**[0355]** 60. The composition of any one of embodiments 57-59, wherein the first antigen is NY-ESO-1 and the second antigen is MAGE-A3.

**[0356]** 61. The composition of embodiment 57, wherein the first and second antigen are expressed from a bi-directional promoter.

## EXAMPLES

**[0357]** The following examples are provided for illustration and are not intended to limit the scope of the disclosure.

### Example 1

### Lentiviral vector particles pseudotyped with Sindbis virus glycoproteins produced in the presence of kifunensine efficiently infect DC-SIGN-expressing cells

**[0358]** The goal of the following experiments was to attempt to produce and characterize pseudotyped lentiviral vectors with highly mannosylated envelope glycoproteins. In so doing, the inventors unexpectedly discovered that kifunensine was far more effective at producing pseudotyped lentiviral vectors with the capability to efficiently infect cells expressing DC-SIGN (e.g., dendritic cells) using significantly smaller concentrations as compared to other mannosidase I inhibitors including DMNJ.

**[0359]** 293T cells were transfected with four separate plasmids encoding the lentiviral genome, the Gag/Pol, Rev, and the Envelope, respectively, using polyethyleneimine (PEI). Five hours after transfection, mix+media was removed. Media was added back to the vessel along with the indicated amount of mannosidase inhibitor (i.e., DMNJ, kifunensine, and swainsonine). 48 hours later, supernatant (containing vector) was collected and filtered with a .45μm filter. HT1080 cells stably expressing the human DC-SIGN receptor were then transduced with the indicated volumes of vector. The parental HT1080 cells (lacking DC-SIGN), were used as controls, and were not transduced by any of the vectors. 48 hours after transduction, cells were analyzed for GFP expression (gfp%). The results are shown in Figures 1A (HT1080 expressing DC-SIGN) and 1B (parental HT1080).

**[0360]** Lentiviral vector particles pseudotyped with Sindbis virus glycoproteins and produced in the presence of low concentrations of kifunensine (1 μg/ml) unexpectedly transfect cells expressing DC-SIGN significantly better than those produced in the presence of higher concentrations of DMNJ (400 μg/ml) or swainsonine (10 μg/ml). Accordingly, production of lentiviral vector particles pseudotyped with Sindbis virus glycoproteins in the presence of the mannosidase I inhibitor kifunensine results in significantly enhanced infection of DC-SIGN-expressing cells as compared to particles produced in the presence of other mannosidase I inhibitors.

**Example 2**

**Low amounts of kifunensine are required to generate pseudotyped lentiviral vector particles that efficiently infect DC-SIGN-expressing cells**

**[0361]** The goal of this experiment was to determine the concentration of kifunensine most effective at producing pseudotyped lentiviral vector particles with the capability of infecting DC-SIGN-expressing cells.

**[0362]** 293T cells were transfected with the plasmids described in Example 1 using PEI. Five hours after transfection, mix+media was removed. Media was added back to the vessel

along with the indicated amount of Kifunensine (μg/ml), or with 400 μg/ml of DMNJ. 48 hours later supernatant (containing lentiviral vector particles) was collected and filtered with a .45μm filter. HT1080 cells stably expressing the human DC-SIGN receptor were then transduced with the indicated volumes of supernatant containing vector. The parental HT1080 cells, which are not transduced by the vector, were used as controls. 48 hours after transduction, cells were analyzed for gfp expression (gfp+%). The results are shown in Figures 2A (HT1080 cells expressing DC-SIGN) and 2B (parental HT1080 cells).

**[0363]** Particles produced in the presence of 0.125 μg/ml kifunensine matched the ability of particles produced in the presence of 400 μg/ml DMNJ to infect DC-SIGN-expressing cells (Figure 2A). Particles produced in the presence of all kifunensine concentrations exceeding 0.125 μg/ml infected DC-SIGN-expressing cells much more efficiently that particles produced in the presence of 400 μg/ml DMNJ. The titration of kifunensine revealed that the ability of lentiviral vector particles pseudotyped with Sindbis virus glycoproteins to infect DC-SIGN-expressing cells peaks with particles produced in the presence of 0.25 μg/ml.

**Example 3**

**[0364]** The goal of this experiment was to characterize the glycosylation profile of pseudotyped lentiviral particles produced in the presence of DMNJ or kifunensine.

**[0365]** Lentiviral vector particles pseudotyped with Sindbis virus glycoproteins were prepared according to Example 1 in the presence of 1 μg/ml kifunensine, DMNJ, or no mannosidase I inhibitor. The particles were incubated with either PNGaseF or EndoH for 1 hour. PNGaseF is a general endoglycosidase that will cleave all N-linked glycosylation regardless of glycosylation profile (see Figure 3A). EndoH is a specialized endoglycosidase that will only cleave high-mannose N-linked glycosylation (see Figure 3A). When viral particles are produced in the presence of a mannosidase I inhibitor, the viral envelope would be expected to have glycoproteins with high $Man_9$ content and susceptible to cleavage by EndoH. Samples were analyzed using a gel-shift assay by running on an SDS-PAGE gel and immunoblotting with antibody against the Sindbis viral envelope. The results are illustrated in Figure 3B.

**[0366]** The degree of mobility of the viral envelope (SIN-Var1) of virus produced in the presence or absence of kifunensine or DMNJ, combined with the treatment of PNGaseF or EndoH, is indicative of the degree of glycosylation of Var1. Control virus (lane 1) is

glycosylated (consequently running slower on the gel) and this glycosylation can be completely removed by PNGaseF (as evidenced by the faster mobility seen in lane 2). As expected due to the ability of PNGaseF to cleave any N-linked glycosylation, virus produced in the presence of either DMNJ or Kifunensine is sensitive to PNGaseF treatment (lanes 5 and 8). However, only virus produced in the presence of mannosidase I inhibitors (Var1+ DMNJ or +kifunensine) are sensitive to EndoH treatment (lanes 6 and 9) whereas the control virus (Var1) is only partially sensitive to EndoH. The partial sensitivity likely comes from sites in E2-Var1 that are normally not exposed to mannosidase I during production and do not contribute to binding to dendritic cells. These results indicate that the efficiency of the mannosidase I inhibitor kifunensine in producing viral particles with high-mannose glycoproteins can be measured using a gel-shift assay after EndoH treatment and comparing its efficiency to particles produced in the presence of DMNJ.

**Example 4**

**Mannose content in envelope glycoproteins correlates with kifunensine concentration in media used to prepare viral particles**

**[0367]** The goal of this experiment was to characterize the glycosylation profile of pseudotyped lentiviral particles produced in the presence of varying concentrations of kifunensine.

**[0368]** Lentiviral vector particles pseudotyped with Sindbis virus glycoproteins were prepared according to Example 1 with varying concentrations of kifunensine or 400 μg/ml of DMNJ. The particles were incubated with EndoH for 1 hour. Samples were then analyzed using a gel-shift assay and immunoblotting with antibody against the Sindbis virus envelope. In parallel, HT1080 cells stably expressing the human DC-SIGN receptor were transduced with the indicated volumes of pseudotyped lentiviral vector particles prepared with or without kifunensine or DMNJ. 48 hours after transduction, cells were analyzed for GFP expression (shown on the y-axis as percent of GFP positive cells) to create the graphs. The results are illustrated in Figure 4.

**[0369]** The degree of mannose content correlates with the degree of transduction of HT1080 DC-SIGN cells, as indicated by the degree of shift on the gel of EndoH treated samples (Figure 4A) and the percent GFP transduction graphs (Figure 4B). I.e., increasingly higher kifunensine concentrations in the media used to prepare viral particles resulted in higher mannose content envelope glycoproteins, as demonstrated by greater shifts with

EndoH treatment and higher GFP expression (i.e., infection) in HT1080 cells expressing DC-SIGN. These results indicate that kifunensine directly affects the degree of mannose content on the viral envelope and this correlates directly with the ability to transduce HT1080 cells expressing the human DC-SIGN receptor.

**Example 5**

**Confirmation of Vpx expression in pseudotyped lentiviral vector particles**

**[0370]** The goal of this experiment was to determine if SIVmac Vpx could be expressed and detected in pseudotyped lentiviral vector particles.

**[0371]** SIVmac Vpx with an N-terminal HA tag was cloned into a mammalian expression vector driven by a CMV promoter (construct named pENV-SIVmacVpx). To confirm that the Vpx protein was expressed, 293T cells were transfected with this construct and lysed 24 hours after transfection. Lysates were analyzed via immunoblotting using anti-HA antibody (Figure 5A). To confirm that Vpx was packaged into lentivirus particles, lentiviruses were prepared using four plasmids transfected into 293T packaging cells. These four plasmids encode the lentiviral genome, the Gag/Pol (either integration competent [Int+], or integration-defective [Int-]), Rev, and the Envelope. A fifth plasmid was either included for Vpx or not. Virus was collected two days after transfection and concentrated using centrifugation. 100ng of p24 was loaded per well onto a gel for immunoblotting with anti-HA antibody (Figure 5B). As a loading control anti-p24 antibody was used.

**[0372]** In 293T cells transfected with the plasmid encoding the Vpx gene, Vpx protein is efficiently expressed (Figure 5A). Similarly, Vpx is packaged into both integration-competent (Int+) and integration-defective (Int-) lentivirus particles (Figure 5B).

**Example 6**

**Vpx is necessary for efficient transduction of human dendritic cells by VSV-G-pseudotyped integration-deficient lentiviral vector particles**

**[0373]** The goal of this experiment was to determine if Vpx was required for a productive infection of dendritic cells by VSV-G-pseudotyped integration-deficient lentiviral vector particles.

**[0374]** Human peripheral blood mononuclear cells (PBMCs) were enriched for CD14+ monocytes, followed by enrichment for dendritic cells using GMCSF and IL-4. These PBMC-derived human dendritic cells were transduced with increasing amounts VSV-G-

pseudotyped integration-deficient lentiviral vector particle (0.2 ng, 2 ng, 20 ng or 200 ng of p24) constructs which either did or did not contain Vpx. Five days after infection, transduction events were measured by gating on cells that were positive for CD11c, and assessing percent of cells positive for GFP (x-axis) with DC-SIGN on the y-axis. AZT (a reverse-transcriptase inhibitor) was used on the highest dose of lentiviral vector particles (200ng).

**[0375]** The results are illustrated in Figure 6. Vpx was required for integration-deficient VSV-G-pseudotyped lentiviral particles to transduce human dendritic cells derived from PBMCs. Efficient transduction is dependent on reverse transcription because it was inhibited by AZT.

**Example 7**

**Vpx improves transduction of human dendritic cells by VSV-G-pseudotyped integration-competent lentiviral vector particles**

**[0376]** The goal of this experiment was to determine if Vpx was required for a productive infection of dendritic cells by VSV-G-pseudotyped integration-competent lentiviral vector particles.

**[0377]** Human PBMCs were enriched for CD14+ monocytes, followed by enrichment for dendritic cells using GMCSF and IL-4. These PBMC-derived human dendritic cells were transduced with increasing amounts of VSV-G-pseudotyped integration-competent lentiviral vector particle (0.2 ng, 2 ng, or 20 ng of p24) constructs which either did or did not contain Vpx. Five days after infection, transduction events were measured by gating on cells that were positive for CD11c, and assessing percent of cells positive for GFP (x-axis) with CD11c on the y-axis. Nevirapine (Nev, a reverse-transcriptase inhibitor) was used on the highest dose of lentiviral vector particles (20ng).

**[0378]** The results are illustrated in Figure 7. Vpx enhanced the ability of integration-competent lentiviral vector particles to transduce human dendritic cells derived from PBMCs. The improved transduction is dependent on reverse transcription because it was inhibited by Nevirapine.

## Example 8

### Vpx and highly mannosylated envelope glycoproteins are necessary for efficient transduction of human dendritic cells by lentiviral vector particles pseudotyped with Sindbis virus envelope glycoproteins

**[0379]** The goal of this experiment was to test the capability of Sindbis virus E2 glycoprotein pseudotyped lentiviral vector particles comprising a Vpx protein and produced in the presence of kifunensine to productively infect dendritic cells.

**[0380]** Human PBMCs were enriched for CD14+ monocytes, followed by enrichment for dendritic cells using GMCSF and IL-4. These PBMC-derived human dendritic cells were transduced with varying amounts SINvar1-pseudotyped integration-defective lentiviral vector particle (0.2 ng, 2 ng, or 20 ng of p24) constructs which either did or did not contain Vpx, or were produced in the presence or absence of the mannosidase I inhibitor, kifunensine. Five days after infection, transduction events were measured by gating on cells that were positive for CD11c, and assessing percent of cells positive for GFP (x-axis) with either DC-SIGN or CD11c on the y-axis. Nevirapine (Nev, a reverse-transcriptase inhibitor) was used on the highest dose of lentiviral vector particles (20ng).

**[0381]** As shown in Figure 8, unexpectedly, both Vpx and production of the viral particles in the presence of kifunensine are required to efficiently transduce human dendritic cells using a lentivirus pseudotyped with Sindbis virus glycoproteins. Accordingly, these results show that particles comprising the combination of highly mannosylated glycoproteins (a result of particle formation in the presence of kifunensine) and Vpx act synergistically to efficiently infect and express lentiviral genome-encoded proteins. I.e., if either one of Vpx or highly mannosylated glycoproteins are missing from the Sindbis envelope glycoprotein-pseudotyped integration-defective lentiviral particles, dendritic cells are not efficiently transduced.

## Example 9

### Quantifying the mannosylation of the lentiviral vector particle envelopes

Lentiviral vector particles pseudotyped with Sindbis virus glycoproteins were prepared according to Example 1 with no treatment (Figure 9A, lanes 1-3), 400 μg/ml of DMNJ (Figure 9A, lanes 4-6), or 1 μg/ml of kifunensine (Figure 9A, lanes 7-9). The particles were not treated (lanes 1, 4, 7), incubated with EndoH for 1 hour (lanes 2, 5, 8), or incubated with

PNGaseF for 1 hour (lanes 3, 6, 9). Samples were then analyzed using a gel-shift assay and immunoblotting with antibody against the Sindbis virus envelope.

**[0382]** Analysis of the gel shift data was performed using Quantity One software from Biorad. In brief, using the "Lane" function, vertical lines were drawn through each of the 9 lanes shown in Figure 9A. This specifies the area to be analyzed to the program. Next, using the "Band attributes" function, the peak intensity for each band was determined. These values are also shown in Figure 9A. This gives us the peak intensity value of each band on the gel through the previously indicated "lane."

**[0383]** Next, graphs were assembled from the intensity profile of each band and its location on the lane. The results are shown in Figure 9B (no mannosidase treatment), Figure 9C (DMNJ treatment, and Figure 9D (kifunensine treatment).

**[0384]** Each graph depicts each of the envelope types digested with no enzyme, Endo H, or PNGaseF, as indicated. The Y-axis is the intensity of the band and the X-axis is the location of the band along the described lane (i.e., the "relative front" (rf) value; the rf value is the distance of the band from the top of the gel over the total length of the lane).

**[0385]** To quantify the shift, the peak intensity of a band that was not cut with a digestive enzyme (i.e., full glycosylation) was compared with a band that was cut with the PNGaseF enzyme (i.e., all glycosylation sites removed). Thus, a peak intensity that is equal to a band that has not been digested with any enzyme will be a 0% shift and a peak intensity that is equal to a band that has been digested with PNGaseF will be considered a 100% shift. Without the addition of kifunensine (Lane 2), the EndoH gel shift is 36% of a PNGaseF shift. Significantly, the kifunensine-treated sample digested with EndoH (i.e., high-mannose-specific digestion) shifted 90% of the distance of the PNGaseF shift. Accordingly, nearly all of the glycosylated sites on the viral vector envelope are in a high-mannose state after treatment with 1 μg/ml of kifunensine.

**[0386]** All of the quantitative analysis is shown in Table 1.

Table 1

| Envelope | Digestion enzyme | Peak intensity value | Spectrum intensity value | % shift |
|---|---|---|---|---|
| var1 | None | 0.387 | 0 | 0 |
| var1 | endoH | 0.5 | 0.113 | 36.10224 |
| var1 | PNGaseF | 0.7 | 0.313 | 100 |
| var1 + DMNJ | None | 0.338 | | |
| var1 + DMNJ | endoH | .412, .6, .712 | | |
| var1 + DMNJ | PNGaseF | 0.65 | | |
| var1 + kif | None | 0.425 | 0 | 0 |
| var1 + kif | endoH | 0.663 | 0.238 | 90.4943 |
| var1 + kif | PNGaseF | 0.688 | 0.263 | 100 |

**[0387]** Spectrum intensity value is peak intensity value minus the peak intensity value of the envelope digested with no enzyme. This is done to normalize the values in a spectrum from 0% shift to 100% shift, as explained above. %shift is the spectrum intensity value divided by the spectrum intensity value of PNGaseF treated samples multiplied by 100. This generates a percentage that quantifies the shift of a band cut with EndoH as related to bands treated with no enzyme or with PNGaseF. DMNJ treated envelopes were excluded from this analysis because they had heterogenous N-linked glycosylation patterns.

**Example 10**

**Viral vectors with integration-deficiency design elements**

**[0388]** For clinical applications that require the direct administration of viral vectors but do not require sustained expression of the vector-delivered gene, such as for vaccines and antigen-directed immunotherapies, integration-deficient lentiviral vectors represent an appropriate and viable alternative to fully integration-competent lentiviral vectors for delivery of their genetic payload. The D64V integrase mutation within the *gag/pol* gene and the cPPT deletion within the vector genome were tested alone and in combination for their impact on integration rate of a viral vector.

**Materials and Methods**

*Quantification of integration by Alu-PCR.*

**[0389]** 293T huDC-SIGN cells seeded at 5E5 cells/well in 6-well plates were transduced in triplicate with 2E9 genomes per well of vector. At 48 hours post-transduction, cells were harvested and genomic DNA extracted using the DNeasy Kit (Qiagen, Valencia, CA). Genomic DNA was analyzed using an Alu-LTR based nested-PCR assay, which amplifies

only provirus sequences that have been integrated into the host genomic DNA. The following modifications were introduced into the previously published method of Brussel et al., *Methods Mol. Biol.* 304, 139 (2005). Platinum Taq (Life Technologies, Grand Island, NY) was used for the first round of amplification in a final reaction volume of 25 µl. The first-round PCR cycle conditions were as follows: a denaturation step of 2 min at 95°C and then 20 cycles of amplification (95°C for 30 s, 55°C for 30 seconds, 72°C for 90 seconds). Nested PCR was performed using EXPRESS qPCR Supermix Universal (Life Technologies) and 100 nM of probe MH60310 in a final volume of 25 µl. The nested PCR protocol began with a 2 minute hold at 50°C and a 10 minute denaturation step at 95°C, followed by 40 cycles of amplification (95°C for 15 seconds, 60°C for 30 seconds). All amplification reactions were performed using the Bio-Rad CFX (-96 or -384 model, Bio-Rad Laboratories, Hercules, CA). The copy number of integrated provirus was calculated in reference to a standard curve generated by parallel nested Alu-PCR of a reference 293T cell line containing integrated provirus of known copy number, diluted over a 5-log range. The total genomic DNA in the standard curve was normalized by mixing with genomic DNA from non-transduced cells; each standard and unknown sample contained 100 ng total genomic DNA. This assay allowed the detection of 58 proviruses (Experiment 1) or 4 proviruses (Experiment 2) in 100 ng of genomic DNA.

*Quantification of integration by neomycin resistance.*

**[0390]** Vectors encoding GFP-T2A-NeoR antigen were independently analyzed for integration rate by neomycin resistant colony formation. HT1080 huDC-SIGN cells were transduced in 6-well plates with 0.5 ml of serially diluted vector (normalized by genomes) for 2 hours, after which 2 ml of complete medium was added. At 24 hours post-transduction, cells were fed with medium containing 800µg/ml G418 (Life Technologies, Grand Island, NY). Cells were then grown without passaging for 11-13 days under G418 selection, after which colonies were visualized by staining with crystal violet (BD Biosciences, Rockville, MD). Total integration events were calculated as follows: (# of colonies) × (dilution factor) = Integration Events.

*Quantification of integration by GFP expression.*

**[0391]** For vectors encoding GFP-T2A-NeoR antigen, relative integration rate was measured by GFP expression over time in bulk culture. HT1080 huDC-SIGN cells were transduced in 6-well plates with equal amounts of WT/703 or D64V/704 vector (normalized by genomes) in 0.5 ml for 2 hours, followed by the addition of 2 ml of complete medium.

Transduced cells were maintained in medium without drug selection for up to 30 days, passaging at regular intervals. During this period, cells were periodically analyzed for GFP expression by flow cytometry (Guava EasyCyte Plus, Millipore, Billerica, MA).

**Results**

**[0392]** 293T huDC-SIGN cells were transduced with WT- or D64V-integrase VSV-G pseudotyped vectors packaging WT ("703") or cPPT-deleted genomes ("704"). At 48 hours post-transduction, cells were analyzed for the presence of integrated provirus by nested Alu-PCR analysis. As shown in Figure 10A, the WT/704 and D64V/703 vectors each had integration rates that were decreased by approximately 2 logs as compared to WT/703 vector. In comparison, the integration rate of the D64V/704 vector was decreased by greater than 2 logs. These results demonstrate that the ID-VP02 (Sindbis virus E2 glycoprotein pseudotyped lentiviral vector particles with SIVmac Vpx and highly mannosylated envelope glycoproteins and prepared using packaging cells comprising the rev-independent *gag/pol* system described in Example 12) genome has significantly reduced integration potential, and that the D64V and 704 elements independently contribute to this phenotype.

**[0393]** To complement the nested Alu-PCR analysis, two additional methods were employed to investigate the integration rate of the viral vector genome. In both methods, HT1080 huDC-SIGN cells were transduced with WT/703 or D64V/704 vector encoding GFP and neomycin resistance (NeoR) separated by a self-cleaving T2A linker (GFP-T2A-NeoR). Transduction with either of these vectors results in both GFP and NeoR expression. Integration rate was measured as a function of antigen expression, either by outgrowth of neomycin-resistant colonies following G418 selection or by GFP expression over time in bulk culture.

**[0394]** In the first method of measuring integration rate (i.e., neomycin resistance), HT1080 huDC-SIGN cells were transduced with serial dilutions of vector and grown without passaging in the presence of G418 selection. Input vector was normalized by genome copy number. Cells that expressed NeoR and survived prolonged exposure to G418, forming colonies, were presumed to harbor integrated provirus. These colonies were counted and total integration events were calculated. Using this experimental approach, the integration rate of D64V/704 vector was decreased by 3 logs relative to that of WT/703, in two independent experiments (Figure 10B).

**[0395]** In the second method (i.e., GFP expression), transduced cells were serially passaged in the absence of selection and analyzed by flow cytometry at varying times post-transduction. At day 2 post-transduction, approximately 40 percent of the cells transduced with WT/703 vector were GFP-positive (Figure 10C). This population remained consistent for the duration of the experiment, suggesting that GFP expression was primarily from integrated provirus. In contrast, the percent of GFP-positive cells transduced with D64V/704 vector dropped approximately 100-fold by day 6 post-transduction and remained low, albeit higher than the mock-transduced control, for the remainder of the experiment. These results suggest that the majority of D64V/704 transduction events yielded non-integrated vector DNA, which expressed GFP at early times post-transduction, but was lost during subsequent cell divisions. The small percentage of GFP-expressing cells remaining by day 9 post-transduction likely represents the minority of transduction events that yielded integrated provirus. At the completion of the experiment (day 30) it was calculated that the D64V/704 vector was 386-fold decreased in its ability to undergo integration, compared to the WT/703 vector. These findings are comparable to the results from nest Alu-PCR analysis.

**[0396]** Taken together, the results from all three methods of measuring integration rate (nested Alu-PCR, NeoR colony outgrowth, and %GFP expression) demonstrate that the integration rate of the viral vector genome is 2-3 logs reduced relative to that of the standard, integration-competent 3rd generation lentiviral vector (WT/703).

**Example 11**

**Pseudotyped lentiviral vector particles specifically transduce dendritic cells in a homogenous population of cells**

**[0397]** Viral vector specificity for dendritic cells was assessed within the context of a heterogenous population of potential target cells. Human PBMCs were placed in culture in the presence of GM-CSF and IL-4 for three days to generate a pool of primary cells that included a sufficient number of monocyte-derived DCs expressing DC-SIGN. On day three, 20 ng p24 of pseudotyped lentiviral vector encoding GFP that were produced in the presence of kifunensine and that contained Vpx were added to the culture. Three days after the introduction of the vector into the culture, cells were analyzed for the expression of GFP as a measure of transduction within the major populations of cells present at the time of analysis: DCs ($CD11c^{pos}$) 6%, B-cells ($CD11c^{neg}$, $CD19^{pos}$) 10%, and T-cells ($CD11c^{neg}$, $CD3\varepsilon^{pos}$) 80%. As shown in Figure 11, 42% of the cells within the $CD11c^{hi}$, $DC\text{-}SIGN^{+}$ population were transduced compared to 0.1% for both the B and T cell populations present within the

culture. Transduction was completely ablated in all cell populations when the reverse transcriptase inhibitor nevirapine (RT inhibitor) was included in the culture. These results demonstrate that in a heterogeneous population of human cells of which DCs are a minority, the pseudotyped lentiviral vector specifically transduces DC-SIGN expressing DCs.

**Example 12**

**Design of a Rev-independent gag/pol plasmid**

**[0398]** Of the four plasmid system typical of pseudotyped third-generation LVs, two of the plasmids contain sequences within their transcripts that have the potential for recombining. Namely, the transfer vector (referred to here as the LV genome) and the *gag/pol* plasmid. There are two regions of sequence homology between transcripts of the LV genome and *gag/pol* (Figure 12). First, the LV genome has a partial *gag* sequence following the psi packaging signal that consists of 354 base pairs (bp) that are identical to the 5' end of the *gag* sequence in the *gag/pol* plasmid. Recombination events that take place from this sequence overlap are referred to as psi-gag recombination events. Second, both the LV genome and *gag/pol* contain the Rev-responsive element (RRE), which consists of 234 bp that form a secondary RNA structure allowing Rev-dependent nuclear export of RRE-containing transcripts into the cytoplasm. These two homologous sequences were removed by deleting the RRE from the *gag/pol* plasmid and by codon-optimizing the *gag/pol* open reading frame (ORF), with the exception of a frame-shift region between *gag* and *pol* that is required for translation of pol protein products (Figure 12). The frameshift region forms a secondary RNA structure at the *gag* and *pol* junction that causes a -1 register shift of the ribosome during translation that is essential for translating *pol* gene products. Watts et al., *Nature*, 460:711-716 (2009). For these experiments, a 282 bp region between base pairs 1228 and 1509 of the *gag/pol* ORF was not codon-optimized This region starts at bp 1563 of the pNL4-3 sequence of Wild Type HIV-1 which encodes Lysine409 of the Gag protein and extends to include the stop codon of Gag. The remaining regions (bp 1-1228 and bp 1510-4307 of gag/pol) were codon optimized based on the human codon table. Nakamura et al., *Nucleic Acids Res,* 28:292 (2000). The complete ORF of RI *gag/pol* was synthesized at Genscript and was cloned in place of the ORF consisting of WT *gag/pol* and the RRE.

**[0399]** Deletion of the RRE is known to eliminate Rev-dependent export of *gag/pol* transcripts from the nucleus because the RNA secondary structure of gag/pol retains transcripts in the nucleus. Banchereau and Steinman, *Nature*, 392(6673), 245 (1998). Therefore the codon-optimization serves both to eliminate these retentive secondary

structures and to minimize sequence homology with the partial *gag* in the LV genome. Due to the fact that these modifications hypothetically relieve the *gag/pol* transcript from requiring Rev, the scheme is referred to as Rev-independent *gag/pol* (RI *gag/pol*), even though Rev is still required during vector production.

**Example 13**

**Nuclear export of RI gag/pol does not require Rev**

**[0400]** In order to demonstrate that the RI *gag/pol* transcript is indeed Rev-independent, 293T cells were transfected with either the Wild Type (WT *gag/pol*) or the RI *gag/pol* plasmids, in the presence or absence of a Rev encoding plasmid.

**Materials and Methods**

*Expression of Gag protein.*

**[0401]** 293T cells were plated in a 6-well dish at $1x10^6$ cells/well. Twenty-four hours later, cells were transfected with 0.5 µg of either WT *gag/pol* or RI *gag/pol* plasmids in the presence of either 0.5 µg of Rev plasmid or 0.5 µg of empty backbone plasmid using Lipofectamine 2000 (Invitrogen). Twenty-four hours later, cells were lysed with cell extraction buffer (Invitrogen, catalog # FNN0011) and analyzed via SDS-PAGE using 4-12% NuPAGE Bis-Tris precast gels (Invitrogen, catalog # NP0321PK2) followed by transfer onto a nitrocellulose membrane. Blots were then probed with either anti-p24 antibody (Abcam, catalog # ab9071) or anti-actin antibody (Santa Cruz Biotech, catalog # sc-130656).

**Results**

**[0402]** Cell lysates were analyzed for expression of gag protein products using SDS-PAGE and Western blotting with anti-p24 antibody. The RI *gag/pol* plasmid was able to express p24 and its precursors whether or not Rev was present, whereas the WT *gag/pol* transcript required Rev for protein expression (Figure 13). The processing of p55 Gag protein appeared different between RI and WT *gag/pol* transcripts based on the ratio of p55:p24 protein, suggesting effects of codon-optimization on protein expression and/or processing. These results indicate that transcripts can undergo nuclear export in the absence of Rev, confirming that design changes to the RI *gag/pol* construct relieve the requirement for Rev.

**Example 14**

**RI *gag/pol* produces infectious vector with comparable titers to WT *gag/pol***

**[0403]** Previous studies have described reductions in titers of vectors produced in the absence of Rev. *See* Gasmi et al., *J.Virol.* 73:1828-1834(1999); Lucke et al., *J.Virol.* 79:9359-9362 (2005). Vector made with the "rev-independent" *gag/pol* construct was tested to determine if it would generate infectious particles with comparable titers to that of WT *gag/pol.*

**Materials and Methods**

*Vector production*

**[0404]** Vector was produced in either large scale (CF10) or small scale (10cm dish). For large scale production, 293T cells were seeded at 5E8 cells/1L in a 10-layer cell factory (Nunc, catalog#140400) in DMEM media containing 5% serum, L-glutamine, and antibiotics. Three days later, cells were transfected using PEI (stock 1 mg/mL) and total plasmid DNA at a ratio of 3:1 (mL PEI:mg DNA). Per 10-layer cell factory, 1 mg of vector genome plasmid and 0.5 mg of remaining plasmids (gag/pol, Rev, and VSV-G) were used. Five hours later, media was replaced with 1 L of serum-free media (Transfx-293 media, Hyclone catalog# SH30860.LS). Vector was harvested 2 and 3 days after transfection. Harvests were clarified using a pre-filter and 0.45 μm stericup filter (Millipore). Vector was concentrated by spinning in a 1 L centrifuge bottle at 16,000g for 5 hours. Pellet from each liter harvest was either resuspended in 1 mL of HBSS and aliquoted for storage at -80°C, or was resuspended in 1 mL of buffer for benzonase treatment (50 mM Tris-HCL pH7.5, 1 mM MgCl2, 5% v/v Sucrose). Benzonase nuclease was added at a final of 250 U/mL and incubated overnight at 4°C in order to degrade any left-over plasmids from the transfection. Benzonase-treated vector preps were re-concentrated using a sucrose cushion (30% sucrose top, 5% sucrose bottom) and centrifuged at 116,000g in an ultracentrifuge for 1.5 hours at 4°C. Vector pellet was resuspended in 1 mL HBSS, aliquoted and stored in -80°C. For small scale vector production, 293T cells were seeded in a 10cm plate at 2.5E5 cells/plate and transfected the next day using PEI similar to as described above, but with 6 μg of vector genome plasmid and 3 μg of remaining plasmids, except varying amounts of *gag/pol* plasmids when comparing vector production. Small scale transfections were done in triplicates for accuracy. Five hours later, media was replaced with 4 mL of DMEM media containing 5% serum, L-glutamine, and antibiotics. Vector was harvested 2 and 3 days after transfection and was clarified using 0.45 μm filter. Vector was stored at -80°C.

*Vector quantification – p24 assay*

**[0405]** Quantification of p24 was performed using the HIV-1 p24 ELISA kit by Advanced Bioscience Laboratories (Rockville, MD), following the manufacturer's directions.

*Vector quantification – GFU assay*

**[0406]** 293T cells were plated at 2E5 cells/well in a 12-well plate in 1 mL DMEM media containing 5% serum, L-glutamine, and antibiotics. Twenty-four hours later, cells in each well were transduced with 2-fold dilutions of vector encoding GFP. Each amount of vector is prepared in a 1 mL final volume in DMEM complete media. Five 2-fold serial dilutions of supernatant containing vector were prepared starting from 200 µL of vector per well. As a control to rule out pseudo-transduction, 10 µM of the reverse-transcriptase inhibitor nevirapine was used with the highest volume of vector in a parallel well. Forty-eight hours after transduction, cells were analyzed for GFP expression on a Guava machine (Guava technologies, now Millipore). Green Fluorescence Units (GFU) per mL was calculated by using a best fit (least squares) linear regression model based on the volumes of vector and the resulting percent GFP values in order to predict the number of GFP-positive cells per mL of vector using the FORECAST function in EXCEL. Events that resulted in less than 1% of GFP positive cells were set as the limit of quantification (LOQ).

**Results**

**[0407]** Two parallel vector preps pseudotyped with VSV-G were generated using a vector genome encoding green fluorescent protein (GFP) as a marker, and with two input DNA amounts of either the WT *gag/pol* or the RI *gag/pol* constructs. Both vector preps were assayed for p24 and were shown to have comparable physical particle titers, regardless of the *gag/pol* plasmid used to produce them (Figure 14A). These preps were then assayed for their ability to transduce target cells. When normalized by volume, RI *gag/pol* vector resulted in transduction events comparable to WT *gag/pol* for both of the amounts of input *gag/pol* plasmid (3 µg or 6 µg) used during vector production (Figure 14B). These results indicate that design elements introduced to generate the rev-independent *gag/pol* construct did not reduce the physical particle yield or infectivity of the lentiviral vector.

**Example 15**

**RI and WT *gag/pol* vectors generate equivalent immune responses**

**[0408]** LVs are commonly used to deliver protein-encoding nucleic acids to various cell types *in vitro* for research applications and in clinical settings. However, directly injectable LVs are also being developed for both gene therapy and antigen-directed immunotherapy. To

test whether a RI *gag/pol* vector would serve as an appropriate LV for immunotherapy applications, immune responses generated against an antigen transgene encoded by the RI *gag/pol* vector was evaluated.

## Materials and Methods

*Vector quantification – TU assay*

**[0409]** Transduction units (TU) was determined using an assay in which transduction events in a target cell line are measured using a quantitative PCR assay that amplifies reverse-transcribed vector RNA sequences. Serial dilutions of test samples and reference material were incubated in duplicate in 96-well tissue culture plates in the presence of target 293T cells. The transduction step was performed both in the presence and absence of the reverse transcriptase inhibitor nevirapine as a means to asses background signal that may be contributed by residual plasmid DNA. At one day post-transduction, mock- or vector-transduced cells were lysed by the addition of a buffer containing sodium deoxycholate, Tween-20, sodium dodecyl sulfate (SDS), and proteinase K. The cell lysates were then incubated sequentially at 37°C, 55°C, and 95°C to ensure proteolysis and DNA denaturation. Denatured cell lysates were then analyzed by qPCR using a primer/probe set that was designed to amplify a vector genome sequence of approximately 400-bp located upstream of the antigen promoter (EXPRESS qPCR Supermix Universal, Life technologies). The infectivity titer was calculated in reference to a standard curve comprised of linearized plasmid DNA containing the target sequences diluted over a 7-log range (5.3 copies – $5.3 \times 10^6$ copies).

*Immunizations*

**[0410]** C57BL/6 mice were immunized subcutaneously in the tail base on day 0 with either $2 \times 10^7$, $1 \times 10^8$, or $5 \times 10^8$ TU of LV encoding LV1b, a polyepitope construct containing the OVA257 (SIINFEKL) (SEQ ID NO: 24) H-2Kb-restricted epitope, or HBSS vehicle. Aliquots of LV stored at -80°C were thawed at room temperature and then kept on ice. Vector was serially diluted in cold sterile HBSS and transported to the animal facility for injection. Mice were placed in a conventional slotted restrainer with the tail base accessible. Vector was administered via 50 μL injection using a 29-gauge 0.3 mL insulin syringe (Becton Dickenson [BD]) inserted subcutaneously on the right side of the tail base, approximately 1 cm caudal to the anus, leading to minor but notable distension of the skin around the tail base.

*Intracellular Cytokine Staining (ICS)*

**[0411]** Spleens were homogenized by pressing through a 70 μM nylon filter. Red blood cells were lysed by hypotonic shock by brief exposure to ice-cold ultrafiltered water followed by immediate isotonic restoration with 10x PBS. For analysis of cytokines, cells were stimulated a 96-well with peptides are a concentration of 1 μg/mL per peptide in complete RPMI (10% FCS, 10 mM HEPES, 2 μM β-mercaptoethanol, and L-glutamine) for 5 hours at 37 °C, 5% $CO_2$. OVA257 (SIINFEKL) peptide was manufactured at 95% purity by AnaSpec (Fremont, CA). After stimulation, surface staining was carried out in FACS buffer (PBS, 1% FCS, 2 mM EDTA, 0.01% sodium azide) in the presence of FcR blocking antibody 2.4G2 and LIVE/DEAD® Fixable Near-IR (L/D NIR, Invitrogen). Antibodies used for surface staining in *in vivo* experiments included anti-mouse CD4-PerCP-Cy5.5 (eBioscience) or CD4-Alexa Fluor 700 (eBioscience), CD8-Pacific Blue (eBioscience), and B220-V500 (BD). After surface staining, cells were fixed with Cytofix® (BD) and stored at 4 °C overnight in FACS buffer. Cells were then permeabilized with Perm/Wash™ buffer (BD) containing 5% rat serum (Sigma Aldrich). Antibodies for intracellular staining were diluted Perm/Wash™ buffer containing 5% rat serum and added to permeabilized cells. Antibodies included anti-mouse TNF-α-FITC (eBioscience), IFN-γ-PE (eBioscience), and IL-2-APC (eBioscience). Cells were washed twice with Perm/Wash™ buffer and resuspended in FACS buffer and analyzed on a 3-laser LSRFortessa with High Throughput Sampler (BD). Data were analyzed using FlowJo software (TreeStar,Ashland, OR). Viable CD8 T cells were gated as follows: lymphocytes ($FSC^{int}$, $SSC^{lo}$), single cells (SSC-A = SSC-H), live ($L/D\ NIR^{lo}$), $B220^-$ $CD4^-$ $CD8^+$. Cytokine gates were based on the 99.9th percentile (0.1% of positive events in unstimulated cells).

**Results**

**[0412]** Mice were immunized with a dose range of WT or RI *gag/pol* vectors, containing either a Wild Type (INT(+)) or D64V mutant integrase (INT(-)), encoding a polyepitope construct termed LV1b which contains the $OVA_{257}$ (SIINFEKL) (SEQ ID NO: 24) H-2Kb-restricted CD8 T cell epitope. At 12 days post immunization, $OVA_{257}$-specific CD8 T cell responses in the spleen were measured by ICS for IFN-γ (Figure 15). For both integration-competent and integration-deficient vectors, RI *gag/pol* and WT *gag/pol* vectors generated comparable CD8 T cell responses, confirming that codon optimization of the *gag/pol* gene did not negatively impact LV function as an immunotherapy vehicle.

## Example 16

*RI and WT gag/pol vectors both induce protective anti-viral immunity*

**[0413]** While it was observed that primary LV-induced CD8 T cell responses were equivalent with RI *gag/pol* vectors, the following experiments were performed to determine whether functional immunity induced by these was vectors was also similar. To address this, a recombinant live vaccinia virus challenge was employed as a model of viral infection.

### Materials and Methods

*Vaccina virus challenge*

**[0414]** C57BL/6 mice were immunized subcutaneously in the tail base on day 0 with $5 \times 10^8$ TU of vector encoding LV1b or HBSS vehicle. Four weeks later, mice were challenged intraperitoneally with $1 \times 10^7$ $TCID_{50}$ recombinant vaccinia virus expressing OVA (rVV-OVA), 1E7 $TCID_{50}$ wild-type vaccinia virus (VV-WT), or HBSS vehicle. Five days after challenge ovaries were harvested for quantitation of viral load by $TCID_{50}$ assay.

### Results

**[0415]** Mice were vaccinated with integration-deficient (INT(-)) LV vectors encoding $OVA_{257}$ with either a WT or RI *gag/pol*, and then challenged 4 weeks later with recombinant vaccinia virus encoding OVA (rVV-OVA) or wild type vaccinia virus (VV-WT) as a control (Figure 16). Mice vaccinated with RI *gag/pol* and WT *gag/pol* vectors both showed dramatic reductions in viral load after challenge with rVV-OVA. Confirming that protection was antigen specific, the viral load after VV-WT challenge was similar between vehicle and LV treated groups. These data indicate that RI *gag/pol* LVs can induce memory CD8 T cells that respond to viral challenge and provide functional immunity.

## Example 17

### RI gag/pol modifications eliminate psi-gag recombination, but not other recombination events between vector genome and gag/pol transcripts

**[0416]** The RI *gag/pol* was designed to attempt to eliminates psi-gag recombination, thus further minimizing the chances of RCL formation for third generation LVs. A nested PCR based approach was utilized to screen genomic DNA of cells transduced with integrating vector in order to detect psi-gag recombination.

## Methods and Materials

*Vector quantification – Genomes assay*

**[0417]** Genomic RNA was isolated from vector particles using the QIAamp Viral RNA Mini kit (Qiagen, Valencia, CA). To eliminate contaminating DNA, the extracted nucleic acid was then digested with DNAseI (Invitrogen) following the manufacturer's directions. Two dilutions of each DNAseI-treated RNA sample were then analyzed by quantitative RT-PCR using the RNA Ultrasense One-Step Quantitative RT-PCR System (Invitrogen) and previously-described vector-specific primers and probe. The RNA genome copy number was calculated in reference to a standard curve comprised of linearized plasmid DNA containing the target sequences, diluted over a 7-log range (10 copies – $1.0 \times 10^7$ copies). The genome titer as expressed here reflects the number of physical vector particles, calculated based on genomes, with each vector particle predicted to contain two single-stranded copies of genomic RNA.

*Psi-gag recombination assay*

**[0418]** 293T cells were plated at 2E6 cells in a 10 cm plate. Next day cells were transduced with 1E11 genomes of concentrated VSV-G pseudotyped vector made with either WT *gag/pol* or RI *gag/pol*. The titers for these vectors were 1.2E13 genomes/mL and 1.5 genomes/mL respectively. Forty-eight hours after transduction, cells were harvested and genomic DNA was isolated using a blood and cell culture DNA kit (Qiagen, catalog # 13323). 100 ng of genomic DNA was used as template for the first round of PCR using high-fidelity platinum *taq* polymerase (Invitrogen, catalog # 11304-011) and the following cycling parameters: 1 cycle at 94°C for 2 minutes; 40 cycles at 94°C for 30 seconds, 55°C for 30 seconds, 68°C for 90 seconds; 1 cycle at 68°C for 5 minutes. 1µl (out of 50µl) of the first PCR was used as template either undiluted (1:1) or 1:100 diluted or 1:1000 diluted for the nested PCR. The nested PCR cycling parameters were identical to that used in the first round. No primer controls were included for all reactions. Primers used for PCRs were 378 (TAAGGCCGAGTCTTATGAGCAGC) (SEQ ID NO: 60), 709 (AGGACTCGGCTTGCTGAAG) (SEQ ID NO: 61), 710 (AGCCTGTCTCTCAGTACAATC) (SEQ ID NO: 62), 835 (TGTCTTATGTCCAGAATGCT) (SEQ ID NO: 63), 863 (GCACGGCAAGAGGCGAGG) (SEQ ID NO: 64), and 864 (GCCGGATGTCCAGGATGCTG) (SEQ ID NO: 65). 25µl of total 50µl of the nested PCR was visualized on a 1% agarose gel made with 1xTAE buffer

and ethidium bromide. Bands were extracted and DNA was purified using a gel extraction kit (Qiagen, catalog # 28704) followed by cloning into a TOPO-TA vector (Invitrogen, catalog # K4500-02) and sequencing (Davis Sequencing, CA) using M13 forward and reverse primers.

**Results**

**[0419]** Using the nested PCR approach, a first round of PCR was performed using a forward primer (709) that binds the LV genome 5' of the psi packaging signal and a reverse primer (710) that binds within the frameshift region of both RI *gag/pol* and WT *gag/pol* (Figure 12). The PCR product from this first round was then diluted and used as template for a second PCR using a nested forward primer (863) that binds the LV genome, and a nested reverse primer (835 or 864) that binds to the *gag* region within either the WT *gag/pol* or the RI *gag/pol*, respectively. These two reverse primers were designed to bind the same region in both constructs, with the only differences being due to codon-optimization. The amplicon size from a hypothetical psi-gag recombinant would be 937 bp when using either primer pairs 863 and 835, or primer pairs 863 and 864.

**[0420]** Vector preps encoding the LV1b polyepitope were generated with either the RI *gag/pol* or the WT *gag/pol* plasmids, and were used to transduce 293T cells. Forty-eight hours after transduction the genomic DNA was harvested and PCR was performed followed by analyzing on an agarose gel. First, a positive control PCR was performed using primers that bind only within the LV genome (primers 709 and 378). The predicted LV genome amplicon size with these primers is predicted to be 1697 bp. Cell cultures transduced with either WT *gag/pol* or RI *gag/pol* vector both yielded the expected amplicon size, thus confirming that transduction and integration of provirus are comparable for both vectors (Figure 17A).

**[0421]** Next, the nested PCR was performed for psi-gag recombination as described above. Genomic DNA from cells transduced with the WT *gag/pol* vector produced a band at the expected size of 937 bp, consistent with psi-gag recombination (left half, Figure 17B). In contrast, genomic DNA from cells transduced with RI *gag/pol* produced a larger, but fainter band at 1329 bp (right half, Figure 17B). To determine the nature of the PCR bands, the 937 bp band from WT gag/pol as well as the 1329 bp band from the RI *gag/pol* were extracted and cloned into TOPO-TA plasmids. Sequencing revealed that the WT *gag/pol* band was consistent with a psi-gag recombinant in that the first half of the sequence aligned with the vector genome and the second half aligned with the *gag/pol* transcript that extended beyond

the partial *gag* sequence (Figure 17C). The fainter 1329 bp band from the RI *gag/pol* encoded a sequence that consisted of the first 1253 bp aligning with the LV genome but the last 77 bp aligning with a region of the RI *gag/pol* (Figure 17D). These results indicate that psi-gag recombination was detectable in cells transduced with the WT *gag/pol* vector, but not in cells transduced with the RI *gag/pol* vector. Furthermore, these results present evidence that recombination, though apparently not dependent on psi-gag sequences, was still detectable in cells transduced with the RI *gag/pol* vector.

**Example 18**

**Identification of the DC-SIGN homolog SIGNR1 as a mouse receptor for SINvar1**

**[0422]** ID-VP02 vector particles were investigated to determine whether they could utilize an endogenous mouse receptor for binding and entry. While humans encode DC-SIGN and one paralog, DC-SIGNR, mice have 8 homologs of DC-SIGN (termed SIGNR1 through SIGNR8). Of these, six are predicted to be membrane bound, namely SIGNR1, -R3, -R4, -R5, -R7, and -R8. Based on functional studies, SIGNR1, SIGNR3, and SIGNR5 (also referred to as mouse DC-SIGN), are reported to be the closest functional orthologs of human DC-SIGN. The ability of SINvar1 to mediate binding and entry via these receptors was therefore tested.

**[0423]** HT1080 cells stably expressing either mouse SIGNR1, SIGNR3, or SIGNR5 were generated. These cells were incubated with varying concentrations of integration-deficient GFP-encoding vector that was pseudotyped with SINvar1, kifunensine-modified high mannose SINvar1, or with pantropic VSV-G. In Example 8, it was established that a SINvar1 envelope produced in the presence of the mannosidase I inhibitor kifunensine is required for DC-SIGN binding and human DC transduction. In this experiment, therefore, HT1080 cells over-expressing human DC-SIGN were used as a positive control. Of the three mouse DC-SIGN orthologs tested, SINvar1-pseudotyped vector transduced only mouse SIGNR1 expressing cells and did so in a kifunensine-dependent manner (Figure 18A-D), as had been observed for the human receptor. The transduction efficiency of kifunensine-modified SINvar1 vector on human DC-SIGN- and mouse SIGNR1-expressing cells was remarkably similar (Figure 18A,B), indicating that SIGNR1 is a functionally orthologous receptor for ID-VP02 vector particles in the mouse.

## Example 19

### SIGNR1 is expressed on mouse DCs *in vivo*

**[0424]** In order to further investigate the utility of the mouse model for functional studies that were reflective of the intended mechanism of action in humans, experiments were undertaken to determine whether SIGNR1 was expressed on mouse dendritic cells.

### Materials and Methods

*SIGNR1 and 5 expression* in vivo

**[0425]** Cells from individual spleens or pools of 10 popliteal lymph nodes from 5 mice were stained in FACS buffer (PBS, 1% FCS, 2 mM EDTA, 0.01% sodium azide) in the presence of FcR blocking antibody 2.4G2 and LIVE/DEAD® Fixable Near-IR (L/D NIR, Invitrogen). Antibodies used for surface staining included anti-mouse CD4-PerCP-Cy5.5 (eBioscience) or CD4-Alexa Fluor 700 (eBioscience), CD8-Pacific Blue (eBioscience), and B220-V500 (BD). After surface staining, cells were fixed with Cytofix® (BD) and analyzed on a LSRFortessa multiparametric flow cytometer. Live, single cell events (L/D $NIR^-$, SSH=SSA) were subdivided into B cells ($B220^+$ $TCR\beta^-$), T cells ($TCR\beta^+$, $B220^-$), and DCs ($B220^-$ $TCR\beta^-$ MHC-$II^+$ $CD11c^{hi}$). Gates for SIGNR5 and SIGNR1 expression each of these subsets was set using negative control stains lacking SIGNR1- and SIGNR5-specific antibodies, such that frequencies of positive events were $\leq 0.00$.

### Results

**[0426]** Single cell suspensions from three individual spleens or three pools of popliteal lymph nodes each were analyzed for SIGNR1 and SIGNR5 expression on T cells, B cells, and DCs. SIGNR5 expression was relatively rare in the steady state, being detected only on a small population of B cells (Figure 19). By contrast, while SIGNR1 expression was limited on lymphocytes, approximately 10-12% of MHC-$II^+$ $CD11c^{hi}$ DCs expressed SIGNR1 (Figure 19). Since SIGNR1 is also a functional receptor for ID-VP02 vector particles, these data led us to evaluate whether ID-VP02 vector particles could specifically target mouse DCs *in vivo*.

## Example 20

### [0332] ID-VP02 vector particles target mouse draining lymph node DCs *in vivo*

**[0427]** In order to determine whether the product of a Sindbis virus E2 glycoprotein pseudotyped lentiviral vector particle-encoded transgene could be detected in DCs after direct

administration, particles encoding GFP or a non-fluorescent negative control protein were injected into the right footpad of recipient BALB/c mice.

**Materials and Methods**

*[0332] ID-VP02-GFP transduction* in vivo.

**[0428]** BALB/c mice (n=15/group) were injected subcutaneously in the footpad with $3\times10^{10}$ genomes of ID-VP02 vector particles encoding GFP, control particles encoding NY-ESO-1, or left untreated. Four days later, the draining popliteal or non-draining cervical lymph nodes from were pooled from 5 mice (3 pools per treatment group) and live (L/D singlet events (L/D NIR-, SSH=SSA) were analyzed for the presence of GFP. The phenotype of $GFP^+$ cells was determined by co-staining with anti-mouse CD11c-PE-Cy7 (eBioscience), MHC-II-Pacific Blue (eBioscience), SIGNR5-PE (eBioscience), and SIGNR1-APC (eBioscience).

**Results**

**[0429]** Four days after injecting ID-VP02 vector particles encoding GFP, the draining popliteal or non-draining cervical lymph nodes from 5 mice were pooled (3 pools per treatment group) and analyzed for GFP expression. Injection of ID-VP02 vector particles encoding GFP, but not a non-fluorescent control protein, led to detection of $GFP^+$ cells in the draining popliteal lymph node but not in the distal lymph node (Figure 20A). Upon further surface marker analysis, approximately 90% of transduced cells were identified as DCs as indicated by CD11c and MHC-II expression (Figure 20B), and more than one third of these $GFP^+$ DCs were $SIGNR1^+$ (Figure 20C), supporting a likely role for this receptor in mouse DC transduction *in vivo*.

**Example 21**

**ID-VP02 vector particle DNA has limited biodistribution**

**[0430]** While analysis of lymph node cells was consistent with specific targeting of mouse DCs *in vivo*, biodistribution studies were performed to establish whether transduction events could be detected in other, particularly non-lymphoid, tissues and to characterize the clearance kinetics at positive tissue sites.

**Materials and Methods**

*Vector biodistribution*

**[0431]** C57BL/6 mice (n=3/group) received $3 \times 10^{10}$ genomes of ID-VP02 encoding the polyepitope construct LV1b subcutaneously at the base of the tail. The presence of reverse transcribed vector DNA was analyzed by qPCR at 1, 4, 8, 21, or 42 days post-injection in the following tissues: site of injection (tail base), spleen, liver, heart, ovaries, brain, and draining (inguinal) and non-draining (cervical) lymph node. Tissues were processed in Fastprep Lysing Matrix D tubes using a Fastprep-24 homogenizer (MP Biomedicals, Santa Ana, CA) and genomic DNA was isolated from homogenates using the Qiagen DNeasy Blood & Tissue Kit (Qiagen Inc., Valencia, CA). Eluted DNA (200 ng per sample) was analyzed by qPCR in quadruplicate using EXPRESS qPCR Supermix Universal (Life Technologies, Carlsbad, CA) and a primer/probe set designed to amplify a target sequence of 85-bp within the LV1b cassette. All reactions were performed using the Bio-Rad CFX384 and analyzed using Bio-Rad CFX Manager software (Bio-Rad Laboratories, Hercules, CA). The vector DNA copy number was calculated in reference to a standard curve comprised of plasmid DNA containing the target sequences diluted over a 7-log range ($10^1$ copies – $10^7$ copies).

**Results**

**[0432]** ID-VP02 vector particles encoding a polyepitope model antigen construct designated as LV1b was utilized to determine biodistribution of the particles. After vector injection, the presence of reverse-transcribed vector genomes (vector DNA) can be measured by qPCR using a set of primers and probe specific for the LV1b cassette. Mice were administered $2.8 \times 10^{10}$ genomes of pseudotyped vector particle-LV1b in a single subcutaneous injection at the base of the tail. On a timecourse between 1 and 42 days post-injection, vector DNA was quantified at the injection site (tail base), draining (inguinal) and non-draining (cervical) lymph nodes, spleen, heart, liver, brain, and ovaries. At early time points after administration, vector DNA was detected exclusively at the injection site and in the draining lymph node. The vector signal in these tissues decreased over time, with no quantifiable signal at 8 days in draining lymph node and signal barely above the limit of quantitation (LOQ; 10 copies) at 42 days at the injection site (Figure 21). These results indicate that the dispersal of ID-VP02 vector particles outside the injection site is limited to the draining lymph node, where its biological activity would be hypothesized to occur, and over 99% of vector DNA was cleared within three weeks.

## Example 22

## ID-VP02 vector particles induce polyfunctional primary and secondary CD8 T cell responses

**[0433]** The following experiments were undertaken to measure the ability of Sindbis virus E2 glycoprotein pseudotyped lentiviral vector particles to generate an antigen-specific immune response *in vivo*.

### Materials and Methods

*Intracellular Cytokine Staining (ICS)*

**[0434]** Spleens were homogenized by pressing through a 70 μM nylon filter. Red blood cells were lysed by hypotonic shock by brief exposure to ice-cold ultrafiltered water followed by immediate isotonic restoration with 10x PBS. For analysis of cytokines, cells were stimulated a 96-well with peptides are a concentration of 1 μg/mL per peptide in complete RPMI (10% FCS, 10 mM HEPES, 2 μM β-mercaptoethanol, and L-glutamine) for 5 h at 37 °C, 5% $CO_2$. Peptides, including $OVA_{257}$ (SIINFEKL) (SEQ ID NO: 24), LCMV $GP_{33}$ (KAVYNFATM) (SEQ ID NO: 66), AH1 (SPSYVYHQF) (SEQ ID NO: 67), and AH1A5 (SPSYAYHQF) (SEQ ID NO: 25) were manufactured at 95% purity by AnaSpec (Fremont, CA). In some experiments, as noted, anti-mouse CD107a-PerCP-eF710 (eBioscience) was included in the stimulation cocktail to capture translocated CD107a on the surface of degranulating T cells. After stimulation, surface staining was carried out in FACS buffer (PBS, 1% FCS, 2 mM EDTA, 0.01% sodium azide) in the presence of FcR blocking antibody 2.4G2 and LIVE/DEAD® Fixable Near-IR (L/D NIR, Invitrogen). Antibodies used for surface staining in *in vivo* experiments included anti-mouse CD4-PerCP-Cy5.5 (eBioscience) or CD4-Alexa Fluor 700 (eBioscience), CD8-Pacific Blue (eBioscience), and B220-V500 (BD). After surface staining, cells were fixed with Cytofix® (BD) and stored at 4 °C overnight in FACS buffer. Cells were then permeabilized with Perm/Wash™ buffer (BD) containing 5% rat serum (Sigma Aldrich). Antibodies for intracellular staining were diluted Perm/Wash™ buffer containing 5% rat serum and added to permeabilized cells. Antibodies included anti-mouse TNF-α-FITC (eBioscience), IFN-γ-PE (eBioscience), and IL-2-APC (eBioscience). Cells were washed twice with Perm/Wash™ buffer and resuspended in FACS buffer and analyzed on a 3-laser LSRFortessa with High Throughput Sampler (BD). Data were analyzed using FlowJo software (TreeStar,Ashland, OR). Viable CD8 T cells were gated as follows: lymphocytes ($FSC^{int}$, $SSC^{lo}$), single cells (SSC-A = SSC-H), live (L/D

$NIR^{lo}$), $B220^-$ $CD4^-$ $CD8^+$. Cytokine gates were based on the 99.9$^{th}$ percentile (0.1% of positive events in unstimulated cells) and the CD107a gate was based on the 99$^{th}$ percentile.

**Results**

**[0435]** To assess the immunological activity of ID-VP02 vector particles *in vivo*, a dose range of vector encoding full length chicken ovalbumin (ID-VP02-OVA) was administered subcutaneously to C57BL/6 mice and the $OVA_{257}$-specific CD8 T cell response in the spleen was measured by intracellular cytokine staining (ICS) (Figure 22A). The frequency of IFN-γ+ effectors among splenic CD8 T cells range from a mean of around 15% at a dose of $7.0 \times 10^{10}$ genomes to around 1% at $2.7 \times 10^8$ genomes, indicating that ID-VP02 induces CD8 T cell responses in a dose-dependent manner across at least a 2-log dose range.

**[0436]** To address whether priming with ID-VP02 vector particles induced memory T cells that could be recalled through the administration of ID-VP02 as a homologous boost, animals were primed with a midrange dose of $1.0 \times 10^{10}$ genomes and then boosted with an equivalent dose 35 days post prime. At various timepoints post-prime and boost, the CD8 T cell response was measured by ICS. By analyzing the frequency of IFN-$\gamma^+$ CD8 T cells, it was found that boosting with ID-VP02-OVA induced an $OVA_{257}$-specific recall response that was both more rapid and of a more than two-fold greater magnitude than the primary response (Figure 22B). These data indicate that the application of ID-VP02 is not limited to a single administration by vector-specific immunity, which is known to be a problem for other viral vectors, such as adenovirus-based vectors.

**[0437]** In addition to staining for IFN-γ, the quality of the primary and secondary CD8 T cell responses was analyzed by simultaneous staining for two additional cytokines, TNF-α and IL-2, as well as surface translocation of CD107a, a correlate of cytotoxic activity. After both the prime and boost, most of the responding CD8 T cells had a multifunctional phenotype, as evidenced by elucidation of CD107a, TNF-α, and IL-2 (Figure 22C,D). Notably, 35 days after the boost, essentially 100% of the IFN-$\gamma^+$ cells were $CD107a^+$, a majority also expressed TNF-α, and a substantial fraction of these "triple-positive" cells also produced IL-2, indicating the formation of memory T cells with high functional quality.

**[0438]** The markers KLRG1 and CD127, when measured around the peak of a virus-specific CD8 T cell response, have been associated with a short-lived effector cell (SLEC) and memory precursor cell (MPEC) fates, respectively. As observed during infection with LCMV, when the phenotype of antigen-specific H-$2K^b$-$OVA_{257}$ multimer-binding CD8 T

cells was analyzed at day 9 post-immunization, a fraction of cells were polarized into either the KLRG1$^+$ CD127$^-$ SLEC or KLRG1$^-$ CD127$^+$ MPEC phenotype (Figure 22E). Interestingly, 35 days after both the prime and boost immunizations, while the majority of cells had CD127$^+$ memory phenotype, they were roughly equally divided between KLRG1$^+$ and KLRG1$^-$ subsets, both of which are reported to increased recall potential over SLEC.

**Example 23**

**Memory CD8 T cells induced by Sindbis virus E2 glycoprotein pseudotyped lentiviral vector particles expand and exhibit anti-viral function**

**[0439]** To directly evaluate the function of memory CD8 T cells induced by SINVar1 immunization, an alternative antigen cassette termed LV1b, that encodes both the minimal $OVA_{257}$ and LCMV $GP_{33}$ peptide sequences, two robust H-2Kb-restricted epitopes was employed.

**Materials and Methods**

*MHC-I multimer and memory phenotype analysis*

**[0440]** Splenocytes prepared as described above were stained with H-2K$^b$-$OVA_{257}$ MHC-I pentamers (ProImmune, Oxford, UK) in room temperature FACS buffer for 10 minutes in the presence of 2-4G2 antibody. Cells were washed once and stained with surface antibodies plus L/D NIR for 20 minutes on ice. Antibodies included CD127-FITC, CD44-PerCP-Cy5.5, KLRG1-APC, CD8-Alexa Fluor 700 (all from eBioscience), and B220-V500 (BD). Cells were washed, fixed with Cytofix®, and analyzed as above. Within the viable CD8 T cell population, CD44$^{hi}$ H-2K$^b$-$OVA_{257}$ pentamer$^+$ events, gated based on the 99.9$^{th}$ percentile in unimmunized mice, were analyzed for their expression of KLRG1 and CD127.

*Vaccina virus challenge*

**[0441]** C57BL/6 mice were immunized subcutaneously in the tail base on day 0 with a dose range of ID-VP02 encoding LV1b, a polyepitope construct containing the $OVA_{257}$ (SIINFEKL) (SEQ ID NO: 24) and LCMV $GP_{33}$ (KAVYNFATM) (SEQ ID NO:66) H-2K$^b$-restricted epitopes, or HBSS vehicle. Five weeks later, mice were challenged intraperitoneally with $1x10^7$ $TCID_{50}$ recombinant vaccinia virus expressing OVA (rVV-OVA), 1E7 $TCID_{50}$ wild-type vaccinia virus (VV-WT), or HBSS vehicle. Five days after challenge, spleens were harvested for $OVA_{257}$- and $GP_{33}$-specific ICS as described above, and ovaries were harvested for quantitation of viral load by $TCID_{50}$ assay.

**Results**

**[0442]** As depicted schematically in Figure 23A, 35 days post-immunization with ID-VP02-LV1b, mice challenged with recombinant vaccinia virus expressing OVA (rVV-OVA), but not wild-type vaccinia virus (VV-WT), showed dramatic expansion of $OVA_{257}$-specific CD8 T cells (Figure 23B,C), indicating that these memory cells were recalled in an antigen-specific manner. Further, rVV-OVA did not expand $GP_{33}$-specific memory cells (Figure 23B), confirming the requirement for antigen-specificity within the same animal. Corresponding to the dose-dependent induction of CD8 T cells that responded to infection, there was a clear dose-dependent reduction in the viral load of rVV-OVA in the ovaries of infected mice (Figure 23D). Importantly, the sole antigenic sequence shared between the LV1b antigen construct and the rVV-OVA challenge strain was the SIINFEKL MHC class I epitope, indicating that the protection was mediated by CD8 T cells. Confirming that protection was indeed antigen-specific, infection with VV-WT was not impacted by immunization.

**Example 24**

**SINVar1 immunization provides both prophylactic and therapeutic anti-tumor efficacy**

**[0443]** The CT26 tumor cell line is derived from a spontaneous colon carcinoma in BALB/c mice. An endogenous epitope that can mediate rejection of implanted CT26 tumors is the AH1 peptide. While the MHC-TCR interaction is relatively weak with the AH1 epitope, the altered peptide ligand AH1A5 can stabilize this interaction, leading to greater CD8 T cell expansion and anti-tumor responses. To generate SINVar1 encoding this epitope, an antigen cassette was generated in which the AH1A5 sequence was inserted into full length OVA sequence (OVA-AH1A5), as previously reported. Brockstedt et al., *Proc. Natl. Acad. Sci. U. S. A* 101(38), 13832 (2004).

**Materials and Methods**

In vivo *cytotoxicity assay*

**[0444]** BALB/c mice (3 per group) were immunized subcutaneously at the tail base with ID-VP02 encoding OVA-AH1A5. Twelve days later, dye-labeled, peptide-pulsed target cells were transferred intravenously via the retroorbital sinus into immunized and untreated control mice. Target cells were prepared from naïve splenocytes by lysing red cells by hypotonic shock, then splitting the cells into three populations that were pulsed with 1 μg/mL of either AH1 (SPSYVYHQF) (SEQ ID NO: 67), AH1A5 (SPSYAYHQF) (SEQ ID NO: 25), or

negative control NY-ESO-181-88 (RGPESRLL) (SEQ ID NO: 68) peptides. Cells were washed and then labeled with 2 μM CFSE (Invitrogen) plus one of three concentrations of Cell Trace Violet (Invitrogen): 2 μM, 0.2 μM, or 0.02 μM. Target cells were combined at a 1:1:1 ratio and $5 \times 10^6$ total cells were transferred to recipients. The following day, spleens were harvested and the relative recovery of each population was compared between naïve and immunized mice to calculate specific killing as previously described. Wonderlich et al., *Curr. Protoc. Immunol.* Chapter 3, Unit (2006).

*CT26 tumor challenge*

**[0445]** For prophylaxis experiments, BALB/c mice (10 per group) were immunized subcutaneously at the tail base with ID-VP02 encoding OVA-AH1A5, an antigen that contains a defined MHC-I-restricted rejection epitope for CT26 tumor cells. Four weeks later, immunized and untreated control mice were injected subcutaneously with $8 \times 10^4$ CT26 tumor cells on the right flank. Tumor growth was monitored three times per week and mice were euthanized when tumor area exceeded 100 $mm^2$. Experiments testing ID-VP02 in the therapeutic mode were performed the same way, with the exception that immunization with ID-VP02 was delayed until four days post tumor implantation.

**Results**

**[0446]** When BALB/c mice were immunized with ID-VP02 encoding OVA-AH1A5, we observed dose dependent induction of multifunctional AH1A5-specific CD8 T cells, approximately half of which cross-reacted with the endogenous AH1 sequence (Figure 24A). The ability of ID-VP02 induced CD8 T cells to acquire cytolytic capacity was directly analyzed by *in vivo* cytotoxicity assay. Three splenocyte target cell populations were simultaneously labeled with CFSE plus varying concentrations of Cell Trace Violet, then pulsed with AH1, AH1A5, or a negative control peptide. Target cells were mixed at a 1:1:1 ratio, then co-transferred into recipient mice immunized 12 days earlier with ID-VP02 or left untreated. After 1 day, the relative recovery of AH1 and AH1A5 pulsed targets was reduced in ID-VP02 immunized mice, with specific killing rates over 90% against AH1A5 and about 25% against AH1 (Figure 24B), indicating that ID-VP02 induces functional cytotoxic CD8 T cells against the immunizing antigen.

**[0447]** As a first test for anti-tumor efficacy, mice immunized subcutaneously with ID-VP02-OVA-AH1A5 or vehicle were challenged 28 days later with CT26 tumor cells implanted in the flank. Whereas all control mice had lethal tumor growth (>100 $mm^2$) by day

21, 70% of ID-VP02 immunized mice were able to reject the implanted tumors and these surviving mice were tumor-free for at least 60 days (Figure 24C). These findings were extended by applying ID-VP02 as a therapy to previously implanted CT26 tumors. In this model, tumors were allowed to grow for 5 days, then animals were treated with ID-VP02-OVA-AH1A5 or vehicle control. As in the prophylactic experiments, all control animals succumbed to tumor growth within approximately three weeks (Figure 24D). By contrast, all mice treated with ID-VP02 showed impacts on tumor progression, ranging from a delay in the growth kinetics to outright rejection. Tumors either failed to grow to a palpable size (2/10) or completely regressed (3/10) in the immunized group, leading to 50% of the mice being tumor-free out to at least day 60. These data show that ID-VP02 can exert anti-tumor cytotoxic activity in both the prophylactic and therapeutic settings, supporting the evaluation of ID-VP02 as a therapeutic for cancer in humans.

**WHAT IS CLAIMED:**

1. A composition comprising pseudotyped lentiviral vector particles comprising (a) a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity, (b) an exogenous polynucleotide encoding an antigen, and (c) a plurality of envelope glycoproteins that preferentially bind cells expressing DC-SIGN, wherein said composition is more highly mannosylated compared to a control composition of the same pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor.

2. The composition of claim 1, wherein the envelope glycoproteins are alphavirus glycoproteins.

3. The composition of claim 2, wherein the envelope glycoproteins are Sindbis glycoproteins.

4. The composition of any of claims 1-3, wherein high mannosylation is characterized by being more EndoH-sensitive than a control composition prepared in the absence of a mannosidase inhibitor.

5. The composition of any of claims 1-3, wherein EndoH sensitivity is determined by assessing the molecular weight of the envelope glycoproteins by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) after EndoH treatment.

6. The composition of any one of claims 1-3, wherein the molecular weight of the envelope glycoproteins after treatment with EndoH has shifted about 45% or more of the distance between (a) envelope glycoproteins not treated with an endoglycosidase, and (b) envelope glycoproteins treated with PNGase F.

7. The composition of claim 6, wherein the molecular weight of the envelope glycoproteins after treatment with EndoH has shifted approximately 70% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F.

8. The composition of claim 6, wherein the molecular weight of the envelope glycoproteins after treatment with EndoH has shifted approximately 90% or more of the distance between (a) envelope glycoproteins not treated with endoglycosidase, and (b) envelope glycoproteins treated with PNGase F.

9. The composition of any one of claims 1-8, wherein at least 30% of the envelope glycoproteins in said composition have an increased amount of EndoH-sensitive

glycan as compared to control glycoproteins having the same amino acid sequence(s) in a control composition of pseudotyped lentiviral vector particles prepared in the absence of a mannosidase inhibitor.

10. The composition of any one of claims 1-9, wherein a majority of the envelope glycoproteins are highly mannosylated.

11. The composition of any one of claims 1-10, wherein the pseudotyped lentiviral vector particles are integration deficient.

12. The composition of any one of claims 1-11, wherein the composition comprises a Sindbis E2 glycoprotein.

13. The composition of claim 12, wherein the E2 glycoprotein is 90% identical to SEQ ID NO: 30 [SIN-Var1].

14. The composition of claim 12 or 13, wherein (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein.

15. The composition of claim 14, wherein the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

16. The composition of any one of claims 1-15, wherein the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx [SEQ ID NO: 44].

17. The composition of any one of claims 1-15, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

18. The composition of any one of claims 1-14, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

19. The composition of any one of claims 1-18, wherein the antigen is a tumor-specific antigen or a virus-specific antigen.

20. The composition of claim 19, wherein the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, and alpha-fetoprotein.

21. The composition of claim 19, wherein the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

22. The composition of any one of claims 1-21, wherein the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen.

23. The composition of claim 22 wherein the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens.

24. The composition of claim 23, wherein self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57.

25. The composition of any one of claims 22-24, wherein the first antigen is NY-ESO-1 and the second antigen is MAGE-A3.

26. The composition of claim 22, wherein the first and second antigen are expressed from a bi-directional promoter.

27. The composition of claim 1 wherein the envelope glycoproteins bind cells expressing mouse SIGNR1.

28. The composition of claim 1, wherein the pseudotyped lentiviral vector particles more efficiently transduce cells expressing mouse SIGNR1 compared to cells not expressing mouse SIGNR1.

29. A method of generating a pseudotyped lentiviral vector particle comprising:

(a) culturing in a culture medium comprising kifunensine a virus packaging cell comprising:

(1) a lentiviral vector genome comprising a polynucleotide encoding an exogenous antigen,

(2) a polynucleotide encoding a Sindbis E2 glycoprotein that preferentially binds dendritic cells expressing DC-SIGN, and

(3) a polynucleotide encoding a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity; and

(b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN.

30. The method of claim 29, wherein the E2 glycoprotein is 90% identical to SEQ ID NO: 30 [SIN-Var1].

31. The method of claim 29 or 30, wherein (i) residue 160 of the E2 glycoprotein is absent or is an amino acid other than glutamic acid, (ii) one or more of residues 70, 76, or 159 of the E2 glycoprotein variant is a non-basic residue, and (iii) the E2 glycoprotein variant is not part of a fusion protein with Sindbis virus E3 glycoprotein.

32. The method of claim 30, wherein the E2 glycoprotein is SEQ ID NO: 30 [SIN-Var1].

33. The method of any one claims 29-32, wherein the Vpx protein comprises an amino acid sequence that is at least 80% identical to SIVmac Vpx [SEQ ID NO: 44].

34. The method of any one of claims 29-32, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVmac Vpx (SEQ ID NO: 44), SIVsm Vpx (SEQ ID NO: 45), SIVrcm Vpx (SEQ ID NO: 46), or HIV-2 Vpx (SEQ ID NO: 47).

35. The method of any one of claims 29-32, wherein the Vpx protein comprises an amino acid sequence at least 90% identical to SIVdeb Vpr (SEQ ID NO: 48) or SIVmus Vpr (SEQ ID NO: 49).

36. The method of any one of claims 29-35, wherein the antigen is a tumor-specific antigen or a virus-specific antigen.

37. The method of claim 36, wherein the tumor-specific antigen is selected from the group consisting of NY-ESO-1, MAGE, MART-1/Melan-A, BAGE, RAGE, gp100, gp75, mda-7, tyrosinase, tyrosinase-related protein, renal cell carcinoma antigen, 5T4, SM22-alpha, carbonic anhydrase I, carbonic anhydrase IX (also known as G250), HIF-1alpha, HIF-2alpha, VEGF, prostate specific membrane antigen (PSMA), prostate-specific antigen (PSA), prostatic acid phosphates, six-transmembrane epoithelial antigen of the prostate (STEAP), NKX3.1, telomerase enzyme, survivin, mesothelin, mutated ras, bcr/abl rearrangement, Her2/neu, mutated p53, wild-type p53, cytochrome P450 1B1, N-acetylglucosaminyltransferase-V, human papilloma virus protein E6, human papilloma virus protein E7, carcinoembryonic antigen, and alpha-fetoprotein.

38. The method of claim 36, wherein the virus-specific antigen is an HIV antigen, an SIV antigen, an adenovirus antigen, an enterovirus antigen, a coronavirus antigen, a calicivirus antigen, a distemper virus antigen, an Ebola virus antigen, a flavivirus antigen, a hepatitis virus antigen, a herpesvirus antigen, an infectious peritonitis virus antigen, an influenza virus antigen, a leukemia virus antigen, a Marburg virus antigen, an orthomyxovirus antigen, a papilloma virus antigen, a parainfluenza virus antigen, a paramyxovirus antigen, a parvovirus antigen, a pestivirus antigen, a picorna virus antigen, a poliovirus antigen, a pox virus antigen, a rabies virus antigen, a reovirus antigen, a retrovirus antigen, or a rotavirus antigen.

39. The method of any one of claims 29-38, wherein the lentiviral vector genome further comprises a nucleotide sequence encoding a second antigen.

40. The method of claim 39 wherein the first and second antigen are expressed as a fusion protein that comprises a self-cleaving A2 peptide between the two antigens.

41. The method of claim 40, wherein self-cleaving A2 peptide comprises the amino acid sequence of SEQ ID NO: 56 or SEQ ID NO: 57.

42. The method of any one of claims 39 to 41, wherein the first antigen is NY-ESO-1 and the second antigen is MAGE-A3.

43. The method of claim 39, wherein the first and second antigen are expressed from a bi-directional promoter.

44. The method of any one of claims 29-43, wherein the kifunensine is present in the culture medium at a concentration of about 0.1 μg/ml to about 10 μg/ml.

45. The method of claim 44, wherein the kifunensine is present in the culture medium at a concentration of about 0.25 μg/ml to about 2 μg/ml.

46. The method of any one of claims 29-45, wherein the virus packaging cell further comprises:

(i) a polynucleotide comprising gag and pol genes; and

(ii) a polynucleotide encoding a rev protein.

47. The method of claim 46, wherein the gag and pol genes are human codon optimized and comprise a non-optimized window around position 1228 to 1509 of SEQ ID NO: 54.

48. The method of claim 46 or 47, wherein the polynucleotide comprising gag and pol genes lacks a functional rev responsive element (RRE).

49. The method of any one of claims 46 to 48, wherein the pol gene encodes an inactive integrase enzyme.

50. The method of claim 49, wherein the integrase enzyme has a D64V mutation.

51. The method of any one of claims 46 to 50, wherein the polynucleotide encoding the Vpx protein is on the same or different plasmid as the polynucleotide encoding the rev protein, or the polynucleotide comprising the gag and pol genes.

52. The method of any one of claims 29 to 51, wherein the lentiviral vector genome is derived from HIV-1.

53. The method of any one of claims 29 to 52, wherein the lentiviral vector genome has an inactivated 3' long terminal repeat (LTR) or a self-inactivating 3' long terminal repeat (LTR).

54. The method of claim 53, wherein the lentiviral vector genome comprises a U3 element lacking at least one of an enhancer sequence, a TATA box, an Sp1 site, an NK-kappa B site, or a polypurine tract (PPT).

55. The method of any one of claims 29 to 54, wherein the lentiviral vector genome comprises the nucleotide sequence of any one of SEQ ID NOs: 21, 22, or 23.

56. The method of any one of claims 29 to 55, wherein the lentiviral vector genome further comprises a nucleotide sequence encoding a dendritic cell maturation/stimulatory factor.

57. The method of claim 56, wherein the dendritic cell maturation/stimulatory factor is selected from the group consisting of GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-15, IL-21, IL-23, TNFα, B7.1, B7.2, 4-1BB, CD40 ligand, and drug-inducible CD40.

58. The method of any one of claims 29 to 57, wherein the nucleotide sequence encoding an antigen is operably linked to a promoter selected from the group consisting of the human Ubiquitin-C promoter (UbiC), the cytomegalovirus immediate early promoter (CMV), the Rous sarcoma virus promoter (RSV), and the tetracycline-responsive promoter.

59. The method of claim 58, wherein the promoter is an intron-deficient promoter.

60. The method of claim 59, wherein the intron-deficient promoter is a UbiC promoter.

61. The lentiviral vector particle produced by the method of claim 29-45.

62. The lentiviral vector particle produced by the method of claim 46-60.

63. A method of generating a pseudotyped lentiviral vector particle comprising:

(a) culturing in a culture medium comprising kifunensine a virus packaging cell comprising:

(1) a lentiviral vector genome comprising a polynucleotide encoding MAGE-A3 and NY-ESO-1, wherein a polynucleotide encoding a self-cleaving TA2 peptide is positioned between the polynucleotide encoding MAGE-A3 and NY-ESO-1, wherein the lentiviral genome lacks a polypurine tract (PPT), and wherein expression of MAGE-A3 and NY-ESO-1 is controlled by a UbiC promoter lacking an intron,

(2) a polynucleotide encoding a Sindbis E2 glycoprotein that preferentially binds dendritic cells expressing DC-SIGN,

(3) a polynucleotide comprising human codon optimized gag and pol genes, wherein the polynucleotide lacks a functional rev responsive element (RRE) and wherein the pol gene encodes an inactive integrase enzyme,

(4) a polynucleotide encoding a Vpx protein or a Vpr protein that retains SAMHD1-inhibiting activity; and

(b) isolating a pseudotyped lentiviral vector particle that preferentially binds dendritic cells expressing DC-SIGN.