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## (54) RECOMBINANT CEDAR VIRUS CHIMERAS

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CPC ..... *C07K 14/005* (2013.01); *CI2N 15/86* (2013.01); *A61K 39/00* (2013.01); *A61K 2039/70* 2039/5254 (2013.01); *A61K 2039/70* (2013.01); *CI2N 2760/18222* (2013.01); *CI2N 2760/18234* (2013.01); *CI2N 2760/18243* (2013.01); *CI2N 2760/18244* (2013.01)

## (57) ABSTRACT

Described herein are replication-competent recombinant Cedar virus chimeras are described that are engineered to express antigenic surface or soluble proteins/polypeptides of a non-CedV henipavirus, such as of a pathogenic henipavirus, such as Nipah virus or Hendra virus. Vaccine compositions containing the recombinant Cedar virus chimeras are also described, as are therapeutic methods and uses for protecting against pathogenic henipavirus infection.

Specification includes a Sequence Listing.

## A

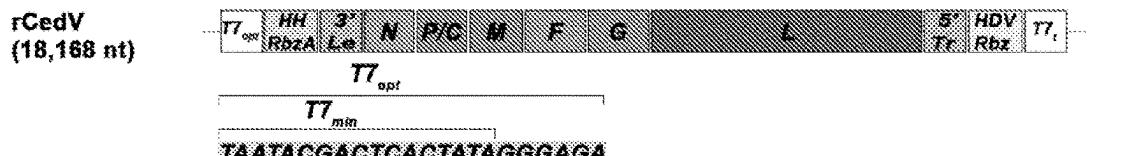


## B

rCedV-NiV-B (18,072 nt)	T7 <sub>opt</sub>   HH   3'   N   P/C   M   NiV   NiV   L   5'   HDV   Rbz   T7 <sub>i</sub>
rCedV-NiV-B-GFP (18,774 nt)	T7 <sub>opt</sub>   HH   3'   N   P/C   GFP   M   NiV   NiV   L   5'   HDV   Rbz   T7 <sub>i</sub>
rCedV-NiV-B-Luc (19,758 nt)	T7 <sub>opt</sub>   HH   3'   N   P/C   GFP   M   NiV   NiV   L   5'   HDV   Rbz   T7 <sub>i</sub>
rCedV-HeV (18,078 nt)	T7 <sub>opt</sub>   HH   3'   N   P/C   M   HeV   HeV   L   5'   HDV   Rbz   T7 <sub>i</sub>
rCedV-HeV-GFP (18,786 nt)	T7 <sub>opt</sub>   HH   3'   N   P/C   GFP   M   HeV   HeV   L   5'   HDV   Rbz   T7 <sub>i</sub>
rCedV-HeV-Luc (19,714 nt)	T7 <sub>opt</sub>   HH   3'   N   P/C   GFP   M   HeV   HeV   L   5'   HDV   Rbz   T7 <sub>i</sub>

FIG. 1

**A**



*HHRbzA*

*GGGAGATTGGTCTGATGAGTCCGTGAGGACGAAACGGAGTCTAGACTCCGTC*

**B**

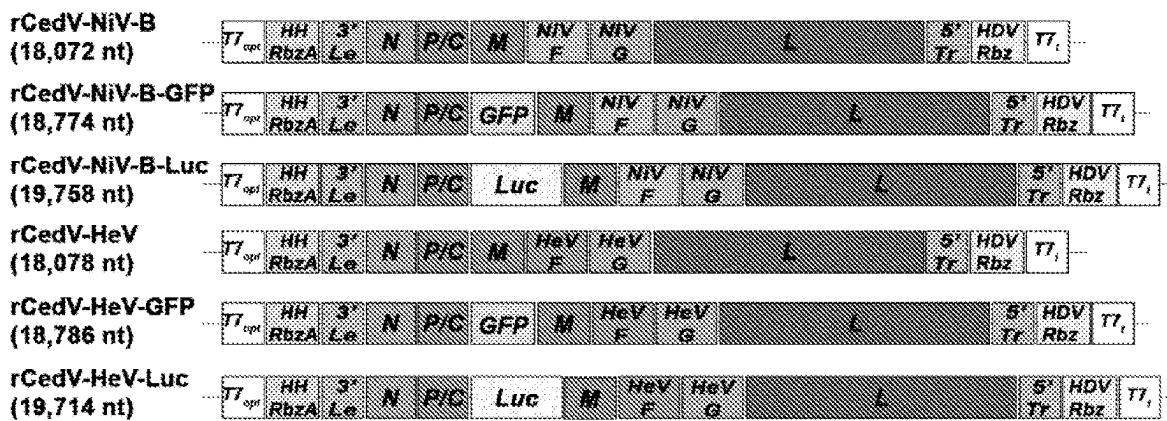


FIG. 2

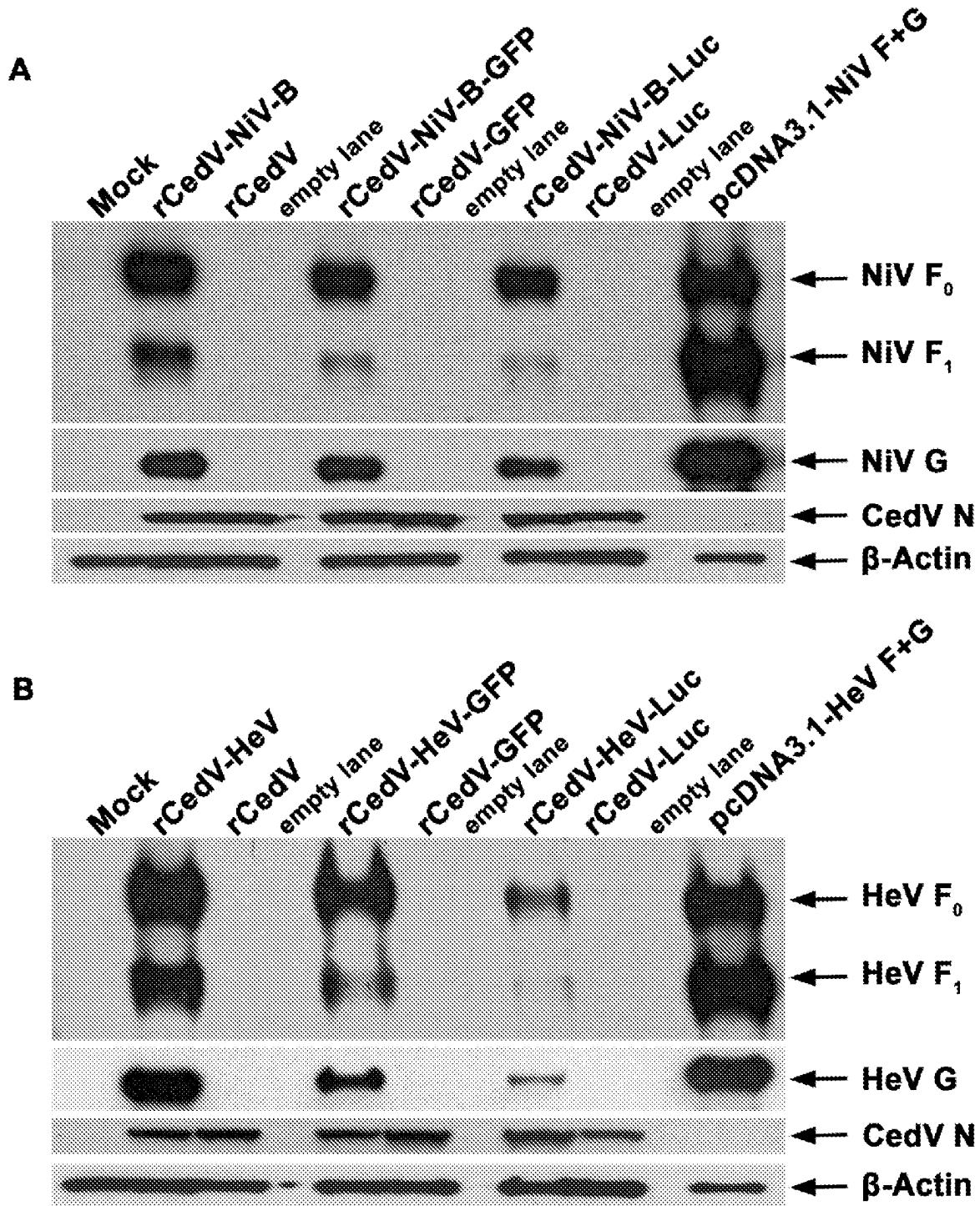


FIG. 3

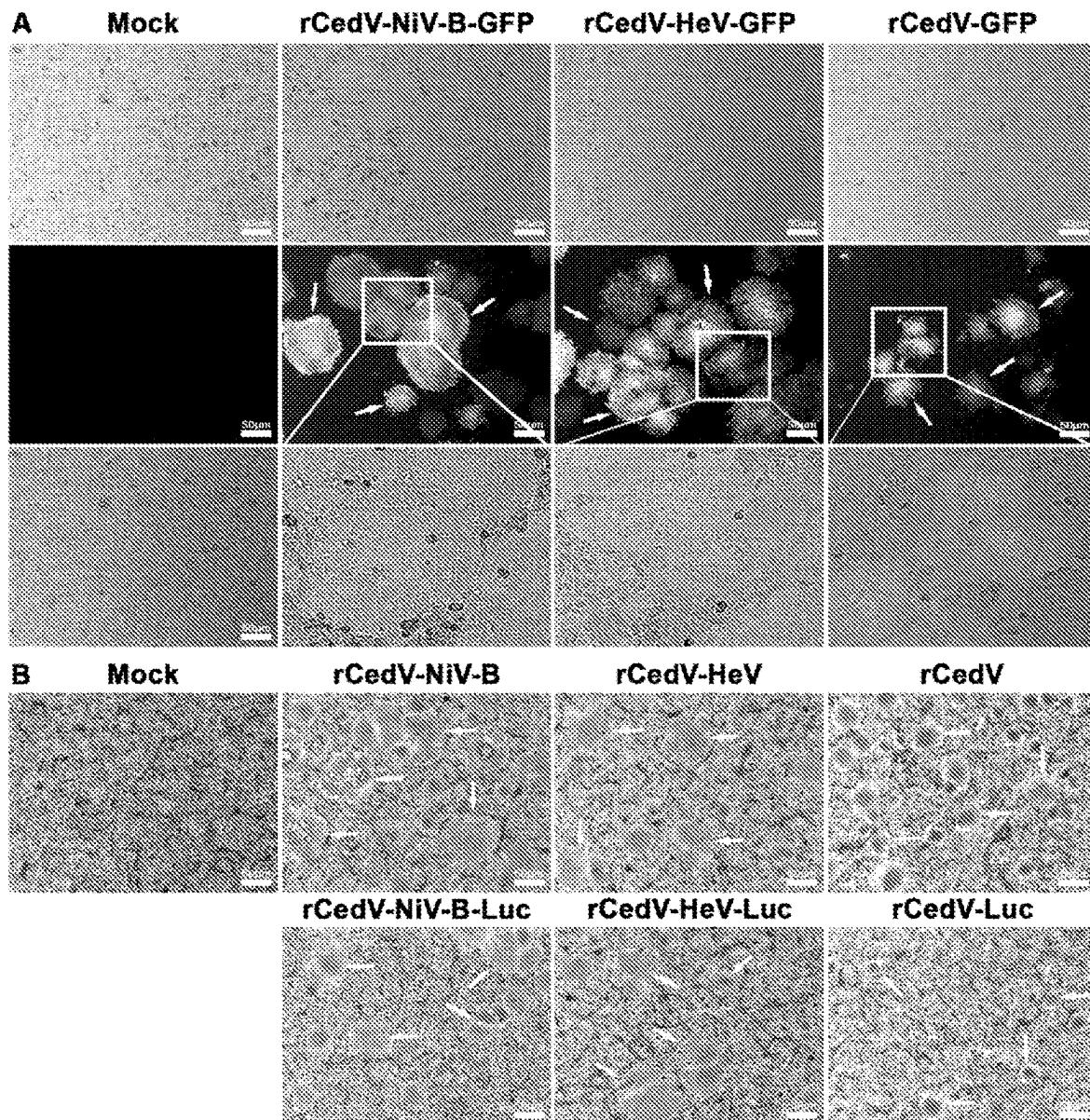


FIG. 4

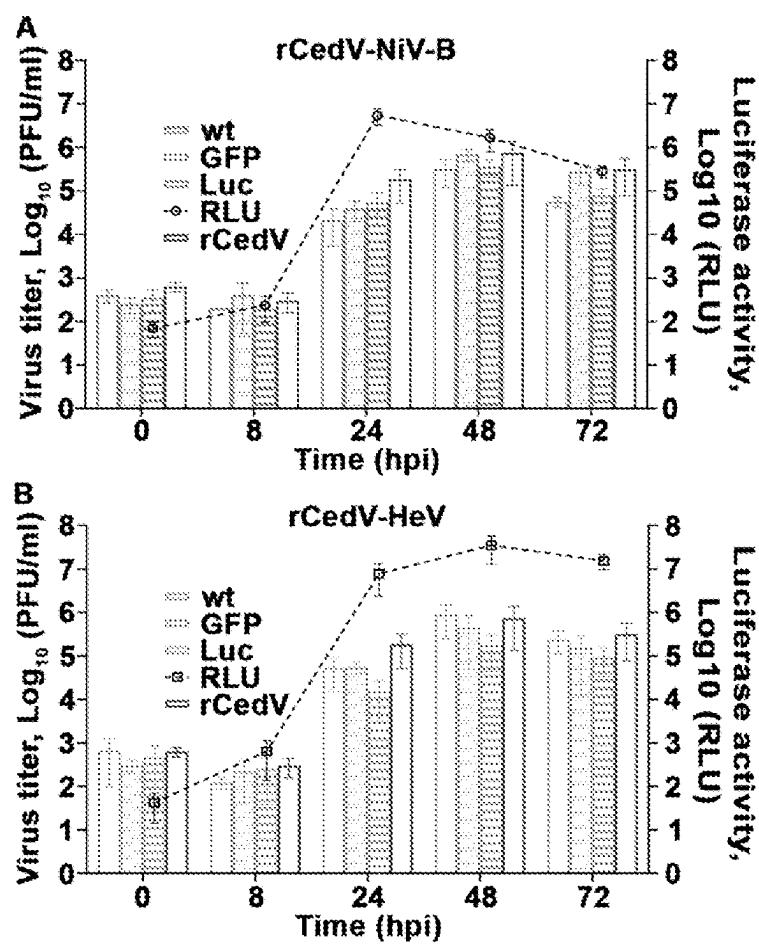


FIG. 5

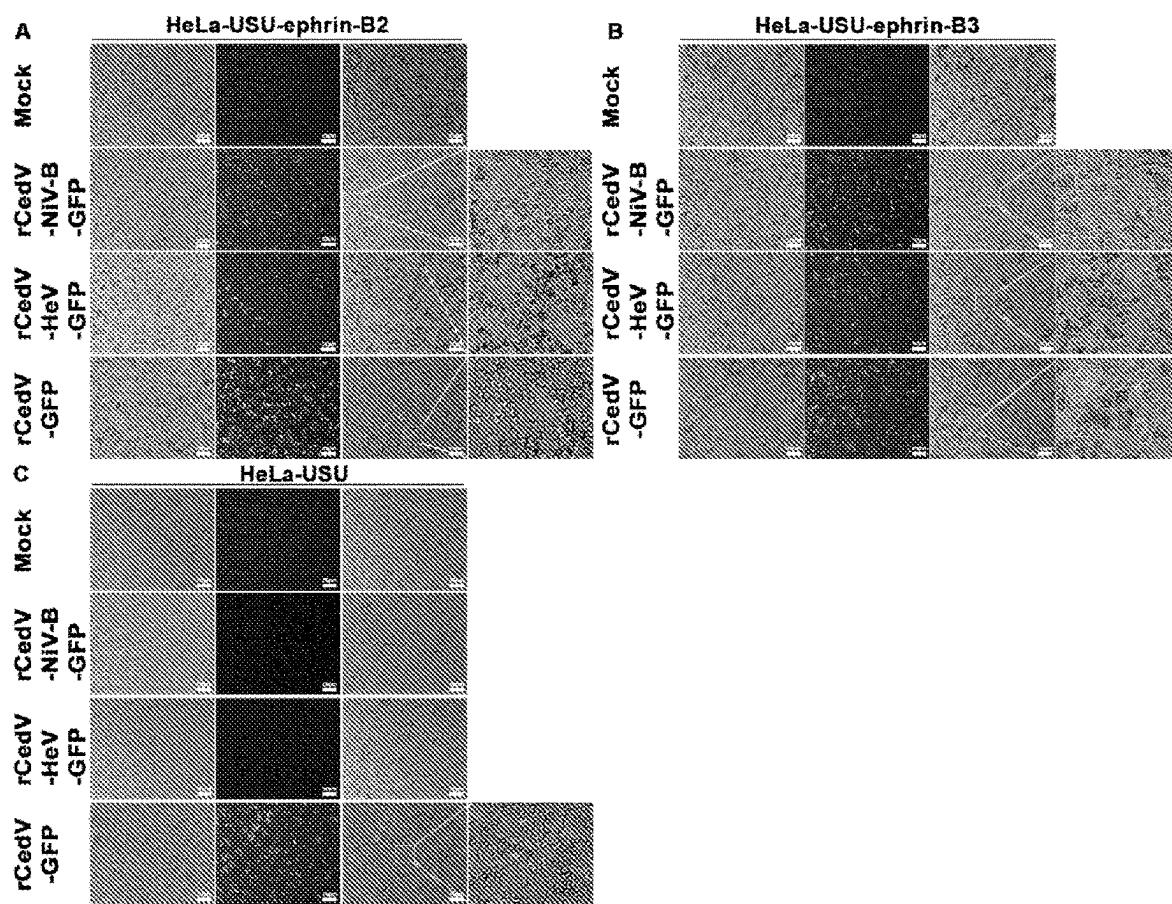


FIG. 6

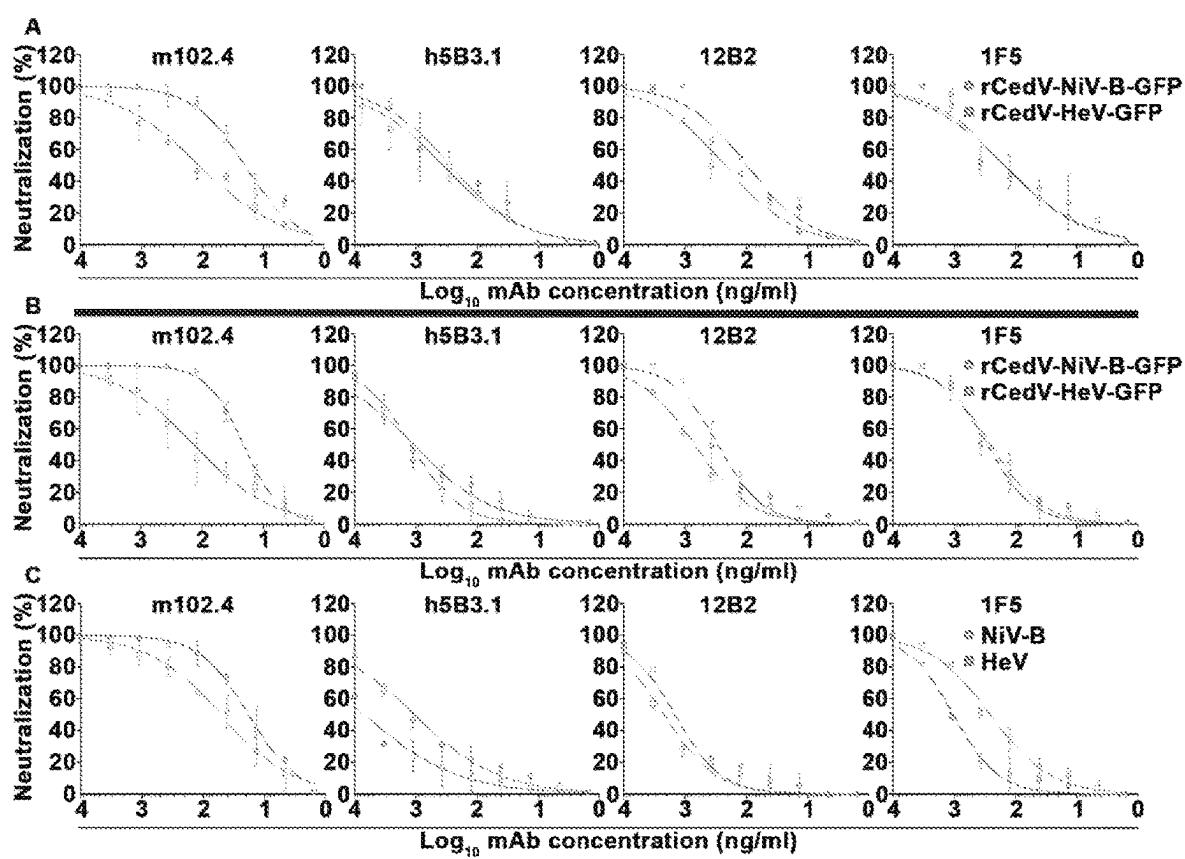


FIG. 7

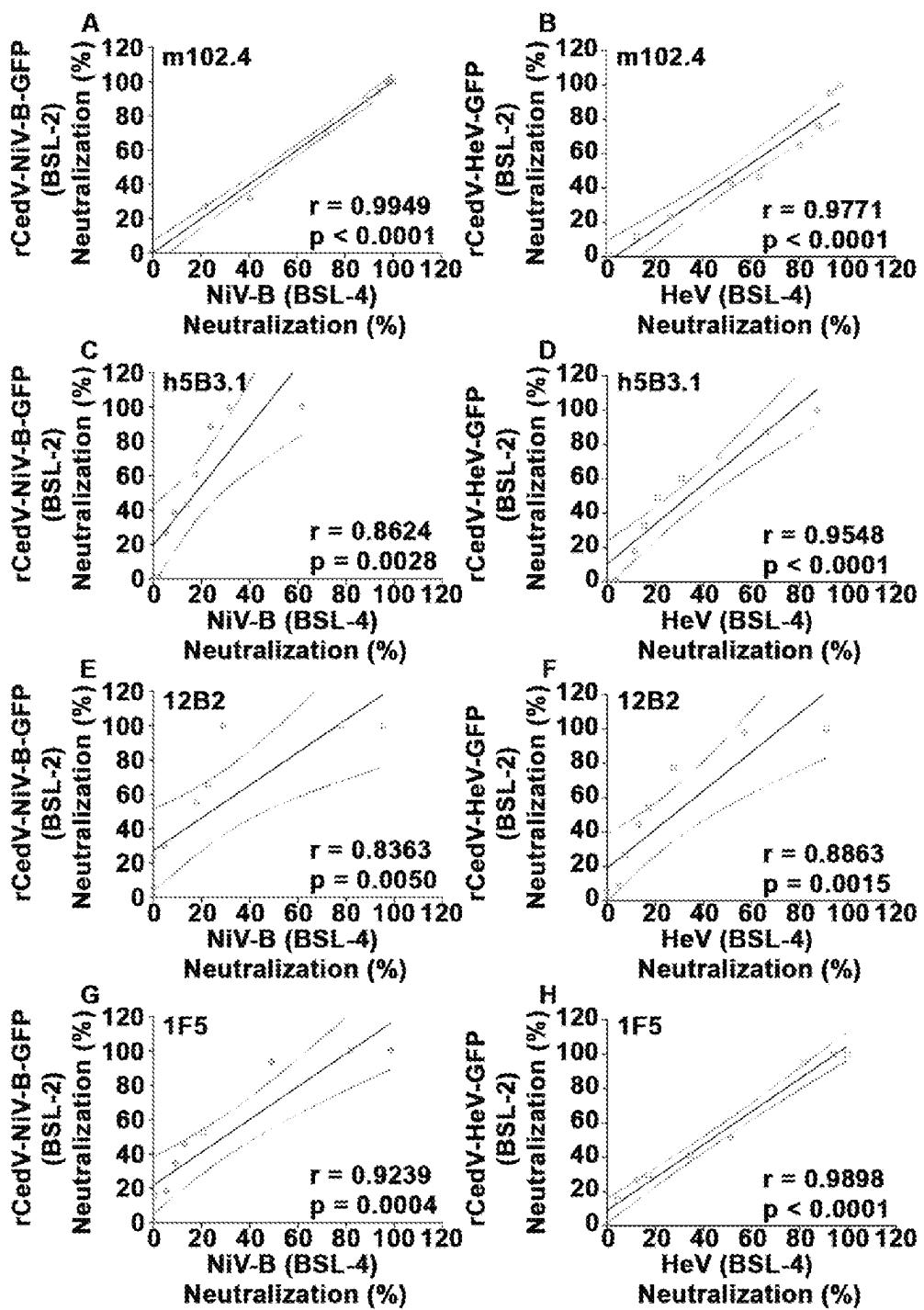


FIG. 8

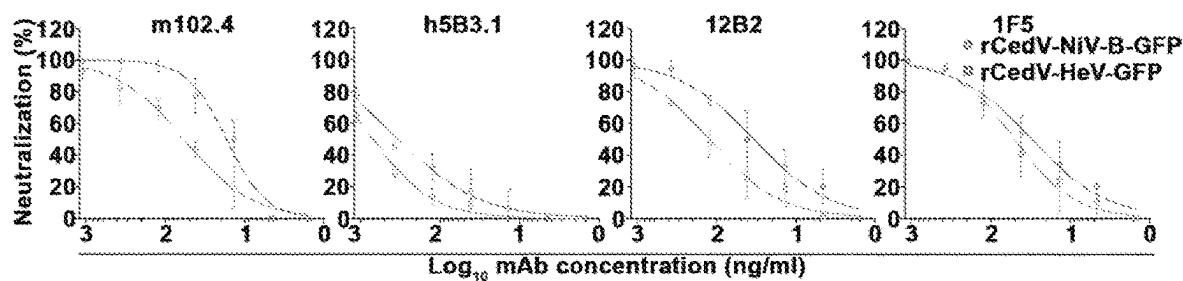


FIG. 9

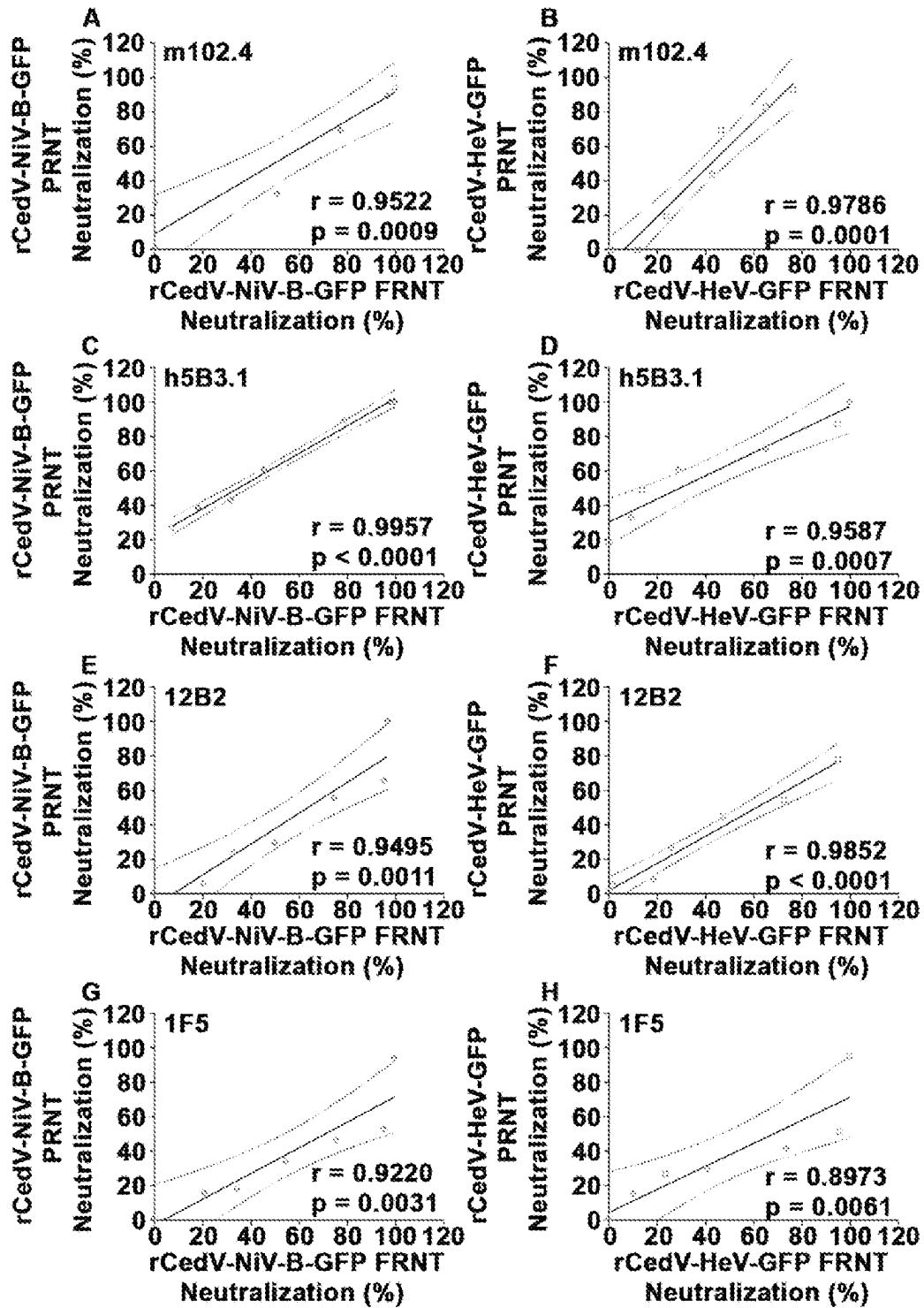
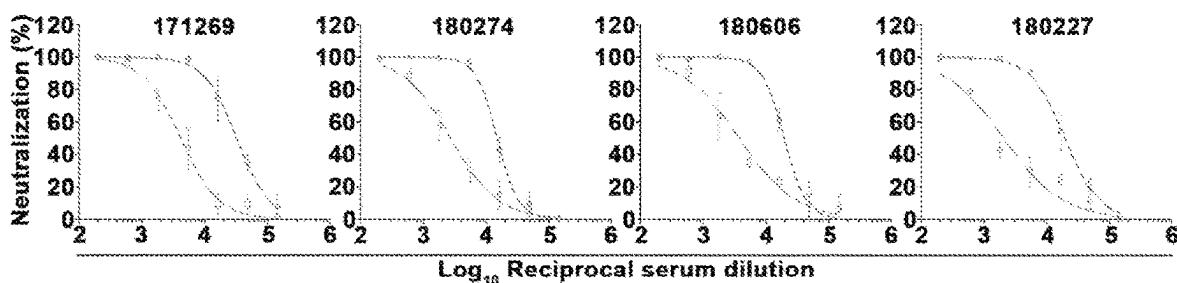


FIG. 10



**FIG. 11**

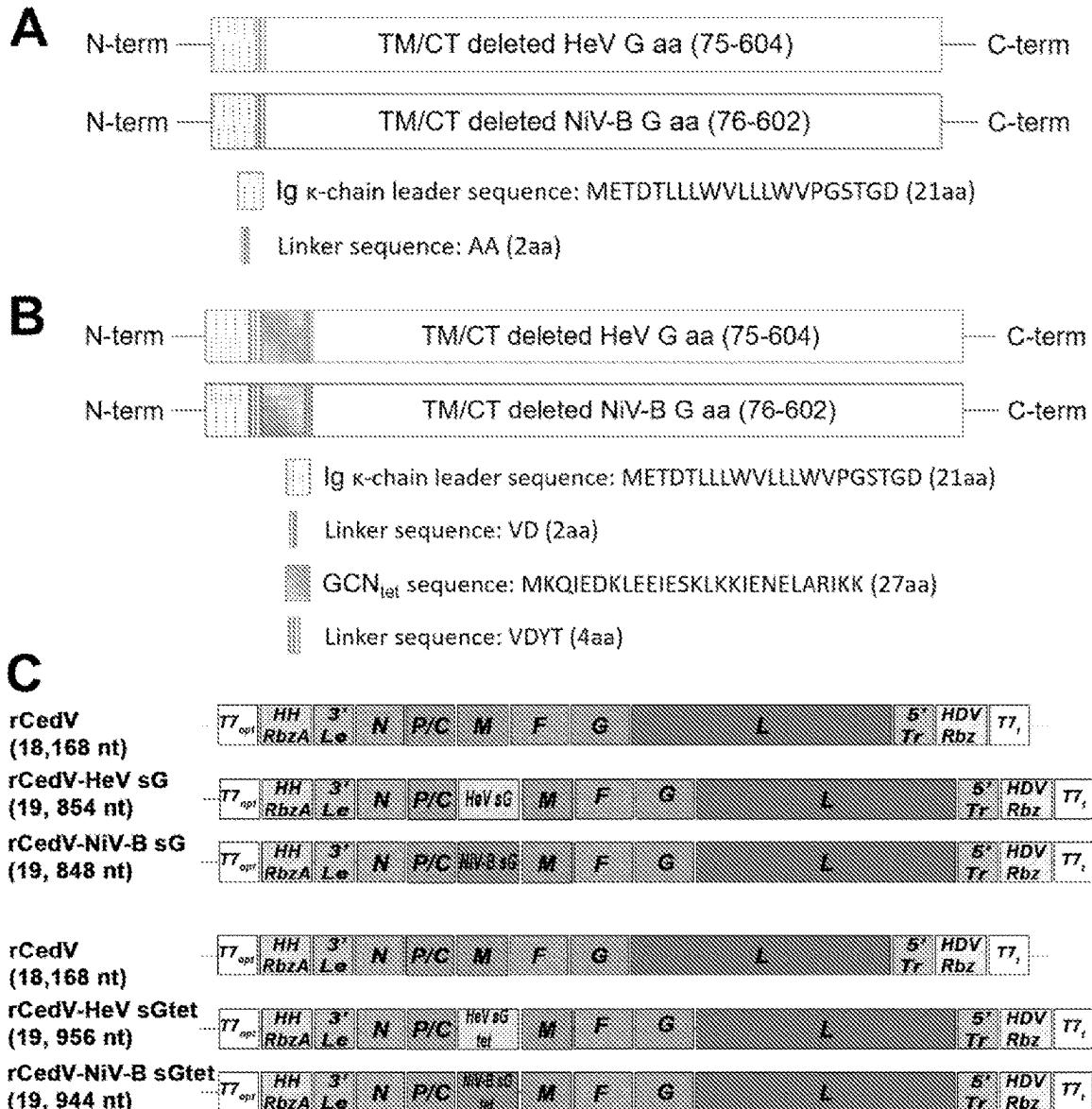


FIG. 12

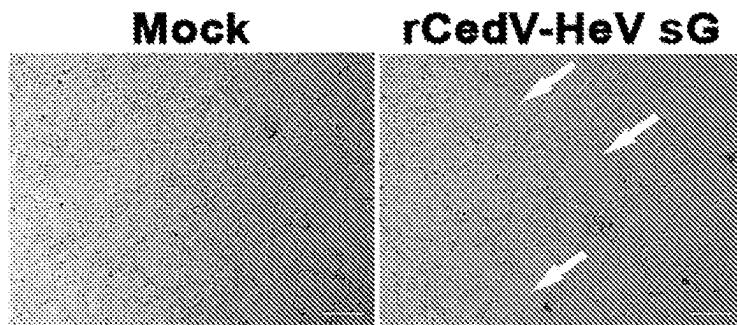


FIG. 13

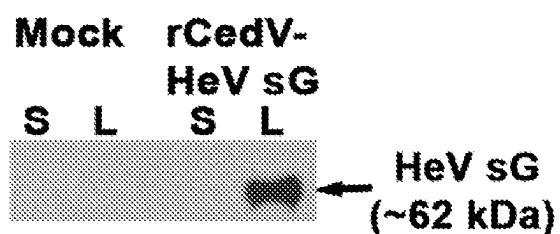
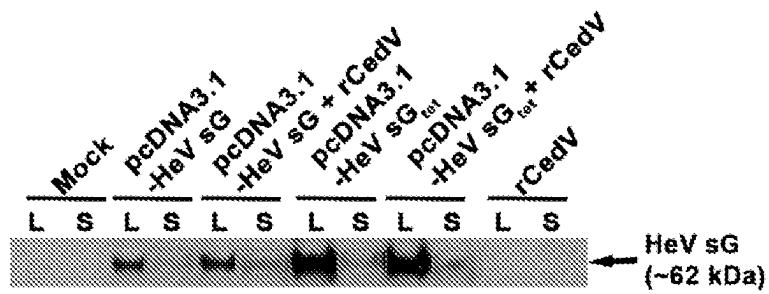


FIG. 14



**RECOMBINANT CEDAR VIRUS CHIMERAS****CROSS-REFERENCE STATEMENT**

[0001] This application is the U.S. National Stage of International Application No. PCT/US2022/026456, filed Apr. 27, 2022, and claims priority under 35 U.S.C. § 119(e) to U.S. Provisional Application 63/180,516 filed Apr. 27, 2021. The entire contents of each application is incorporated herein by reference.

**STATEMENT OF GOVERNMENT SUPPORT**

[0002] This invention was made with federal support under U19 AI142764 01 awarded by the National Institutes of Health. The United States government has certain rights in the invention.

**SEQUENCE LISTING**

[0003] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Jun. 18, 2024, is named “103783-0347\_SL.txt” and is 130,244 bytes in size.

**FIELD**

[0004] The present disclosure relates to recombinant virus chimeras. More specifically, the disclosure relates to recombinant henipavirus chimeras.

**BACKGROUND**

[0005] The following discussion is provided to aid the reader in understanding the disclosure and is not admitted to describe or constitute prior art thereto.

[0006] Henipaviruses are unique members of the Paramyxoviridae family (6). The prototypical henipavirus species, Hendra henipavirus, Hendra virus (HeV) and Nipah henipavirus, Nipah virus (NiV), are highly pathogenic Biological Safety Level-4 (BSL-4) select agents that emerged in the 1990s in Australia and peninsular Malaysia, respectively. They possess a broad host range spanning six mammalian orders (7) and cause infections that can result in severe respiratory illnesses and/or encephalitis with associated high fatality rates in humans (40-100%) (8) and other mammals, such as horses and pigs (2).

[0007] Presently, the well-characterized and well-accepted animal models of NiV (both the Malaysian (NiV-M) and Bangladesh (NiV-B) strains) and HeV infection and pathogenesis that replicate features of human henipavirus disease are the hamster, ferret, and African green monkey (7). There are no licensed NiV and HeV therapeutics or vaccines approved for human use currently available. A licensed equine vaccine for use in Australia (Equivac® HeV) was launched by Zoetis, Inc., in November 2012 on a minor use permit by the regulatory authority, the Australian Pesticides and Veterinary Medicines Authority (APVMA). All vaccinated horses are microchipped, and a database is maintained, and Equivac® HeV received full registration by the APVMA in 2015 (37, 40).

[0008] The genus Henipavirus also includes three additional species, two of which include viruses that were detected in, or isolated from, individual bats. The species, Ghanaian bat henipavirus, includes Ghana virus (GhV), which was identified by targeted RNA sequencing of fecal

samples collected from straw-colored fruit bats (*Eidolon helvum*) (9). Cedar virus (CedV) (Cedar henipavirus), a non-pathogenic virus, was isolated from fruit bat urine samples in Australia (1). The third additional Henipavirus species, Mojjiang virus (MojV) (Mojjiang henipavirus), was discovered in 2012 specimens collected from yellow-breasted rats (*Rattus flavipectus*) in the Tongguan mine in Mojjiang, Yunnan, China, where three miners had died of pneumonia of unknown etiology (10). No viral isolates of GhV and MojV have been recovered to date. GhV and MojV are known only from genetic sequence data and the pathogenic potential of either of these henipaviruses in animals or humans remains unknown.

[0009] Products of the P gene of NiV and HeV inhibit both double-stranded RNA signaling and interferon signaling. The P, V, W and C proteins all antagonize the host interferon response, and have now been demonstrated to play roles in the modulation of henipavirus pathogenicity (11). The NiV W protein is the most potent interferon antagonist and P protein the least (12). Infectious virus studies have shown that interferon signaling remains functional during henipavirus infection of human cell lines while interferon production was inhibited (13). NiV has been central to understanding the V, W, P and C protein's roles in antagonizing the innate immune responses via a diverse set of mechanisms. Notably, recombinant NiV lacking either the V or C protein suppressed the interferon response to similar levels as observed by wild-type NiV, but were significantly less pathogenic in hamsters suggesting that their roles in pathogenicity can also be independent of their interferon antagonist activity (14). Studies with recombinant NiV variants in the ferret model further detailed the relative importance of the V, W, C and P proteins in pathogenesis, revealing that their absence (with the exception of V) or disruption in their STAT1-binding capacity leads to an altered, but still lethal, pathological outcome in comparison to wild-type NiV, whereas only a recombinant NiV lacking the V protein resulted in a non-lethal productive infection in ferrets (15-17). Thus, the inhibition of viral recognition and innate immune signaling induction may be the major role of NiV P, V, and W proteins in NiV-mediated disease, and the inhibition of IFN signaling is less important (15).

[0010] In contrast, CedV does not cause pathogenesis following infection in ferrets, guinea pigs or hamsters (1, 18), or African green monkeys (Geisbert, T. W. and Broder, C. C., unpublished). Unlike HeV and NiV, CedV does not possess the RNA editing site within the phosphoprotein gene (P) that results in the expression of the V and W proteins (1). CedV infection of human cells elicits an interferon- $\beta$  response (1). In contrast to the BSL-4 requirements for NiV and HeV (and potentially for additional henipaviruses, such as GhV and MojV), CedV can be used and manipulated at a lower biocontainment level (BSL-2) (4, 5). Cedar virus can thus serve as a novel, recombinant, henipavirus platform using BSL-2 containment for countermeasure developments against pathogenic henipaviruses.

[0011] CedV is a novel virus platform that has allowed the development of henipavirus targeted technologies for use in antiviral drug discovery, assays and diagnostics development, and live-attenuated vaccine development strategies. A reverse genetics system was previously developed to manipulate and generate novel recombinant CedV (rCedV) that has been used in antiviral discovery programs (e.g.,

anti-henipavirus therapies) (4,5). The genomic sequence of CedV is disclosed in U.S. Pat. No. 10,227,664.

**[0012]** The henipavirus virion bears surface projections composed of the F (fusion) and G (attachment) glycoproteins that are anchored in the viral membrane and are the major structural protein targets of neutralizing antibodies and the antigens employed in various vaccine strategies (7). Within the paramyxovirus family the attachment glycoproteins are also known as the receptor-binding protein (RBP). Infection of host cells by henipaviruses is mediated by the F and G glycoproteins (41). The F glycoprotein facilitates membrane fusion between the virus and host cell. The G glycoprotein consists of a characteristic stalk with a globular head that engages entry receptors on host cells leading to the fusion activation of F and virus infection. The native structure of G is a tetramer, while F is a trimer, and together they are the key determinants of infection and tropism (42). NiV and HeV utilize the host cell proteins ephrin-B2 and ephrin-B3 for entry (43-46). Ephrin-B2 and -B3 are members of a large family of ligands that bind to Eph receptors and are highly sequence conserved among mammals (47). In contrast, CedV has a uniquely broad ephrin tropism and can utilize mouse ephrin-A1, as well as human ephrin-A2, -A5, -B1 and -B2 as entry receptors (4).

**[0013]** Currently existing technology that has been extensively used as a surrogate assay or pseudovirus system or vaccine platform for henipaviruses are the recombinant Vesicular Stomatitis Virus (VSV) (a rhabdovirus) platform that has been used as a replication-incompetent pseudovirus whereby VSV with a deletion of its G glycoprotein is prepared by production in cell culture in which the F (fusion) and G (attachment) glycoproteins of NiV or HeV are transiently expressed in the cells so that progeny virions produced bud from the cells and acquire the F and G glycoproteins that are expressed on the cell surfaces (26-28). This is a tedious method of production, difficult to produce in large quantities, and although is suitable to measure antibody activity or neutralizing titers in sera against NiV and HeV, the measured titers are often quite different to those measured titers or neutralizing antibody activity when compared to assays conducted with authentic live NiV and HeV. Also, a replication competent VSV whereby its G glycoprotein is genetically replaced with NiV F and G, had enhanced pathogenicity in animals (29). Pseudoviruses using retroviruses have also been produced as surrogate neutralization assay systems for NiV and HeV, and these also have the same limitations described for VSV (30).

**[0014]** In regards to vaccines, recombinant VSV vectors have also been a widely used vaccine platform for NiV (31-36). Other viral vectors have also been used, but none are based on an authentic henipavirus that is naturally attenuated (reviewed in (37)).

**[0015]** Thus, there remains a need for constructs useful in vaccines against henipaviruses, and useful in antiviral drug discovery, assays and diagnostics development.

## SUMMARY

**[0016]** Described herein are novel chimeric forms ("chimeras") of Cedar virus that express one or more pathogenic henipavirus proteins (e.g., F protein, G protein, or a combination thereof) and methods and uses of the same for treating, reducing the risk of, or preventing henipavirus infections or stimulating an immune response to henipaviruses. Additionally, the disclosed Cedar virus chimeras can

be used to safely and effectively study or test vaccines and therapeutic agents against pathogenic henipaviruses.

**[0017]** In a first aspect, the present disclosure provides replication-competent recombinant Cedar virus (rCedV) chimeras wherein one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes, respectively, of a non-CedV henipavirus. The non-CedV henipavirus can be a pathogenic henipavirus, such as Hendra virus (HeV), Nipah virus (NiV), Ghana virus (GhV), or Mojjiang virus (MojV). The non-CedV henipavirus can be the Malaysian strain of NiV (NiV-M) or the Bangladesh strain of NiV (NiV-B). In some embodiments, one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes of HeV (rCedV-HeV). In some embodiments, one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes of NiV (rCedV-NiV). In some embodiments, one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes of NiV-M (rCedV-NiV-M). In some embodiments, one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes of NiV-B (rCedV-NiV-B). The rCedV chimera can further comprise a reporter sequence, such as a reporter sequence that encodes a green fluorescent protein (GFP) or a luciferase protein (Luc).

**[0018]** In a second aspect, the present disclosure provides replication-competent recombinant Cedar virus (rCedV) chimeras, comprising the F and G envelope glycoprotein genes of CedV, and further comprising a coding sequence for one or both of (i) a soluble F envelope glycoprotein (sF) of a non-CedV henipavirus and (ii) a soluble G envelope glycoprotein (sG) of a non-CedV henipavirus. The sF and sG coding sequences can be coding sequences of any pathogenic henipavirus, such as NiV, HeV, GhV, or MojV.

**[0019]** In a third aspect, the present disclosure provides replication-competent recombinant Cedar virus (rCedV) chimeras, comprising one or both of (i) a gene encoding a henipavirus F envelope protein fusion protein, and (ii) a gene encoding a henipavirus G envelope protein fusion protein, wherein the fusion protein comprises the ectodomain and transmembrane domain of a non-CedV henipavirus F envelope protein or G envelope protein, respectively, fused to the cytoplasmic tail domain of CedV F envelope protein or G envelope protein, respectively, or (iii) a gene encoding a henipavirus G envelope protein fusion protein, wherein the fusion protein comprises the ectodomain of a non-CedV henipavirus F envelope protein or G envelope protein, respectively, fused to the cytoplasmic tail and transmembrane domains of CedV F envelope protein or G envelope protein, respectively. The non-CedV henipavirus can be a pathogenic henipavirus, such as HeV, NiV, GhV, or MojV. In some embodiments, the non-CedV henipavirus is Hendra virus (HeV) or Nipah virus (NiV). In some embodiments, the non-CedV henipavirus is the Malaysian strain of NiV (NiV-M) or the Bangladesh strain of NiV (NiV-B).

**[0020]** In a fourth aspect, the present disclosure provides vaccine compositions, comprising a rCedV chimera as disclosed herein and a pharmaceutically acceptable carrier. Such a vaccine composition may optionally further comprise an adjuvant. A vaccine as disclosed herein may further comprise one or both of (i) a soluble F envelope glycopro-

tein (sF) of a non-CedV henipavirus and (ii) a soluble G envelope glycoprotein (sG) of a non-CedV henipavirus. The non-CedV henipavirus sF and sG can be those of any pathogenic henipavirus, such as NiV, HeV, GhV, or MojV.

[0021] In a fifth aspect, the present disclosure provides methods of treating, reducing the risk of, or preventing henipavirus infection in a subject in need thereof, comprising administering to the subject an effective amount of a vaccine composition as disclosed herein.

[0022] In a sixth aspect, the present disclosure provides methods of inducing an immune response against a pathogenic henipavirus in a subject in need thereof, comprising administering to the subject an effective amount of a vaccine composition as disclosed herein.

[0023] In a seventh aspect, the present disclosure provides uses of a vaccine composition as disclosed herein for treating, reducing the risk of, or preventing henipavirus infection in a subject.

[0024] In an eighth aspect, the present disclosure provides uses of a vaccine composition as disclosed herein for inducing an immune response against a pathogenic henipavirus in a subject.

[0025] In a ninth aspect, the present disclosure provides vaccine compositions as disclosed herein for treating, reducing the risk of, or preventing henipavirus infection in a subject.

[0026] In a tenth aspect, the present disclosure provides vaccine compositions as disclosed herein for inducing an immune response against a pathogenic henipavirus in a subject.

[0027] In the context of the disclosed methods and uses, the target henipavirus may be any pathogenic henipavirus, including HeV, NiV (including NiV-M or NiV-B), GhV, or MojV. In the context of the disclosed methods and uses, the subject can be a human or a non-human mammal, including but not limited to livestock.

[0028] The foregoing general description and following detailed description are exemplary and explanatory and are intended to provide further explanation of the disclosure as claimed. Other objects, advantages, and novel features will be readily apparent to those skilled in the art from the following brief description of the drawings and detailed description of the disclosure.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0029] The present invention may be better understood by reference to the drawings, which are incorporated in and constitute a part of this specification. The drawings are included to provide a further understanding of the disclosure and are merely exemplary to illustrate certain features that may be present or used singularly or in combination with other features. The present invention is not limited to the embodiments shown.

[0030] FIGS. 1A-B show a schematic representation of the rCedV chimeric antigenome plasmids described herein. FIG. 1A discloses SEQ ID NOS: 38 and 39, in order of appearance.

[0031] FIGS. 2A-B show western blots demonstrating intracellular expression of NiV-B (FIG. 2A) and HeV (FIG. 2B) envelope glycoproteins in infected Vero E6 cells as described herein.

[0032] FIG. 3A-B shows representative syncytia formation (giant cells) by rCedV chimeras rCedV-NiV-B-GFP and

rCedV-HeV-GFP, rCedV-NiV-B-Luc and rCedV-HeV-Luc, and no reporter gene containing rCedV-NiV-B and rCedV-HeV (Scale bar, 50 m).

[0033] FIGS. 4A-B show a comparison of rCedV-NiV-B (FIG. 4A) and rCedV-HeV (FIG. 4B) progeny virus production.

[0034] FIGS. 5A-B show ephrin-B2 and ephrin-B3 are recognized as entry receptors by rCedV-NiV-B and rCedV-HeV and comparison to rCedV controls (Scale bar, 50 m).

[0035] FIGS. 6A-C show a comparison of rCedV chimeras described herein and live NiV-B and HeV by plaque reduction neutralization test (PRNT).

[0036] FIGS. 7A-H show correlation analysis of neutralization values shown in FIGs 6A-C.

[0037] FIG. 8 shows neutralization of rCedV-NiV-B-GFP and rCedV-HeV-GFP by NiV and HeV cross-reactive monoclonal antibodies by fluorescence reduction neutralization test (FRNT).

[0038] FIGS. 9A-H show correlation analysis of neutralization assays using the GFP expressing rCedV chimeric viruses from PRNT (y-axes) and FRNT (x-axes).

[0039] FIG. 10 show the analysis of sera from Rhesus macaques immunized with a mixture of NiV-B and NiV-M sG using the rCedV chimeras described herein by fluorescence reduction neutralization assay (FRNT).

[0040] FIG. 11A-B are a schematic representation of recombinant Cedar virus chimeric antigenome plasmids described herein comprising coding sequences for soluble G (sG) proteins of HeV or NiV-B. FIG. 11A discloses SEQ ID NOS: 40. FIG. 11B discloses SEQ ID NOs: 40, 41, and 42, in order of appearance.

[0041] FIG. 12 shows syncytia induced by rCedV expressing HeV sG glycoprotein.

[0042] FIG. 13 shows western blot data demonstrating the intracellular expression of the HeV sG glycoprotein in cell infected with rCedV-HeV sG.

[0043] FIG. 14 shows western blot data demonstrating that rCedV does not affect expression and secretion of HeV sG or new versions of HeV sG tetrameric (tet) constructs.

#### DETAILED DESCRIPTION

[0044] The following detailed description is presented to enable any person skilled in the art to make and use the invention. For purposes of explanation, specific nomenclature is set forth to provide a thorough understanding of the present invention. However, it will be apparent to one skilled in the art that specific details disclosed may not be required to practice the invention. Descriptions of specific applications are provided only as representative examples. The present invention is not limited to the embodiments shown, but is to be accorded the widest possible scope consistent with the principles and features disclosed herein.

[0045] Described herein are novel rCedV chimeras that are far superior constructs for any heretofore described assays or vaccine systems for henipaviruses, at least because CedV is non-pathogenic and is an authentic henipavirus that is closely related, genetically and structurally, to the other henipavirus species within the genus, including other pathogenic henipaviruses, such as HeV and NiV. As noted above, in some aspects, there are provided replication-competent rCedV chimeras wherein one or both of the F and G envelope glycoprotein genes of CedV are replaced with the F and G envelope glycoprotein genes, respectively, of a non-CedV henipavirus. As noted above, in other aspects,

there are provided replication-competent rCedV chimeras comprising the F and G envelope glycoprotein genes of CedV, and further comprising a coding sequence for one or both of a soluble F envelope glycoprotein (sF) and a soluble G envelope glycoprotein (sG) from a non-CedV henipavirus. As noted above, in yet other aspects, there are provided rCedV chimeras comprising a gene encoding a chimeric fusion henipavirus F or G envelope glycoproteins, wherein, in the fusion protein, the ectodomain and transmembrane domain, of a non-CedV henipavirus F or G envelope glycoprotein is fused to the cytoplasmic tail of a CedV F or G envelope glycoprotein, respectively. There are also provided rCedV chimeras comprising a gene encoding a chimeric fusion henipavirus F or G envelope glycoproteins, wherein, in the fusion protein, the ectodomain of a non-CedV henipavirus F or G envelope glycoprotein is fused to the transmembrane domain and cytoplasmic tail of a CedV F or G envelope glycoprotein, respectively.

### I. Definitions

[0046] In order that the present invention may be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0047] Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present disclosure pertains, unless otherwise defined.

[0048] As used herein, the singular forms “a,” “an,” and “the” designate both the singular and the plural, unless expressly stated to designate the singular only. Reference to an object in the singular is not intended to mean “one and only one” unless explicitly so stated, but rather “one or more.”

[0049] As used herein, “about” when used with a numerical value means the numerical value stated as well as plus or minus 10% of the numerical value. For example, “about 10” should be understood as both “10” and “9-11.”

[0050] As used herein, the term “henipavirus” refers to all viruses and strains thereof in the genus Henipavirus, which is a genus of negative-strand RNA viruses in the family Paramyxoviridae, including but not limited to Nipah virus (NiV), Hendra virus (HeV), Cedar virus (CedV), Ghana virus (GhV) and Mojiang virus (MojV). Further, as used herein, the terms “Nipah virus,” “NiV,” “Hendra virus,” “HeV,” “Cedar virus,” “CedV,” “Ghana virus,” “GhV,” “Mojiang virus,” and “MojV” are inclusive of any strains or sub-types of the respective virus species.

[0051] As used herein, the term “recombinant,” when used in reference to a virus, generally refers to a virus that is produced using genetic engineering techniques and is distinct from a naturally occurring virus.

[0052] As used herein, the term “chimera,” when used in reference to a virus, generally refers to a virus that encodes a gene expression product that the corresponding naturally occurring, or wild-type, virus does not express.

[0053] As used herein, the term “vaccine” refers to a preparation of a chimera as described herein, that, upon administration to a subject, stimulates one or both of antibody production and cellular immunity against a target virus, but is incapable of causing severe infection.

[0054] As used herein, the term “treat,” and variations thereof, refers to a reduction of the level of infection or viral load, including reduction to an undetectable level or elimination of infection, by administration of a chimera, composition, or vaccine as described herein. However, “treatment” does not require the achievement of a complete elimination of infection.

[0055] As used herein, the terms “reduce the risk of,” “prevent,” and variations thereof, refers to elimination or reduction of the incidence or onset or progression of infection by administration of a chimera, composition, or vaccine as described herein, as compared to that which would occur in the absence of the measure taken.

[0056] Alternatively stated, the treatments disclosed herein slow, delay, control, or decrease the likelihood or probability of infection or progression of infection in the subject, as compared to that which would occur in the absence of the measure taken.

[0057] As used herein, the term “immune response” generally refers to innate and acquired immune responses including, but not limited to, both humoral immune responses (mediated by B lymphocytes) and cellular immune responses (mediated by T lymphocytes).

[0058] As used herein, a “therapeutically effective” or “effective amount” designates a dose that causes a specific pharmacological effect for which the chimera, composition, or vaccine described herein is administered to a subject in need of such treatment, e.g., to reduce the risk of, prevent, or reduce infection, as may optionally be assessed through clinical testing and evaluation, patient observation, and/or the like. “Therapeutically effective amount” or “effective amount” can further designate a dose that causes a detectable change in biological or chemical activity. The detectable changes optionally may be detected and/or further quantified by one skilled in the art for the relevant mechanism or process. Moreover, “therapeutically effective amount” or “effective amount” can designate an amount that maintains a desired physiological state, i.e., reduces viral load, or prevents significant increase in viral load, and/or promotes improvement in the condition of interest (e.g., infection status). As is generally understood in the art, the dosage will vary depending on the administration routes, symptoms and body weight of the patient, but also depending upon the compound (e.g., chimera) or composition (e.g., vaccine) administered.

[0059] As used herein, the term “adjuvant” refers to a substance that can enhance or increase an immune response to an antigen. In general, an adjuvant as described herein will be pharmaceutically acceptable for use in the subject to which it is administered by the intended route of administration.

[0060] As used herein, the term “subject” refers to any animal in whom protection from pathogenic henipaviruses is intended, including but not limited to, vertebrates, such as mammals and birds. As used herein, the term “mammal” refers to any animal classified as a mammal, including humans and non-human primates, domestic/pet and farm/livestock animals (such as dogs, cats, horses, cows, pigs, sheep, goats, etc.), weasels, rodents, bats, and zoo or sports animals, etc. The terms “individual,” “subject,” and “patient” are used interchangeably herein.

## II. Cedar Virus Chimeras

[0061] Cedar virus (CedV) is a non-pathogenic henipavirus that can function as a platform for the development of pathogenic henipavirus-targeted technologies for use in anti-viral drug discovery, assay and diagnostics development, and vaccine development strategies. Described herein are novel recombinant Cedar virus (rCedV) chimeras based on the non-pathogenic CedV, and engineered to express antigenic surface or soluble proteins/polypeptides of a non-CedV henipaviruses including pathogenic henipaviruses, such as Hendra virus (HeV), Nipah virus (NiV), Ghana virus (GhV), and Mojiang virus (MojV). The rCedV chimeras described herein have properties that make them advantageous as assay reagents and immunogenic agents (e.g., vaccines) because they are based on an authentic, non-pathogenic henipavirus (rCedV) that is selectively altered with chosen proteins from another henipavirus, such as a pathogenic henipavirus.

[0062] In general, the rCedV chimeras of the present disclosure are designed to either: (1) express a full length F envelope glycoprotein from a non-CedV henipavirus, a full length G envelope glycoprotein from a non-CedV henipavirus, or both, in place of the naturally occurring F, G, or both glycoproteins of CedV; (2) express a soluble form of a F envelope glycoprotein (sF) from a non-CedV henipavirus, a soluble form of a G envelope glycoprotein (sG) from a non-CedV henipavirus, or both, in addition to the naturally occurring F and G glycoproteins of CedV; or (3) express a henipavirus F envelope protein fusion protein, a henipavirus G envelope protein fusion protein, or both, in place of the naturally occurring F or G, or both, glycoproteins of CedV (respectively), wherein the fusion proteins comprise the ectodomain and transmembrane domain of a non-CedV henipavirus and the cytoplasmic domain of CedV, or the ectodomain of a non-CedV henipavirus and the transmembrane domain and cytoplasmic tail domain of CedV. Each of these designs provides a non-pathogenic chimeric virus that is replication-competent. The chimeric viruses can be used for study of the non-CedV henipavirus of which the F/G proteins are expressed. Additionally or alternatively, the chimeric viruses can be used for eliciting an immune response against henipaviruses, including against the non-CedV henipavirus of which the F/G proteins are expressed (e.g., in the form of a vaccine).

[0063] The non-CedV henipavirus can be any henipavirus, including any pathogenic henipavirus. For example, the non-CedV henipavirus can be Hendra virus (HeV), Nipah virus (NiV), Ghana virus (GhV), Mojiang virus (MojV), or any other henipavirus.

[0064] A chimera as disclosed herein may further comprise a reporter sequence, such as a reporter sequence that encodes green fluorescent protein (GFP) or luciferase protein (Luc). Such a reporter sequence may facilitate study of the chimera, be useful in assays using the chimera, or permit tracking of the chimera after administration.

[0065] The genome sequences of a CedV isolate and an exemplary recombinant CedV are provided in Table 9 at the end of the specification. Certain modifications including a

C7A substitution, a C395A substitution, a C4816A substitution, and incorporations of a *Mlu*I restriction site (ACCGCT; SEQ ID NO: 27) are shown in bold and underlined in Table 9 (SEQ ID NO: 2). The C395A and C4816A substitutions remove internal *Sma*I restriction sites. The *Mlu*I restriction site can be inserted between the P and M genes at nucleotide position 4531, after the M transcriptional start sequence, to facilitate insertion of a modified turbo Green Fluorescent Protein (GFP) gene or a firefly luciferase protein (Luc) gene, or the soluble F or soluble G gene sequences from a non-CedV henipavirus. The genome sequences of HeV, NiV, GhV, and MojV are published and available on Genbank. Each of the foregoing chimera designs are described in more detail below.

### A. Chimeras Expressing Full-Length Non-CedV Proteins

[0066] One aspect of the present disclosure is directed to replication-competent, recombinant Cedar virus (rCedV) chimeras wherein one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes, respectively, of a non-CedV henipavirus. While not wanting to be bound by theory, it is believed that in order for this type of rCedV chimera to remain replication-competent, the virus can comprise only one gene encoding a full-length F protein and one gene encoding a full-length G protein. Thus, in these embodiments, if the rCedV chimera expresses a non-CedV F protein, then the gene encoding the CedV F protein is deleted, and if the rCedV chimera expresses a non-CedV G protein, then the gene encoding the CedV G protein is deleted. If the rCedV expresses both F and G non-CedV proteins, then the genes encoding the CedV F and G proteins are deleted.

[0067] For example, the gene encoding the F envelope glycoprotein of CedV may be replaced by a gene encoding a F envelope glycoprotein of a non-CedV henipavirus (e.g., HeV, NiV, GhV, or MojV) while the G envelope glycoprotein of the rCedV remains unaltered; the gene encoding the G envelope glycoprotein of CedV may be replaced by a gene encoding a G envelope glycoprotein of a non-CedV henipavirus (e.g., HeV, NiV, GhV, or MojV) while the F envelope glycoprotein of the rCedV remains unaltered; or the genes encoding both the F envelope glycoprotein and the G envelope glycoprotein of CedV may be replaced, respectively, by a gene encoding a F envelope glycoprotein and a gene encoding a G envelope glycoprotein of a non-CedV henipavirus (e.g., HeV, NiV, GhV, or MojV). In some embodiments, when both the F and G envelope glycoprotein genes are replaced, both replacement genes are from the same non-CedV henipavirus (e.g., HeV, NiV, GhV, or MojV). In other embodiments, when both the F and G envelope glycoprotein genes are replaced, each replacement gene is from a different non-CedV henipavirus.

[0068] Coding sequences for exemplary F and G proteins of various Henipaviruses (SEQ ID NOs: 3-12) that can replace the F and G proteins of CedV (SEQ ID NOs: 28 and 29) are shown in Table 1 below.

TABLE 1

F and G Protein Coding Sequences for Henipaviruses		
Name	SEQ ID NO:	Sequence
NIV-B F coding sequence GenBank: JN808864.1 Predicted TM domain underlined	3	ATGGCAGTTACTAACAGAGATATTATCTTAATCTCTTGTGATGATC TCGGAGTCAGTGTGGGATTTGCATTATGAGAAATTGAGTAAGATTGGCTGTCAA AGGAATAACAAAATACAAAGATCAAACGATCTCTCACAAAAGACATTGTTATT AAATGATCCGAATGTCACCATGCTCAATGCAACGGGGAGTGTATGGAAACTAT AAAACAGATTAACCGTATCTAACGCCATAAAGGGGCAATTAGAGATTAAAGAA CAACACTCATGACCTGTGCGGTGATGTAAGACTGGCGGAGTTATAATGGCAGGAGTTG CTATTGGAATTGCAACCGCAGCTCAAATTACTGCAAGGTGAGCATTATATGAGGCAATG AAAACAGATTCGACAACATCAAACACTCAAAGCAGCATAGAATCAACTATGAAGCTG TTGTTAAGCTCAAGAGACTGCAGAAAAGACAGTCTATGACTGACCGCTTGAGGAT TACATTAATACTAACTGGTACCGACAATTGACAAGATAAGCTGCAAACAGACCGGAACT CTCATTAGATCTAGCACTATCAAAGTACACTCTCTGATTGCTTTGTTGATTTGGTCCCAC CTTCAGGACCCAGTTTCAATTCAGTCAATGACTATACAGGCTATATCTCAGGCATTGGTGG ATTATGAAACACTGCTAAGAACGTTGGGTTACGCTACAGAAGACTTTGATGATCTTCT AGAAAGTGCAGCATAACGGGTCAAATTATCTACGTTGATTTAAGTGGCTACTACATAA TTGTCAGGGTTATTTCTATCCCTGACTGAAATCAAACAGGGCTATATCCAAGAATTGT TGCAGTGGCTTAACTGACAATTGACAATTGAGATCAGCATGGCATTGCCCCAAATTCTCATAT TGGTAAGGAACACATTAAATCAAATATGAGATTGGATTGGCTTAATTACAAAGAGG AGTGTGATCTGCAACCAAGATTATGCAACACCCATGACAACAAATATGAGGGATGTT GACGGGGTCGACTGAGAAGTGTCCCTGAGAGCTGGTGGTTCATCACACGTTCCAGAT TTGCACTATCTAACGGGTTTGTGCTAATTCAGTCAATGCAAAAGCTGTCACATGCCAGTGTCAA CAACAGGTAGGGCAATTCTCACAGTCAAGGAGAACAAACTCTGCTGATGATGATAACACC ACCTGTCCTACAGCCGACTCGGTAATGTGATCATCAGCTGGGAAATATCTGGGTC GTAAAATTATAACTCTGAAGGCATTGCTATTGTCCTCTGCTCTTACTGATAAAGTTGAC ATATCAAGTCAAATATCTAGCATGAACTGATCCTAACAAATCTAAGGACTATATCAA AGAAGCTCAACGACTCTGATGACTGTTAACCCGTCATTAAAGCATGTTGCTATGAT CATACTGTATGACTATCAATTGCAATTGTTGATAGGATTGATTACATTATCAGTTT ATCATTGTTGAGAAAAAAAGAACACCTATAGCAGATTAGAGGACAGGAGACTCAGAC CTACAAGTAGTGGGATCTATTACATTGGGACGTAG
NIV-B G coding sequence GenBank: JN808864.1 Predicted TM domain underlined	4	ATGCCGACAGAAAGCAAGAAAGTTAGATTCGAAAATACTGCTCAGACAAGGGAAAA ATCCTAGTAAAGTTATTAAAGAGCTACTACGGAACATGGACATTAAGAAAATAATGAA GGTTATTGGACAGAACGATATAAGTGCCTTCAACACAGTGTAGCAGTCTGGATC CATTGTAATCATAGTGTGAATATAATGATCATCCAAACTACACAAGATCAACAGATA ATCAGGCCATGATCAAAAGATGCATTGCAAGTATCAGCAGCAGTCAGGGCTGCC GACAAAATTGGCACAGAGATAGGGCGAAAGTACTACTGTTGATACATCCAGTACTAT CACTATCCGCTAATATTGGGCTTGTAGGTTCAAGAGTCAAGGAGCTAACCTGCAAGTAT AAATGAGAATGTAATGCAATTGAAAATTACACTTGCCTCCCTGAAAATTCACGAAT CTAACATTCTGGCTTAACCCACTCCCTTTAGAGAGTATAAGCCAGACAGAAGGA GTGAGCAATCTGGTAGGATTACCTAATAATATCTGCTGAAAAGACATCTAATCAGAT ACTGAAAGAACGACTCTACACCTTACCCGCTAGTCGGTCAAAGTGGCACCTGTA TCACAGACCCACTGCTGGCTATGGATGAGGGTACTTGTGATATGCCACCTGGAAAAAA ATCGGATCATGTCAGAGGGGCTCCAAACAAAGAATAATAGGAGTTGGAGAGGACT AGACAGAGGTGACGAAGTACCTCTTGTATGACTAACGTCGGACCCCATCAAATCC AAACACCGTTTACATTGCACTGGCCGTGACACAAATGAAATTCTATTATGCTTTGTC AGTGTGAGTTGGAGACCCATTCTGAAATAGCACCTACTGGTCCGGGATCAATGAT GACTGTCAGCTGAAACACTAAGAATAATGTTGAGAGTTACAATCAACATCAATTG CCTTACGGAATTGAGAAAGGGAGTATGATAAAGTTATGCAATATGGCACCTCAGGC ATCAAACAAGGTGACACCCCTGACTTCTGCTGAGGATTGGTCAAGGACAGAGTT ACATACAATGATCTCAAATGTCCTACGGGATGTCATAACAGCAAAACTGAAAATG CAGGCTATCTAGGGGATTGACCAACAGTCATTATCTTCGATCTGGACTACTAAA ATACAATCTACGGATGAGGAGAACTCTAAATTGTTGATGAAATCTGATCAA GACTATCTATTGGATCTCTGACAAATCTATGATTCTTGGGTCAACCTGTTTCTACCA AGCATCTTCTGAGGAGACTATGATAATTGGAGAGTGTCAAACAGTTAACCTTT AGTTGTAATTGGCGTGACACACGGTAATCTCAAGACCTGGGAATCAATGCCCTA GATTCAACAAGTGGCCAGAGGTTGCTGGGAAGGGGTTATAATGATGCTTCTGATTG ATAGAATCAATTGGATAAGGGGGGTGATTCTTGTGACAGCAACAGACGGCAGAGAAT CTCTGTTTACTGATTCAAGATAATGAGTACTTACAGAGCACAACACTGCTTCCGAG GACACCAATGCAACAAACAAATACTAATTGCTCTTTGAGAATAAGATCTGGTG TATATCACTGGTGAGATATAGCAGACACAGGAGACAATGTTATAAGACCTAAACTATTG CATTTAAGATACCAAGAGCAATGTACATA
HeV F coding sequence GenBank: JN255801.1 Predicted TM domain underlined	5	ATGGCTACACAAGAGGTTAGGCTAAAGTGTGCTCTGGGATCATAGTCTGGTTTG TCATTAGAAGGGCTAGGAATACTACATTATGAGAAACTTAGTAAGATAGGGCTGGTTAA AGGTATTACAAGAACTACAGGATTAAGAGTAACCCCTTGACCAAGGATATTGTAATCA AAATGATCCCTAATGTTGCAAGTGTCTCAAAGTGCACCGGGACTGTTATGGAGAATTAC AAAAGCAGACTCAAGGAGATTCTCTACCAATCAAGGGCCCATGAACTGTACAATAA TAACACGGCATGACCTAGTTGGTGTGTCAGGCTTGCAAGGTGTGGTGTGGCAGGGATTG CAATCGGGATACTGCTGACAAATCACAGCAGGAGTGTGGCTTATATGAGGCAATG AAGAACGCAGACAATCAATAACTCAAGAGCAGCATAGAGTCTACAAATGAGGCTG TTGTCAAATTACAGGAAACAGCTGAGAAAACAGTCTACGTCCTTACTGCTCTCAAGATT ACATCAACACTAACCTGTTCTACATAGATAACAGTCAAATTAGCTGCAAGAACAGAACTC

TABLE 1-continued

F and G Protein Coding Sequences for Henipaviruses		
	SEQ ID	Name NO : Sequence
		GCATTAGACTTGGCGTTGCTAAGTATCTGCTGATCTGCTTTGTTTCGGACCTAAC TACAGGATCAGTCTCTAACTCCATGACTATCCAAGCAATATCTAAGCATTGGGGCA ATTACGAAACCTTAATCTGAGAACGCTGGTTACGCCAGGAGGATTGACGACCTTTA GAAAGTGATGACATAACAGGCCAGATAGCTATGTAGATCTAGCTAGCTATTACATAAT AGTAAGGGTGTATTTCCTATACTAACAGAGATCCAACAGGCTTATGTGAGGAGTTGC TTCCAGTGAGTTAATAACGATAATTCAAGATGGATCAGCATTGCTCCGAATTTCGTC TGATAGGAACACGCTGATTCAAATATAGAAGTGTAGCTGCTATACCAAGAAA AGTGTGATTGTAATCAAGCATATGCTACACCCATGACGCCAGCTAGGCTAGAGAATGCT GACAGGATCCACAGATAAGTGCCAAGGGAGTTAGTAGTCTATCCCAGTTCAGAG TTGCCCTCTCAGGAGGAGTCTGTTGCAATTGATAAGTGACATGTCAGTGTGAGA CTACTGGGAGGGCAATATCTCACTACAGGCCACAGACTAGTGATGACAATACT ACCTGCAACAACTGTTCTAGGAAACATAATCAGCTGGGCAATTGCTGATCATTCAAG ATAAAATTACAACTTCAGGAGCATTGCTGCGCAGTGTGATTGGCTGATCATTCAAG ATATCTCAAGTCAGATATCTAGTATGAATCAACTACAAACATCTAAGGATTACATTA AGAGACTCAGGAAAGTCTGGACACTGTGAATCTGCTGTTGATAAGTGTGATCT ATCATCCTTATGTTGTCATTGCGCAGTGTGATTGGCTGATCATTCAAG TTGAATAGTTGAGAAAAGAGGAAATTACAGCAGGCTAGATGATAGGCAGGTGCG ACCGTCAGTAATGGTGATCTGATTATATTGGACATCAA
HeV F coding sequence GenBank: MN062017.1 Predicted TM domain underlined	6	ATGGCTCACACAGAGGTCAGGCTAAAGTGTGCTCTGGGATCATAGTCTGGTTTG TCATTAGAAGGGCTAGGGATACTACATTATGAGAACTTAGTAAGATAGGGCTGGTTAA AGGTATTACAAAGAAAGTACAAGATTAAGAGTAACCCCTTGACCAAGGATATTGATCA AAATGATCTCTAATGTCGATGCTCAAGTGACCCGGACTGTATTGAGAAATTAC AAAGCAGACTCTACAGGATCTCCTACCAATCAAGGCCACATGAACTGTACAATATA TAACACCATGACCTAGTGGTGTGATCAAGCTTGCAGGTGTTGATGGCAGGGATTG CAATCGGGATAGCTACTGTCACAAATCACAGCAGGTTGCTCTTATATGAGGCAATG AGAACCCAGACAATATCAAAACTCAAGAGCAGCATAGAGTCTACAAATGAGGCTG TTGTCAAATACAGGAAACAGCTGAGAAAACAGTCTACGCTTCTACTGCTCTCAAG ACATCAACACTAACCTTGTCTACAAATAGTCAAAATTAGTGTGACGAAACAGACTC GCATTAGACTTGGCTGTTGCTAAGTATCTGCTGATCTGCTCTTGTGACCTAAC TACAGGATCAGTCTCTAACTCATGACTATCCAAGCAATATCTAAGCATTGGGGCA ATTACGAAACCTTAATCTGAGAACGCTGGTTACGCCAGGAGGATTGACGACCTTTA GAAAGTGATGACATAACAGGCCAGATAGCTATGTAGATCTAGCTATTACATAAT AGTAAGGGTGTATTTCCTATACTAACAGAGATCCAACAGGCTTATGTGAGGAGTTGC TTCCAGTGAGTTAATAACGATAATTCAAGATGGATCAGCATTGCTCCGAATTTCGTC TGATAGGAACACGCTGATTCAAATATAGAAGTCAAGTGTGTTAATCACAAGAAA AGTGTGATTGTAATCAGGACTATGCTACACCCATGACGCCAGCTAGGCTAGAGAATGCT GACAGGATCCACAGATAAGTGCCAAGGGAGTTAGTAGTCTATCCCAGTTCAGAG TTGCCCTCTCAGGAGGAGTCTGTTGCAATTGATAAGTGACATGTCAGTGTGAGA CTACTGGGAGGGCAATATCTCACTACAGGCCACAGACTAGTGATGACATGACAATACT ACCTGCAACAACTGTTCTAGGAAACATAATCAGCTGGGCAATTGCTGAAATTGATC ATAAAATTACAACTTCAGGAGCATTGCTGCGCAGCATTCTACAGACAATGAGGATT ATATCTCAAGTCAGATATCTAGTATGAATCAACTACAAACATCTAAGGATTACATTA AGAGACTCAGGAAAGTCTGGACACTGTGAATCTGCTGTTGATAAGTGTGATCT ATCATCCTTATGTTGTCATTGCGCAGTGTGATTGGCTGATCATTCAAG TTGAATAGTTGAGAAAAGAGGAAATTACAGCAGGCTAGATGATAGGCAGGTGCG ACCGTCAGTAATGGTGATCTGATTATATTGGACATCAA
HeV G coding sequence GenBank: JN255805.1 Predicted TM domain underlined	7	ATGATGGCTGATTCCAATTGGTAAGCCTGAACAATAATCTATCTGGTAAATCAAGGA TCAAGGTAAGTTCAAGAAATTACAGGCCAAATGGACATCAAGAAAATTACAGATG GGTTATTAGATAGTAAGATACTGGGGCTTAAACACAGTGATAGCTTGTGTTGGGATCA ATCATCATCATGGTGTGATGAATCATGATAATTCAAATTACACAGAACGACTGATAA TCGAGCACTAATCAAGAGTCACTCCAGAGGTGATCACGACAAATCAAAGCTTAAACAG ACAAAGATCGGACAGAGATAGGCCCAAAAGTCTCACTGTGATGACATCACGCCACATC ACAATTCTGCTAACATAGGGTTACTGGGATCCAAGATAAGTCACTGCTACAGCAGTAT TAATGAGAACTGTTAACGATAATGCAAAATTACTCTCCCTTAAAGATTGATGAGGT TAATATCTCTGTCGAATTCTGGCTTCTAGAGAAATCCGACAACTCTACAAAGGGGT GAGTGATCTGTAGGAGTCTGCCAAACAGATCTGTCTACAGAGAACACATCACAC TAAAGGCCAGGCTGATATCTATACTCTACCAATTAAATACAGAGAAGGGGTTGCGATC ACTGCCCACTTTGGCTGTTGATAATGGCTCTCCGCCATTAGGCATCTGAAAGATC GGATCATGTAAGTGGAGAACAAAGGAAATTAGGGTGGGTGGAGGTATTGG ATAGGGGTGATAAGGGTCCCATCAATGTTTGTGACCAATTGTTGGACACCAACATCCA AGCACCATCCATATTGCACTGACGCTCACTTACCATGAGAATTATTACACATTGCGCA GTGTCCTCATGGTGGAGATCTCATCTTAAACAGTACTCTCTGGACAGAGTCACTGTC ATTGCTCTGTGTTGAGAACAAAAGTGTAGTGGAGAGTACAATCAGAAATACATGC TATAACTAAAGTGAAGAGGGAGATGACGATAAGGAAATTGCTTACGGTCTACAGGTA TCAAGCAAGGGGATACATTGACTTCTGGCCGTCGGTTCTGCAAGGACCGAATTTC ATAATACTGACTCTAATTGCCCCATAATTCAATTGCAAGTACAGCAAGCAGAAAATGT AGGGCTTCAATGGGTGCACTCCAAAAGTCATTATATTGGAGATCAGGACTATGGAAG TATAATCTGTCCTGGTGGAGACATCATCTACCAATTATTCGAGATGTCAGACATAGA TTGCACTGGGTTCTCTAGTAAGGAAATTACAACTCCCTAGGTCAGCTGCAACATAGA

TABLE 1-continued

F and G Protein Coding Sequences for Henipaviruses		
Name	SEQ ID NO :	Sequence
		GCATCATATTCTGGATAACGATGATTAATTAGCGATGTTGATACCGTTGACCCCTA AGAGTACAGTGGAGAAAACAGTGTGATTCTAGACCTGGACAGTCACAGTGTCTCG ATTGCTAAACTGGGTTAGCTGGGAAGGGACATATAATGATGTTTCTAATAGA TCGGCTAAACTGGGTTAGCTGGGTATTAAACAGTAACCAAACCTGCAGAGAAC CTGTGTTGCCATTCAAGGATAACGGAGATCCTTACCAAGTCTTGTGAGGATG ACACAAATGCACAAAAACCATCACAGATTGCTTGTGAGAATGTCATATGGT ATATCACTAGTAGAAATATACGATACGGAGACAGTGTGATAAGACCAAAACTGTTG AGTCAAGATACTGCCAATGTCAGAGAGTTGA
HeV G coding sequence GenBank: MN062017.1 Predicted TM domain underlined	8	ATGATGGCTGATTCCAATTGGTAAGCCTGAACAATACTATCTGGTAAAATCAAGGA TCAGGTAAACTTACAGGAAATTACGGGACATGGACATCAAGAAAATTAAACGATG GGTTATTAGATACTGGGCTTAAACAGTGTAGCTTGTGTTGGGATCA <u>ATCATCATATTGTGATGAAATATCATGATAATTCAAAATTACACAGAACGACTGATAA</u> <u>TCAGGCACTAATCAAAGAGTCACCCAGAGTGTACAGCAACAAATCAAAGCTTAAACAG</u> ACAAAATCGGGACAGAGATAGGCCAAAGTCTCACTAATTGACACATCCAGCACCATC ACAAATTCTGCTAACATAGGGTACTGGGATCAAGATAAGTCAGTCTACCAAGCAGTAT TAATGAGAAATGTAACGATAATGCAAATTACTCTTCTCTTAAAGATTCAATGAGTG TAATATCTCTGTCGAATCTTGCCTTCAGAGAAATACCGACCAATCTCACAAAGGGGT GAGTGTCTTGTAGGACTGCCAACAGATCTGCTACAGAAAGACAACATCAAATCT TAAGGCGAGGTGATATCTTACTCTACCAATTACAGGAAATACCGAGAAGGGGTTGATC ACTGACCCACTTTGGCTGTGATAATGGCTTCTGGCTTATAGCCATCTGAAAAGATC GGATCATGACTAGAGGAATTGCAAACAAAGGATAATAGGGGTGGGTAGGTATTGG ATAGGGGTGATAAGGTGCCATCAATGTTATGACCAATGTTGGGACACCACCAATCCA AGCACCATCCATCATTGCAACTTACCATGAGATTATTACATTTGCGCA GTGCCCCATGTCGGAGATCTTACCTTAAGCTACTCTGAGAGTCACTGCTCTG ATTGCTTGTGAGACAGGAAAGTGTAGTGGAGACTACAATCAGAAATACATCGC TATAACTAAAGTGAAGAGGGAAAGTACGATAAGGTGATGCCATTGGCATCAGGTA TCAGGAAAGGGGATACATGTCATTCTGGCGCTGGTTTTGCGCAAGGGACGAATTTC ATAATAATGACTCTAATTGTCCTAAATTCAATGCAAGTACAGCAAAGCAGAAAATGT AGGCTTCAATGGGTGTCACCTCAAAGTCTTATTTGAGATCAGGACTATTGAG TATAATCTCTTGGAGGAGACATACATCTCAATTATTCGAGATTGTCAGAAATAGA TTGACCATCGTCTCTCTAGTAAGATAACAAATTCTAGGTCAACCCGTTTCTACAG GCATCATATTCTGGGATACGTTAGGAAATTAGCGATGTTGATACCGTTGACCCCTCA AGAGTACAGTGGAGAAAATACAGTGTGATTCTAGACCTGGACAGTCAGTGTCTCG ATTAAATGTCTGCCCAGGGTATGCTGGGAAGGGACATATAATGATGTTTCTAATAGA CCGGCTAAACTGGGTTAGTGTGGTTATTAAACAGTAACCAAACCTGCAGAGAAC CTGTGTTGCCATTCAAGGATAACGGAGACTTACAGTGTGAGGATG ACACAAATGCACAAAAACCATCACAGATTGCTTGTGAGAATGTCATATGGT ATATCACTAGTAGAAATATACGATACAGGAGACAGTGTGATAAGACCAAAACTATTG AGTCAAGATACTGCCAATGTCAGAGAGTTGA
MojV F coding sequence GenBank: KF278639.1 Predicted TM domain underlined	9	ATGGCACTAAATAAAATATGTCAGTCACTGTCCTTGGTATCTATTAGTGTACGCT ACGACTGTTCACTAGTATAACACTATGACTCCTTATCAAGGTCGGTGTCTTAAGGGT CTGACATACAACTATAAGATCAAGGGTCGCCATCTACAAGGTAATGGTGTCAAATT GATACCTAACATTGATAGTGTAAAAACTGTACTCAGAACAGTATGATGAAATACAAGA ACTTAGTAAAGGAAAGCCTTAGAACCGGTAAATGCTTACGACCCATGCTCAATAAT GTAAAGTGGGTTAAACAAGGATCAGGTTGCAATTATGGCTGGAGTTGCGCT CGGTGTTGCCACAGCAGCCACTGTTACAGCAGGGATAGGCTTCCATAGATCAAATGAAA ATGCACAGGAAATTGCAAACATGAAGAGTCATCTAAATACAATGAGGCACTAA GCAATTGCAATTGCCAATAACAAACACTAGCTGTGATTGACACCATAGGGAGAG ATCAAAACAAATATAACCGGTTAAATCAATTGAGCTGTGACACAAATTGGCTCAG TGTAGGTATAAGACTCACTGACTACTCTGAAATAACTGTCATTGGCCAGCTTT GCAGAACTCAGTAAATAACAGGATTACCAAGCAATATCTAGTGTGTTAAATGGCA ACCTTGTGAACTGTCAGGATATGGGTTACAGGTTGATGTTGAGATGTCAGGATACAGCT ATAGTGAATTAAATTAGAGGCAACATTATAGACGTTGATGAGATGTCAGGATACAGCT CTAGAAATAGAAATTCCCAACTCAACATTGTCACCTAATGCTGTAGTACAGGAGTTAAT GCTCATCTAGTATAACATAGAGGGGATGACTGGGTCACACTTGTGCAAGGGTTGTC TTACAGGAACTACACTGTTATCAAAATATTGATACGAGTAGATGTCACATCACAGATAGT AGTGTGATATGTCAGGACTACGCTTGCCTATGTCACAGGCTTATTGGCTGCTTA CAGGGAGATACTCAAGTGTGTCAGAGAGAAGGGTAGTCTCAAGTGTGCTTAAATT TCCGTTGCTGTGAGGGTTAGTGTATGCAAAATTGCTCAATACTATCTGCCATGTATGGA TACAGATACTCCTACAAAGTCTGGAGGCCACTGTTACTAGACAAACAAGA GGTGTGTCAGTATCAGGTTAGGAGATGTCATTGATTCGTCAGGATCATATCTAGGAGATG GAGAATAATACTGCTGATAATGTCAGGCTTGCCTTACAGTGTGAGGATG ATAGGAAATCAGCTGGCAGGTAAATCAAACCTTACAAGAGGAGAGGAGATCATTGA GAAGTCAGAAGAGTTCTAAAGGGGTTAACCTTCAATTATCACTCTGTTCCATGGT ATTAATAACAGTAAAGGTAACGTTGCAAGGAGCAGTCAGTATACTCAGCATGT TCCTAGCATGGAGAATATCAATTATGTCAGGAGTTGA

TABLE 1-continued

F and G Protein Coding Sequences for Henipaviruses		
Name	SEQ ID NO:	Sequence
MojV G coding sequence GenBank: KF278639.1 Predicted TM domain underlined	10	ATGGCAACGAATAGAGACAATACCACATCACAGCAGAGGTCTCCAAGAAGATAAGG <u>TTAAAAAATATTATGGAGTGGAAACTGCTGAGAAGGGCTGCAGACATAAGTGTAAT</u> <u>AGGTATCATATGTAATACACTCTGTACTGACAGGGCTAAAGTCACAGAAATATGCTGAA</u> <u>CTAAATATCACCACCTGACAGCGCTAAAGTCACAGAAATATGCTGAAAATATCCA</u> <u>AGATGACGTGAATGCCAATTAGAAATGTCGTGAATCTTGATCAATTGGTGAAGGGTG</u> <u>AAATTAAGCCAAAAGTGTCACTCATAAAATACAGCAGTGAACGCTGACAGCTACCCGGTCAG</u> <u>ATCTCAAACCTCAGACCAAAATTCTGCAAAATATGTTACTTAGAAGAATCTATTACT</u> <u>AAGCAGTGCACTGCAACCCATTATCTGGATATTCCAACATCAGGCCAACCTACCC</u> <u>CCAACGTATAAACACCAGACGTATAACCACAGATGTGACAAAGTGGACACCACGATTA</u> <u>AGCCATTGAGTACCCCAAGCGGATGGGTCAATAGAACCTGGGACCAATTTCACGATG</u> <u>GAGCCCGAGCTAACTTTATACTGTGCTCTAACCTAGGACGGCAAGGTTCTAATTCTGAC</u> <u>GAGTGTAACTAACACCCCTTTTCAATTGGTCTCCATCTATATGTTCTCAAGAG</u> <u>ATTAGAAAACGGACTGACAGCAGGAGAGATATTATCAATTCACTCGTCTAGGCCG</u> <u>ATATGAGACAAGGGTCAAGCAGGGTCTCAAGCAGCACCCATTAGTATGGCGTCC</u> <u>CAAATCCAAGATCATAAACTCTGTGCTGAGCTGGAGACAGAGATGGATGGTG</u> <u>TTATGCTCAGTGACATTAAGTCAGCATCAGGGAGCCATACCTCACATGTTGATGG</u> <u>GTTCTGGTTGATAAGTTAGAACCTGACACCGAAGTTGATCTATAGAATCACAGGCTA</u> <u>TGCTTATCTTAGATAAAACATATGACTCTGCTTATAGTTAGGCAAGGGCGTGGTATTCA</u> <u>GAAGAGTAACGATCTACTTCAGATGTGATTGGTCCAGAAAATAGGAAAGATTTTA</u> <u>AGGCACTGTGAAACATGATCATGCCACTGGCAGTGGAGGTGAGGTTCAAGTGTG</u> <u>TGTGACAGGGCTGTGATGCTTTCGGGAGTGAAAGACTAATTACAAATGCAATATCT</u> <u>GAAGGTAATGATCTGGCAAGTGGAAACCTGTGATAATAGGACAGACATTCGCCCT</u> <u>CAGATTCTTATAAAAGGCTCAATGGTGGATGTACACTATAGGTGATAAAATGGTCTG</u> <u>TATCTGCTCCGTCATCTGGACAGATATCTAGATTGGGATAACACAGATATTCT</u> <u>GTAAAGATCAACACCTGGTAAAGTCAGATCCGATAATGAAGATTGTCACATG</u> <u>CACGAACACTGATAGAGATACTGTCCTGAAATTACATAGGCAACTCTAAATAATG</u> <u>GTGGAACATAAAACTTGTGGCGTACGTGACTCAGATGGTCAATAGCATCATTGAT</u> <u>ATTTCACAAAATTATAGTATCACCTCACTACTATAAGCTGTTCATGTACAAAGAT</u> <u>GAGATTGGTGTATTGCAATCAGAGAGGAAAACAGAAAAGACAATCTCACCGA</u> <u>TATATGCACTTCTACAAATAGGCAAATGTGTTATAATGAGTCGCCACAGTGA</u> <u>CTGTGGGTAATGCCAAAATATCACACAGGAGGTATTA</u>
GhV F coding sequence GenBank: HQ660129.1 Predicted TM domain underlined	11	ATGAAGAAAAGACGGACAATCCCACAATATCAAAGAGGGTCACAACCATTCTGAG GAATCAATCTAGAGGCTACTCAGAGAGACAGATAATTATGCCATGGCTAAAGTT GAGAATTAGTTAGAACATGTCATCCAAAGTAAGAACATCTAAACTACTAAAGAC ACAAAAAAAGGATTCTACAATCCCTTATCGTGTGGAGAGAGAAAAGGACATTATCAA AGATTAAACATCTTATTGATAAAATCTACAAGCATATAAAAGAGGGAGAGAAA TGGTCATAATGGCACTTAACTACTAATTCTGTTGTTATTAAAGGACACA GATGAGTGAAGGCTATCCATACAGGACTCTAAGTAAGATCCGATTAATAAAGGGAA TCACCAAGAGACTCAAAGGAACTCCGTCAGTAAGACATAGTCATCAAATTG ATTCCAATGTACCGGCTTCAACAGTCAGCAACATATCAATGCAAACATATAAAGA ACAACATTGACAAAATACTAACTCTTAAACACATAATTGAAATTGATGCAACTCAA CTAAATCAGCCCCCTGGGAATCAGTTGCTGGCTTATAATTGCAAGGAGTGGCATT GGTGTGAGCCGAGCAGCCAAAATAACTGCGCAGTCAGTCAGTCAGAGCTCGACAGAA TGCAGAGAGAATTAACTCTTAAAGGATAGCATTCTGCCACTAACACGAGTAGCAG AACTCCAGGAAGCACTGGTGGAACTAGTAAATGTCATTACAGGAATGCAAGATTACATC ATAACAAATCTAGTCCCGCAGATTGACAAACTGCAATGTCAGATCAAACGGCATT AGACATATCTCTCCAAATCTATTCAAGAAATTTAACAGTGTGTTGGTCCAAACCTTCA AAATCCAGTAACTACTCTCCATGTCATACAAAGCCATATCACAACTTGGGGAAAATA TAGATTGCTCTAAACACTACTGGTAACTGCAACAGACTTATGGATTGCTGAAA CTAAAAGTATAACAGGCCAAATAACATACATAAACTTGAACATTACTCATGGTAACT AGAGTATATTATCTTAAATGACAACATCAGCAATGCTTATGTCAGGAATTGTC ATTAGCTTCAATGTCGATGCCAGTGAATGGTATCTCTGTACCCCTGTATATTGAT TAGAAACTCATATCTCCAAACATAGACATATCAGAAATCTGCTCATAAACAAAATTCA TGATATGCTGTCATGTCATGTCAGTCAGTCGGCAATGAGTTACACCTTAAGGAATGCCAACTG GAGACACTGAAAAGTGTGGAGAGGGCTGTTGAACTCTCATATGCTCAAGATTGCT ATCTCGGGGGAGTGTATTGCTAATTGTCAGTACAACATGTCATGTCATCAA GCCAAAGTAATTGCTCAAGACGGCAGCCAAACATTGATGATGATAATCAAACATG TTCAATGAGTAAGAAATTGAGAAATCTCATATCAACAGGGAAATATCTGGAGACTCAG AGTACAATACGATGTCAGTCAGTCGGCAATTCTGCTTCACTGACAAGCTGGACATA ACAAAGTCAAAATTCCAACATCAACAACTTGTGAAACAATCCAATTCTAGATAA GTCTAAGGCTATACTGACAAGATAATCTCAACTTAAATTGGCTCTGTACCGATATCAAT ACTTTCTATAATGCGATCTTATGATCTCTTATTATAACTTTGTGATGATGATG ATAATTGTCAGAGAGTATAACAAATACACTCTCTTATAACTCTGATCCATCCAGTAG AGGAGTACTATACAGGACGTATATCATCCCGAACCCCGGAGAACATTGATTAGATC AGCTGCTCGATCAATTGACAGAGATCGAGATTGA

TABLE 1-continued

F and G Protein Coding Sequences for Henipaviruses		
Name	SEQ ID NO:	Sequence
GhV G coding sequence GenBank: HQ660129.1 Predicted TM domain underlined	12	ATGCCGCAGAAGACTGTGGAATTCACTAACATGAATTCCCTCTAGAAAGAGGGTCAG CACTTTCAAGATAAGAACCTCAATCAATCTAAAATCACCAAGCAGGGTATTTG GGTTAGGATCCCACAGTGAGAGAAATTGGAAGAAGCAGAAGAATCAAATGATCATT <u>CATGACTGTTCAACCATGATTCTTGAGATATTAGTGTCTGGCATCATGTTAATCTC</u> <u>ATAGTTTAACATATGGTATTATCAGAATGACAACATCAATCAAGGATGGCAGAACT</u> <u>TACAAGCAATATCACAGTGCTTAAATCTTAAATCATTGACAATTGACAAACAAATTCAA</u> <u>GAGAAATTATTCTTAGGACTCTTATTGACACAGCAACCACATTACAATTCTTAGTG</u> <u>CCATTACTCATATTAGCACTCTGACAACAGAACTCTCGAAATTATTGCGTCATCA</u> <u>ACCAAAAGTGTGAGTTCAAGACACCGACACTTGTCTGAATGACTGCAGAATAACTGT</u> <u>ACCCCAACCTAAACCCGCTGTGATGGAGTGAATTGAGTTCTTGCCTACTAATTGGTT</u> <u>GCACATGGGCCCTCCCTGTAGAAACTTTCATCCGTACCTACAATTACTATTATCGG</u> <u>ATCCAGGATTATAACATAGAACAGATTGACGAAGAGTGTACTAAACCCGAGATT</u> <u>GACAATAAGCAGTACAAAATTGCTTATGCACTCTGAATATGATAAAATTGACCCA</u> <u>GAGGATTCAAATACTGATTGATGACATTGGAGAAATACTGGAGGGTCCGAAAAAA</u> <u>GAACCCAGAATGTTCTAGGTCATTATTGCCCCACAATGCTGTGAATCATATTCT</u> <u>TGTACGCCGATGTCAGTGACTGCAATGAAGGATATTCTTGCCTGAATGACCTCCTCA</u> <u>GATCCCTGTACAAGCAATCTATCTAAATAGCACATTCCATTGGTGTACTGAGGCAT</u> <u>AACAAGGATGAGAAAATAGTTCAATGCCCTAGCTTAACCTTCTACTGATCAAGAGTA</u> <u>TGTCAGATAATCCCTGCAGAACGGTGGCGCACAGCAGAGGTGGCAATCTTACTTCC</u> <u>CTTGTATTGGAGGCTTACACAAACAGACTCACCCATCCTTATGCAAAAGTCAAATT</u> <u>GTCGCGAACTGTGATGTAATTGCTGAAAGTTTACATCAATCAAGGGTCGCCCTCA</u> <u>CACCAAGTAGTCACACTGTCGATAAGGATCAGAAATGCAAGAGAGATAATCAACCTG</u> <u>GGATGTTATCACAGTGTGACTAATACATACCCAGGATCAAGGAGCAGGATTTG</u> <u>GAAGCTTCTCAAACCGATGTTTACATCATCGATCATGGCATACTCTTCTCAGG</u> <u>TAGCAGAGATAACAGACCTAGATAAGTATCAATTGACTGTTGGATACACCTATATA</u> <u>TCTCGTCTGGAGGATCTGAGTGCCTTCCGGAAATTATTGCTCAACCGGTATGCTGGAA</u> <u>GGGACATATAATGATGCTTATAGCTTAACCTCAAATACGATCTTTGTCACTGTTAT</u> <u>TGAAAGAGTGAACAGTCAGAGAACCCATTTCGCAATCTTCCGGATCAAAT</u> <u>CTTGAAGAAATCCCCTTGTGATGCACTGGATAAGCAGTGCACGAACTACGACAATATCGT</u> <u>GCTTCATGTTCAACAATGAAATTGGTGTAGCTGATTAGAGATCACAAGATTGAAT</u> <u>GATGACATCATAAGACCAATTATTACTCTTCTGGCTGCCTACTGATTGCGGACACCA</u> <u>TATCCCCACACGGTAAGATGACCAGGGTCCCTGCGCTCCACATATAACTAA</u>
CedV F coding sequence GenBank: JQ001776.1 Predicted TM domain underlined	28	ATGTCTAACAAAGAGGACAACAGTATTGATCATAATAAGCTATACTTTATTGAAAT <u>ATGCAAGCAATTGTAGGGTTGATTGATAAAATTGAAATAAAATAGGTGTGGTCAAGG</u> <u>GAGAGTCCTAAATTATAAAATTAAAGGAGATCCAATGACAAAAGACCTGCTTGAAAT</u> <u>TTATCCCTAACATAGTGAATATCACTGAATGTTGAGAGAGCCCTGAGTAGGTACAAT</u> <u>GAGACCGTGAGGAGATTGCTTACCTATACACACATGCTGGGTTATACTGAAATAAC</u> <u>ACAAATGCTAAATGACTGGGTGATGATGCCGGTGTGATCATGGTGGGATAGCAAT</u> <u>AGGTATAGCCACAGCAGCTCAGACAGCAGGTTGCTTTATGAGGCAAAAGA</u> <u>ACACAGAAAATTACGAAATTACAGACACATCATGAAAACACAGGACTCGATTGA</u> <u>TAAAACTTACTGACAGTGTGGGACAGCATACTTATATTGAAATAAGCTACAGACATACA</u> <u>TCAACAACTCAACTGGTACCAAACTAGAGCTTCTATCCTGCCGACAAAACAAATTGAG</u> <u>TTTGATCTAATGTTAACAGTATTGGTGGATCTTATGACTGTTATTGGTCTAAATCA</u> <u>ATAATCCTGTTATAAAGATATGACTATTCAATCTTGTCACTTCTTTGATGCCAATT</u> <u>TGATATAATGTCAGAACCTGGTATACACTCAGGATTCTTAGATTTGATAGAGAG</u> <u>TAAGAGTAAACAGGCAAAATTATTTGTTGATATGGAAAACCTGATGTTGATGCA</u> <u>GGACATATCTACCTAACCTAAATGAGTACCTGATGCCAAATATATGATGTTCAACAAA</u> <u>ATAACTATGAGTAGCAATGGAGGAGAAACTTGTCAACCATACCTAATTCTATTAAT</u> <u>AAGAGGTAATTATATGTCATAATATAGATGTTGCAACATGTTATGACCAAAGCAAGCG</u> <u>TAATTGTAATCAAGATTATTCACTCCCGATGAGGCAAAACTTAAGAAGCTTATCAAG</u> <u>GTGAGACAGAGATACTGCTCTGTGAGGCAGTCATCCGTCACACTCTCAAGATTGCTC</u> <u>TTACAAATGGGATTATTGCTCAATTGATAACAAATCAATTGTTAGGTGTCAAGACAATG</u> <u>GTAAGAGACTATCACTAAACACAAACATTCGTAAGCATGATGACAAACAGTACTTGT</u> <u>ATGATGTCATGTTAGATAATTCACTTAAAGTAGGAAATAATGGGGAGAAAAG</u> <u>ATATCAATAATTAAATATCAGATAGGACCGCAGATCATAATTGATAAGGTTGACTTG</u> <u>TCTAATGAAATAACAGATGAATCAATCTTAAAGATAGTATTCTACCTGAGAGA</u> <u>AGCCAAGAGAATTAGACTCAGTAATATCAGTCTTATATCTCAAGGTTCAATTGTT</u> <u>TCTAATAATAATATCAGTCTCTATTATATTGATGTTATCATAGTATACTTGTAC</u> <u>TGTAATCAAAACATTCAATAAATATAACAAATTATAGATGATGCTGATTATTACAAT</u> <u>GATTACAAAAGAGAAGCTTAAATGGCAAGCCAGTAAGAGTAACAATATATTATGTT</u> <u>AGGTGATTAAC</u>

TABLE 1-continued

F and G Protein Coding Sequences for Henipaviruses		
Name	SEQ ID NO:	Sequence
CedV G coding sequence GenBank: JQ001776.1 Predicted TM domain underlined	29	ATGCTTCTCAGCTCCAAAAAAATTACTTAGACAACCAAACCAAGGTGATAAAT GAACAACCAAGATAAGAAAATTAGTGTCAACTCAACCCTTAGAATTAGATAAGGTC AAAAGAGTCTCAATAAGTCTTATTATGTTAAAACAAGAATTATAACGTTCAAATCTAT TAATGAAAGTCTGCACGATATCAAGTTGTATTATTGTATACTCTACTGCTAATTAT <u>CATTACAATAATCAATAATCACAAATATCAATTGTATAACTCGTCTGAAAGTACATGA</u> AGAGAATAATGGCATGGAATTCTCTAATTCAACATCTATTCAAGATAGTCTCATCTCT TACTAACATGATCATCACAGAGATAACTCCTAGAATAGGGATTAGTTACAGGCCACTT CTGTTACTCTCTTCATCTATCAATTATGTCGGACTAACAGAAATCACTGGTCAATG ATTAAAAGATTATAACAAAAGTTGTGGCTTAAGGTCCTGAATTAAAGTTACAT GAATGCAACATAAGTGTGATCCAAAATTAGCAAATCTGCAATGTACAGCACCAA TGCCTATCCGGAGCTGGTCCACCTAAAGATATTGTAAAAGTGTATCCAAAGACCC COAGTTAGACTGAAGCAGATAGATTATGTAACCAAGTGTACAGGCCACTT GTATGAAACAACCTTATTGGATATTCTGATGGTTTTACCTACATACATTATGAAG GAATAATAGTGTAAAAATCAGATTCAATTAAAGTGTCTGTACATGGTAAATA GTGTGAGGGTGAATTATCGACATCATATTATCTATTATCAAGTCATTACATCCTTAT TCATGAGGTTAAACTGTGTACCTGTGACTTGAACCGATCATCCTTGATTCCTGT CATATCTCAACAAACACTAAACATGGACAATTCAAGATTACTCGTCAGACGAGACTA CATAAACATATTCAATGGCATAGATCGTCCAAAACCAGAAAGATCCCATTAAACAA TGACAGCAGACAATTCGTTATCCATTACATTCTCAGGTGGGGAGGTATGTTAG GTGAAGAATTATTATTCCTGTACACAGTCATCAATAGTGTATTACGGCATGATT ATTGTGAGAGTTCACTGTICAGTCCAAACGGTAAAGTCTAAAGGAGATACTCT GAGTCATTAAGATCTCCAACGAACTCATCGGATAACATTAAACGGAATCATGTTAT AAGTCAAACACATGACAGATTTAAGATTAGTGTGAATGGTATAACTTAAACAAAC TGTCAATTGGAGACTCTGGAGACTGAGCAAGACACTGGCCAGGTCTTATTACCAA TCTCAATGAGTGGGAACTTATCTAAAGGAGGATTGTGAGAAATGAAACCCCTT ACCCCGAATTGGATGAACAATACTGTGATATCAGACCTAACCAAGGTATTGTC GTATCATTAACATGCCCGAGATATGTTATGGAGGGACATACAATGATATTGCT ATCTAGGAAAGAGCATGTATGTTAGCGTTATTCTAGATTCACTGTCAGAGAAT CCAGAGTTACAGTATTAAACTCTACTATACATTATAAGGAGAGTATC TGAACAAACACAAGAAGTACTAACAGAGCTTTCTTCTAGATGAACCTGGT TATATCAGTATTAGAAACAAACAGATTAAACGGCAAATCTATTAGGCCAGATTATT CATACAAAATTCTAAGTATTGTTAA

[0069] The non-CedV henipavirus that can be chimerized with CedV (i.e., the henipavirus whose F and/or G proteins are expressed) may be selected from Hendra virus (HeV), Nipah virus (NiV), Ghana virus (GhV), and Mojave virus (MojV). In specific embodiments, the non-CedV henipavirus may be a strain of NiV selected from the Malaysian strain of NiV (NiV-M) and the Bangladesh strain of NiV (NiV-B). Other henipaviruses may similarly be chimerized with CedV.

[0070] In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of a non-CedV henipavirus (e.g., HeV, NiV, GhV, MojV, or any other pathogenic henipavirus). In some embodiments, the rCedV chimera comprises the F and G envelope glycoprotein genes of a non-CedV henipavirus (e.g., HeV, NiV, GhV, MojV, or any other pathogenic henipavirus). For instance, none limiting examples include a rCedV chimera may comprise a MojV F envelope glycoprotein gene and a GhV G envelope glycoprotein gene or a GhV F envelope glycoprotein gene and a MojV G envelope glycoprotein gene, or any other combination of non-henipavirus F and G envelope glycoprotein genes.

[0071] In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of HeV. In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes of HeV (designated herein as chimera rCedV-HeV). In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a HeV G envelope glyco-

protein gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a HeV F envelope glycoprotein gene.

[0072] In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of NiV. In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes of NiV (designated herein as chimera rCedV-NiV). In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a NiV G envelope glycoprotein gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a NiV F envelope glycoprotein gene.

[0073] In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of NiV-M. In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes of NiV-M (designated herein as chimera rCedV-NiV-M). In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a NiV-M G envelope glycoprotein gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a NiV-M F envelope glycoprotein gene.

[0074] In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of NiV-B. In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes of NiV-B (designated herein as chimera rCedV-NiV-B). In some embodiments, the rCedV chimera comprises a CedV F

envelope glycoprotein gene and a NiV-B G envelope glycoprotein gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a F envelope glycoprotein gene.

**[0075]** In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of GhV. In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes of GhV. In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a GhV G envelope glycoprotein gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a GhV F envelope glycoprotein gene.

**[0076]** In some embodiments, the rCedV chimera comprises one or both of the F and G envelope glycoprotein genes of MojV. In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes of

MojV. In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a MojV G envelope glycoprotein gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a MojV F envelope glycoprotein gene.

**[0077]** In some embodiments, the rCedV comprises a modified version of a gene encoding a non-CedV henipavirus F or G protein. For example, to maintain the “rule of 6,” a feature of henipaviruses to promote replication initiation, the F coding region of NiV-B can be modified. For example, the last 3 nucleotides (ACG) before the stop codon (TAG) of the NiV-B F coding region may be deleted in the chimeric design, as deletion of this amino acid (Threonine) does not interfere with endocytosis, trafficking, or fusion, and therefore would not impede the successful rescue of the chimeric virus nor interfere with the functionality of the NiV-B F protein. An example of a modified NiV-B F protein coding sequence is set forth below:

Modified NiV-B F Protein Coding Sequence  
(SEQ ID NO: 13)

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ATGGCAGTTACTAACAGAGATATTATTCTAATCTCTTAATCTGATTTGATGA
TCTCGGAGTCAGTGCGGGATTTGCATTATGAGAAATTGAGTAAGATTGGGCTTG
TCAAAGGAATAACAAGAAAATACAAGATCAAAGCAATCCTCTCACAAAAGACATT
GTTATTAATGATTCGAATGTGTCAACATGTCTCAATGCACGGGAGTGTATG
GAAAACATAAACACGATTAAACGGTATCTAACGCCTATAAAGGGGCATTAGA
GATTTACAAGAACACACTCATGACCTGTGGTGTGAGACTGGCCGGAGTTAT
AATGGCAGGAGTTGCTATTGGAATTGCAACCGCAGCTAAATTACTGCAGGTGTAGC
ATTATATGAGGCAATGAAAAATGCTGACAACATCAACAAACTCAAAGCAGCATAG
AATCAACTAATGAAGCTGTGTTAAGCTTCAAGAGACTGCAGAAAAGACAGTCTAT
GTTACTGACCGCTTGCGAGGATTACATTAACTAATCTGTTACCGACAATTGACAAG
ATAAGCTGAAACAGACGGAACCTCTCATTAGATCTAGCACTATCAAAGTACCTCT
GATTTGCTTTGTATTGGTCCAACCTCAAGACCAGTTCTAAATTCAATGACTA
TACAGGCTATATCTCAGGCATTGGTGGAAATTATGAAACACTGCTAAGAACGTTGG
GTTACGCTACAGAAGACTTGTGATGTTCTAGAAAGTGACAGCATAACGGGTCAA
ATTATCTACGTTGATTAAGTGGCTACTACATAATTGTCAGGGTTATTTCTATCC
TGACTGAAATCCAACAGGCCTATATCCAAGAATTGTTGCCAGTGACCTTAACAATG
ACAATTCAAATGGATCAGCATTGTCCTAACATTGTAAGGAACACATTAA
TATCAAATATAGAGATTGGATTTGCTTAATTACAAAAGAGGAGTGTGATCTGCAACC
AAGATTATGCAACACCCATGACAAACAAATATGAGGGAAATGTTGACGGGGTCGACT
GAGAAGTGCCTCGAGAGCTGGTGGTTCATCACACGTTCCAGATTGCACTATCT
AACGGGTTTGTGCTAATTGCTAAGCGTCACATGCCAGTGTCAAACACACAGGT
AGGGCAATCTCACAGTCAGGAGAACAAACTCTGCTGATGATTGATAACACCACTG
TCCTACAGCCGTACTCGGTAATGTGATCATCAGCTGGAAAATCTGGTCAAGT
AAATTATAACTCTGAAGGCATTGCTATTGGCCTCTGTCTTACTGATAAGTTGAC
ATATCAAGTCAAATATCTAGCATGAATCAGCTTACAACAACTCAAGGACTATAC
AAAGAAGCTCAACGACTCCTTGATACTGTTAACCCGTCAATTAAAGCATGTTGTCT
ATGATCATACTGTATGTAATCAATTGCACTATTGTTAGGATTGATTACATTAA

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- continued

TCAGTTTATCATTGTTGAGAAAAAAAGAAACACCTATAGCAGATTAGAGGCAGG  
AGAGTCAGACCTACAAGTAGTGGGATCTCTATTACATTGGGTAG

**[0078]** In a further example, to maintain the “rule of 6” an extra stop codon (TAA; bolded and underlined below), can be added to the end of F coding region from HeV, as shown below. The HeV F amino acid sequence encoded by the sequence below is identical to the amino acid sequence of

the HeV 2008 Redlands isolate (GenBank: JN255805.1) and protein sequence GenBank: AEQ38070.1. The exemplary rCedV-HeV clones set forth herein use the F coding sequence of the HeV genomic sequence (GenBank: MN062017.1).

Modified HeV F Protein Coding Sequence  
(SEQ ID NO: 14)

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ATGGCTCACACAGAGGTCAAGGCTAAAGTGTGCTCTGGGATCATAGTTCTGGTT
TTGTCATTAGAAGGGCTAGGGATACTACATTATGAGAAAATTAGTAAGATAGGGCT
GGTTAAAGGTATTACAAGAAAGTACAAGAGATTAAGAGTAACCCTTGACCAAGGATA
TTGTGATCAAATGATCCCTAATGTCTCGAATGTCTCAAAGTGCACCGGGACTGTTA
TGGAGAATTACAAAAGCAGACTCACAGGGATTCTCTCACCAATCAAAGGCGCCATC
GAACTGTACAATAAACACAGCATGACCTAGTTGGTATGTCAAGCTTGCAAGGTGTG
GTGATGGCAGGGATTGCAATCGGGATAGCTACTGCTGCACAAATCACAGCAGGTGT
TGCCTTATATGAGGCAATGAAGAACGCAGACAATATCAATAAACTCAAGAGCAGCA
TAGAGTCTACAAATGAGGCTGTTGTCAGGAAACAGCTGAGAAAACAGTC
TACGTCCTTACTGCTCTTCAAGATTACATCAACACTAACCTGTTCTACAATAGATC
AAATTAGCTGCAAGAACAGAGCTCGCATTAGACTTGGCGTTGTCTAAGTATCTGT
CTGATCTGCTCTTGTGTTTCCGGACCTAACTTACAGGATCCAGTCTCTAATTCCATGAC
TATCCAAGCAATATCTCAAGCATTGGGGCAATTACGAAACCTTACTGAGAACGCT
TGGTTACGCGACCGAGGACTTCGACGACCTTTAGAAAGTGTAGCATAACAGGCC
AGATAGTCTATGTAGATCTCAGTAGCTATTACATAATAGTAAGGGTGTATTTCCCA
TACTAACAGAGATCCAACAGGCTTATGTCAGGAGTTGCTCCAGTGAGTTAAATA
ACGATAATTCTCAGAATGGATCAGCATTGTCGGAAATTCTGCTGATTAGGAACACGC
TGATTTCAAATATAGAAGTCAAGTACTGCTTAATCACCAAGAAAAGTGTGATTTGTA
ATCAGGACTATGCTACACCCATGACGGCTAGCGTGAAGAGAATGCTGACAGGATCC
ACAGATAAGTGCCAAGGGAGTTAGTAGTCTCATCCCAGTCTCAAGATTGCCCTC
TCAGGAGGAGTCTGTTGCAAATTGATAAGTGTGACATGTCAGTGTCAAGACTACT
GGGAGGGCAATATCTCAATCAGGGGAACAGACACTACTGATGATTGACAATACTAC
CTGCACACAGTTGTTCTAGGAAACATAATCATAAGCCTGGAAAATATTGGGATC
AATAAAATTACAATTCTGAGAGCATTGCTGTTGGGCCACCAGTCTATACAGACAAAGT
TGATATCTCAAGTCAGATATCTAGTATGAATCAATCACTACAACAATCTAAGGATTA
CATTAAGAAGCTCAAAGATCTGGACACTGTGAATCCGTCGTTGATAAGTATGCT
ATCAATGATCATCCTTATGTTGTCATTGCAAGCAGTGTGCAATTGGTCTGATCACT
TTCATAAGCTTGTAAAGTTGAGAAAAGAGAGGGAAATTACAGCAGGCTAGTGA
TAGGCAAGTGCACCGGTCAAGTAATGGTGTCTGTATTATATTGAAACATAAATAA
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**[0079]** In a further example, a single nucleotide (T1593A; bolded and underlined below), which does not result in an amino acid change, can be modified to remove an internal PstI site from a HeV G-encoding sequence. The HeV G amino acid sequence encoded by the sequence below is

identical to the amino acid sequence of the HeV 2008 Redlands isolate (JN255805.1), and protein sequence GenBank: AEQ38071.1. The exemplary rCedV-HeV clones set forth herein use the G coding sequence derived from the HeV genomic sequence (GenBank: MN062017.1).

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Modified HeV G Protein Coding Sequence
(SEQ ID NO: 15)
ATGATGGCTGATTCCAATTGGTAAGCCTGAACAATAATCTATCTGGTAAATCAAG
GATCAAGGTAAAGTTATCAAGAATTATTACGGCACAATGGACATCAAGAAATTAA
CGATGGGTTATTAGATAGTAAGATACTGGGGCGTTAACACAGTGATAGCTTGT
GGGATCAATCATCATCATTGTGATGAATATCATGATAATTCAAATTACACCAGAAC
GACTGATAATCAGGCACTAATCAAAGAGTCACTCCAGAGTGTACAGCAACAAATCA
AAGCTTTAACAGACAAATCGGGACAGAGATAGGCCAAAGTCTCACTAATTGAC
ACATCCAGCACCATCACAATTCTGCTAACATAGGGTACTGGGATCCAAGATAAGT
CAGTCTACCAGCAGTATTAAGTGAGTGTAAGATAATGCAAATTACTCTT
CCTTAAAGATTCATGAGTGTAAATATCTCTGTCCGAATCCTTGCCTTCAGAGAAAT
ACCGACCAATCTCACAAGGGTGAGTGTACTTGTAGGACTGCCAACAGATCTG
TACAGAACACATCAACAATCTTAAAGGCCAGGCTGATATCCTACTCTACCAA
TTAATACAGAGAAGGGTTTGCATCAGTGACCCACTTGGCTGTTGATAATGGCT
TCTCGCCTATGCCATCTTGAAAGATCGGATCATGTACTAGAGGAATGCAAAAAC
AAAGGATAATAGGGTGGGTGAGGTATTGGATAGGGTGATAAGGTGCCATCAATG
TTTATGACCAATGTTGGACACCACCCACTCAAGCACCATCCATTCATCGCAGCTCA
ACTTTACCATGAGAGATTTTTATTACACATTGCGCAGGTCCCATGGGGAGATCCT
ATCCTTAACAAGTACTTCCGGACAGAGTCACTGCTCTGATTCGTCTGTGTAAGAC
CAAAAGTGTAGTGGAGACTACAATCAGAAATACATCGCTTATAACTAAGGTGAA
AGAGGGAAGTACGATAAGGTGATGCCTTACGGTCCATCAGGTATCAAGCAAGGG
TACATTGTACTTCCGGCGTCGGTTTGGCCAAGGACCGAATTCAATATAATGAC
TCTAATTGTCCCATAATTCATGTGCAAGTACAGCAAAGCAGAAACTGTAGGCTTCA
ATGGGTGTCAACTCCAAAGTCATTATTTTGAGATCAGGACTATTGAAGTATAA
CTATCTCTGGAGGAGACATCAACTCCAATTTATCGAGATTGCTGACAATAGATTG
ACCATCGGTTCTCCTAGTAAGATATACAATTCCCTAGGTCAACCCGTTTCTACCA
GCATCATATTCTGGGATACGATGATTAAATTAGGCATGGTGATACCGTGGAC
CTAAGAGTACAGTGGAGAAATACAGTGTGATTTCTAGACCTGGACAGTCACAGTG
TCCTCGATTTAATGTCTGCCGAGGTTATGCTGGTTATTTAAACAGTAACCAAAC
AGCAGAGAACCCCTGTTTGCCTATTCAGGATAACGAGATCCTTACCAAGTTCC
ACTGGGTGAAGATGACACAAATGCACAAAAAACCATCACAGATTGCTCTGCTGTG
AGAATGTCATATGGTGTATATCACTAGTAGAAATACGATACAGGAGACAGTGTG
ATAAGGCCAAACTATTGCAGTCAGATACCTGCCATGTTCAGAGTTGA

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**[0080]** In a further example, a single nucleotide (C924A; bolded and underlined below), which does not result in an amino acid change, can be modified to remove an internal AleI site from a MojV F-encoding sequence. Further, to

maintain the “rule of 6” an extra stop codon (TAA; bolded and underlined below), can be added to the end of the MojV F coding region.

Modified MojV F Protein Coding Sequence  
(SEQ ID NO: 16)

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ATGGCACTAAAAAAATATGTCAGTCACTGTTCCTGTTATCTATTAGTGACC
CTACGACTGTTCAGTCTAGTATAACTATGACTCCTATCTAAGGTCGGTGTCATTAA
GGGTCTGACATAAACTATAAGATCAAGGGTCGCCATCTACAAAGCTAATGGTGGT
CAAATTGATACTAACATTGATATGTAAAAACTGTACTCAGAACAGTATGATGA
ATACAAGAACTAGTAAGGAAAGCCTAGAACCGGTCAAATGGCTATTGACACCA
TGCTCAATAATGTTAACTGTCGGGTAATAACAAGTACAGAGGTCATTGACATTG
CTGGAGTTGCCTCGGTTGCAACACCCAGCACTGTACAGCAGGGAGGTAGCTC
ATAGATCAAAATGAAATCCACAGGCATTCAAACATAGAAAGAGTGCTATTCAAA
ACAAAATGAGGCAGTAAGCAATTCCAATTGGCAAAACAACTAGGTGTGAT
TGACACCATAAGAGGGAGAGTCAAACAAATATAACCCGTTATAAATCAATGA
GCTGTGACACAATTGGCTCAGTGTTAGGTATAAGGACTCACTCAGTACTACTTGTGAA
TAATAACTGCATTGGCCAGTTGCAGAATCCAGTAAATAAGGATTACCATTG
AAGCAAAATCTAGTGTTTAAGGCAATTGATGAACTGCAGGATTAGGGGT
ATACAAGTGGGTATTTTGAAATTCACATGTATTAGGGCAACTTTA
TAGACGTTGTAGTGCAGGATACAGGTCTAGGATTCCCAATCAA
CATTGGTACATGCTGTAGTCAGGGTTTAAGGACTCACAGGTGTGAA
GGGATGAGTGGGTAACATTTGCCAAGGTTTGTACTAGGACTACTTGTTAT
CAAATTTGATCGAGGTAGTGTACAATCACAGATAGTTGTCATTGACAAC
GATACGCTTCCTAGTGCAACGGCTTATTGGCTGCTAAGGGAGATACTT
AAAGTTCTAGAGAGAGGTGTCTAAGTTATGTCCTAAAATTTGGGTTGTGAT
GGGTTAGTGTTATGCAATTGCTCAACTATTCTGCCGATGTAGGATACAGAT
CCAATCTCACAAGTCTCGGGCCACTTGTATCATACTAGACACACAAAGGGTTCA
GTTATTCAGGTGGAGAGTTGTTGTATTTCTGCGGATCATACTAGGAGTGGGAA
TATAAGTCTGATAGTTAGAGGTGTTGGCCACCTATTTGTATAAGGAATTGACATA
GGAAAATCGCTGGCAGGTTTAAATCAAACCTTACAAGGAGGCAGAGGATTACTTGA
GAAGTCAGAAGTCTTAAAAGGGGTTAACCCTTCAATTACTCCTTGGGTCAT
GGTTGCTTTATATTTTGATTTAATAGCCATTTGTGTCAGTAAATCGACTAGTGTA
TTGTCAATTAAATAACGTAAAAGGTAACGTGGTAAGGCGAGTTCACGTTATCT
CAGCATTGTTCTCTGATGGAATATCATTTGTAAGTGTCATATAATAA
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**[0081]** In a further example, to maintain the “rule of 6” an extra stop codon (TGA; bolded and underlined below), can be added to the end of F coding region from GhV, as shown below.

Modified GhV F Protein Coding Sequence  
(SEQ ID NO: 17)

ATGAAGAAAAAGACGGACAATCCCACAATATCAAAGAGGGGTCACAACCATTCTCG  
AGGAATCAAATCTAGAGCGCTACTCAGAGAGACAGATAATTATGCCAATGGGCTAA  
TAGTTGAGAATTAGTTAGAAACTGTCATCATCCAAGTAAGAACAATCTAAACTATA  
CTAACGACACAAAAAAGAGATTCTACAATCCCTTATCGTGTGGAAGAGAGAAAAGGA  
CATTATCCAAGATTAAACATCTTATTGATAAACTTACAAGCATAAAAAAGAGGG  
AAGAGAAGAAATGGTCATAATGGGAACATTATAACTATAATTCTGTTGTTGATTTA  
ATTTGAAGACACAGATGAGTGAGGTGCTATCCATTACGAGACTCTAAGTAAGATC  
GGATATAAAAGGAATCACCAGAGAGTACAAAGTCAAAGGAACTCCGTCAAGTAA  
AGACATAGTCATCAAATTGATTCCGAATGTCACCGGTCTAACAGTGACGAACAT  
ATCAATGGAAAACTATAAGAACACTTGACAAAACTAATCCTTAAACACA  
TAATTGAATTGATGCAAACTCAACTAAATCAGCCCTGGGAATGCACGTTGCTG  
GCGTTATAATTGCAGGAGTGGCATTAGGTGTTGCAGCGCAGCCAAATACTGCC  
GCATTGCACTGCATGAAGCTCGACAGAATGCAGAGAGATTAATCTCTTAAAGGA  
TAGCATTCTGCCACTAACACCGCAGTAGCAGAACTCCAGGAAGCACTGGTGGAA  
TAGTAAATGTCATTACAGGAATGCAAGATTACATCAAACAAATCTAGTCCC  
GAGTTGACAAACTGCAATGTAGTCAGATAAAACGGCATTAGACATATCTCT  
CCAAACTATTCAGAAATATTAACAGTGTCGGTCAAACCTTCAAATCCAGTAACTACTT  
CCATGTCAATACAGCCATATCACAACTTGGGAAATATAGATTGCT  
CTAAACCTACTAGTTACACTGCAAACGACTTATTGGATTGCTCGAAAGTAAAGTATAAA  
CAGGCCAAATACATACATAAATCTGGAACATTACTTCATGGTAATCAGAGTATATT  
ATCCTATAATGACAACAATCAGCAATGCTTATGCCAGGAATTGATCAAAAATTAGCT  
TCAATGTCGATGGCAGTGAATGGTATCTCTGTACCCCTCGTTATATTGATTGAA  
ACTCATATCTCTCAAACATAGACATATCAGAATGTCTCATAACCAAAATTCACTGA  
TATGTCGTCATGACTTTGCAATGCCAATGAGTTACACCTTAAAGGAATGCCTAACTG  
GAGACACTGAAAGTGTCCGAGAGAGGCTGTTGTAACCTCATATGCCAAAGATTG  
CTATCTCCGGGGAGTGATTTGCTAATTGCTAAAGTACACATGTCAATGCTATC  
AAACTGGCAAAGTAATTGCTCAAGACGGCAGCCAAACATTGATGATCGATAAT  
CAAACATGTTCAATAGTAAGAATTGAAAGAAATCCCTCATATCAACAGGGAAATATCT  
GGGAAGTCAGGAGTACAATACGATGCATGTCAGTCGGCAATCCTGTCTTCACTGA  
CAAGCTGGACATAACAGTCAAATTCCAAACATCAACCAATCCATTGAACAATCCA  
AATTTTATCTAGATAAGTCTAAAGGCTATACTTGACAGAAGATAAAATCTCAACTTAATTG  
GCTCTGTACCGATATCAATACTTTCATATTGCGATCTTATCATTGATTCTCT  
ATAACTTTGTGATTGTGATGATAATTGTCAGAAGATAAAACAAATACACTCCCTT

-continued

ATAAAACCTGATCCATCCAGTAGGAGGAGTACTATACAGGACGTATATCATCCG

AACCCCGGGAAACATTGATTAGATCAGCTGCTGATCAATTGACAGAGATCGAGA

**TTGATGA**

**[0082]** In a further example, two nucleotide changes (T321C to remove an internal SwaI site and C1653A to remove an internal SmaI site; both bolded and underlined below) can be made. These changes do not result in any amino acid changes.

Modified ChV G Protein Coding Sequence  
(SEQ ID NO: 18)  
ATGCCGCAAGAAGACTGTGGAATTCAATTAACATGAATTCCCCTCTA  
GAAAGAGGGGTCACTTTAGATAAGAACCCCTAAATCAA  
TCTAAATCACCAAGCAGGGGTATTTGGGTTAGATCCACAGT  
GAGAGAAATTGGAAGAACAGAAGAATCAAATGATCATTACATG  
ACTGTTCAACCATGATTCTTGAGATATTAGTTGCCTGGGCATC  
ATGTTAACTCATAGTTAACTATGGGTATTATCAGAATGAC  
AACATCAATCAAAGGATGGCAGAACTTACAAGCAATATCACAGTC  
CTGAAACTTAAATCTTAATCAATTGACAAACAAAATTCAAAGAGAA  
ATTATTCTTAGATCACTTTATTGACACAGCAACCACATTACA  
ATTCCTAGGCCATTACTACATATTAGCAACTCTGACAAACAGA  
ATCTCGGAATTATTGCCGTCATCAACCAAAAGTGTGAGTTCAAG  
ACACCGACACTGTCTGAAATGACTGCAGAAATAACTGTACCCCCA  
CCACTAAACCGTCTGATGGAGTGAAATGAGTTCTTGCCT  
AACTTGGTTGCACATGGGCCCTCTCCCTGTAGAAACTTTCATCC  
GTACCTACAATTACTATTATCGGATTCCAGGATTACAATAGA  
ACAGCATGGACGAAAGATGTATACTAAACCGAGATTGACAATA  
AGCAGTACAAAATTGCTTATGTCCACTCTGAATATGATAAAAAT  
TGCACCAGAGGATTCAAATACTATGAATTGATGACATTGGAGAA  
ATACTGGAGGGTCCGGAAAAAGAACCCAGAATGTTCTAGGTCA  
TTTATTGCCACAAATGCTGTGAACATCATTCTGTACGCCG  
ATCGTCACTGTCAATGAAGGATATTCTTGCCTGATGCCACC  
TCCTCAGATCCCTTGTACAAAGCAAATCTATCTAAAGCACATT  
CATTGGTGATACTGAGGCATAACAAGGATGAGAAAATAGTTCA  
ATGCCCTAGCTTAACCTTCACTGATCAAGAGTATGTTCTAGGATA  
ATCCCTGAGAGGTGGGGCACAGCAGAGAGTGGCAATCTTAC  
TTCCCTGTATTGGAAGGGCTTACACAAACGAGTCACCCATCCT  
TTATGCAAAAGTCAAATTGTCGCGAAGTGTGATGATGAACTTGC  
CTGAAAAGTTTACAATCAAGGGTGCCTCAGCACCAAGTAGTC  
AACTGTCTGATAAGGATCAGAAATGCACAGAGAGATAATCCAACC  
TGGGATGTTATCACAGTTGATCTGACTAATACATACCCAGGATCA

-continued

AGGAGCAGGATCTTGGAAAGCTCTCCAAACCGATGCTTATCAA  
TCATCAGTATCATGGCATACTCTCTCAGGTAGCAGAGATAACAA  
GACCTAGATAAGTATCAATTGGACTGGTTGGATACACCCCTATATA  
TCTCGTCTGGAGGATCTGAGTGCCCTTCGGAAATTATTGTCCA  
ACGGTATGCTGGGAAGGGACATATAATGATGTCTATAGCTTAAC  
CCAAATAACGATCTTTGTCACTGTGTATTGAAGAGTGAACAA  
GTTGCAGAGAACCTTATTGCAATCTTCACGGATCAAATC  
TTGAAAGAATTCCCTCTTGTGATGCAATGGATAAGCAGTGCACGAACT  
ACGACAATATCGTGCCTCATGTTCAACATGAAATTGGTGTATA  
GCTGCATTAGAGATCACAAGATTGAATGATGACATCATAAGACCA  
ATTTATTACTCTTCTGGCTGCCTACTGATTGCCGACACCATAT  
CCCCACACGGTAAGATGACCAGGGTCCCTGGCTCCACATAT  
AACTACTAA

**[0083]** The present disclosure includes other variations to non-CedV coding sequences for F and G proteins. In some embodiments, a rCedV chimera may comprise a gene encoding a non-CedV F protein, a gene encoding a non-CedV G protein, or both, in which the gene encoding the non-CedV F protein and/or the gene encoding the non-CedV G protein may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more substitutions, insertions, or deletions, so long as the resulting virus is replication-competent. For instance, the gene encoding the non-CedV F protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to any one of SEQ ID NOS: 3, 5, 6, 9, 11, 13, 14, 16, or 17. Similarly, the gene encoding the non-CedV G protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to any one of SEQ ID NOS: 4, 7, 8, 10, 12, 15, or 18.

**[0084]** In any embodiments of the chimeras described herein, the chimera may further comprise a reporter sequence. For example, the reporter sequence may encode green fluorescent protein (GFP) or luciferase protein (Luc).

**[0085]** As described in more detail below, such recombinant Cedar virus (rCedV) chimeras in which one or both of the F and G envelope glycoprotein genes of CedV are replaced with a corresponding F and/or G envelope glycoprotein from a non-CedV henipavirus may be used to elicit an immune response to a non-CedV henipavirus, e.g., in a vaccine optionally comprising a pharmaceutically acceptable carrier and, further optionally, an adjuvant.

#### B. Chimeras Expressing Soluble F and G Proteins

**[0086]** Another aspect of the present disclosure is directed to replication-competent, recombinant Cedar virus (rCedV)

chimeras comprising the F and G envelope glycoprotein genes of CedV, and further comprising a coding sequence for one or both of (i) a soluble F envelope glycoprotein (sF) of a non-CedV henipavirus and (ii) a soluble G envelope glycoprotein (sG) of a non-CedV henipavirus. In some embodiments, the non-CedV coding sequences are NiV coding sequences encoding NiV sF and/or NiV sG. In some embodiments, the non-CedV coding sequences are HeV coding sequence encoding HeV sF and/or HeV sG. In some embodiments, the non-CedV coding sequences are MojV coding sequences encoding MojV sF and/or MojV sG. In some embodiments, the non-CedV coding sequences are GhV coding sequences encoding GhV sF and/or GhV sG.

**[0087]** When both non-CedV sF and sG genes are inserted into the rCedV genome, both genes may come from the same non-CedV henipavirus (e.g., HeV, NiV, GhV, or MojV) or each may come from a different non-CedV henipavirus.

**[0088]** Without wishing to be bound by theory, these chimeras may be advantageous because a sF or sG may be

superior to that of full-length, membrane-bound protein when used as a vaccine immunogen when administered to subjects. Additionally, chimeras comprising HeV sF and/or sG may induce an immune response that can provide protection against not only HeV, but also NiV-M and NiV-B. **[0089]** The soluble form of a non-CedV F or G protein can comprise the full ectodomain or an immunogenic fragment thereof. In some embodiments, the sF or sG of the non-CedV henipavirus comprises or consists of the full ectodomain sequence of the protein. In some embodiments, the sF or sG comprise or consist of a fragment of the ectodomain that is about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% of the length of the full ectodomain sequence of the F or G protein of the given non-CedV henipavirus. In some embodiments there is a GCNtet amino acid sequence inserted to promote tetramerization.

**[0090]** Exemplary sF and sG coding sequences are provided below in Table 2.

TABLE 2

Exemplary soluble F (sF) and G (sG) Sequences

Name	SEQ ID NO: Sequence
NiV-M SF coding sequence Genbank: AY816748.1	<p>19 ATGGTGGTGATCCTGGACAAGAGGTGCTACTGCAACCTGCTGATCCTGATCTGATGATC            AGCGAGTCAGCGTGGCATCTGCACATACGAGAACGCTGTCCAAGATCGGCCCTGGTGAAG            GGGTGACCAGGAAGTACAAGATCAAAGAACCCCCCTGACCAAGGACATCGTGTATCAAG            ATGATCCCAACCTGAGCGACATGAGCCAGCTGACCGCTGAGCTGATGGAGAACTACAG            ACCAGGTGAACCGCATCTGACCCATCAAGGGCCCTGGAGATCTAAGAGAACACAC            ACCCACCGACCTGGTGGCGAGCTGAGCTGAGAGCTGATGAGACGGCTGAGCTGGCAG            ACCCGACACCCACCGCATCTGGTGGCGAGCTGAGCTGAGAGCTGATGAGACGGCTGAG            GGGTGAACACCCACCGCATCTGGTGGCGAGCTGAGCTGAGAGCTGATGAGACGGCTGAG            ACCATCACCGGCGAGATCATCTACGTTGACCTGAGCAGCTACTACATCATGTAAGGGGTG            TACTTCCCACATCTGAGCGAGATCCACGGAGCTACATCCAGGAGCTGCTGCCGTCAGC            TTCAACACGAGCACGAGCGAGCTGAGATCGACATCTGAGCTGAGAGCTACATCTGGCAG            CTGAGACACCCACCGCATCTGGTGGCGAGCTGAGCTGAGAGCTGATGAGACGGCTGAG            ACCCTGAGCAACATCGAGATCGGCTTTTGCTGATCACCAAGAGAACGGTGTATCTGC            AACCAAGGACTACGCCACCCCATGACCAACACATGAGAGAGTGCTGAGCCAGCACC            GAGAAGTGCCTCGGAACTGGTGGTGCAGCCACGTGCCCAGGTTGCCCTGTCCAAC            GCCGTGCTGTTGCCAACCTGAGCATCGCGTCACTGCGCAGACCAACGGCAGGGCC            ATCTCCCAGAGCGCGAGACACTGCTGATGAGCAACACACCACCTGCCAACCGGCC            GTGCTGGCAACGTGATCATCGAGCTGGAAAGTACCTGGCAGCGTGAACGAAACAGC            GAGGGCATGCCATGCCCTCGTGTACCGACAAGGGTGACATCAGCAGCCAGATC            ACCAGGATGAACCGAGCCCTGAGCGAGCAAGGATTAACATCAAGGGAGGCCAGAGCTG            CTGGACACCGTGAACCCACGATGAAGCAGATCGAGGACAAGATCGAGGAGATCTGAGC  <u>AAGATCTACACACATCGAGAACAGAGATGCCAGGATCAAGAACAGTGTATCGGCCAGGCCCC GGCGC</u></p>
HeV sF coding sequence Genbank: AY816747.1	<p>20 ATGGCCACCCAGGAGGTGCGGCTGAAAGTGCCTGCTGCGGCATCATCGTGTGGCTG            TCCCTGGAGGGCTGGCATCTGCACATACGAGAACGCTGTCCAAGATCGGCCCTGGTGAAG            GGCATCACCAGGAAGTACAAGATCAAAGAACCCCCCTGACCAAGGACATCGTGTATCAAG            ATGATCCCAACCTGAGCAACGCTGCAAGTGCACCGCACCCTGATGGAGAACTACAG            AGCAGGCTGACGGCATCTGGCCACATCGAGCCATCAAGGGCCCATCGAGCTGACCAAC            ACCCACCGACTGGTGGCGAGCTGAGCGACATCGGCCCTGGTGAATGGCCGATCGCCATC            GGAATCCCAACAGCGGCCAGATCACAGCGCGCTGCCCTGTACCGAGGCGATGAGAAC            GCCGACAACATCAAAGCTGAAGAGCAGCATCGAGAGCAGCAACCGAGGGCTGGTAAG            CTGCAGGAGACGCCGAAAAGACCGTGTACCTGCTGACCGCCCTGAGGACTACATCAAC            ACCAACACTGGTCCCAACCATCGACCAAGATCGCTGAGCGAGACGGAGCTGGCCCTGGAC            CTGGCCCTGAGCAAGTACCTGAGCGACCTGCTGTTGCTGAGCTGCCCAACCTGCGAG            CCCGTGAGCAACAGCATGACCCATCGAGCCATCGCCAGGCTTCCGCGGCCACTACAG            ACCCTGCTGAGGACCTGGCTACGCCACGGAGACTCGACGGCCCTGCTGGAGAGCGAC            AGCATCACGGCAGATCGTGTACCTGAGCGACCTGAGCGAGCTACATCATGTAAGGGGTG            TACTTCCCACATCTGAGCGAGATCCACGAGCTACGAGCTGAGCTGAGGAGCTGCTGCCGTCAGC            TTCAACACGACAACAGCGAGTGGATCAGCATCTGAGCTGAGGAGCTGCTGCCAACCTGAGC            ACCCTGATCAGCAACATCGAGGAGTACTGCCCTGATCACCAAGAAAAGCGTGTATCTGC</p>

TABLE 2 -continued

<u>Exemplary soluble F (sF) and G (sG) Sequences</u>	
Name	SEQ ID NO: Sequence
NIV-B sF coding sequence GenBank: JN808864.1	<p>AACCAAGGACTACGCCACCCCCATGACCAGCAGCTGAGAGAGTGCCTGACCGGCAGCACC GACAAGTGCCCTCGGAACGTGGTGTCCAGCCACGTGCCAGGTTGCCCTGAGCGGC GGAGTGTGTTGCCAACACTGCATCAGCGTGACCTGCCAGTGCAGCACACCCGGCAGGGCC ATCTCCAGAGCGCCGAGCAGACACTGCTGATGATCAGCACAAACACCCTGCACCACCGTG GTGCTGGGCAACATCATCATCAGCTGGAAAGTACCTGGGAGCATCAACTACAATCC GAGAGCATCGCCGAGCCGGACATCAGCAGCACAGGATTACATCAAGGGAGGCCAGAAAATC AGCAGCATGAACCAGCGCTGCAGCAGAGCAAGGATTACATCAAGGGAGGCCAGAAAATC CTGGCACACCGTAGACAGAGATCGAGGACAAGATCGAGGAGATCTGAGC <b><u>AAGATCTACCACATCGAGAACGAGATCGCCAGGATCAAAGACTGATCGGCAGGGCCCT GGCGC</u></b></p> <p>The foregoing sF coding sequences (for NiV-M and HeV) are both codon optimized and contain an optional GCN4t sequence (bold and underlined) to promote trimerization of the expressed protein.</p>
NIV-B sF coding sequence GenBank: JN808864.1	<p>30 ATGGCAGTTACTAACAGAGATATTCTTAATCTCTTAATACTGATTTGATGATC TCGGAGTCAGTGTGGGATTTCGCTATTGAGAATTGAGTAAGATTGGGCTTGTCAAA GGAATAACAAGGAAATACAAGATCAAAGCAATCCTCACAAGAACATTGTTATTAAA ATGATTCCGAATGTCAAACATGTCATCAGCAGGGAGTGTCTATGAAAATCTAAA ACACGATTAAACGGTATCCTAACGCCTATAAAGGGGCATTAGAGATTACAAGAACAAAC ACTCATGACCTTGTGGTGTAAAGACTGGCCGGAGTTAAATGGCAGGAGTTGCTATT GGAAATTGCAACCCGAGCTCAAATTACTGCAGGTGTAGCATTATATGAGGAATGAAAAT GCTGACAAACATCAAACACTCAAAGCAGCATAGAATCAAATATGAGCTGTGTTAAG CTTCAAGAGACTGCAGGAAAGCAGTCTATGTTACTGACCGTTGAGGATTACATTAAAT ACTAACTTGGTACCGACAATTGACAAGATAAGCTGCAAACAGACGGAACACTCATTAGAT CTAGCACTATCAAAGTACCTCTGTGATTGCTTTGTATTGGTCCAACCTCAAGAC CCAGTTCTATTCATGACTATACAGGCTATATCTAGGATTTCGTTGGAATTATGAA ACACTGCTAAGAACGCTGGGTTACGCTACAGAAGACTTTGATGATCTTAGAAAGTGAC AGCATAACGGTCAAATTATCTACGTTGATTAAAGTGGCTACTACATAATTGTCAGGGTT TATTTCTATCTGACTGAAATCAAACAGGCTATATCAGAAATTGTCAGTGTGAC TTAACAAATGACAATTGAGATCAGCATTGTCACATTGTCACATTGTCAGGAAAC ACATTAATATCAAATATGAGATTGAGATTGCTTAATTCAAAGAGGAGTGTGATCTG AACCAAGATTATGCAACCCATGACAACAAATATGAGGGAAATGTTGACGGGTCGACT GAGAAGTGTCTCGAGGAGCTGGTTTACACAGCTTCCAGATTGCAACTATCAAC GGGGTTTGTGCTAATTGCAAGCGTCACATGCCAGTGTCAAACACAGGTAGGGCA ATCTCACAGTCAGGAGAACAAACTCTGTGATGATTGATAACACCCTGTCTACAGCC GTACTCGGTAATGTGATCATCAGCTGGGAAATATCTGGGTCACTAAATTATAACTCT GAAGGCATTGCTATTGGCTCTCTGTCTTACTGATAAAAGTTGACATATCAAGTCAAATA TCTAGCATGAATCAGCTTACAACAACTCAAGGACTATATCAAAGAGCTAACCGACTC CTTGATACTGTTAACCGTCATGAAGCAGATCGAGGACAAGATCGAGGAGATCTGAGC <b><u>AAGATCTACCACATCGAGAACGAGATCGCCAGGATCAAAGACTGATCGGCAGGGCCCT GGCGC</u></b></p> <p>The NiV-B sF coding sequence contains an optional GCN4t sequence (bold and underlined) to promote trimerization of the expressed protein.</p>
NIV-B sG coding sequence Genbank: JN808864.1	<p>21 <b><u>ATGGAAACCGACACTGCTGTGGGCTCGCTGTGGGCCCTGGCTCAACTGGC GACGCCAGCATCACAGATAATCAGGCCATGATCAAAGATGCTGGAGAGTATCCAGCAG CAGCATCAAGGGGCTGCCGACAAAATTGGCACAGAGATAGGGCCGAAAGTATCAGTATT GATACATCCAGTACTACTACATTCAGCTAAATTGGCTGTTAGGTTCAAAGATCAGC CACTCAACTGCAAGTATAAATGAGAATGTAATGAAAAATGCAAATTACTGCTCCC TTGAAAATCCACGAATGTAACATTCTGTCTAACCCACTCCCTTTAGAGAGTATAAG CCCGAGACAGAAGGAGTGAACATTGCTGAGGATTACCTAATAATCTGTCTGCAAAG ACATCTAACATGACATGAAACCAAAAGCTGATTCTACACCTTACCCGTAGTCGGTCAA AGTGGCACCTGTACAGCACAGGACTCGCTGGCTATGGATGAGGGCTACTTGCATATAGC CACCTGGAAAAAAATCGGATCATGTTCAAGAGGGCTCCAAACAAAGAATAATAGGAGTT GGAGAGGTTACTAGACAGAGGTGACGAAGTACCTCTTGTGTTAGACTAACGCTGGGACC CCATCAAATCCAAACACCGTTTACCATGTCAGTCAGTCAGTCAACAAATGAAATTCTATTAT GTGCTTGTGCTGAGTGTGAGGACCCATTCTGAATAGCACCCTACTGGTCCGG TCACAAATGATGACTCGCTAGCTGTTAAACCTAAAGAATAATGGTGAAGAGTTACATCAA CATCAATTGCTTACGGAAATTGAGAAAGGGAGTATGATAAAGTTATGCCATATGGA CCCTCAGGCATCAAACAAAGGTGACACCCGTACTTCTGCTGTAAGGATTGGTCA ACAGAGTTCACATCACATGATTCAAATTGTCCTACGCAAGTGTCAATACAGCAAACCT GAAAATCGAGGCTATCTATGGGATTAGACCAAAAGCTCAATTATCCTCGATCTGGA CTACTAAATACAATCTATCGGATGAGGAGAACTCTAAATTGTTACATGAAATATCT GATCAAAGACTATCTATTGGATCTCTAGCAAATCTATGATTCTGGGCAACCTGTT TTCTACCAAGCATTTTCTAGGGACACTATGATAAATTGGAGATGTCACAAACAGTT AACCCCTTGGTAAATTGGCGTACAACACGGTAATCTCAAGACCTGGCAATCACAA</u></b></p>

TABLE 2-continued

<u>Exemplary soluble F (sF) and G (sG) Sequences</u>	
Name	SEQ ID NO: Sequence
	<p>TGCCCTAGATTCAACAAAGTGCCCAGAGGTTTGTGGGAAGGGGTTATAATGATGTTTC      CTGATTGATAGAATCAATTGGATAAGCGGGGTGATTCCCTGACAGCAACCAGACCGCA      GAGAACCTCTGTTTACTGTATTCAAAGATAATGAACTACTTTACAGAGCACAACTAGCT      TCCAGGAGCACACAAATGCACAAAAAAACAATAACTAAATTGCTCCTTTGAAGAATAAGATC      TGTTGATATCAGTGGTGGAGATATAACGACACAGGAGACAATGTTATAAGACCTAAACTA      TTCGCAAGTTAACAGATACCGAGCAATGTACATAATAA  <i>The attachment glycoprotein's signal sequence for endoplasmic reticulum targeting is located at the N terminus of the protein, which also overlaps with the molecule's transmembrane anchor domain. To create a soluble and secreted form of NiV-B sG, the Ig κ leader sequence (bold and underlined) was added to the N-terminus of NiV-B sG. A short linker sequence (GCAGCA) was inserted between the Ig κ leader sequence and the NiV-B sG sequence (underlined). To maintain the "rule of 6" an extra stop codon (TAA; bolded italics) was added to the end of the NiV-B sG coding region. Both of these modifications are optional.</i></p>
HeV sG coding sequence Genbank: MN062017.1	<p>22 <b>ATGGAAACCGACACTCTGCTGTGGGTCCTGCTGTGGGTCCTGGCTCAACTGGC</b>  <u>GACGCAGCAAGAACGACTGATAATCAGGCACTAACTAAAGAGTCACCTCCAGAGTGTACAG</u>      CAACAAATCAAAGCTTTAACAGACAAAATCGGGACAGAGTAGGGCCCAAAGTCTCACTA      ATTGACACATCAGCACCATCACAATTCTGCTAACATAGGGTTACTGGGATCCAAGATA      AGTCAGTCTAACAGCAGTATTAAATGAGAATGTTAACGATAATGCAAAATTACTCTCCT      CCTTTAAAGATTGAGTGTAAATATCTTGTCCGATCCTTGCCTTCAGAGAAATAC      CGACAATCTCACAAGGGGTGAGTGATCTGTAGGACTGCCAACAGATCTGTCTACAG      AAGACAAACATCACAATCTTAAAGGCCAGGCTGATATCCTAACTCTACCAATTAAATACC      AGAGAAGGGGTTGCTACTGACCCACTTTGGCTGTGATAATGGCTTCTCGCCATT      AGCCATCTGAAAAGATCGGATCATGACTAGAGGAATTGCAAAACAAAGGATAATAGGG      GTGGGTGAGGTATTGGATAGGGGTGATAAGGTGCCATCAATGTTTACGAAATGTTGG      ACACACCAAACTCAAGCACCATTGACATTGCAACTTACCATGAGATTTTTAT      TACACATTGCGCAGCTGCTCATGTGGAGATCCTACCTTAACAGTACTTCCTGGACAA      GACTCACTGCTCTGATTGCTTGTGTAAGACAAAAGTGTAGTGTGGAGACTACAAT      CAGAAATACATCGTATAACTAAAGTTGAAAGAGGGAACTGATAAGGTGATGCCATTAC      GGTCATCAGGATCAACAGGGATACATTGACTATTCCGGCTCGGTTTTTGCCA      AGGACCGAATTTCATTAATGACTCTAATTGTCACATTGCAAGTACAGCAGGAA      GCAGAAAATCTGAGGTTCAATGGGTGTCACCTCAAAGTCATTATTTGAGATCA      GGACTATTGAAGTATAATCTATCTTGGAGGACATCATACTCCAATTATCGAGATT      GCTGACAAATGAGTGGACCATCGGTTCTCTAGTAAGATATACTCCATTGTCACCC      GTTTCTACCGGCACTATATTCTGGATACGATGTTAAATTAGGGATGTTGATACC      GTTGACCCCTCTAAGAGTACAGTGGAGAATAACAGTGTGATTTCAGACCTGGACAGTCA      CAGTGTCTCGATTAAATGTCGTGCTCGAGGATGCTGGGAAGGGACATATAATGATGCT      TTCTAAATAGACCGCTAAACTGGTTAGTGTGGTTTATTTAAACAGTAACCAAACAA      GCAGAGAACCTGTGTTGGCTATTCAAGGATAACGAGCTTCAACAGTGTGGAGATGTC      GCTGAAGATGACACAAAACCATCACAGATTGCTTGTGGAGATGTC      ATATGGTGTATATCACTAGTAGAAATATACTGACATACAGGAGACAGTGTGATAAGGCCAAA      CTATTGCAAGTACCTGCCATTGTTAGAGAGTGA</p> <p><i>The attachment glycoprotein's signal sequence for endoplasmic reticulum targeting is located at the N terminus of the protein, which also overlaps with the molecule's transmembrane anchor domain. To create a soluble and secreted form of HeV sG, the Ig κ leader sequence (bold and underlined) was added to the N-terminus of HeV sG. A short linker sequence (GCAGCA) was inserted between the Ig κ leader sequence and the NiV-B sG sequence (underlined). There is a single nucleotide change (T1593A; bold and underlined) in the above sequence of HeV G, which does not result in an amino acid change. The HeV sG amino acid sequence is identical to the amino acid sequence of the HeV 2008 Redlands isolate, protein sequence GenBank: AEQ38071.1. Both of these modifications are optional.</i></p>
NiV-B sGtet coding sequence Genbank: JN808864.1	<p>31 <b>ATGGAAACCGACACTCTGCTGTGGGTCCTGCTGTGGGTCCTGGCTCAACTGGC</b>  <u>GACCTGCACATGAAAGCAGATCGAGGACAAAGCTGGAGGAGATCGAGAGCAAGCTGAAGAAG</u>  <b>ATCGAGAAACGAGCTGCCAGGATCAAGAACGAGTCAGACTACACCTCAACAGATAATCAGGCC</b>      ATGATCAAAGATGCATTGCGAGTATCCAGCAGCAGATCAAGGGCTTGCCGACAAAATT      GGCACAGAGATAGGGCGGAAAGTACTGATGATTGACATCCAGTACTATCACTATTCCA      GCTAATATTGGCTGTTAGGTCAAAGATCAGCAGCTCAACTGCAAGTATAATGAGAAT      GTGAATGAAAATGCAAAATTACACTGCCCTCTGAAAATCCACGATGTAACATTCT      TGTCCTAACCCACTCCCTTTAGAGAGTATAAGCCAGACAGAAGGAGTGGCAACTCTG      GTAGGATTACCTAATAATCTGCTGTCGAAAGAGACATCTAATCAGATACTGAAACCAAAG      CTGATTTCATACACCTTACCCGTAGTCGCTCAAAGTGGCACCTGTTACACAGACCCACTG      CTGGCTATGGATGAGGGTACTTTGCACTATGACCCACTGGAAAAATCGGATCATGTTCA      AGAGGGCTCTCAAACAAAGAATAATGGAGTTGGAGGGTACTAGACAGAGGTGACGAA      GTACCTCTTTGTTATGACTAACGCTGGACCCATCAAATCCAACACCGTTACCAT      TGCACTGCCGTGACAACTGAATTCTATTATGTCCTTGTGCACTGTCAGTTGTTGGA      GACCTATTCTGAATAGCACCCTACTGGTCCGATCACTATGATGACTCGTCTAGCTGTA</p>

TABLE 2 -continued

Exemplary soluble F (sF) and G (sG) Sequences

Name	SEQ ID NO : Sequence
	<pre> AAACCTAAGAATAATGGTGGAGAGTTACAATCAACATCAATTGCCCTACGGAATATTGAG AAAGGGAAAGTATGATAAAGATTATGCCATATGGACCTCAGGCATCAAACAAAGGTGACACC CTGCTACTTCCTGCTGAGGATTTCGGTCAGGACAGAGTTCACATACAATGATTCAAAT TGTCCCATCGCAGAGTGTCAATACAGCAAACACTGAAACACTGAGGTCTATGGGATT AGACCAAAACAGTCATTATATCCTTCGATCTGGAACACTAAATACATCTATCGGATGAG GAGAACACTAAATGGTATTGAAATATCTGATCAAAGACTATCTATTGGATCTCCT AGCAAAATCTATGATTCTTGCGGTCACCTGTTTACCAAGCATTTCATGGAC ACTATGATTAAATTGGAGATGTCAAACAGTTAACCTTTAGTTGTAATTGGCGTGCAC AACACGGTAATCTCAAGACCTGGGCAATCACAATGCCCTAGATTCAACAAGTGCAGAG GTTTGCCTGGGAAGGGGTTATAATGATGCTTCTGATTGATAGAATCAATTGGATAAGC GCGGGTGTATTCTTGAGCAGCACCCAGCAGAGGAACTCTGTTTACTGTATTCAA GATAATGAAGTACTTACAGAGCACAACTAGCTTCGAGGACACCAATGCAACAAAAAAACA ATAACTAATTGTTCTTGTGAAGAATAAGATCTGGTGTATATCAGGTTGAGATATAC GACACAGGAGACAATGTTATAAGACCTAAACTATTGCGAGTTAAGATACAGAGCAATGT ACATAA </pre> <p>This is a sG protein with a tet (tetramerization) peptide sequence. The attachment glycoprotein's signal sequence for endoplasmic reticulum targeting is located at the N terminus of the protein, which also overlaps with the molecule's transmembrane anchor domain. To create a soluble and secreted form of NiV-B sG, the Ig κ leader sequence (bold and underlined) was added to the N-terminus of NiV-B sG. The NiV-B sG contains a GCNtet sequence to promote tetramerization (bold and italic). Short amino acid linker sequences were included between the Ig κ leader sequence and the GCNtet sequence (GTCGAC; underlined) and the GCNtet sequence and the NiV-B sG sequence (GTCGACTACACC (SEQ ID NO: 37); underlined).</p>
HeV sGtet coding sequence Genbank: MN062017.1	<pre> 32 ATGGAAACCGACACTCTGCTGTGGGTCCTGCTGTGGGTCCTGGCTCAACTGGC GACCTGCACATGAGCAGATCGAGGAGAAGCTGGAGAGATCGAGAGCAACCTGAAAG ATCGAGAACAGAGCTGGCAGGATCAAGAAGGTCGACTACACCCGGACACCGACAACAG GCCCTGATCAAAGAGTCCTGAGAGCGCTCAGCAGCAGATCAAGGCCCTGACCGACAAG ATCGGCACCGAGATCGGCCCCAAAGTGTCCCTGATCGACACCGCAGCACCATCACCAC CCCGCACAATCGGGCTGCTGGGCTCAAGATCAGCCAGAGCACCAGCTCCATCAACGAG AACGTGAAACGAAAGTCAAGTCCAGGTTACCCCTGGCCCCCTGAAGATTCACGAGTGCACATC AGCTGCCCAACCCCTGCCCTCCGGAGATCGCTGAGAAAACACCTCCACCATCTGAAGCCC CTGGGGGCTGCCAACAGATCGCTGAGAAAACACCCCTGAGCTGATCACCGGACCC CGGGTGTACGCTACACCCCTGCCCTCAACACCCGGAGGGGGTGTGTCATCACCGGACCC CTGCTGGGCTGGACAACGGCTCTCCCTACAGCCACCTGGAAAAGATCGGAGCTGC ACCGGGGATTGCCAAGCAGCGGATCATCGGGTGGCGAGGTGCTGGACCGGGGAC AAGGTGCCAGCATGTTCATGACCAAGCTGTGGACCCCCCCCACCCAGACAATCCAC CACTGAGCAGGACACTTACCCAGGAGACTTCACTACACCCCTGTGCCCGTGAAGCCACGTG GGCAGGACACAGCAGCAGCGGACTACAAACAGAGTATATCGCATACCAAGGTG GTGGGCCAAGAGCGACAGCGGCACTACAACAGAGTACGAGTACCGGCTGACCATCGGAGC GAGCGGGCAAGTACGACAAAGTGTGCCCCACGGGGCATCAAGCAGGGCAG ACACTGTACTCCCGCGTGGGCTCTGCCCGGACGGACTTCAGTACAACGACAGC AACTGCCCATCATCCTACTGCAAGTACAGCAAGGCCAGAAGTGCAGACTGAGCATGGC GTAAACAGCAAGGCCATACATCTGGGAGGGCTGCTGAAGTACAACCTGTCTG GGCGGCACATCATCTGAGTTATCGAGATGCCGACAACCGGCTGACCATCGGAGC CCAGCAAGATCTACAGCTGGGCAGCCGCTGTTCTACCGGGCAGCTACAGCTG GACACCATGATCAAGCTGGGGACGTGGACCCCTGCGGGTCCAGTGGCGG AAACACAGCGTATCAGCAGAGCCGGCAGAGCCAGTGGCCCGTCAACGTGTGCC GAAGTGTGCTGGAGGGCACCTACACGACGGCTTCTGATCGACGGCTGAACGGTG TCCGGCGAGGTACTCTGAACCTCAACACAGCCGAGAACCCCTGTTCCCGTGTTC AAGGACAACGGAGACTCTGTACACAGGTGCCCCCTGGCCAGGAGCACCAACGCCAGAAA ACCATCACCGACTGCTTCTGCTGGAAAAGCTGATCTGGCATCACCTGGTGGAGATC TACGACACCGGGGACTCCGTGATCCGGCCAAGCTGTTGGCGTGAAGATCCCCGGCCAG TGCAGCGAGAGCTGATGA </pre> <p>This is a sG protein with a tet (tetramerization) peptide sequence. The attachment glycoprotein's signal sequence for endoplasmic reticulum targeting is located at the N terminus of the protein, which also overlaps with the molecule's transmembrane anchor domain. To create a soluble and secreted form of HeV sG, the Ig κ leader sequence (bold and underlined) was added to the N-terminus of HeV sG. The HeV sG coding sequence is codon optimized and also contains a GCNtet sequence to promote tetramerization (bold and italic). Short linker sequences were included between the Ig κ leader sequence and the GCNtet sequence (GTCGAC; underlined) and between the GCNtet sequence and the HeV sG sequence (GTCGACTACACC (SEQ ID NO: 37); underlined). The HeV sG sequence has the NCBI Reference sequence: NP_047112.2. To maintain the "rule of 6", a feature of henipaviruses to promote replication initiation (Halpin et al., 2004), an extra stop codon (TGA; bold) was added to the end of the HeV sG coding region.</p>

[0091] The present disclosure includes additional variations to non-CedV coding sequences for sF and sG proteins, beyond those illustrated above (e.g., the optional GCN4t sequence on sF proteins, the optional Igk leader sequence on sG proteins, and optional point mutations shown in Table 2). In some embodiments, a rCedV chimera comprises a gene encoding a non-CedV sF protein, a gene encoding a non-CedV sG protein, or both, in which the gene encoding the non-CedV sF protein and the gene encoding the non-CedV sG protein may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more substitutions, insertions, or deletions relative to the naturally-occurring sequence, so long as the resulting protein is capable of eliciting an immune response. For instance, the gene encoding the non-CedV sF protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to nucleotides 1-1,461 of SEQ ID NO: 19, nucleotides 1-1,461 of SEQ ID NO: 20, or nucleotides 1-1,461 of SEQ ID NO: 30. In some embodiments, the gene encoding the non-CedV sF protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to any one of SEQ ID NOs: 19, 20, or 30. Similarly, the gene encoding the non-CedV sG protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to nucleotides 64-1,647 of SEQ ID NO: 21 or 31, or nucleotides 64-1,656 of SEQ ID NO: 22 or 32. In some embodiments, the gene encoding the non-CedV sG protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to any one of SEQ ID NOs: 21, 22, 31, or 32.

[0092] The coding sequences for sF, sG, or both, can be incorporated into the rCedV genome between the P/C gene and M gene, as shown in FIG. 11. Indeed, it was determined that reporter genes (e.g., GFP and Luc) were well-tolerated when inserted between the P/C gene and M gene as well, making this a particularly useful site for insertion. Paramyxoviruses have what is known as a gradient of transcription, whereby more mRNA transcripts are made from the 5' end (N protein the most) to the 3' end (L protein the least), and therefore incorporation between P/C and M leads to a high level expression of the non-CedV gene(s) inserted in this location. In this way, the more sG or sF antigen made and secreted from the rCedV chimera, the better the immune response to sG or sF antigen. Nevertheless, the coding sequences for the sF, sG, or both, may be inserted in other locations as well, so long as the virus remains replication-competent.

[0093] As described in more detail below, recombinant Cedar virus (rCedV) chimeras that express non-CedV henipavirus sF, sG, or both, may be used to elicit an immune response to a non-CedV henipavirus.

[0094] Another aspect of the present disclosure is directed to a method of producing a non-CedV henipavirus sF protein, a non-CedV henipavirus sG protein, or both, using a rCedV as disclosed herein. In some embodiments, the method comprises culturing cells capable of being infected by a henipavirus with a rCedV chimera as described herein comprising a coding sequence for a sF, sG, or both, of a non-CedV henipavirus, and isolating the non-CedV henipavirus sF, sG, or both, from the culture. In some embodi-

ments, the sF and/or sG are NiV (e.g., NiV-M or NiV-B) sF and sG. In some embodiments, the sF and/or sG are HeV sF and sG.

### C. Chimeras Expressing Fusion Proteins

[0095] Another aspect of the present disclosure is directed to rCedV chimeras comprising one or both of (i) a gene encoding a henipavirus F envelope protein fusion protein and (ii) a gene encoding a henipavirus G envelope protein fusion, wherein the fusion protein comprises the ectodomain and transmembrane domain of a non-CedV henipavirus F envelope protein or G envelope protein, respectively, fused to the cytoplasmic tail domain of CedV F envelope protein or G envelope protein, respectively. Or the fusion protein comprises the ectodomain of a non-CedV henipavirus F envelope protein or G envelope protein, respectively, fused to the transmembrane domain and cytoplasmic tail domain of CedV F envelope protein or G envelope protein, respectively.

[0096] Chimeras comprising these fusion constructs exhibit the predicted interaction of CedV matrix protein (M) (which forms the virus particle) with the internal cytoplasmic tail domains of CedV F and G, and display the functional ectodomains of the non-CedV F and G envelope proteins on the virus particle. Those ectodomains of the non-CedV F and G envelope proteins are anchored by their respective transmembrane domains and the CedV F and G cytoplasmic tail domains, or by the respective transmembrane domains and cytoplasmic tails of the CedV F and G envelope glycoproteins, which allows the ectodomains of the non-CedV F and G proteins to be exposed and serve as antigens, e.g., if the chimera is administered to a subject.

[0097] In some instances, particularly with MojV and GhV, expressing the full length sequence of a non-CedV F protein, G protein, or both, in a rCedV chimera (as disclosed herein above) may not result in a replication competent chimera. Chimeras comprising these fusion constructs instead may avoid this problem, and result in replication competent chimeras that effectively display the non-CedV F and/or G envelope protein ectodomains on the virus particle, where they can serve as antigens. Thus, chimeras comprising these fusion constructs may be advantageous for chimeras of certain species of non-CedV henipaviruses, such as MojV or GhV, and may result in the production of more robust and replication-competent rCedV chimeras (which may exhibit better virus production capacity) than chimeras in which a full-length non-CedV F protein or G protein was inserted.

[0098] In any embodiments, the fusion proteins may comprise all or a portion of the ectodomain and transmembrane domain of the non-CedV henipavirus. For example, a fusion protein may comprise the full ectodomain or an immunogenic fragment thereof. In some embodiments, the fusion F protein or fusion G protein comprises the full ectodomain sequence of the non-CedV henipavirus. In some embodiments, the fusion F protein or fusion G protein comprises a fragment of the ectodomain that is about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% of the length of the full ectodomain sequence of the F or G protein of the given non-CedV henipavirus. In some embodiments, the fusion F protein or fusion G protein comprises the full transmembrane domain sequence of the non-CedV henipavirus. In some embodi-

ments, the fusion F protein or fusion G protein comprises a fragment of the transmembrane domain that is about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% of the length of the full transmembrane domain sequence of the F or G protein of the given non-CedV henipavirus.

**[0099]** The non-CedV henipavirus ectodomain and transmembrane domain sequences can be from any henipavirus, including from any pathogenic henipavirus, including from HeV, NiV, GhV, or MojV. In some embodiments, the non-CedV henipavirus ectodomain and transmembrane domain sequences are MojV ectodomain and transmembrane domain sequences. In some embodiments, the non-CedV henipavirus ectodomain and transmembrane domain sequences are GhV ectodomain and transmembrane domain sequences. In some embodiments, the ectodomains of non-CedV henipavirus F and G glycoproteins are fused to the transmembrane domains and cytoplasmic tail domains of CedV F and G glycoproteins.

**[0100]** In some embodiments, the rCedV chimera comprises F and/or G fusion genes derived from GhV (i.e., a fusion comprising a GhV ectodomain and GhV transmembrane domain with the cytoplasmic domain of CedV). In some embodiments, the rCedV chimera comprises F and G fusion genes derived from GhV (designated herein as chimera rCedV-GhV). In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a GhV G fusion gene. In some embodiments, the rCedV chimera comprises a CedV G envelope glycoprotein gene and a GhV F fusion gene.

**[0101]** In some embodiments, the rCedV chimera comprises F and/or G fusion genes derived from MojV (i.e., a fusion comprising a MojV ectodomain and MojV transmembrane domain with the cytoplasmic domain of CedV). In some embodiments, the rCedV chimera comprises both F and G fusion genes derived from MojV (designated herein as chimera rCedV-MojV). In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a MojV G fusion gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a MojV F fusion gene.

**[0102]** In some embodiments, the rCedV chimera comprises F and/or G fusion genes derived from HeV (i.e., a fusion comprising a HeV ectodomain and HeV transmembrane domain with the cytoplasmic domain of CedV). In some embodiments, the rCedV chimera comprises both F and G fusion genes derived from HeV. In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a HeV G fusion gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a HeV F fusion gene.

**[0103]** In some embodiments, the rCedV chimera comprises F and/or G fusion genes derived from NiV (i.e., a fusion comprising a NiV ectodomain and NiV transmembrane domain with the cytoplasmic domain of CedV). In some embodiments, the rCedV chimera comprises both F and G envelope glycoprotein genes derived from NiV. In some embodiments, the rCedV chimera comprises a CedV F envelope glycoprotein gene and a NiV G fusion gene. In some embodiments, the rCedV comprises a CedV G envelope glycoprotein gene and a NiV F fusion gene.

**[0104]** Exemplary F and G fusion coding sequences are provided below in Table 3.

TABLE 3

Exemplary Fusion F and G Sequences		
Name	SEQ ID NO:	Sequence
MojV Fusion F coding seq. Genbank: KF278639.1	23	ATGGCACTAAATAAAAATATGTTAGTTCACTGTTCTGGTTATCTATTAGTG TACGCTACGACTGTTCAGTCAGTCTAGTATACACTATGACTCTTATCTAAGGTCGGT GTCATTAAGGGTCTGACATAACAATATAAGGTCAGCCATCTACAAAG CTAATGGTGGTCAAATTGTACCTAACATTGTAGATGTGTTAAAAGCTGTACTCAG AAACAGTATGATGAATAACAAGAACTTAGTAGAAGGAAAGCTTAGAACCCGTCAA ATGGCTATTGACACCATGCTCAATAATGTTAAGTCGGGATAAACAAAGTACAGA TTTGCAGGTGCAATTATGGCTGGAGTTGCCCTCGGTGTTGCAACAGCAGCACT GTTACAGCAGGGATAGCTCCATAGATCAAATGAAAATGCACAGGCAATTGCA AACATGAAGAGTGTATTCAAATACAAATGAGGCACTGAAAGCAATTGCAATTG GCCAATAAACACTAGCTGTGATTGACACATAAGGGAGAGATCAAATAC AATAATAACCGTTATAATCAATTGAGCTGTGACACAAATTGGGCTCAGTGT GGTATAAGACTCACTCGTACTACTCTGAATAATAACTGCAATTGGGCCAGCT TTGCAGAATCCAGTAAATACAAGGATTACCAATTCAAGCAATTCTAGTGTGTT AATGGCAACTTGTGAAGTGTGAAGATTATGGGTATACAAGTGGTGTCTT TATGAAATTCTACATAGTGAATTAATTAGAGGCAACATTATAGACGTTGATGTA GATCAGGGATACATAGCTAGAAATAGAAATTCCCACATCTAACATTGGTACCT AATGCTGTTAGTGTGCAAGGAGTTAATGCTTACAGTATAACATAGACGGGGATGAG TGGGTAAACACTTGTGCCAAGGTTGTACTTACAAGGACTACACTGTTATCAAAT ATTGATACAGGTAGATGTACAAATCACAGATAGTAGTGTCTATGTGACAACGAC TACGCCCTGCTTATGTCACACGAGCTTATGGCTTACAGGGAGATACATCT AAGTGTGCTAGAGAGAAGGTAGTCTCAAGTATGTCCCTAAATTGCGTTGCT GATGCTGTTAGTGTGCAAAATTGCTCAATACTATCTGGCGATGTATGCGATACA GATACTCCAATCTCACAAAGTCTGGAGGCACTGTATCATTAACAGACAACAG AGGTGTTCACTATCACAGTAGGAGATGCTTGTGATTCTGCGATCATATCTA GGAGATGGAGAATATAATGCTGATAATGCTGAGGCTTGGCCACCTATAGTTATA GATAAGATTGACATAGGAAATCAGCTGGCAGGTATTAATCAAACCTTACAAGAG

TABLE 3-continued

Exemplary Fusion F and G Sequences

Name	SEQ ID NO:	Sequence
GhV Fusion F coding seq. Genbank: HQ660129.1	24	GCAGAAGATTACATGAGAAGTCAGAAGAGTTCTAAAAGGGGTTAACCTTCA ATTATCACTCTGGTTCATGGTGTCTTATATATTATGATATAAGCC <u>ATTGTGTCAGTAATAGCACTAGTATTGTCAATTAAACAGTAAAAAATAT</u> <u>AACAAATTATTAAGATGATCCTGATTATTACAATGATTACAAAAGAGAACGTATT</u> <u>AATGCCAAGCCAGTAAGAGTAACAATATAATTATGTTAGGTGATTGA</u>
Moj-V Fusion F coding sequence, GenBank: KF278639.1	33	ATGAAGAAAAAGACGGACAATCCCACAATATCAAAGAGGGTCACAACCATTCT CGAGGAATCAAACTAGAGCCTACTCAGAGAGACAGATAATTATCCAATGGG CTAATAGTGAGAATTAGTAGAACTGTCTCATCCAAAGTAAGAACATCTA AACTATACTAACAGACACAAAAAGAGATTCTACAATCCCTTATCGTGTGGAGAG AGAAAAGGACATTATCAAAGGAAATGGTCATAATGGGAACATTATAACTATAATT ATAAAAGGGAGAGAAGAGAAATGGTCATAATGGGAACATTATAACTATAATT CTGTTGTTGATTATAATTGGAGACACAGATGAGTGAGGTGCTATCCATTAC GAGACTCTAAGTAAGATCGGATTAATAAGGGAATCACAGAGAGTACAAGTC AAAGGAACTCCGTCAAGTAAGACATAGTCATCAAATTGATTCGAATGTACC GGTCTTAACAGTCAAGCAGAACATATCAATGGAACAACTATAAGAACAACTTGAC AAAATACTAATTCTTAAACACATAATTGAAATTGATGAACTCAACTAA TCAGCCCCCTGGAATGCAGTTGCTGGCGTTATAATTGAGGAGTGGCATT GGTGTGAGCAGCGGAGGCCAAATAACTGCCGCCATTGCACTGCATGAAGGCTGA CAGAATGCAAGGAGAGAATTATCTTAAAGGATAGCATTCTGCCTAACAAC GCAGTAGCAGAACACTCCAGGAACGAACTCGTGAATAGTAAATGTCATTACAGGA ATGCAAGATTACATCAATACAAATCTAGTCCCGCAGATTGACAAACTGCAATGT AGTCAGATCAAACGGCATTAGACATATCTCTCCAAATACTATTGAGAATA TTAACAGTGTCCAAACCTTCAAATCCAGTAACTATTCCATGTCATA CAAGCCATATCACAATCTTGGGGAAATATGAGATTGCTCTTAAACCTACTA GGTACACTGCAACGACTTATTGGATTGCTGAAAGTAAAGTATAACAGGC CAAATAACATACATAATCTGAACATTACTCATGGAATCAGAGTATATTAT CCATAATGCAACAACTCAGGAATGCTTATGTCAGGAATTGATCAAATTAGC TTCAATGTCGATGGCAGTGAATGGGTATCTTGTAACCTCTGTATATATTGATT AGAAACTCATATCTCAAAACATAGACATATGAGATGTCATAACCAA TCAGTGTATGTCGTATGCAATTGCAATGCCAATGAGTTACACCTTAAAGGAA TGCCCTAATGGAGACACTGAAAGTGTCCAGGAGAGGCTGTTGTAACCTCATAT GTCCCAAGGATGCTATCTCCGGGGAGTGAATTATGCTAATTGCTAAGTACA ACATGTCATGCTATCAAACACTGCGAAAGTAATTGCTAAGCGGCAGCCAAACA TTGATGATGATGATAATCAAACATGTCATAGTAAGAATTGAGAAATCCTC ATATCAACAGGAAATATCTGGGAAGTCAAGGAGTACAATACGATGCACTGTC GTGGCAATCTGCTTCACTGACAACGCTGGACATAACAGTCAAATTTCACAC ATCAACCAATCCATTGAAACAACTCAAATTATCTAGATAAGTCAAGGCTATA CTTGACAGATAAAATCTCAACTTAATTGGCTCTGTACCGATATCAAACTTTTC ATAATTGCGATCTTATGATTGATCTCTCTTAACTTTGATGTTGATG ATAATTAAATAACAAATTATAGATGATCCTGATTATTACAATGATTACAAA <u>AGAGAACGTATTAAAGCCAAAGCAGTAAGAGTAACAATATAATTATGAGT</u> <u>GATTGATGA</u>

TABLE 3-continued

Exemplary Fusion F and G Sequences

Name	SEQ ID NO:	Sequence
		ATTATCACTCCAAGCGTTCAATTGTTCTAAATAATAATATCAGTCCTCTCATTT ATTATATTATGATTATCATAGTATACTGTACTGTAAATCAAACATTCAAT AAAATAACAAATTATAGATGATCCTGATTATTACAATGATTACAAAGAGAA <u>CGTATTATGGCAAAGCCAGTAAGAGTAACAATATATTATGTAGGTGATTAA</u> <b>TAA</b>
GhV Fusion F coding sequence GenBank: HQ660129.1	35	ATGAAGAAAAAGACGGACAATCCCACAATATCAAAGAGGGGTCAACACCATTCT CGAGGAATCAAATCTAGAGCCTACTCAGAGAGACAGATAATTATCCAATGGG CTAATAGTTGAGAATTAGTTAGAAACTGTCACTCATCCAAGTAAGAACATCTA AACTATACTAACAGACACAAAAAGAGATTCTACAATCCCTTACGTGTGGAGAG AGAAAAGGACATTATCAAAGGAAATGGTCAATGGGAAACATTATAACTATAATT ATGAAAAGGGAGAGAGAAGAAATGGTCAATGGGAAACATTATAACTATAATT CTGTTGTTGATTATAATTGGAGACACAGATGAGTGAGGTGCTATCCATTAC GAGACTCTAAGTAAGATCGGATTAATAAGGGAATCACAGAGAGTACAAGTC AAAGGAACTCCGTCAAGTAAGACATAGTCATCAAATTGATTCGAATGTCA GGTCTAACAGTCAAGGCAGAACATATCAAAGGAAACATTATAAGAACACTTGAC AAATAACTAATTCTTAAACACATAATTGAAATTGATGCAAACACTCAACTAAA TCAGCCCCCTGGAATGCAGTTGCTGGCGTTATAATTGAGGAGTGGCATTAA GGTGTGAGCAGCGGAGGCCAAATAACTGCCGGCATTGCACTGCATGAAGGCTGA CAGAATGCAAGGAGAGAATTATCTTAAAGGATAGCATTCTGCCTAAACAAC GCAGTAGCAGAACACTCCAGGAAGCAACTGGGAATAGTAAATGTCATTACAGGA ATGCAAGATTACATCAATACAAATCTAGTCCCGCAGATTGACAAACTGCAATGT AGTCAGATCAAACGGCATTAGACATATCTCTCCAAATACTATTGAGAAATA TTAACATGTCAGGAAACCTTCAAATCTTAAAGGAAATATTGCTCTAAACCTACTA CAAGCCATATCACAATCTTGGGGAAATATAGATTGCTCTAAACCTACTA GGTACACTGCAAACGACTTATTGGATTGCTGAAAGTAAAGTAAACAGGC CAAATAACATACATAATCTGAAACATTACTCATGGAATCAGAGTATATTAT CCATAATGACAACAACTCAGGAATGCTTATGTCAGGAATTGATCAAATTAGC TTCAATGTCGATGGCAGTGAATGGGTATCTGTACCTCGTATATATTGATT AGAAACTCATATCTCAAAACATAGACATATGAGATGTCATAACCAAAAT TCAGTGTATGTCGTATGACTTGTCAATGCCATGAGTTACACCTTAAAGGAA TGCCCTAAGTGGAGACACTGAAAAGTGTCCAGGAGAGGCTGTTGTAACCTCATAT GTCCCAAGATTGCTATCTCCGGGGAGTGAATTATGCTTAATTGCTTAAGTACA ACATGTCATGCTATCAAACACTGGCAAAGTAATTGCTCAAGCGGCAGCCAAACAA TTGATGATGTCGATAATCAAACATGTCATAGTAAGAATTGAGAAATCCTC ATATCAGGAAATATCTGGGAAGTCAAGGAGTACAATACGATGTCGATGTC GTGGCAATCTGCTTCACTGACAACGCTGGACATAACAGTCAAATTTCAC ATCAACCAATCCATTGACAATCCTAAATTGCTGAACTTGTCAATTGTTCTAATA CTTGACAAGATAAACTCTCAACTTAATTGGCCAAGCGTTCAATTGTTCTAATA ATAATATCAGTCTCTTATTATATTGATTATCATGTAATCTGTC TGTAAATCAAACATCTATATAATAAACAAATTATAGATGATCCTGATTAT <b>TACAATGATTACAAAAGAGAAGCTATTAAAGCCAAAGCCAGTAAGAGTAACAAAT</b> <b>ATATTATGTAGGTGATTGATG</b>
MojV Fusion G coding seq. Genbank: KF278639.1	25	ATGTTCTCAGCTCCAAAAAAATTACTTAGACAACCTCAAACCAACAAGGTGAT <u>AAAATGAAACACCCAGATAAGAAATTAAAGTGTCAACTCTCAACCCCTTGTAGATTA</u> <u>GATAAAGGTCAAAAGATCTAAAGTCTTATTGTTAAACAAAGAAATTAT</u> <u>AACCTTTCAATCTTAAATGAAAGTGTGTTAAAGGTATTCAATTGATG</u> <u>AATACACTCTGTACTGACAGGTGCTTATTACAATAACACTAAATATCACC</u> <u>AAACCTGACAGCGGCTAAAGTCACAGAAATATGCTGAAATATCAGATGAC</u> <u>AAAGTGGCACCCAGATAAGGCTTATTGAGTACCTTGTGAAATTGTTGAAAGGGTGA</u> <u>ATTAAAGCCAAAAGTGTCACTCATAAACAGCAGTGAAGCGTCAGCATACCCGT</u> <u>CAGATCTAAACCTCCAGACCAATTCTGCAAAATATGTTACTTAGAGAA</u> <u>TCTTATTACTAAGCAGTGCACTTGCAACCCCTTATCTGGGATATTCCAACATCA</u> <u>GGCCCAACCTACCCCTCAACTGATAAAACCAAGCAGTACACAGATGATGAC</u> <u>AAAGTGGCACCCAGATAAGGCTTATTGAGTACCTTGTGAAAGGGTGA</u> <u>AGAACCTGGGACCATTTACAGATGGAGCCGGAGCTAATTCTATGTCCTT</u> <u>AACTTAGGACCGGCAAGTCTAAATTCTGACGAGTGTACACAAACCCCTCTTT</u> <u>TCAATTGGGTCCTCCATCTATGTTTCTCAAGAGATTAGAAAAAAAGGACTGC</u> <u>ACAGCAGGAGAGATTATCAATTGCACTGCTTGTGAGACAGATGTTGAT</u> <u>GGTCAGCAGGGTCTCAAGCATCACCTTATTAGTATGGGGTCCAAATCCA</u> <u>AAGATCATAAACTCTGTTGCTGAGCAGTACGGGAGCCATACCTCACATGTTGAT</u> <u>TGCTCAGTGACATTAACCTGCAAGCATCAGGGAGCCATACCTCACATGTTGAT</u> <u>GGGTTCTGGTTGTATAAGTTAGAACCTGACACCGAAGTTGATCCTATAGAATC</u> <u>ACAGGGCTATGCTTATCTCTAGATAAAACATATGACTCTGTTATAGGTAAAG</u>

The cytoplasmic tail of CedV F protein coding sequence is bolded and underlined. The predicted transmembrane domain of the non-CedV F protein coding sequences is underlined.

A single nucleotide (C924A; bold and underlined), which did not result in an amino acid change, was modified to remove an internal AleI site in the MojV fusion F protein.

To maintain the "rule of 6" an extra TGA or TAA was added at the end of CedV F cytoplasmic tail (bold italicics) of the GhV fusion F protein.

TABLE 3-continued

Exemplary Fusion F and G Sequences

Name	SEQ ID NO:	Sequence
GhV Fusion G coding seq. Genbank: HQ660129 .1	26	<p>GGCGGTGGTATTCAAGAAAGGTAAACGATCTATACTTTAGATGTATGGATTGTCC      AGAAAATAGGCAGAAGTTTAAGGCACTGTGTGAACATGGATCATGCCCTCGGCACT      GGAGGTGGGGGTATCAAGTGTGTGTGACAGGGCTGTGATGTCCTTCGGGAGT      GAAGAACATCAATTACAAATGCATATCTGAAGGTGAATGATCTGGCAAGTGGG      AAAACCTGTGATAATAGGACAGACATTTCGCCCTCAGATTCTATAAAGGCTCA      AATGGTCGGATGTACACTATAGGTGATAAATATGGTCTGTATCTTGCTCCGTC      TCTCTGGAACAGATATCTTAGATTGGATAACCCAGATATTCTGTAAGATCA      ACACACTGGTGGAAAGTCAGAGTCAGATAATGAAAGATTGGTCAACATGCAAG      AACACTGTAGAGATATGTCTGTGAAATTGCAATACTAGAGGTTATCAAGAT      ATTTTCCATTGTCGGAGGATTCAGAGTATTATACATACATAGGCATAACTCCT      AATAATGGTGAACAAAAACTTTGTGCCCTGACTCAGATGGTCAATA      GCATCATTGATATTACAAAAATTATATAGTATCACCTCAGCTACTATAAGC      TGCTTCATGTAACAAAGATGAGATTGGTGTATTCGAATCACAGAAGGGAAAAAA      CAGAAAGACAATCCTCAACGGATATATGCACATTCTACAAATTAGGCAAATG      TGTATAATATGAAGTCTGCACAGTGAATGTGGGTAATGCCAAAATATCACA      ATCAGGAGGTTAA  <u>ATGCTTTCTCAGTCCAAAAAAATTACTTAGACAACCTCAAACCAACAAGGTGAT</u>  <u>AAAATGAACAACCCAGATAAGAAATTAAAGTGTCAACCTCAACCTTGTAGAATTA</u>  <u>GATAAAAGGTCAAAGATCTCAATAAGTCTTATTATGTTAAAAAACAAGAATTAT</u>  <u>AAACGTTCAAACTATTAATTAAGTCAAACATGATCATTACATGACTGTTCA</u>  <u>ACCATGATTCTTGAGATATTAGTTGTCTGGCATCATGTTTAACTCTAGTT</u>  <u>TTAACTATGGTGTATTATCAGAATGACAACATCAATCAAAGGATGGCAGAACCT</u>  <u>ACAAGCAATATCACAGTCTGTAACCTAAATCTTAATCAATTGACAACAAACAAATT</u>  <u>CAAAGGAAATTATTCAGGATCTTATTGACACAGCAACCCACATTACA</u>  <u>ATTCTCTAGTCCATTACTTACATATTAGCAACTCTGACAACCCAGAATCTCGGAA</u>  <u>TTATTGCGCTCAATCAACCAAAAGTGTGAGTCAAGACACCGACACTTGCTTG</u>  <u>AATGACTGCAGAATAAAACTGTACCCCACCAACAAACCGTCTGATGGAGTGA</u>  <u>AACTGAGTTCTGCACTAACTTGGTGTGACATGGGCCCCCTCCCTGTAGAAC</u>  <u>TTTCATCGTACCAATTACTTATCGGATTCCAGGATTATACAATAGA</u>  <u>ACAGCATTGGACAAAGATGTACTAAACCCGAGATTGACAATAAGCAGTACA</u>  <u>AAATTGCTTATGCACTCTGAATATGATAAAATTGCAACAGGAGATTCAA</u>  <u>TACTATGATGATGACATTGGAGAAATACTGGAGGGTCCGAAAAAGAACCC</u>  <u>AGAATGTTCTGAGGTCTTATTGCCCCAACATGCTGTGAACTATCATTCT</u>  <u>TGTCAGGCCATCGTCACTGCAATGAGGATTTCTTCGCTTAATGACC</u>  <u>TCCTCAGATCCCTGTACAAGCAAATCTATCTAATAGCACATTCCATTGGT</u>  <u>AAATGACTGAGTCAAGAGTCTGAGATAATCCTCCAGAAGGTCGGGCACAGCA</u>  <u>GAGAGTGGCAATCTTACTTCCCTGTATTGAAAGGCTTACACAAACGAGTC</u>  <u>ACCCATCCTTATGCAAAAGTCAAATTGTCGCGAACTGTGATGATCTTG</u>  <u>CTGAAAGTATTACAACTCAAGGGTCCCTCAGCACCAAGTAGTCAACTGCTG</u>  <u>ATAAGGATCAGAAATGACAGAGAGATAATCCAACCTGGGATGTTATCAGTT</u>  <u>GATCTGACTTAACATACCCAGGATCAAGGAGCAGGATTTGGAGCTTCTCC</u>  <u>AAACCGATGCTTTATCAATCATCAGTATCATGGCATACTCTTCTCAGGTGCA</u>  <u>GAGATAACGACCTAGATAAGTATCAATTGGACTGGTTGGATACACCCATATA</u>  <u>TCTCGTCTGGAGGATCTGAGGTGCCCCCTTCCGAAATTATTGTCACCGGTATGC</u>  <u>TGGGAGGGACATATAATGATGTCATAGCTTAACCTCAAATAACGATTTTT</u>  <u>GTCACTGTGTTATGAAAGAGTGAACAAGTTGCGAGAGAACCTTATTCGCAATC</u>  <u>TTCTCAGGGGATCAAATTGAAAGAATTCCCTCTGATGATGATAAGGAGT</u>  <u>GCACGAACTACGACAATATCGTGTCTCATGTCACAAATGAAATTGGTGTATA</u>  <u>GTCGATTAGAGATCACAAGATTGAATGATGACATCATAAGACCAATTATAC</u>  <u>TCTTCTGGCTGCCACTGATTGCGGACACCATATCCCCACACCGGTAAGATG</u>  <u>ACCAGGGTCCCTGCGCTCACATATAACTAA</u> </p>
Moj-V Fusion G coding sequence, GenBank: KF278639 .1	34	<u>ATGCTTTCTCAGTCCAAAAAAATTACTTAGACAACCTCAAACCAACAAGGTGAT</u> <u>AAAATGAACAACCCAGATAAGAAATTAAAGTGTCAACCTCAACCTTGTAGAATTA</u> <u>GATAAAAGGTCAAAGATCTCAATAAGTCTTATTATGTTAAAAAACAAGAATTAT</u> <u>AAACGTTCAAACTATTAATTAAGTCAAAGTCTGCACTGAGTCAAGTGTGTTTAT</u> <u>TGTTATATTCTCAGTCAATTATCATTACAAATAATCAATATAATCACAATATCA</u> <u>ATTGTTATAACTCGTCTGAAAGTACAACAGAATATGCTGAAATAATCCAAGAT</u> <u>GACCTGAACTGCAAAATTAGAAATGTTCTGTAATCTGATCAATTGGTGAAGGGT</u> <u>GAATTAAGCAGAAAGTGTCACTCATATAACAGCAGTGGCAGTCAGCATACCC</u> <u>GGTCAGATCTCAACCCCTCAGACCAATTCTGCAAAATATGTTACTTAGAA</u> <u>GAATCTATTACTAAGCAGTGCACCTGCAACCTTATCTGGGATATTCCAACA</u> <u>TCAGGCCAACCTACCCCTCAACTGATAAAACAGACGATGATACCAACAGATGAT</u> <u>GACAAAGTGGACACACAGATTAGCCTATTGAGTACCCCAAGCCGGATGGTGC</u> <u>AATAGAACTGGGACCATTCACGATGGAGCCGGAGCTAACTTTTATCTGTC</u> <u>CCTAACCTAGGACGGCAAGTCTTAATCTGACGAGTGTACACAAACCCCT</u> <u>TTTCACATTGGGCTCCATCTATGTTCTCAAGAGATTAGAAAAACCGAC</u> <u>TGCACAGCAGGAGAGATATTCAATTGAGATGTCGCTTAGGCCGAATAGTAGAC</u> <u>AAGGGTCAAGGGTCCCTCAAGCATCACCCATTAGTATGGGCGTCCCAAAT</u> <u>CCAAAGATCATAAACTCGTGTGCGAGCAGAGATGGGATGGGT</u>

TABLE 3-continued

Exemplary Fusion F and G Sequences

Name	SEQ ID NO:	Sequence
		TTATGCTCAGTGACATTAAC TG CAGCATCAGGGAGGCCATACCTCACATGTT GATGGGTTCTGGGTGATAAAGTTAGAACCTGACACCAGTGTATCCTATAGA ATCACAGCTATGCTTATCTTAGATAAACAAATATGACTCTGTCTTATAGT AAGGGCGGTGATTTCAGAAAGGAACGATCTACATTCAGATGTGGATTG TCCAGAAAATAGGCAAAGTTAAAGGCACTGTGTAACATGGATCATGCCCGC ACTGGAGGTGGAGGGTATCAAGTGTGACAGGGCTGTGATGTCTTCGGG AGTGAAGAATCTACTAATTACAAATGCAATCTGAAGGTGAATGATCTGGCAAGT GGAACCTGTTGATAATAGGACAGACATTCGCCCTCAGATTCTTAAAGGC TCAATGGTGGATGTACACTATAGGTGATAAATATGGTCTGTATCTGCTCG TCATCCGGAACAGATATCTAGATTTGGATAACACCAGATATTCGTAAAGA TCAACAACTGGTGTGAAAAGTCAGATAATGAAGATTGTGCAACATGC ACGAACACTGATAGAGATATGTGCTCTGAAATTGCAAAACTAGAGGTTATCAA GATAATTTCCTCATTGTCGGGATTCAAGAGTATTACATACATAGGCATAACT CCTAATAATGGTGGAACTAAAATCTGTGCCGTACGTGACTCAGATGGTCAT ATAGCATCCATTGATATTACAAAATTATTATAGTATCACCTCAGCTACTATA AGCTGCTACTGTGAAAGATGAGATTGGTGTATTGCAAACTACAGAAGGGAAA AAACAGAAAGAACATCTCAACGGATATATGACACATTCTACAAAATTAGGCAA ATGTGTTAATATGAAGTCTGCCACAGTGCAGTGTGGTAAATGCCAAAATATC ACAATCAGGAGGTATTAA
GhV Fusion G coding sequence GenBank: HQ660129.1	36	<u><b>ATGCTTTCTCAGCTCCAAAAAAATTACTTAGACAACCTCAAACCAACAAGGTGAT</b></u> <u><b>AAAATGAACAACCCAGATAAGAATTAAGTGTCAACTTCAACCTTTAGAATTA</b></u> <u><b>GATAAAGGTCAAAAGATCTCAATAAGTCTTATTATGTTAAAACAAGAATTAT</b></u> <u><b>AACTTTCATGTTAAATGAAAGTCTGCAACGATATCAAGTTGTATTAT</b></u> <u><b>TGTATATTCTCACTGCTAATTATCATTACAATAATCAATACAATATCA</b></u> <u><b>ATTGTTATAACTGCTGAAAGTAATGACAACATCAATCAAAAGGATGGCAGAA</b></u> <u><b>CTTACAAGCAATATCACAGTCTGAACTTAAATCTTAATCAATTGACAAACAAA</b></u> <u><b>ATTCAAAAGGAAATATTCCCTAGGATCACTCTTATTGACACAGCAACCCATT</b></u> <u><b>ACAATTCCCTAGGCTCATTACTACATATTAGCAACTCTGACAACCAAGAATCTG</b></u> <u><b>GAATTATTGCCGTCATAACCAAAAAGTGTGAGTTCAAGACACCGACACTTGT</b></u> <u><b>CTGAATGACTGCGAGAATAAACGTACCCCCACACTAAACCGCTGTGGAGTG</b></u> <u><b>AAAATGAGTTCTCTGCCACTAATTGTTGACATGGCACATGGCCCTCTCCTGTAGA</b></u> <u><b>AACTTTTCCCGTACACTACAATTACTATTATCGGATTCCAGGATTATAACAT</b></u> <u><b>AGAACAGCATGGACGAAGATGTATACTAAACCCGAGATTGACAATAAGCAGT</b></u> <u><b>ACAAAATTGCTTATGTCACACTCTGAATATGATAAAAATTGCAACAGAGGATT</b></u> <u><b>AAATACTGATGAGATTGATGACATTGGAGAAAATACTGGAGGTTCCGGAAAAAGAA</b></u> <u><b>CCCGAAATGTTCTAGTCATTTCCTCCACAAATGCTGTGAACATATCAT</b></u> <u><b>TCTTGTACGCCGATCGTCACTGTCAATGAAGGATATTTCCTGCTTGATGC</b></u> <u><b>ACCTCCCTCAGATCCCTGTACAAGCAAATCTATCTAATAGCACATTCCATTG</b></u> <u><b>GTGATGACTGAGGCTACAAGGATGAGAAAATAGTTCAATGCCCTACGTTAAC</b></u> <u><b>CTTCTACTGCTAAGAGTATGTCAGATAATCCTCTGCGAGAGGTGGCGGACA</b></u> <u><b>GCAGAGACTGGAATCTTACTTCCCTGTATGGAAAGGCTTACACAAACGA</b></u> <u><b>GTCACCCATCCTTATGCAAAAGTCAAATTGTCGCAACTGATGATGAATCT</b></u> <u><b>TGCTGAAAGTTTACATCAAGGGTCGCCCTCAGCACCAAGTGTCAACTGT</b></u> <u><b>CTGATAAGGATCAGAAATGCAACAGAGAGATAATCCAACCTGGGATGTTATACA</b></u> <u><b>GTGATGACTAATAATACACCCAGGATCAAGGAGCAGGATCTTGGAGGTTTC</b></u> <u><b>TCCAAACCGATGCTTATCATCATCAGTATCATGGCATACTCTTCAGGT</b></u> <u><b>GCAGAGATAACAGACCTAGATAAGTATCAATTGGACTGGTGGATACACCCAT</b></u> <u><b>ATATCTCGTCTGGAGGATCTGAGTGCCTCTGGAAATTATTGTCACCGTA</b></u> <u><b>TGCTGGGAAGGGACATAATGATGTTAGCTTAACTCCTAAACGATCTT</b></u> <u><b>TTTGTCACTGTTGATTGAAAGAGTGAACAAGTTGCAAGAGAACCTTATTGCGCA</b></u> <u><b>ATCTTCTACGGGATCAATCTGAAAGAATTCCCTTGTGATGCAATGGATAAGC</b></u> <u><b>AGTGCACGAAACTACAGACAATATCGTCTGCTGTTCAACAAATGAAATTGTTG</b></u> <u><b>ATAGCTGCTTCAAGGATCACAAGATTGATGACATCATAAAGACCAATTAT</b></u> <u><b>TACTCTTCTGGCTGCTACTGATTGCCGACACCATATCCCCACACGGTAAAG</b></u> <u><b>ATGACCAAGGGTCTCTGGCTCACATATAACTACTAA</b></u>

The cytoplasmic tail of CedV G protein coding sequence is bolded and underlined.

The predicted transmembrane domain of the non-CedV G protein coding sequences is underlined.

Two nucleotide changes were made in SEQ ID NOS: 26 and 36 (T321C to remove an internal SmaI site and C1653A to remove an internal SmaI site; bold and underlined), which did not result in an amino acid changes, were made in the GhV fusion G coding sequence.

[0105] As is evident from Table 3, Paramyxoviridae F proteins are type I membrane glycoproteins, which means the cytoplasmic domain is at the 3' end of the sequence. In contrast, Paramyxoviridae G proteins are type II membrane glycoproteins, which means the cytoplasmic domain is at the 5' end of the sequence.

[0106] The present disclosure includes additional variations to non-CedV coding sequences of the F and G proteins, beyond the optional point mutations shown in Table 3. In some embodiments, a rCedV chimera comprises a gene encoding a fusion F protein, a gene encoding fusion G protein, or both, in which the gene encoding the fusion F protein and the gene encoding the fusion G protein may

comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more substitutions, insertions, or deletions relative to the naturally-occurring sequence, so long as the resulting protein is capable of eliciting an immune response and the virus remains replication-competent. For instance, the gene encoding the fusion F protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to any one of SEQ ID NOs: 23, 24, 33, or 35. Similarly, the gene encoding the fusion G protein may comprise a sequence that is about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to any one of SEQ ID NOs: 25, 26, 34, Or 36.

[0107] As described in more detail below, such recombinant Cedar virus (rCedV) chimeras, in which one or both of the F and G envelope glycoprotein genes of CedV are replaced with a corresponding F envelope glycoprotein fusion protein and/or G envelope glycoprotein fusion protein, comprising an ectodomain with or without a transmembrane domain from a non-CedV henipavirus, may be used to elicit an immune response to a non-CedV henipavirus.

### III. Vaccine Compositions

[0108] Because CedV is naturally attenuated and non-pathogenic, the disclosed rCedV chimeras can be used as vaccines to elicit an immune response or establish immune protection against pathogenic strains of henipavirus.

[0109] In one aspect, a vaccine composition as disclosed herein comprises a recombinant Cedar virus (rCedV) chimera as disclosed herein, wherein one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes, respectively, of a non-CedV henipavirus, as described in more detail above.

[0110] In another aspect, a vaccine composition as disclosed herein comprises a rCedV chimera as disclosed herein comprising the F and G envelope glycoprotein genes of CedV, and further comprising a coding sequence for one or both of (i) a soluble F envelope glycoprotein (sF) of a non-CedV henipavirus and (ii) a soluble G envelope glycoprotein (sG) of a non-CedV henipavirus, as described in more detail above.

[0111] In another aspect, a vaccine composition as disclosed herein comprises a rCedV chimera as disclosed herein comprising one or both of a gene encoding a fusion protein of a henipavirus F envelope protein and a gene encoding a fusion protein of a henipavirus G envelope protein, wherein the fusion protein comprises the ectodomain and transmembrane domain of a non-CedV henipavirus F envelope protein or a non-CedV henipavirus G envelope protein fused to the cytoplasmic tail domain of the CedV F envelope protein or CedV G envelope protein, respectively, or the fusion protein comprises the ectodomain of a non-CedV henipavirus F envelope protein or a non-CedV henipavirus G envelope protein fused to the transmembrane domain and cytoplasmic tail domain of the CedV F envelope protein or CedV G envelope protein, respectively, as described in more detail above.

[0112] In another aspect, a vaccine composition as disclosed herein may comprise or further comprise (in addition to a chimera as described herein) a non-CedV sF, a non-CedV sG, or both. The non-CedV henipavirus can be selected from HeV, NiV, GhV, or MojV or any other

pathogenic henipavirus. In some embodiments, the sF and/or sG is HeV or NiV (e.g., NiV-B or NiV-M).

[0113] The immune response elicited by immunization with a chimera or vaccine as disclosed herein is expected to induce production of antibodies that bind henipavirus and provide broad spectrum immune protection against henipaviruses. For example, as noted above, a chimera displaying a non-CedV ectodomain of one species of henipavirus, such as HeV, may induce a protective immune response against other species of henipavirus, such as NiV-M and NiV-B.

[0114] In accordance with any embodiments, a vaccine as disclosed herein may comprise a pharmaceutically acceptable carrier suitable for the intended subject and route of administration. Pharmaceutically acceptable carriers for various dosage forms and routes of administration are known in the art. For example, solvents, solubilizing agents, suspending agents, isotonicity agents, buffers, and soothing agents for liquid preparations are known. In some embodiments, the disclosed vaccine compositions include one or more additional components, such as one or more preservatives, antioxidants, and the like.

[0115] In accordance with any embodiments, a vaccine as disclosed herein may be formulated for injection and administered parenterally, such as intravenously, intramuscularly, subcutaneously, or intradermally. Thus, a vaccine as disclosed herein may be formulated for intravenous injection or infusion. Alternatively, with any embodiments, a vaccine as disclosed herein may be formulated for administration by inhalation. Vaccine compositions disclosed herein can be formulated according to standard methods (see, for example, Remington's Pharmaceutical Science, Mark Publishing Company, Easton, USA).

[0116] In accordance with any vaccine composition embodiments described herein, a vaccine composition as described herein optionally may further comprise an adjuvant. An adjuvant is an ingredient used in some vaccines that helps create a stronger immune response in people receiving the vaccine. Adjuvants typically help the body produce an immune response strong enough to protect the person from the disease he or she is being vaccinated against. Adjuvants suitable for use in vaccine compositions are known in the art, including adjuvants suitable for use in henipavirus vaccine compositions. Any such adjuvants can be used in the vaccine compositions described herein.

[0117] Any of the vaccine compositions disclosed herein can be used for treating, reducing the risk of, and/or preventing a henipavirus infection. Optimal doses and routes of administration may vary. The administration methods can be properly selected according to the patient's age, weight, and condition.

[0118] The disclosed vaccines may be formulated to be administered alone or concurrently with another therapeutic agent for treating henipavirus (i.e., an antiviral agent). The vaccines may be formulated to be administered in sequence with another therapeutic agent or concurrently with another therapeutic agent. For example, the vaccine may be administered either before or after the subject has received a regimen of an antiviral therapy. The disclosed vaccines may be administered as a single dose or an initial dose followed by one or more booster doses.

#### IV. Methods and Uses

##### A. Treatments, Reductions of Risk, and Prevention

**[0119]** The vaccines and chimeras disclosed herein can be used for treating henipavirus infections, reducing the risk of henipavirus infections, or preventing henipavirus infections. Accordingly, in another aspect, the present disclosure provides uses of the chimeras and vaccine compositions described herein in methods of treating, reducing the risk of, or preventing a pathogenic henipavirus (e.g., HeV, NiV, GhV, or MojV) infection in a subject in need thereof, comprising administering to the subject an effective amount of a chimera or vaccine composition as described herein.

**[0120]** Administration may be via an injection. The injection may be given, for example, intravenously, intramuscularly, subcutaneously, or intradermally. Alternatively, administration may be via an inhalation.

**[0121]** The targeted henipavirus may be any known, presumed, or suspected pathogenic henipavirus, such as HeV, NiV, GhV, or MojV. In some embodiments, the target henipavirus is HeV. In some embodiments, the target henipavirus is NiV (e.g., NiV-B or NiV-M).

**[0122]** The subject may be any subject in need of treatment of, reduction of risk of, or prevention of henipavirus infection. In some embodiments, the subject is a mammalian subject. In some embodiments, the subject is a human subject. In some embodiments, the subject is a non-human mammal. In some embodiments, the subject is a livestock mammal.

**[0123]** Another aspect of the present disclosure is directed to uses of the chimeras and vaccine compositions described herein in methods of inducing an immune response against a pathogenic henipavirus in a subject, comprising administering to the subject an effective amount of a chimera or vaccine composition as described herein.

**[0124]** Dosage regimens for the disclosed methods and uses can be adjusted to provide the optimum desired response. For example, in some embodiments, a single bolus of a vaccine or rCedV may be administered, while in some embodiments, several doses may be administered over time, or the dose may be proportionally reduced or increased as indicated by the situation. In some embodiments, a subject may be administered more than one distinct rCedV, such as two or three or more distinct rCedV disclosed herein.

##### B. Assay Reagents

**[0125]** Another aspect of the present disclosure is directed to uses of the chimeras described herein as assay reagents. The replication competent rCedV chimeras described herein can be used under BSL-2 containment (as opposed to the BSL-4 containment required for pathogenic henipaviruses), making them ideal for use in studying henipaviruses and agents being developed to target them. For example, the rCedV chimeras described herein can be used as the virus component of a virus neutralization assay to assess and characterize virus-neutralizing antibodies or antibody responses, such as for studies of vaccines against NiV or HeV. The rCedV based chimeras disclosed herein also may be used to study henipavirus entry mechanisms and in entry receptor studies, and in entry inhibitor antiviral drug discovery studies of other henipaviruses.

**[0126]** The following examples are given to illustrate the present disclosure. It should be understood that the invention is not to be limited to the specific conditions or details described in these examples.

#### EXAMPLES

##### Example 1—Rescue of Replication-Competent rCedV Chimeras

###### Rescue of rCedV Stock

**[0127]** In order to rescue replication-competent rCedV chimeras, such as rCedV-NiV-B, rCedV-HeV, rCedV-GhV, rCedV-MojV, or other yet to be described henipaviruses, a stock preparation of each rCedV chimera antigenome plasmid was prepared and sequenced.

**[0128]** BSR-T7/5 cells that stably express T7 RNA polymerase were transfected with four plasmids: first; with the individual rCedV antigenome clone, and three support plasmids expressing CedV nucleoprotein (N), phosphoprotein (P), and polymerase protein (L) required for encapsidation and replication. Four to five days post transfection, GFP expression (if included in the genome construction) or syncytia formation were monitored. After seven days, the supernatant was passaged to fresh Vero E6 cells to amplify rescued virus. Alternatively, six hours post-transfection, the media was changed, and Vero E6 cells were co-cultured with transfected BSR-T7/5 cells. GFP expression and syncytia were monitored, and after seven days supernatant was passaged to fresh Vero E6 cells, which was monitored for syncytia and GFP expression. When maximal GFP expression and syncytia was observed, supernatants were purified by centrifugation and stored or used for experimentation. For virus stock storage, rCedVs are stored at -80° C. as single use aliquots. The virus was removed and thawed and diluted for infection immediately prior to use.

###### Construction of Genetic Cassettes

**[0129]** Novel genetic cassettes with various intergenic regions for the cloning and manipulations of the full-length rCedV antigenome clones were individually designed and constructed to accommodate additional reporter genes, such as green fluorescent protein (GFP) or luciferase protein (Luc). The CedV intergenic regions between each given F and G henipavirus gene cassette were retained, while also retaining the flanking intergenic sequences on the ends of each cassette to that of CedV.

**[0130]** The F and G gene cassettes of either NiV-B or HeV were individually designed to have CedV F start and stop untranslated intergenic regions flanking the NiV-B or HeV F coding region and the CedV G start and stop untranslated intergenic regions flanking the NiV-B or HeV G coding region. To maintain the “rule-of-six” (a feature employed by the henipaviruses to promote replication initiation (38)), additional modifications to the NiV-B and HeV F coding regions were made. Specifically, for the NiV-B F coding region, the last three nucleotides (ACG) from the NiV-B F coding region were not included in the chimera design, as deletion of this amino acid (Threonine) has been shown not to interfere with endocytosis, trafficking or fusion (39) and therefore would not interfere with the proper maturation and biological activity of the NiV-B F glycoprotein and a rCedV chimera rescue. For the HeV F coding region, an additional TAA (stop codon) sequence was added to the end of the HeV

F coding region, which would not impact protein expression or functionality. These custom designed genetic cassettes were synthesized and various rCedV whole genome clones (the chimeras) encoding the F and G envelope glycoproteins of HeV and NiV-B, both with and without reporter genes, were used to rescue replication competent viruses.

[0131] In addition, an optimized full-length antigenome clone of rCedV for the reverse genetics system was designed to enhance recombinant virus rescue efficiency. This was achieved by modifying the 5-prime end of the antigenome clone by inserting additional nucleotides GGGAGA to the minimal T7 RNA polymerase promoter (T7 min) to create an optimized T7 RNA polymerase promoter (T7opt) followed by a self-cleaving autocatalytic hammerhead ribozyme A (HHRbzA) sequence.

#### Construction of rCedV Chimeric Genome Clones

[0132] A T7 polymerase promoter (T7 min) sequence containing additional nucleotides GGGAGA (T7<sub>opt</sub>) (19) preceding a hammerhead ribozyme A (HHRbzA) sequence was synthesized (Genscript; NJ, USA) and enzymatically inserted before the 3'Le (3' Leader) sequence of the pOLTV5-rCedV antigenome plasmid. The F and G glycoprotein open reading frames from NiV-B 2010 Faridpur isolate (F: NCBI accession number AEZ01396.1 and G: NCBI accession number AEZ013971.1) and HeV 2008 Redlands isolate (F: NCBI accession number AEQ38070.1 and G: NCBI accession number AEQ38071.1) (Table 4) were synthesized separately (Genscript; NJ, USA). The NiV-B F and G open reading frames are from the NiV-B 2010 Faridpur isolate GenBank: JN808864.1, with protein sequences GenBank: AEZ01396.1 and GenBank: AEZ013971.1, for NiV-B F and G glycoproteins, respectively. The HeV F and G open reading frames are derived from the HeV genome GenBank: MN062017.1. The HeV F and G amino acid sequences are identical to the F and G amino acid sequences of the HeV 2008 Redlands isolate (GenBank: JN255805.1) and protein sequences GenBank: AEQ38070.1 and GenBank: AEQ38071.1, for HeV F and G glycoproteins, respectively.

TABLE 4

Genbank accession numbers of envelope glycoproteins from NiV-B and HeV isolates inserted in rCedV antigenome plasmid.			
Henipavirus	Isolate	Protein	Genbank Accession #
NiV-B	2010 Faridpur	F	AEZ01396.1
		G	AEZ01397.1
HeV	2008 Redlands	F	AEQ38070.1
		G	AEQ38071.1

[0133] The synthesized gene cassettes were inserted by standard molecular techniques into the newly generated pOLTV5-rCedV antigenome plasmid. A modified turbo Green Fluorescent Protein (GFP) gene or a Firefly Luciferase protein (Luc) gene as previously described (5) was enzymatically inserted between the CedV P and M genes of the newly generated pOLTV5-rCedV antigenome plasmid. All cloning was performed with *Escherichia coli* Stbl2 cells (Invitrogen; CA, USA). All plasmids were sequenced to obtain at least 2-fold coverage.

[0134] FIGS. 1A-B show the optimized rCedV chimera antigenomes prepared in comparison to rCedV. FIG. 1A

shows sequences of the T7 minimal promoter (T7<sub>min</sub>) with additional GGGAGA nucleotides to generate the T7 optimal promoter (T7<sub>opt</sub>) and the Hammerhead Ribozyme A (HHRbzA) in the context of the rCedV antigenome plasmid. The T7<sub>opt</sub> promoter and HHRbzA sequences were inserted before the 3' Leader (3' Le) sequence of the rCedV antigenome plasmid. The long arrows indicate regions of self-cleavage. Unique restriction sites MluI and SphI used to construct the rCedV chimeric plasmids are shown. FIG. 1B shows the genomes and the lengths of the generated chimeras. CedV F and G glycoproteins were enzymatically replaced with NiV-B or HeV fusion (F) and attachment (G) open reading frames to yield rCedV-NiV-B or rCedV-HeV, respectively. A modified turbo Green Fluorescent Protein (GFP) gene or Firefly Luciferase protein (Luc) gene was inserted between CedV P and M genes to generate rCedV-NiV-B-GFP and rCedV-HeV-GFP, or rCedV-NiV-B-Luc and rCedV-HeV-Luc, respectively. Abbreviations: T7<sub>min</sub>, T7 minimal promoter; T7<sub>opt</sub>, T7 optimal promoter; HHRbzA, Hammerhead Ribozyme A; 3'Le, 3' Leader; 5'Tr, 5' Trailer; HDVRbz, hepatitis delta virus ribozyme; T7<sub>c</sub>, T7 terminator.

#### Rescue of rCedV Chimeras

[0135] BSR-T7/5 cells in a 12-well plate ( $2.5 \times 10^5$  cells/well) were co-transfected with pCMV-CedV helper plasmids pCMV-CedV-N (1.25  $\mu$ g), pCMV-CedV-P (0.8  $\mu$ g) and pCMV-CedV-L (0.4  $\mu$ g) together with each of the rCedV chimera antigenome constructs (3.5  $\mu$ g) using TransIT-LT1 transfection reagent (Mirus Bio; WI, USA) according to the manufacturer's recommendations. After 4-5 days, transfected cells were microscopically observed for syncytia formation and expression of GFP. Supernatants from successful rescue wells were collected and passaged onto naïve Vero E6 cells in a T-75 flask to prepare a master stock of each of the rCedV chimeras. When maximal syncytia or GFP expression was observed (~2-3 days), viral supernatants were collected, clarified by centrifugation at 948xg for 10 mins to pellet cell debris, and transferred to screw cap tubes as single use aliquots stored at -80° C. Viral stocks were titrated by plaque assay (5, 20). Briefly, a ten-fold serial dilution of the virus stock was prepared in DMEM-10, 200  $\mu$ l of which was applied to pre-seeded Vero E6 cells in duplicate ( $5 \times 10^5$  cells/well) in a 12-well plate and incubated for 1 hour at 37° C., 5% CO<sub>2</sub>. A 2 ml overlay of a 1:1 mix of DMEM-5 with 2% carboxymethylcellulose sodium salt (medium viscosity) (Sigma-Aldrich; MO, USA) was applied to all wells and incubated for 4 days at 37° C., 5% CO<sub>2</sub>. Cells were fixed with 4% Formaldehyde in diH<sub>2</sub>O for 1 hour at room temperature and stained with 0.5% crystal violet in 80% methanol for 15 mins at room temperature. The stain was removed and washed with diH<sub>2</sub>O and plaques were counted and expressed as plaque forming units (PFU)/ml. All rCedV chimera virus stocks were deep-sequenced.

#### Western Blot Analysis

[0136] Vero E6 cells in a 6-well plate were infected at a density of  $1 \times 10^6$  cells with each of the rCedV-NiV-B chimeras, rCedV-HeV chimeras or rCedV viruses, at a multiplicity of infection (MOI) of 0.01. In addition, Vero E6 cells were transfected with pcDNA3.1-CMV-NiV-F, pcDNA3.1-CMV-NiV-G, pcDNA3.1-CMV-HeV-F or pcDNA3.1-CMV-HeV-G in a 1:3 ratio (F:G). At 24 hours post infection (hpi), cells were collected and lysed with 1×RIPA (Radioimmu-

noprecipitation assay) buffer containing a protein inhibitor cocktail. Total protein (30 µg) was separated on a 4-12% Bis-Tris gel (Thermo Fisher Scientific) and transferred to a nitrocellulose membrane (Thermo Fisher Scientific). The membranes were blocked in 5% milk in 1×PBS with 0.1% Tween-20 at room temperature. NiV and HeV cross reactive murine monoclonal antibodies (mAbs) specific to G glycoprotein (mAb 48D3) and F glycoprotein (mAb 5G7), polyclonal rabbit sera to CedV-N(CSIRO, Australia), and j-actin (Thermo Fisher Scientific) were used and subsequently probed with a corresponding secondary HRP-coupled antibody and visualized by autoradiography.

[0137] rCedV chimeras for HeV and NiV-B without reporter genes, and with the GFP or Luc reporter genes, are shown in FIGS. 2A-B. Vero E6 cells were uninfected (Mock) or infected at a multiplicity of infection (MOI) of 0.01 with either rCedV-NiV-B, rCedV-NiV-B-GFP, rCedV-NiV-B-Luc (A), rCedV-HeV, rCedV-HeV-GFP, rCedV-HeV-Luc (B), rCedV, rCedV-GFP or rCedV-Luc. As a reference, cells were co-transfected with a total of 2 µg of pcDNA3.1-NiV F+G or pcDNA3.1-HeV F+G. All cells were harvested at 24 hours post infection (hpi), lysates prepared and total protein (~30 µg) resolved by electrophoresis (SDS-PAGE). The subsequent membrane was probed with HeV and NiV cross-reactive mAbs against F glycoprotein (mAb 5G7) and G glycoprotein (mAb 48D3), polyclonal rabbit serum to CedV-N and β-actin. Representative images from two independent experiments are shown. This confirms the identity, by western blot detection, of the NiV-B and HeV species of the F and G glycoproteins being expressed by the rCedV chimeras: rCedV-NiV-B, rCedV-NiV-B-GFP, and rCedV-NiV-B-Luc (FIG. 2A) and rCedV-HeV, rCedV-HeV-GFP, and rCedV-HeV-Luc (FIG. 2B).

#### Cell-Cell Fusion Assay

[0138] Cell-cell fusion mediated by rCedV chimeras was demonstrated by syncytia formation (giant cells) by rCedV chimeras as shown in FIG. 3. The rCedV chimeras bearing NiV-B or HeV envelope glycoproteins form syncytia in infected Vero E6 cells. Vero E6 cells were uninfected (Mock) or infected with either rCedV-NiV-B, rCedV-NiV-B-GFP, rCedV-NiV-B-Luc, rCedV-HeV, rCedV-HeV-GFP, rCedV-HeV-Luc, rCedV, rCedV-GFP or rCedV-Luc at a multiplicity of infection (MOI) of 0.01. All images were taken 24 hpi. (FIG. 3A) Cells infected with GFP expressing viruses. Transmitted light (top row), fluorescence (middle row) and merged (bottom row) images are shown. The respective zoomed in fluorescence images (3rd row) are regions in the boxes. (FIG. 3B) Cells infected with non-reporter or Luc expressing rCedV chimeras were fixed, stained and then imaged for syncytia. The images taken with transmitted light are shown. Images were captured with a Zeiss Axio Observer A1 inverted microscope using a 5× objective. Arrows indicate giant multinucleated cells (syncytia). Representative images from three independent experiments are shown. Scale bar, 50 µm.

#### Example 2—Replication Kinetics of rCedV Chimeras

[0139] Vero E6 cells seeded at a density of 2×10<sup>4</sup> cells/well in a 96-well cell culture plate were infected at a MOI of 0.01 for 1 hour at 37°C., 5% CO<sub>2</sub>. Viral overlay was removed and fresh medium added to all wells. Supernatants

were collected at 0, 8, 24, 48 and 72 hpi and stored at -80°C. until ready to analyze. Viral titers (PFU/ml) were determined by plaque assay. Intracellular luciferase activity was determined with the Steady-Glo® Luciferase Assay System (Promega; Madison, WI) in a 1:1 mixture with cell culture medium. After a 10 minute incubation at room temperature, the homogenate was transferred to a white opaque 96-well cell culture plate, Nunc™ F96 MicroWell™ White Polystyrene Plate (ThermoFisher Scientific) and read using the GloMax® —Multi Detection System (Promega).

[0140] The various rCedVs have similar infection and replication kinetics. FIGS. 4A-B show a comparison of progeny virus production over time by determining infectious virus titers (PFU/ml) from supernatants harvested at the indicated time points from Vero E6 cells infected at a multiplicity of infection (MOI) of 0.01 with the rCedV-NiV-B (clear leftmost bar), rCedV-NiV-B-GFP (dotted bar), rCedV-NiV-B-Luc (striped bar) (A), rCedV-HeV (clear leftmost bar), rCedV-HeV-GFP (dotted bar) or rCedV-HeV-Luc (striped bar) (B). As a reference Vero E6 cells were also infected with rCedV (black rightmost bars) (A and B). Normalized relative light units (RLU) for CedV-NiV-B-Luc (A) and rCedV-HeV-Luc (B) infected cells are represented on the right Y-axes as dashed lines. The data represent mean±standard deviation from three independent experiments. Virus titers and luciferase activity levels at 0 hpi indicate the lower limit of detection for the plaque assay and the luminometer, respectively. Statistical analysis was performed in GraphPad Prism 9 by two-way ANOVA followed by Tukey's post hoc test ( $\alpha=0.05$ ).

#### Example 3—Ephrin Receptor Tropism

[0141] To evaluate and confirm the entry and infection ephrin receptor tropism of the rCedV chimeras for HeV and NiV-B, infection and syncytia formation assays were conducted. A representative experiment with the GFP encoding rCedV chimeras for HeV and NiV-B is shown in FIGS. 5A-C.

[0142] Previously, HeLa-USU cells, which lack expression of ephrin-B2 and ephrin-B3 were used to generate stable cell lines expressing ephrin-B2 (HeLa-USU-ephrin-B2) and ephrin-B3 (HeLa-USU-ephrin-B3) (5). HeLa-USU, HeLa-USU-ephrin-B2 and HeLa-USU-ephrin-B3 cell lines were seeded at a density of 2.5×10<sup>5</sup> cells/well in a 12-well cell culture plate. When confluent, cell culture medium was removed and cells were left uninfected (Mock) or infected at a multiplicity of infection (MOI) of 0.5 with rCedV-NiV-B-GFP, rCedV-HeV-GFP or rCedV-GFP. Infected cells were imaged for fluorescence and syncytia at 24 hpi. In each panel, transmitted light (1st column), fluorescence (2nd column) and merged (3rd column) images are shown. Zoomed in regions are from the boxes. Images were captured with a Zeiss Axio Observer A1 inverted microscope using a 5× objective. Representative images from two independent experiments are shown. Scale bar, 50 µm.

[0143] Of the B class ephrin ligands, CedV utilizes ephrin-B2 and not ephrin-B3; whereas NiV-B and HeV utilize ephrin-B2 and ephrin-B3 (4). Thus, the rCedV-HeV-GFP and rCedV-NiV-B-GFP have the same entry receptor tropism as authentic NiV-B and HeV.

#### Example 4—Neutralization Tests

[0144] The utility of these new rCedV chimeras were tested as viable surrogate viruses for the conduct of authen-

tic NiV-B and HeV neutralization tests. The GFP-encoding rCedV chimeras for NiV-B and HeV were evaluated as tools for determining antibody neutralization activities in both the standard Plaque reduction neutralization test (PRNT) and a new Fluorescent reduction neutralization test (FRNT) utilizing the GFP reporter gene activity. Well-characterized HeV and NiV cross-reactive neutralizing mAbs (human mAb m102.4, humanized mAb h5B3.1, and murine mAbs 12B2 and 1F5 (21, 23-25), and also polyclonal anti-NiV G nonhuman primate sera from animals immunized with recombinant NiV-M and NiV-B sG glycoprotein (Auro Vaccines, LLC) were assayed using the rCedV-NiV-B-GFP and rCedV-HeV-GFP chimeric viruses; these mAbs were also directly compared to authentic NiV-B and HeV in side-by-side virus neutralization tests in the BSL-4 facility at the Galveston National Laboratory (GNL), University of Texas Medical Branch (UTMB), Galveston, TX.

#### Plaque Reduction Neutralization Test (PRNT)

**[0145]** Vero 76 cells were seeded at a density of  $6 \times 10^5$  cells/well in a 6-well plate and incubated overnight at 37°C.,

that target the F glycoprotein of NiV and HeV, against the GFP-encoding rCedV chimeras rCedV-NiV-B-GFP and rCedV-HeV-GFP (FIGS. 6A and 6B) in comparison to authentic NiV-B and HeV (FIG. 6C). The neutralization activity by these mAbs (neutralization inhibitory concentrations for 50% inhibition in comparison to no mAb ( $IC_{50}$ )) against the rCedV chimeras are highly comparable to the neutralization profiles against authentic NiV-B and HeV. The limit of detection for this assay was 50 PFU. Data are plotted as non-linear regression curve fit with variable slope using GraphPad prism and are representative of a single experiment performed in duplicate. Grey circles and lines represent rCedV-NiV-B-GFP or NiV-B and light grey squares and lines represent rCedV-HeV-GFP or HeV.

**[0147]** Table 5 tabulates the  $IC_{50}$  calculations by PRNT for the rCedV-NiV-B-GFP and rCedV-HeV-GFP conducted at BSL-2; and also by PRNT assay carried out in BSL-4 of the rCedV-NiV-B-GFP and rCedV-HeV-GFP chimeras and authentic NiV-B and HeV side-by-side in the same assay.

TABLE 5

IC <sub>50</sub> doses of HeV and NiV cross-reactive specific monoclonal antibodies against rCedV-NiV-B-GFP and rCedV-HeV-GFP infection in Vero 76 cells by plaque reduction neutralization test (PRNT).							
Monoclonal antibody (mAb)	IC <sub>50</sub> (95% CI) (ng/ml)						
	BSL-2		BSL-4		BSL-2		BSL-4
	rCedV-NiV-B-GFP	rCedV-NiV-B-GFP	NiV-B	rCedV-HeV-GFP	rCedV-HeV-GFP	HeV	
m102.4	20.30 (16.58-24.99)	21.20 (18.80-23.89)	18.36 (15.21-22.17)	112.9 (82.82-154.1)	137.0 (89.09-208.8)	52.41 (39.32-70.07)	
h5B3.1	274.8 (185.9-403.7)	1,122 (813.6-1,548)	7,101 (4,323-15,087)	363.5 (241.6-546.3)	1,202 (975.2-1,481)	1,064 (827.4-1,372)	
12B2	130.0 (97.10-174.0)	291.9 (219.9-381.5)	1,467 (1,098-1,925)	502.3 (377.4-658.3)	700.1 (570.0-857.0)	2,202 (1,692-2,846)	
1F5	153.8 (107.0-219.4)	289.4 (229.9-360.9)	1,036 (812.3-1,298)	140.6 (83.29-232.0)	253.2 (200.5-318.8)	259.8 (213.2-315.8)	

Note:

All  $IC_{50}$  values are calculated by a nonlinear fit model and are shown with 95% confidence intervals (95% CI). BSL-2 studies are representative of two independent experiments each performed in duplicate and BSL-4 studies are from a single experiment performed in duplicate.

5% CO<sub>2</sub>. The mAbs, serially diluted 3-fold in DMEM-10 to final concentrations ranging from 10 µg/ml to 0.0046 µg/ml were incubated with a target concentration of 100 PFU of rCedV-NiV-B-GFP or rCedV-HeV-GFP for 1 hour at 37°C., 5% CO<sub>2</sub>. Each of the virus-mAb mixtures (400 µl/well) was added to duplicate wells of the pre-seeded 6-well plate. Following a 1-hour incubation at 37°C., 5% CO<sub>2</sub>, the wells were overlaid with 1:1 mix of 0.8% agarose/DMEM-10 and incubated for 4 days. Neutral red solution was added to each well and incubated for 24 hours at which time plaques were counted. Neutralization percent (%) was calculated based on PFU for each virus without antibody. The 50% inhibitory concentration ( $IC_{50}$ ) was determined as the antibody concentration at which there was a 50% reduction in plaque counts versus untreated control wells. The  $IC_{50}$  values were calculated by non-linear regression curve fit with variable slope with GraphPad prism (GraphPad Software Inc.). The limit of detection for this assay was 50 PFU.

**[0146]** FIGS. 6A-C show the virus neutralization (PRNT) activities of a neutralizing cross-reactive mAb (m102.4) that targets the G glycoprotein of NiV and HeV, and three neutralizing cross-reactive mAbs (h5B3.1, 12B2 and 1F5)

**[0148]** Together, these results show that the rCedV-NiV-B-GFP or rCedV-HeV-GFP chimeras respond to mAb neutralization in a highly similar fashion to that of authentic NiV-B and HeV in the context of a standard virus PRNT and are a remarkably ideal surrogate virus assay system that does not need to be used under BSL-4 containment.

**[0149]** Correlation analysis of plaque reduction neutralization test (PRNT) neutralization values from the data in FIG. 6A-C is shown in FIG. 7A-H. Pearson correlation analysis of PRNT neutralization (%) values of rCedV-NiV-B-GFP versus NiV-B (A, C, E, G) and of rCedV-HeV-GFP versus HeV (B, D, F, H) with mAbs m102.4, h5B3.1, 12B2 or 1F5. The Pearson correlation coefficient 'r', p-value (two-tailed), linear regression line (solid lines) and 95% confidence intervals (dashed lines) are represented. Pearson's  $r \geq 0.8$  and  $p$  value  $< 0.05$  indicate a strong significant positive correlation. Table 6 summarizes the correlation analysis of rCedV chimeric virus BSL-2 PRNT versus NiV-B and HeV BSL-4 PRNT.

TABLE 6

Correlation analysis of rCedV chimeric virus BSL-2 PRNT versus NiV-B and HeV BSL-4 PRNT.

Virus	Monoclonal antibody (mAb)	Pearson's correlation coefficient (r)	Coefficient of determination ( $R^2$ )	Significance (p)	95% confidence interval (CI)
rCedV-NiV-B-GFP vs NiV-B	m102.4	0.9949	0.9898	<0.0001	0.9750-0.990
	h5B3.1	0.8624	0.7437	0.0028	0.4640-0.9706
	12B2	0.8363	0.6994	0.0050	0.3873-0.9647
	1F5	0.9239	0.8536	0.0004	0.6722-0.9842
rCedV-HeV-GFP vs HeV	m102.4	0.9771	0.9547	<0.0001	0.8914-0.9953
	h5B3.1	0.9548	0.9117	<0.0001	0.7945-0.9907
	12B2	0.8863	0.7855	0.0015	0.5400-0.9760
	1F5	0.9898	0.9796	<0.0001	0.9503-0.9979

## Note:

Correlation analysis was performed with the neutralization values from FIGS. 6A and 6C.

## Fluorescent Reduction Neutralization Test (FRNT)

[0150] To highlight the further utility of the GFP-encoding rCedV chimeras rCedV-NiV-B-GFP and rCedV-HeV-GFP as surrogate viruses for authentic NiV-B and HeV, a new more rapid and quantitative neutralization assay measuring GFP fluorescence was established and used to conduct virus neutralization tests by fluorescence quantification.

[0151] Vero 76 cells were seeded at a density of  $2 \times 10^4$  cells/well in black-walled clear bottom 96-well plates (Corning Life Sciences; NY, USA) and incubated overnight at 37°C., 5% CO<sub>2</sub>. The mAbs were 3-fold serially diluted in DMEM-10 to final concentrations ranging from 10 µg/ml to 0.0046 µg/ml or monkey sera were 3-fold serially diluted in DMEM-10 starting with a 1:200 dilution. An equal volume of DMEM-10 containing rCedV-NiV-B-GFP or rCedV-HeV-GFP was added to each dilution for a final concentration of 2000 PFU (MOI: 0.05) and incubated for 2 hours at 37°C., 5% CO<sub>2</sub>. Each of the virus-mAb mixtures (90 µl/well) was added to the pre-seeded Vero 76 cells in triplicate and incubated for an additional 24 hours at 37°C., 5% CO<sub>2</sub>. The plate was then fixed with 4% formaldehyde in 1×PBS for 20 minutes at room temperature and then washed extensively with diH<sub>2</sub>O. The fixed plate was then scanned using the CTL S6 analyzer (Cellular Technology Limited; OH, USA). Fluorescent foci were counted using the CTL Basic Count™ feature. The 50% inhibitory concentration (IC<sub>50</sub>) was determined as the antibody concentration at which there was a 50% reduction in fluorescent foci versus untreated control wells. The IC<sub>50</sub> values were calculated by non-linear regression curve fit with variable slope with GraphPad prism (GraphPad Software Inc.). The limit of detection for this assay was 50 fluorescent foci.

[0152] FIG. 8 show the results of the virus neutralization (FRNT) activities of a neutralizing cross-reactive mAb (m102.4) that targets the G glycoprotein of NiV and HeV, and three neutralizing cross-reactive mAbs (h5B3.1, 12B2 and 1F5) that target the F glycoprotein of NiV and HeV, against the GFP-encoding rCedV chimeras rCedV-NiV-B-GFP and rCedV-HeV-GFP.

[0153] In FIG. 8, mAbs serially diluted 3-fold to final concentrations ranging from 10 µg/ml to 0.0046 µg/ml and a target concentration of 2000 PFU (MOI. 0.05) of rCedV-NiV-B-GFP (left) or rCedV-HeV-GFP (right) were incubated for 2 hours at 37°C., 5% CO<sub>2</sub>. Virus-mAb mixture was added to triplicate wells of black-walled 96-well plates containing pre-seeded Vero 76 cells. After 24 hours, plates were fixed with 4% formaldehyde in 1×PBS for 20 minutes.

The fixed plates were scanned using the CTL S6 analyzer. Fluorescent foci were counted using the CTL Basic Count™ feature. Each mAb was tested in triplicate with 3-fold dilutions of each monoclonal antibody. The limit of detection for this assay was 50 fluorescent foci.

[0154] FIG. 8 shows seven point dose response curves for m102.4, h5B3.1, 12B2 and 1F5 monoclonal antibodies against rCedV-NiV-B-GFP and rCedV-HeV-GFP. Neutralization percent (%) was calculated based on fluorescent foci for each virus without mAb. The data represent mean±standard deviation from three independent experiments each performed in triplicate. Data are plotted as non-linear regression curve fit with variable slope using GraphPad prism and are representative of three independent experiments performed in triplicate. The limit of detection for this assay was 50 fluorescent foci. The gray circles and lines represent rCedV-NiV-B-GFP and light gray squares and lines represent rCedV-HeV-GFP.

[0155] The neutralization profiles of the mAbs by FRNT (Table 7) are remarkably comparable to the IC<sub>50</sub> values calculated by PRNT assays for both authentic NiV-B and HeV and rCedV-NiV-B-GFP and rCedV-HeV-GFP previously determined (shown in FIG. 6 and Table 5).

TABLE 7

IC<sub>50</sub> doses of HeV and NiV cross-reactive specific monoclonal antibodies against rCedV-NiV-B-GFP and rCedV-HeV-GFP infection in Vero 76 cells by fluorescent reduction neutralization test (FRNT).

Monoclonal antibody (mAb)	rCedV-NiV-B-GFP	rCedV-HeV-GFP
m102.4	16.91 (14.72-19.45)	58.12 (49.27-68.70)
h5B3.1	333.0 (255.5-439.9)	700.2 (620.0-798.8)
12B2	34.07 (24.88-46.48)	124.5 (98.17-157.2)
1F5	28.97 (22.86-36.65)	50.16 (40.95-61.07)

## Note:

All IC<sub>50</sub> values are calculated by a nonlinear fit model from three independent experiments each performed in triplicate and are shown with 95% confidence intervals (95% CI).

[0156] Correlation analysis of neutralization assays using the GFP expressing rCedV chimeric viruses. FIG. 9A-H shows the Pearson correlation analysis of neutralization (%) values from plaque reduction neutralization tests (PRNTs) (y-axes) (data from FIG. 6A) and fluorescence reduction neutralization tests (FRNTs) (x-axes) (data from FIG. 8) performed with rCedV-NiV-B-GFP (A, C, E, G) and with rCedV-HeV-GFP (B, D, F, H) with mAbs m102.4, h5B3.1,

12B2 or 1F5. The Pearson correlation coefficient 'r', p-value (two-tailed), linear regression line (solid lines) and 95% confidence intervals (dashed lines) are represented. Pearson's  $r \geq 0.8$  and p value  $< 0.05$  indicate a strong significant positive correlation. Table 8: summarizes the correlation analysis of rCedV chimeric GFP viruses by PRNT versus FRNT.

TABLE 8

Correlation analysis of rCedV chimeric PRNT versus FRNT.					
Virus	Monoclonal antibody (mAb)	Pearson's correlation coefficient (r)	Coefficient of determination ( $R^2$ )	Significance (p)	95% confidence interval
rCedV-NiV-B-GFP vs NiV-B	m102.4	0.9522	0.9067	0.0009	0.7038-0.9931
	h5B3.1	0.9957	0.9914	<0.0001	0.9698-0.9994
	12B2	0.9495	0.9016	0.0011	0.6894-0.9927
	1F5	0.9220	0.8501	0.0031	0.5527-0.9886
rCedV-HeV-GFP vs HeV	m102.4	0.9786	0.9576	0.0001	0.8573-0.9970
	h5B3.1	0.9587	0.9191	0.0007	0.7397-0.9941
	12B2	0.9852	0.9707	<0.0001	0.8997-0.9979
	1F5	0.8973	0.8051	0.0061	0.4448-0.9849

## Note:

Correlation analysis was performed with the neutralization values from FIGS. 6A and 8.

[0157] The GFP-encoding chimeras were then tested by FRNT using anti-NiV G glycoprotein polyclonal antisera. FIG. 10 shows the results of the virus neutralization (FRNT) activities of the sera from four Rhesus macaques that were immunized in a prime boost strategy at 3 weeks apart with a 0.2 mg/ml total of an equal mixture of NiV-B and NiV-M sG proteins AI 3+ Aluminum hydroxide suspension. On day 42, sera from 4 subjects was collected and stored at  $-80^\circ\text{C}$ . Sera was tested for neutralization activity against the GFP-encoding rCedV chimeras rCedV-NiV-B-GFP and rCedV-HeV-GFP.

[0158] In FIG. 10, sera serially diluted 3-fold to final dilutions of 1:200 to 1:437, 400 and a final concentration of 2000 PFU (MOI: 0.05) of rCedV-NiV-B-GFP or rCedV-HeV-GFP were incubated for 2 hours at  $37^\circ\text{C}$ ., 5% CO<sub>2</sub>. Virus-sera mixture were added to triplicate wells of black-walled 96-well plates containing pre-seeded Vero 76 cells. After 24 hours, plates were fixed with 4% formaldehyde in 1×PBS for 20 minutes. The fixed plates were scanned using the CTL S6 analyzer. Fluorescent foci were counted using the CTL Basic Count™ feature. Each serum sample was tested in triplicate with 3-fold dilutions of each serum sample. The limit of detection for this assay was 50 fluorescent foci.

[0159] In FIG. 10, Neutralization percent (%) was calculated based on fluorescent foci for each virus without serum. The seven point dose response curves of sera collected on day 42 post immunization against rCedV-NiV-B-GFP and rCedV-HeV-GFP are shown. The data represent mean±standard deviation from two independent experiments each performed in triplicate. Data are plotted as non-linear regression curve fit with variable slope. The limit of detection for this assay was 50 fluorescent foci. Animal ID numbers are 171269, 180274, 180606 and 180227. Grey circles and lines represent rCedV-NiV-B-GFP and light grey squares and lines represent rCedV-HeV-GFP.

[0160] Here again, rCedV-NiV-B-GFP and rCedV-HeV-GFP performed well as surrogate virus assay systems for

measuring the neutralization potency of all four subject sera samples. The sera cross-neutralized the viruses and the sera was more potent against the homologous surrogate virus (rCedV-NiV-B-GFP) because the sera was generated by NiV sG glycoprotein immunization. Table 9 summarizes the IC<sub>50</sub> titers of each of the sera samples.

TABLE 9

IC <sub>50</sub> doses of NiV-M and NiV-B sG immunized Rhesus macaque sera against rCedV-NiV-B-GFP and rCedV-HeV-GFP infection in Vero 76 cells by fluorescent reduction neutralization test (FRNT).		
Animal ID	IC <sub>50</sub> (95% CI) (Serum titer)	
	rCedV-NiV-B-GFP	rCedV-HeV-GFP
171269	1:32,147 (1:29,414-1:35,182)	1:4,157 (1:3,711-1:4,658)
180274	1:14,860 (1:14,018-1:15,761)	1:2,704 (1:2,375-1:3,082)
180606	1:19,480 (1:18,181-1:20,948)	1:3,739 (1:3,094-1:4,542)
180227	1:19,408 (1:17,817-1:21,158)	1:2,048 (1:1,668-1:2,539)

## Note:

All IC<sub>50</sub> values are calculated by a nonlinear fit model from two independent experiments each performed in triplicate and are shown with 95% confidence intervals (95% CI).

[0161] Taken together, these results show this panel of rCedV chimeras can serve as a highly useful toolset for the study of otherwise highly pathogenic henipaviruses such as NiV and HeV that can be used outside of BSL-4 containment. The GFP-encoding chimeras can also be used in quantitative fluorescence based FRNT assays that can be conducted much faster than the standard PRNT assay. Based on the growth kinetics of all chimeras, the Luc-encoding chimeras and the non-reporter gene containing chimeras would be expected to perform similarly to the GFP-encoding chimeras. In addition, these data provide evidence that rCedV can be used to generate a chimera with any henipavirus G and F envelope glycoproteins or functional combinations of any G or F envelope glycoproteins of any other henipavirus, including GhV or MojV, which are both expected to be pathogenic viruses based on their genome sequences, and which is currently being constructed, or of any henipavirus species, strains or mutants.

## Example 5—Vaccine Platform

[0162] Another aspect of the present disclosure relates to vaccine compositions comprising rCedV chimeras for the treatment of, reduction of risk of, or prevention of infection by pathogenic henipaviruses.

[0163] Wild-type (non-chimeric) rCedV has been shown to be non-pathogenic in non-human primates (8 subjects

infected with  $5 \times 10^5$  TCID<sub>50</sub> of rCedV split equally by intranasal and intratracheal administration) (Geisbert, T. W. and Broder, C. C., Unpublished), adding to the data in-hand that rCedV has been shown to be non-pathogenic in three species (ferrets, hamsters, and African green monkeys (AGMs)), all of which are acutely susceptible to HeV and NiV disease. Back-challenge of previously rCedV-infected AGMs with NiV-B (n=4) or HeV (n=4) resulted in death or severe disease showing that prior rCedV infection offers no cross-protection activity against pathogenic henipaviruses. [0164] Two additional studies carried out in hamsters also showed that infection with rCedV provides no cross-protection against a NiV-B back-challenge. In contrast, initial infection of hamsters with the rCedV-NiV-B chimera described herein provided protection against NiV-B back-challenge (4/4 in one experiment), and initial infection with the rCedV-HeV chimera described herein provided protection against NiV-B back-challenge (8/8 in one experiment). [0165] These data provide evidence that a rCedV chimera as described herein can be used to elicit a protective immune response against NiV-B by prior infection by administering to a subject a rCedV chimera expressing either the NiV-B or HeV G and F glycoproteins, and are indicative of vaccine platform success.

#### Example 6—rCedV Chimera Expressing Soluble G (sG) Glycoproteins

[0166] rCedV chimeras have been developed that comprise the coding sequences for wild-type rCedV F and G glycoproteins, as well as sequences encoding soluble G (sG) from other henipaviruses, including HeV and NiV-B.

[0167] Shown in FIG. 11 is a schematic representation of the rCedV virus chimeric antigenome plasmids encoding soluble G glycoproteins (sG) of HeV or NiV-B either as sG or sGtet versions. (A) The sG of HeV and NiV with the Igκ-chain leader sequence (speckled) and the location on the N-terminal end of HeV and NiV-B sG ectodomain sequence are diagrammed. (B) The sGtet of HeV and NiV with the Igκ-chain leader sequence (speckled), the GCNtet peptide domain (hatched), linker domains (striped), and the location on the N-terminal end of HeV and NiV-B sGtet ectodomain sequence are diagrammed. (C) The antigenomes and lengths of the chimeras are schematically diagrammed as rCedV, rCedV-HeV sGtet and rCedV-NiV-B sGtet. T7<sub>min</sub>, T7 minimal promoter; T7<sub>opt</sub>, T7 optimal promoter; HHRbzA, Hammerhead Ribozyme A; 3'Le, 3' Leader; 5'Tr, 5' Trailer; HDVRBz, hepatitis delta virus ribozyme; T7t, T7 terminator. [0168] The rCedV-HeV sG chimera virus was rescued using the virus rescue protocol and rCedV-HeV sG stocks were amplified and titered as in subsection “Rescue of rCedV Chimeras” in Example 1 above.

[0169] FIG. 12 shows syncytia induced by rCedV expressing HeV sG glycoprotein. Vero E6 cells were uninfected (Mock) or infected with rCedV-HeV sG at a multiplicity of infection (MOI) of 0.01. Images were taken 24 hours post infection (hpi). Images were captured with a Zeiss Axio Observer A1 inverted microscope using a 5x objective. Arrows indicate giant multinucleated cells (syncytia). Scale bar, 50 μm.

[0170] FIG. 13 shows western blot data demonstrating intracellular expression of the HeV sG glycoprotein in cells infected with rCedV-HeV sG. Vero E6 cells were uninfected (Mock) or infected with rCedV-HeV sG, at a multiplicity of infection (MOI) of 0.01. At 24 hrs post infection (hpi),

supernatants and cells were collected. All cells were lysed with 1×RIPA (Radioimmunoprecipitation assay) buffer containing a protein inhibitor cocktail. Total protein (L) (30 μg) and 30 μl of supernatant (S) were separated on a 4-12% Bis-Tris gel and transferred to a nitrocellulose membrane. The membrane was blocked in 5% milk in 1×PBS with 0.1% Tween-20 at room temperature. Cross reactive murine monoclonal antibody (mAb), (48D3), specific to NiV and HeV G glycoproteins was used as the primary antibody and subsequently probed with a corresponding anti-mouse secondary HRP-coupled antibody. A band corresponding to HeV sG (~62 kDa) was observed only in the lysates of infected cells. This data provides proof of concept that heterologous HeV sG glycoprotein (a vaccine antigen) can be expressed and produced from a HeV sG encoding rCedV, and this rCedV-HeV sG could serve as another version of a live-attenuated vaccine for HeV and NiV.

[0171] FIG. 14 shows rCedV does not interfere with expression of HeV sG glycoproteins as determined by western blot. The first generation of rCedV-HeV sG chimera did not appear to produce high levels of secreted sG while high levels of sG was detected in cell lysates. Here, duplicate wells of confluent Vero E6 cells were untreated or transfected with 1 μg of either pcDNA3.1-HeV sG or pcDNA3.1-HeV sGtet, a second generation sG that maintains a native-like tetrameric (tet) structure (4, 22). At 4 hrs post transfection, 1 set of cells was infected with rCedV at a multiplicity of infection (MOI) of 0.01 and the other set remained uninfected. At 24 hrs post infection (hpi), supernatants and cells were collected. All cells were lysed with 1×RIPA (Radioimmunoprecipitation assay) buffer containing a protein inhibitor cocktail. Total protein (L) (20 μl) and 20 μl of supernatant (S) were separated on a 4-12% Bis-Tris gel and transferred to a nitrocellulose membrane. The membrane was blocked in 5% milk in 1×PBS with 0.1% Tween-20 at room temperature then probed with HeV sG polyclonal rabbit serum followed by a corresponding anti-rabbit secondary HRP-coupled antibody. A band corresponding to HeV sG (~62 kDa) was observed in the lysates (L) and supernatants (S) (boxes), of all samples except in the untreated and rCedV only infected cells. These data show that sG and newer versions of tetrameric sG (sGtet) can be expressed and secreted in the context of replicating rCedV, and second generation versions of rCedV-HeV sGtet or rCedV-NiV sGtet viruses could also serve as live-attenuated vaccines for HeV and NiV.

#### Example 7—rCedV Chimera Expressing Fusion F or G Surface Glycoproteins

[0172] rCedV chimeras are created that express chimeric henipavirus F or G envelope glycoproteins, wherein the ectodomain and transmembrane domain of a non-CedV henipavirus (such as NiV, HeV, GhV and MojV) F or G is fused to the cytoplasmic tail domain of CedV F or G, or the ectodomain of a non-CedV henipavirus (such as NiV, HeV, GhV and MojV) F or G is fused to the transmembrane domain and cytoplasmic tail domain of CedV F or G.

[0173] All patents, patent applications, and published references cited herein are hereby incorporated by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention

encompassed by the appended claims. The claims are intended to cover the components and steps in any sequence

which is effective to meet the objectives there intended unless the context specifically indicates the contrary.

TABLE 9

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites		
Virus	SEQ ID NO:	Sequence
CedV Isolate CG1a Genbank: JQ001776.1	1	<pre> ACCAAGACAAAGGAAGTCTAGTCTCGGATAAATCATATTGTATGATTAATCTTAGGAT CCCGGTATCTAGAATCTGGATCTGGATTGGTTAATTGAATTCGATCGTTATAAATT AGAAAGGAGATTACTACTCAAATGCTTGACATTTCAATGAGACTCAATCATTTAGAA ACTATCAGTCACAATCTAGGCAGAGATGCCAGGGGCACTGGCAGCAACGACTACTTGGACAA CTAACAGTGAGGATCTTGTCTTCAAGCAGATAAATATCCTACAGATGGCGTTAACAC TATTCTTGATGGATGTCGTGAGGTACCTGCCCTCCGCAGAGTCTATGAAAGTGGGTGCTG GGATATCCTGGTATCTATGTATGCTGAAAAACCCGGGGCTTGTGAGAGCATTATTGA ATGACCGAGATGTTGAAGGCAATCATGATGTTATGGCTTGTGAGAGTATTCCCTA TAATGGAACGAAGAGGTGATAAAGCTACAGATGACATGGATTCCCTAAGAAAGATTGTTA AAGCTGCACATGATTCTAGCAGAGGAAGGGATTATTGTGATCAAGGGTCCAGGATA TTGTTATGTCAAGATATGGGTCTTGTGATGCTATTACTCCATAGAGACGAGATAT GGATTTGATCGCAAAGGCTGAACTGCCTGGCAGAGTACAGCAGAAAGAGCGAAGGAAGAA GATGGGCAAATATGTCAGCAAAGAGGGTTAATCTTGTCTTGTGATTCTCCAAAT GGATCAATGACATGAGATCCTGATTGGCGCAAGTCCTTGTGAAATTGTTGATGTTG AACTACTGATGGAAGCTAAGAAAGGACGGGGCACAAAAGGAAGAATAATGGAGATTGAT CCGATATCGGAAATACGGTGAAGGAGACAGGAATGGCAGGGTCTTGCCTAAATAAGT TCCGCTTGAGCAGAAATTCCTGCTTGGCAGTAACTGAGCTCCAGAGTGAATTGAAACA CAATGAAAAGTCTCATGATACTGTACAGAGCATAGGACCAAAGGCCCTTATGGTGT TGTGGAAGATTCAATTCTAGCAGCAAATTGTCAGGAAAGCTATCCACTCTTGGAGTT TTGTCATGGGTGTAAGGCAACACTTACAGACAGCTATGGTGTGCTTAACATGAGAA GTTATCTTGAAACCTGTCTATTAGGCTAGGGCAACATCAGCTAAACATCAAGCAGGAA ATGTTGACAAGAAATGGCAGAAAAGTGGATTTGAGATGGAGAAGACGAGTCGTGACCTAT CAGCTAATGTGAAGGATGCAAGTCAGGTAGAGATGCAATCAAATCAACATCCGAGAAG GGAAGTTCAAAATGTTGATGACATCCAGGATCATGCCAGAGTTCCTGAGGATT ACAATCTCTAAAGGATTTCTCAATATGACAGTCACATCCACCTGGTAGATAGTG CTGACAGTAGGTCTGCAATGAAATGAGTCAGTACAAACACATCTTGATGAAATTGAGAC AGAGGCTGGCAGAGAAGAAGGGAGACTCCAAGAACAGTCAGACAGCACCTCCAAAACCAC CCAGAGCAAAGATCAACCCACTGATGAGGTCTCTCATGGATTCAAATATGATCAG AATGATGGTTAAATCAACCAACTAAGGGCGCTAGAGTACCTTCAGATAGAACACTACA TTAATCGGTGAAACAAATAGGATTATGGTTGCTTAATTAACTCTTAACTCTTACTT GCAAAACAGGCAGCTGCTACACTCTGTAACCAACTCTCACAGTAAGGGCAACACGGGTCT AGAACTTATGCCCTAGATTAACCTCTATCTGTTATCTAGCTATGTTAAAATGTAATCT TCTGCTGAGGGTTCTAGCAACAGTCACATTAACTTATGGTATTTTAACTCA ACCTTTTAAATCAAATATACAAAAAACTTAGGATCCTGGTCAAACCTTTTTT GATCAAGAGTCATATTGGCTACTTCTAGGAGGACACTTTAACACAAATTGTTACAAGAGG ATATTCATCAGATGGCAACACTAACATTGAGATGGCTCTACTATCAATTTTA TACAGGAAAATAGGAAAATACAGCATTCTACGGAGATCCTCCATCAGAGGCCAC CCCAAGGTCTGGGTTAGGAGGAGAAATTCTAGGAAAGATCTGGTCTGGACCTG AACAAGTTCAAGGGGAGGACTGAGACTGAGATCACAGGGATAATGGAGATAGGGCA ATTITACCAATCTGATCAGGGAGGCGGAGTCACAGGACAATTGAGAAAGGTTCAA AATGGGGGTCAAGGATTCAGAAATTCAACATTGGGCAACATGGGCTCTACTATCAATT ATGAGCAGAGAAGGGGAAATCCGCACATGGAAAGATGGCAGCTAAAGGGG ATAATATCAGAGAAGGAACACGACAGGATAAGTACAATAATCAGTCAGTGAATTAC TGTCTGCTACAACCCTTCTAAGAACGATCTCAAGAACGATGAAAGTACATCAGTGT CAAATTGCGATTTGAGGAACTAACAGGAGGAACTCTGGCAGGAAACCTTGGACCCACCT CCCAGTCGAAGGACACCAACACCACAGCACAAACAAAATGACCATCGACCCAGATG ATGATTATAAGAATAGAAGATCCAGTGAAGAACACTGAGCTCTGATCATGCCACACAA TGGAAAGACAAACAATTATCCGGCAGCAAAAGGAAGAATGCAATTGAGGCCACCA TATACTGTCAGGTTGGCTCAAACACAGGAGGTTCTCGGGAAAAAGATTATCCACTCC TCAAGGACAACACTGTCAGAAGCGTCAGGGCAGTCCTAGAACACTGCTCAACCC CTGAGGCTCTGCGACCAAGACACAACTGAGTGAAGAACACATGCTGAGCTTC CAAACACTGCTCACAGAGATACAGCAGTCAGGAGGATAACATGATCTGCTC TTGAGGAGCATTAGAGGAGATGGCTCTGAGTAAAGGAGATGGAGCTAAAGGAG CAAGGATGAAATGAGATAGAAGGAGGAACTCAAGAACGAGGAAATGAGATGAA GTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG CTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG GTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG GGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG ACTACGATGAAGGGGAGGAGACTATGAGGCTATGCCGTAGATAGGTTTATAACACATT CAGGTGAAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG AGGGCCAGGTTGGAGAATTACAGCAATGAGATCTCATACTCTATTCTAGATTAGAAACTA CTAATAAGTTGCTTATTGACATATTGAGTCAGCTAAAGAAATGCAAAGGTTAGGAA AAGTGGATAATCTTGAGAGACAGATGGGTAATTGAAATGTTAACCTCACCTTGGAGG GTCAACCTATCTCTGTAATGATTGATACCCGTAAGGATAAGAGCGAAAAGGAAATCC CTAAAAATCCGGACCTGGAGACCAATACTGGGAGAAGCAACACGTCGTTAATGATGTTA TCGACCTAGACCAATTACCCGATATAAGGCTCCAAAGGTTCAAACCAAGTGGATCTGGAG </pre>



TABLE 9-continued

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites		
Virus	SEQ ID NO:	Sequence
		ATATACATATTATCCTTTCCGTGTTATTGATCATTAATAATGCTTCTCAGC TCCAAAAAAATTACTTAGAACACTCAAAACAAACAGGTGATAAAATGAACAACCCAGATA AGAAAATTAAGGTCAACTTCACCCCTTGAAGATTAGATAAAGGTCAAAGATCTCAATA AGTCTTATTATGTTAAAACAGAATTATAACGTTCAAACTTATTAAAGGTCTGC ACGATATCAAGTTGTATTATTGTATATTCTCACTGCTAATTATCATTACAATAATCA ATATAATCACAAATATCAATTGTATAACTCGTCTGAAAGTACATGAAGAGATAATGGCA TGGAAATCTCTTAACTTACAATCTTCAAGATAGTCTCTCATCTTACTAACATGATCA ATACAGAGATAACTCCTAGAATAGGGATTAGTTACAGCACTCTGTGTTACTCTCTT CATCTATCAATTATGTCGGGACTAAGACAATCAACTGGTCAATGAATTAAAAGATTATA TAACCCAAAAGGTGCGTTAAAGGTGAAATTAGGTACATGAATGCAACATAAGTT GTGCTGATCCCCAAAATTAGCAACATCGCAATGTACAGCACAATGCTTATGCCGAGCTTG CTGGTCACCTCAAGATAATTGTAAAAGGTGATTCAGGAACTTAACTGAAGC AGATAGATTATGTAATACCAGTGCAGCAAGATCGGTCTATTGTATGAACAAACCTTAT TGGATATTCTGATGGGTTTTTACCTACATACATTATGAAGGAATAATAGCTGTTAAA AATCAGATTCAATTAAAGGTGCTGCTGACATGGTAAAGATAGTTGACAGGGGTGATTATC GACCATATTATCTATTATCAAGTCATTACCATCTTATTCAATGCAGGTAATAAAGT GTGTACCTGTGACTTGTAAACCAAGTCATCCTTGTATTCTGTATATCTCAACAAACACTA AAACATTGGACAAATTCAGATTACTCGTCAGACGGACTACATAACATATTCAATGGCA TAGATCGTCCCCAAAAGGAAGATTCCCATTAACAAATATGACAGCAGACAATCGTATA TCCATTTCATCTCAGTGGGGAGGTGATGTTAGGTGAAGAATTATTATTCTG TTACACAGTCATCAACTGATGATTACCGCATGATTATGAGAGTTCAACTGTT CAGTCCAACCGTAAAGTCTAAAGGAGATATGCTGAGTCATTAAGATCTCCAAACG ACTCATCGCATACTAACTTAAACGGATCATGATTAAAGTCAAAACACATGACGATT TTAAGATTCAAGTTGAATGTTAACTTAACTTAAACAAACTGTCATTGGAAAG TGAGCAAGACACTGGCCAGGTCTTTTACCAATCTCAATGAGTTGGATACTTATC TAAAGGCAGGATTGTCGAGAAATGGAACCCCTTACCCGATTGGATGAACAATACTG TGATATCCAGACCTAACCAAGGTAAATGTCAGGATCATAAATGCCCGAGATATGTT ATGGAGGGACATACAATGATATTGCTCTTGTAGATCTAGGAAAAGACATGTTAGCG TTATTCTGAGATTCAAGCTTCAGGTCAGAGAATCCAGAGATTACAGTATTAACTCTA CTATACTTTATAAGGAGAGTATCCAAGATGAACTAAACACAAGAAGTACTAACAGA GCTGTTCTTCTCAGTGAACCTGGGTATATCAGTATTAGAAACAAACAGATTAA ACGGCAAACTCTATTAGGCCGAGATTATTCACTACAAATTCTCAAGTATTGTTAATTG ATGAGCTATTCTCCTACTTCATTAACAAATTAAATAACTAATATCAAATGTTGCACT CAGCTATTATAAAACTGGATCATCGACAATAAAAGATGTACAAAGATATATCGAAGA GGGTATTAAAGAAAATTAGATGGCCAGATCTTCAATAAGCAGGCCTGATTGTATC ACCGCTATTACATTAACTCAATTAAACACACTGATTAACTTAACCGAATAACT CCTATTACAGTTAAATTGACTTAATTAAATTGAGGATTTTAACTCTTATAATTGGA GCAGATCTAAACTCTCACCAGATTCTAATCCTTTATAACTAAAGAACAAATTCTA AATAATTGGATGACGTACAGGAGAACGCTGAAAACAAATTAGTTAGAAGGAAGAAC TTTACCGAGATGGAAAGTGTACTTTGATATACTCTTAGGGACGTACTGTACCCAGAA GTCTTGGACACTCTAGTGGCGTAAGCTTACTCTCTTGTAGTATGCAATT TGACTCATAAACCAACCTCATGAAGATCAGACATTGCTGACTAATATAATGTCATAAAA AGAAGAAGATAAAAGTCCTAATAATCCTAAACATCTTATTGGAAATGAGGTAAATA AGGAGATTTCGATCTTAAAAATTATTACCATGTCCTTATCCAGAATGTAACAGAGATT TATTCTTAACTCTGATGACAATAAGCTTACACTCAGTAAATCATGGATAATTCTA ATAAAACTGTTGATGGTTAGAGAGGAAACTGAGTCGCTTAATTGCAATGTTAGATAATC AACTTAAATGCAACCTCTTCTCATAAATAATTCTGAGATGGATCGGAAGGGAAAAGAAC ATCTTGCTTCCCAGAACAGCACAATTGATGATGTAAGACAGCAGAGACAGCAG ATTTCCTAAAGAATTCAACTAGAGAGGGAGATCTCCAAAACACCCCTGATGCCGTCTA CACCTGAAAACAGTGCCTAAAGCTTGCATAGAGACAACACAGACAATATGCCAACAG GCCATAGTTGCGACATCTGAAAAAACTTAAATCTGAGAATATCTGGAAAGGATCTTGT GGCTAGACTCGACAGGATTGGTTCTAAACGATTTCGCAACTTGGGAAGGATGTAT CATGTAAGGGCCATCTGCACACAGACAAGAACACCGATAATAGTCTCTGACACTCGAT ATATCCAAAATCATGAATCTAAACGATATTTCCTTAAAGGAAAGAAAAATTCTGCA AACTTCCACCGTCTCGGATAATTAAACCAAATCATGGTAAATTGAGCTTAAATCTGCA CTTCTCTTGGTTACTGTCAGACTTAACTGAGCTTACTGAGCTGCCAGAAGGAGAACTACA AAAGGAAAACAGAAAATTGGGAAATTATCACATGTTAAAGGTTCTGAGTATAAGTTGA TACTCAACCGAGACTAGTGAATATTGAGGAAAGACAGCAGTGGATACTCAGATCATA AAAAAAGGAAAACAGATGCTACTTCTAAACTCCGAAATGGTCTTATGTTCTCGGATG TAACTGAGGAAAGTGTGATGTTGCAATGAGATTGAGACAAAAAGTACAAAACACTC TAGAGAAAAGGCTTGAATTATGTTCTTATAGACGAGTTATTCTCTTATGGAA ATAGAGTGTATAATATTATCATGCTTGGCCTTGTACTCTCGCGATATTACAGGTTA AGGATGACTCAAGGTTGTGAGAGGTCATTGATGATCATGTTAGGTGACCTCTTCG AAGAACCTTCGAGAGTCCAAGAACACTACCCGGAGAGATGAGATCAAGAGATTGCAACGACC TAATAATGTCATGACCTGTCGGGACATTCTCATTTAGTACAGCAATTCTCTCATTCTTA GGACTTCCGAGATCCAATTGAAACGCTCAAACCTGAGCAGCAGGAAAGTTAGAGGATC TGTGAGCAGATAAAATCTTGTAGTACGAACCTTACATGAAAGGTGATGCGATTCTGTG CTATAATCATAAATGGATTAGAGATAGACATGGAGGAGTTGGCTCCTTGTATCTTC CAAACATTGTCAAAGAACATAATCTCTAAACATACAGGTGAAGGGTAACCTATG AAAGTAGCAATAACAAATTGGAGATCATTTGTCGGGTTAAAGTTCAATGTTATGGTC

TABLE 9-continued

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites		
	SEQ ID NO:	Sequence
Virus		TCAATTAGACAATGATCTCAGCATGTACATGAAAGATAAAGCATTATCACCTTAAGGG ATCTTTGGGATTACATCTATTCACGTGAAGTAAATGTCCTACCAACCACCTAGAAAACAAAA AATCAAGGAGATTGGTGAGGTTCTGTTGATGATCAGGACTTGTGATCCCGTTGATATGAA TAAATTATGTTCTGACCCGGAGAATATCTCAGAGATGATGATTCAATGCTCTTATAGTT TAAAAGAGAAAGACCAAAACAGTTGGCAGGTTGTTGCTAAGATGACTTATAAAATGAA GGGCTGTCAAGTTATTGCTGAGAATTAAATGACATGGGATTGGGAGATATTCATG AAACGGGATTGGTAAAGGATGAGCTAGCAGAAATCAGTGTCAATTGCTATAT CAGGAATACCAAGAGGAACAAAACAACAAATCGACGAAACACAAATCCACGAAAGCA AGATCGAGAATAAACATTCTTAAACATCCAGAATCGATCATTGAAAGACGGATA ACCCATACATAGATTAACTTGTAAACCCAACTTTCTTATCCCCAAACTGTAACCCCA AGTATAACCGTAGAATTAGAGACAAATAGGTATATTCTCTGTCAGAAACCCAAAGCA TGATTAGAGAACAGAAAAGTCAGAGAAAGTCAAATAAATAGCTAGATACTGGCAGTG ATAATGAGAGCAAGGAAAGAGATAGATGCCGCAAGTACAAATCACGGACAAACCAA ATCCACACATAATCTCAAGATCAACCCGGAACTCTGTCAGAAGAACAAAGGCAAGAAG GAGCAAAGTCAGATCTCACAGAACGGCATGAGTTCTGGAGATGCACACACTCTTAAACC CGAGTAAGGGCATATCGAACAAATCTGAATTGGAAAGAGTTCACTTCAAACCCCTG GATTATATCACAAAAGAGAAAAGAGGCAAAACTTATAATGAATCCCATTCACTGGGAA AGTCTCTAAAGGGATGAGAAGAGATACGATGTCATCAGTCATTCTGACAAACAGATT TACGAAAATTCTGTTAAATGGGAGATGAATCAATGGCATTGGTCAAGAAGGATGG ACGAAATCTATGGTTCTGGTTCTTAAATTGGATGCAAGAACAGTACAGCAGTCAG TGTATATGTTGGGACCTCATTGCCCGCTCTATCAATGAACATATCGATCTAAACG ATTACCCGAAAGAGACATATTATACATCATCGAAAGGGGTATAGAAGGATACAGCC AAAACTGCGACAATAGCGACTATCCCTTCTATCCCTCAGTGTCTGACAAACAGATT CCCGGATAGCGCAGTTGACAAAGGTGACAATCAATTGCAATTACACATAAGGTCC ACCCTCATTGCTTACAAAATGAAGAACAGTCTCTGCAATCGAGGCAAAAGGATATT TTCAAGGTTACGGCACAACATGAAGGCATTAGGGCATGAATTGAGGCGACCGAGACTA TCATTAGTACTCATTTCTCATTTCAAGAAAATTCACATGAGCTTGTGTTTAT CACAATCTGAAATCATGGCAAGGTGTATTGGTCAAGAAACCTTGTGATGAA CTAGAGCAGCATGCGATAATATCAGCACAAACATTGCAAGGCTATTGAGATGGTATA GCAGGAGATCTGGTATCTGATAATGTTCTTAAACCATCAACAAATTATATCAT TGAGTTTAAATAAATGAATGACAGATGACATAATCAGACGGTTAGAGATAATC CAAACCTGGGATCAAACATGCCGATTAATCCCGCCAGCTGGGAGGACTCAACTATATGA ACATGTCCTGATTGATGTGAGGAAATAGGGGATCAGTCACAGCATCGATAGCAGATG TTAAGAGAATGATTCTCGTGTGACTACCATTGGAATACTCCAAATATCATGTTG AAGAAGGGTGTGACTTGGGACTGGTGTGATTCTGATCCATACTCCATCAACCTAA ACGAGACTCAAACATACAAAAGTTAAAGAACATAACCGCAAGAGTGAATACTAAGGA ATTGGGTCAATCCACTGCTCAAGGTCTATTTCATGAAGGTGCTTATGAGGAGGACACTG AATTAGCAACATTCTTGGACAGGAGACTCATCTTACACAGCTGGTCACGAGATCT TAAACAACCTCATCACAGGCAAGGAGAAGATCTGGGCTTACTCGGATACCCAAAG GATTGATAAGAATTGGCATAGCAAAGGGAGATTAACTCAGAGAACATTATCTGAATT CCAATTATGATTGAACAATTGGTCAATGAAATATGTTGAAGAACAAAGAACAAA ACAGTGTATTCCCTGTCAGCTGCTGTGACTTGCATAGCTTAAAGAGCAGGA TGTTGGAGGAAATTGGCAAAGGAAGATAATATGTTAGAGGATCCCTGATCCAATAG AAGCAATGATTGGCTTCTCATCCGGAGTGAAGATTTGCTACTCTGATTGAGGAA GCAAAACTATACCTGGTTTCTCATACAAAGGTGACTAGTTGATAAGATTGATAAAAG ATCACGCATCAATAAGGGTACCTATGTCGATCAACTACCGAACAGATCAGAGATAA AGTTAGGATCCTGAAACATCCAGGAAATCCTGGAATATGCTATAAGACTCGCAACTG TGTACACTGGCATTGGCACAAGTGTGATGCTGAATGGTGGGAGGCTGGTACTTGTCTA ATCAACGAGCAAATATACCTTGTGATGCTGAAACACCTTATATCTACTTCAA CGAATATTGCTCATAGATTACGAGACCGATAACACAGTTAAACAGCAGTCACATCTC TTAACAGAGTATCGGGCATGTAACAAATTGTAACGATAACATGAATTGGTGAACG GGGTTAAATGGGATACCAACATTGATTATCAACAGTCATGCTTGGGCTTCTGCT TGGAGAGTTATTCGAAATAGGGAAATGCAAAATAGTTACAAATATGTTGATCATTAC ACGTTCAAGAACATTTGTTGTAAGGGCTCTGAATGATTACCTTATACACCGTCACAC ATTCAGTGCACAAATTATCAGAACAGTTAGAGATAATAGGTTAATTGATCTCCTCAC TATTGAGATTGAGCTAGGATAACATTGCAATTGAGAACACAAAGGAGTTGGGAAAT TTCTATTGGGATACAAAAGAACACTTGTGAGAAATTAGCTCAAAGTTACGGATTACAG TAACGGGATATTGACAAAATCTGATAAAGTCATATTAAAGACCAAGAACAGTATAGATG TTGATGATAATTAAAGACACTAATAACTGAGTTTTTATTAGTAGACCCGAAATTTG CCGTAATTAGGATGCTATATCAATAAATGGTCAATTGATATTCTACTTTAACAGAC CAAGAGGAGCTATAGCATGAGATAACTGACTGATCTTGTGATAACTCTCTC ATGTTTATGAACTCTACTAATGTTATCTCATCCAGGTTATGAGAACATTCACTA ATGCCGGCTACTAGTACCGAAATACGGTCCTACCTTACAAGTCAGGATTCACAAAAGA TGGCGGTAGATTTCATAATAACAGCGTATAACACATTTGACCAATTGGTGAATAATA ACAAGTTTCAATTCTAATACCTGAAACAAGACCTGATATACTTGAATTAGAAAAGACA TCACTCATGCAAGGCAATTATGTTGATCTCGATCTTACTGCTACTCTTCAACGAAAC CTTGGATAAGGGCTTACACCAACAGAGAACATCTCGTCACTGGAGGACTTCAGGCC ATTGTGTTGCTAATGATCAACAAAGTCGGGCTGGAAACATAACGCCCTTAAGAGTTACA ATCTCCCTGTCATGACCAACATCAGGAGAGGATAATAAAACAAATTAGAATCCGTC AAAGCAATGAGCCTATTGATCTGGAAAGATATTAGGATGGTCAAGACCCCGATTGTA

TABLE 9-continued

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites			
Virus	SEQ ID NO:	Sequence	
		ATAAACCTATTGAGTTTGAGCTAGTGAATTGGTACACAATTATAACCTTGAAGAAA TTCTTAATCAATGTCTCAGTGTAAATGAAACATTGACTCCTCACAAAGTAACA ATACTGAAAATCATTTATTAGAAGGGTAGCTGAACTCTACTTCATCTTAAAGCAC TATCTTTAACACCTGTATTAAAAGATATCATCAACAGAACACTAATAGGTGTTATAG GAGAAGGATCAGGGTATGTATCTTACAGAAAACCTGGGGAGACAATATGCT TCTTTAATCGGGAGTTCACTGAAATGAGGATCTGGTCAAAAGGGAAACAATATTAC CGAGTGAATACAGTATCTGTGAAACAAGGGATAAAAAGAAAACCCCTCACCAGGGCATG TTATACCACTATTCAATGGAAAGACCAAGAACACATGGTAGGGCAATGATGATTCTTC AGTATATATTGGAACATACTATAATAGAGACATCGGGCTTGTCACTCCGATATGGAAA CAGGAATAGGGAGGATAATTACTATCTTAAATGAACATGCACATCTTATAGCACTGA GCCCTACAGTAAATGTGATGTTCTGGTCAAAAGGGAAACAATATTAC CGAGTGAATACAGTATCTGTGAAACAAGGGATAAAAAGAAAACCCCTCACCAGGGCATG TTCCACCGTATAGCAATTGGAATCAACTGAATTTCACCTGATTGCTGCAAAAAGTA TACCCGGACCTATCACACCCAGTAGAGCCATCCAACAAACGCAAGCAACTTAGAGAAG AGGATAATAGTAACTATAATATCCTCAAATAAAATCTTGTCAAGAAGAATTAA TCAAAACAGTAAAGAAAATCGAAATCCATCTTGTAACTGTCTATCAACTTC CAAAGGATGATAAATATTAAATGAGTGTGGGTTCAAGCCAATGGCTGATATGATAC GTAAGAGACGGGCTATGACATAGGTAGCAATGAGAATCTCGAGATGCTTAAATCA AGTGTGAGATGAGCTACCTTATGTGATGTCACAAATAAAAAGAATTTTAA ATCCTTATCCAGTCTACAAAGAACCTGATGTTAAATCTGATGGATAAAATATGCAAGA AAAGTCACCTTATACACCTTAATCATATCATGAAAGGATCCAATCAATATTGCTGGAAA TTAAATCCCAAATAAGAAGGATTGTCATACTGATTGAAAAGTAAGGTTTACAA AACTTATCCCAAAGGGATTAGAGAAAGGGTGACTCAAAGGGATGAAGAGCATATGGT TCACTAAACTAACCGATCAAGGGTAAAGAGTGGTGAAGGATGATGATCTACATCGTGA TAATAAGCACTTACACACATCCAACCTGTCACTTAAACACTTAAATACAATAACT TGTCACTGAGATTAAGAAAATTATAATTCCCTTTTAGGT	
rCedV Derived from isolate CGla Genbank: JQ001776.1 Mods. shown in bold & underlined F and G coding regions underlined	2	ACCAGA <u>AAA</u> AGGAAGTCTAGTCTCGGATTAAATCATATTGATGATTAATTCTTAGGAT CCCGTATCTAGAATCTGATCTGGATTGGTTAATTGAAATTGCGATCGTTATAAATT AGAAAGGAGATTACTACTCAAATGCTGACATTTCATGAGACTCAATTTAGAA ACTATCAGTCACTAAGCAGAGATGGCAGGGCAGTGCACAAACGACTACTTTGACAA CTAAAGTGGAGATCTTGTCCAGCGAATAATAATCCTAACACCTCAGATGGCTTAAAC TATTCTTGATGGATGTCAGGTCACCTGCTCCAGACTGCTATGAAAGTGGGCTG GGATATCTTGGTATCTATGTTGCTGAAAAAC <u>AGGGCTTGTGAGAGCATTATTG</u> ATGACCGAGATGTTGAAAGCATATCATAGATGTTATGGCTTGTGAGAGTATTCC TAATGGAACGAAGAGCTATAAGCTACAGATGACATGGATTCCCTAAGAAAGATTGTT AAAGCTGCACATGATTTCAGCAGAGGAAGGAGTTATTGTTGATCAAAGGTTCCAGGATA TTGTTATGTCAGATATGGGTCTTGTGAATGCTATTACTCCATAGAGACGAGATA GGATTTTGTGCGAACAAAGGCTAACTGCCAGATACAGCAGAAGAGAGCGAAGGAAGAA GATGGGAAATAATGTTGCAAAAGGGTTAATCTTGTGATTCTCACAAT GGATCATGACATGAGATCCCTGATTGGCAAGTCTTCTGTTCTGTAATCATGGTT AAACTACTGATGGAAGCTAAGAAAGGACGGGGACAAAAGGAAGAATAATGGAGATTGAT CCGGATGGGAAATTCAGTGGAGAGACAGGAATGGCAGGGTCTCGCTACAATAAAGT TCGGTCTTGAGGCAAAATTCCCTGCTTGGCACTTATGAGCTCCAGAGTGAATTGAAACA CAATGAAAAGTCTCATGATACTGTCAGAAGCATAGGACCAAAAGGCCCTTATGGT TGTGGAGATTCAATTGACACCAATTGTCAGGAAGCTATCCACTTCTGGAGTT TTGGATGGGTAGGACAACACTATTGACAGAGCTATGGGTCCTGAAACATTAAACAGAA GTTATCTTGAACCTGCTATTAGGCTAGGGCAAAACTCAGCTAACATCAAGCAGGAA ATGTTGCAAAAGAATGGCAGAAAAGTAGGATGACAGAAGACAGATCTGCACCTAT CAGCTAATGTAAGGATGCAAGTCAAGGTAGAGATGACAATCAAATCAACATCCGAGAAG GGAAAGTTCACAAATGTTGATGACATCCAGGATCATGCCAGAGTCTCTGAGGATT ACAATCCTAAGGAGGTTCTCAATTGACAGGATCACATCCACCGTAGATAGTG CTGACAGTAGGCTGCAATGAGTCATGACAACACATCCCTGCTGAATTGAGAC AGAGGCTGGAGAGAAGAAAGGGACTCCAAGAACAGTCAGACACACCTCCAAAACAC CCAGAGAAAAGATCAACCCACTGAGGATCTCTCATGGATTCCAATAATGATCAG AATGATGGTTAAACCAACTAAGGGCGGTAGAGTACCTTCAGATAGAAACACTACA TTAATGGGTAAACAAATGAGTTATGGGTTGTCTTAATTATTATCTTACTT GCAAAACAGGCAGCTGCTACACTGTAACCACTCCTCACAGTAAGGGCAACACGGGT AGAACTTATGCCATGATTACCTCTATGTTATCTAGTATGATTAAATGTTAACT TCTGCTGACGGGTTCTAGCAACACTTACATTACTTATGGTATTGTTAATCA ACCTTTATAATCAAATATTACAAAAGGTTAGGATCCAAGTGGTCAAACATT GATCAAGAGTCATATTGGTCACTTACGGAGACACTTTAACACAAATTGTTACAAGAGG ATATTGATGAGGAAACACTACAATTGATGAGATGGCTCTACTATCAATT TACAGGAAAATAGGAAAAAATTACAGCATTCTACGGAAAGATCCTCCATCAGAGAGCCAC CCACAAGTGTGAGGGTGAAGAGTGGGAGAATTATTGAAAGATGCTTCTGGACCTG AACAGTTCAAGGGGGAGGATCTGAGACTGAGATCACAGGGATAATGGAGATAGGGCA ATTTCACCAACTGATCAGGGAGGCGGAGTACAGGACAAATTGAAAGAAGGTATCAA AATGGGGTCAAAAGATTGAGAACTACAATGGACCAATGGTGTACACGATTCTCT ATGACGAGAGAAGGGAGAATCCGACAATGAAAATATGACCGCAGCTCTAAACACGGG ATAATATCAGAGAAGGAAACACGACAGGATAACTACAATCATGTCAGTGAATTAC	

TABLE 9-continued

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites		
Virus	SEQ ID NO:	Sequence
		TGCTCTGCCTACAACCATCTTCAAGAACGATGTCATCAAGAAATGAAAGTACATCAGTGT CAAATTTCAGTGTACAGGAAATAACTGAACTCTGACGCAAAACCCCTTGAACCCACCT CCCAGTCGAAAGAGCACCCAAACCACACAGCACAAACAAAATGACCATCAGACCGATG ATGATTATAAGAATAGAGATCAGTGAAGAACAAATGTGATCTGATCATGCCACACAA TGGAAAGACAACAAACATTATCCCGGCACCAAAAGAAAAGAATGCATTGAGCGAACCCA TATACAGTCAGGTATTGCCCCTAAACACAGAGGGTTCTCGGGAAAAGATTATCCACTCC TCAAGGACAACACTCTGTCAGAAGCGTGAGAGCCAGTCATCTAGAAAACATGCCAACACC CTGCAGGCTCTGCCGACCAAGAGCACAAATCAGATTGAAGAAAACATGCAGTTCACCCCTC CAAACACTGTCACAGAAGATAACAGACGATGAACACAGAGGATAACAAATGATTCCATGCC TTGAGGAAGACATTAGAGAGATGGTTCCATGCTAAAGAGATGGAACCAAAGATATAAGA CAAGGATAGAGATAGATGAGCAGCAATCAGAAGATAATAAGAAATCAAAATAGAA GTCAGGATCTAGAATCAGCGGTTAAGATCAGGGGAGAAGAGATCCATCAGTAGACCTCG GGATTAAGAAAAGAAGGAAGGGCTAAAGGCCGCAATGCAAAAGACAAAAGAGCAATTGT CTATAAAAGTGGAGAGAGGATGGATGTAACGACAGGATATGTCAAAATTGGAAGATG GTACAGAAGAAAATGATATACTGCGGATGGAAGTATGGAGTATGGACAAACAGACTACTG GGTCAGGAGGTCCACAAGGATGGACTCTGATGATGTCAGGTTTACAAACATT ACTACGATGAAGGGGAAGACTATGAGGCTATGCCGTAGATAGGTTTACAAACATT CAGGTGACAAAAGGATAGATTGATCTAGATGCTAACAAATGTCAGTATGACCTCG AGGATGACAAAGGATGAAATATGGAATACTGTGAATGATTACCTCGATGGCAACAA CTAATAAAGTGTCTATTGACATATTAGATCTAGCTAAAGAAATGCCAAAGTTAGTTAGAA AAAGTGGATAATCTTGAGAGACAGATGGTAATTGAAATGTTAACCTTACCCCTTGAGG GTCACCTATCTCTGTAAATGATATTGATACCCGTAAGGATAAGAGCGAAAAGGAATCC CTAAAAATGCCGACATGGTCAAGGACCAAACTGGGAGAAGCACAACAGCTGTTAACAGT TCGACCTAGACCATTAACCTGATAAGGCTTCAAAGGTTACAAACAAAGTGGATCTGGAG ACAGACAGTACATGGCTCTAGAGAGCAATTTCATAATGATGAGTACAATTTC CTCCATACCCATCAGGGACAACTCTATTGCCAGGTTAACAGAGATGACAAAACCAATG CTTCATCGTCATCCAGATGACACGGACAGTCTCAATCTGCTCAAATAATTTC GACAGAACATCCATGTAAGGATGAGGCTACTGTCCATAACTAGAACACATA ACACTGTGGGAAATTGAGATGAAATATGGAATACTGTGAATGATTACCTCGATGGCAAC TCTGATTAACAGATATTGAGATTGATCTTAAACAAAGTAATCTGATAATGATAG TATGGAATAAGAATACTAAACACTATTGACTCTGTGAATGTTAACAGAGTGTCTAA TGTCAAGATTGAGGATGAAACACATAACTAAACTGTAATCTGATATTCTCTTATTCCATT TCTCAGCATTAGAAAAAAACTTAGGATCCAGACCGTGTTCAGATTGCAAAGTCAAAAGGGATCT ACTATCAGGTGTTGGAGCTAACAAATAGCGGAGTCTGTCATAACAAATAGCCTCAAGAAG TTTGAAGAACATGTAAGGATCTGGATCGTCAGATTGAGGAGGATTATAATGGGGATG ATAAGAGTCTGGTCAACATGATGATGACTAACAAAGTGTGTTTCAGAGAAAATCTGG GAGAAGGGAGTAAGATTGACAAGATCACACCAAGAGGTTGATGAAAAGGGAAATATGGTCC CCAAGTACGTGTTCTCAACCCAGGGAAAATGAGGAGAAAACATCGGATATCAATA TGATTTGTTATGGTTATTGAGGATGGACCTATCAATGGCTCAGCAAGAGTCTCAAGGTA ATATCAGAACACCGCTTCTTCCCTTGGGTGTTGGAAAACATTACTCGTCTCCAGAAG AGATCTTACAAGAGCTGACAAACACTAACGATCACTGTCAGAAGGACAGCCGATCAAATG AGAAGTTGGTATGGAATAACGGGCTTAAATCACCTTACCGTGTATAAGTT TGACAGGTGGCTTATTGAGGCTGTGAGGATGTCGATCAAATACTAT TAGACAGCCCCAAATACTTAGAGTATTCTCTAGATAACTAAATTAACAGATAAAG GTGTGTTATGATACCCAAAATGTTCTGACTCATCGGATAATTGATGGCCTTC ATCTGCTTGATCTCAAGATAGACACTGACATCACCAAGCAGGCATCAGAGGGATTG TCAACAAAGAAGGGAGGGATAACAGTCACTTGTGTTAACAGCTTACAGGTTAACAGAA GAGGAGGAGGAAACATTACTCAGGGAGTATTGCAAAAGGAAAATGACAAAATGAAGCTCA CATTGCGCTTACGGCACTATAGGGCTTCAAGGTTACATACAGGATCGATGGAGGATAA GTAAGGGCTCAAGCACAAGTGGCTTCAAGGAAACATTGCTACTCACTAATGGACA CAACACCATGGTGAATAACATTGCAACAAATGTTGAAATACACAAGTCACCG CTGTCATTGCGCATCTGTGCCAAAGGACTCTGTGTTAGGGACATCTTAATAGATA ATAACAGGAAAGATCTTAAATAAGTGGAGGAGTCAGTATTACCCAGTATATTGAAATAC TAATGACAACATTATTAAATCAATTCTATCTCCAGTTACTAGAATTCTAAACAAATTCT ACTGCTCAGCAACGCATCTCAACACATTGTCATCTCAATTATGATCGACGATTGTAATC TATATAGCTTGTGATCTCAAGATAGACACTGACATCACCAAGCAGGCATCAGAGGGATTG TCTCCAAATGCAAAAGCAGCTCAACATCTCAAGCAGCACAATAACACCATCAA TGTGCAACAAGAGCAATGCTAAAGTGTGAAACCAAAATCACAGATCAGAAAGGGCAC ATATTCAGTCCTGTTAAATAACCAAGTGGGATTAATAAGAGGATCAATCTTATCAT TTTAAAGGAAAACATTAGGATCCAGAGATCTTAAAGGCAATTCTTTATATTGATCT TGAGGGCTAGGAGTCAGCTTAAACAGAGGTTGGAGGACACAGGAACATAAGGTT GAAATCACCTTAGCTCAACATCTAATCAATCAAGCTTAAAGTCACTCTAAACTGTATAC AACCAGCAGCGTAGAGAGTGGATTTCGGCACCCCTGGAACTGAAGGCTTACT GCCTGCTTCAATCAGAAATTACATTACCTTACCCATAAAAGTAATCTCAACATGTCTAAC AGAGGACAACAGTATTGATCATATAAGCTTACGTTTTTTGATAATGCAAGCAA TTGTAGGGTTGATTTGATAAAATGAAATAAAATAGGTGTGGTGTCAAGGGAGGACTCTAA ATTATAAAATTAAAGGAGATCCAATGACAAAAGACCTTGTCTTGAATTTACCCCTAAC TAGTGAATATCACTGATGTTGAGAGAGGCCCTGAGTAGGTACAATGAGACCGTGTAGGA GATTGCTTTACCTATACACACATGCTGGGTATACTGAAATAACACAAATGCTAAAA TGACTGGGTTGATGATCGCGGGTGTATGGGTGGGATAGCAATAGGTATAGCCACAG

TABLE 9-continued

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites			
Virus	SEQ ID NO:	Sequence	
		CAGCTCAGATCACAGCAGGGTTTGCTCTTATGAGGCCAAAAGAACACAGAAAATTCA AGAAAATTCAAGCAGCATCGAAAACACAGGACTCGATTGATAAACTTACTGAGCTG TGGGACAAGCATACTTATATTGAATAAGCTACAGACATACTCAAAATCAACTGGTAC CAAATCTAGAGCTCTATCTCGCGACAAAACAAAATTGAGTTGATCTAATGTTAACCA AGTATTGGGGATCTTATGACTGTTATTGGCTTAATATCAATAATCCTGTTAATAAG ATATGACTATTCAATTTGCACTCTTTGTGATGCCAATTATGATATAATGATGTCAG AACTGGTTATACACCTCAGGATTCTTAGATTGATAGAGAGTAAGAGTATAACAGGGC AAATAATTATGTTGATGGAAAATTGTCAGGTTGATCAGGACATATCTACCTACCC TAATTGAAGTACCTGATGCCAAATATATGAGTTCAACAAAATACTATGAGTAGCAATG GAGGAGAACTCTGTCACCATACCTAATTTCATATAAAGAGGTAATTATATGCTA ATATAGATGTTGCAACATGTTATATGCCAAAGCGTAATTGTAATCAAGGATTATT CACTCCGATGAGCCAAAATTCAAGAAGCTGTTCAAGGTGAGACAGAATACTGTCCTG TTGAGGCAGTCATCGCGTCACACTCTCCAAGATTGCTTCAACAAATGGAGTTTTTCG CCAAATTGTTAAACAAATTGAGGTGTCAGGACATGGTAAGGACTATCACTCAAAACA TAACCAATTGCTAAGCATGTCAGAACACAGTACTCTGTAATGATGTCATGGTAGATAAGT TTACTATCAAGGAGAAAATTATGGGGAGAAAAGATACTAAATAATTAAATATCCAGA TAGGACCGCAGATCATAATTGATAAGGTTGACTGTGTTAATGAAATAACAGATGAACTC AACTTTAAAAGATAGTATTCTACCTGAGAGAAGGCCAGAGAATTGACTCAGTAA ATATCAGTCTATATCTCCAAAGCCTTAACTGTTCTAATATAATATCAGTCTCTCAT TTATTATATTGATTATCATGTTACTGTTACTGTTAACTCAATTGCTATATAATGCTT ATAACAAATTATAGATGATCCTGATTATTACAATGATTACAAAAGAGAACGTTAAATG GCAAGGCCAGTAAGAGTAACAAATATAATTATGTTAGGTGATTAACAACTGATAATCTAA GGATTACCTCAACTCAACTTCAACCCCTTGAATTAGATAAAAGGTCAAAAAGATC CATAAACTTAAAGGATAGTATTCTACCTGAGAGAAGGCCAAATCTTCAAAATCTTAA GTCGCACGATATCAAGTTGTTATTTGTTATCTCAGTCACTGCTAATTATCATTACAA TAATCAATATAATCACAATATCAATTGTTATAACTCGTCTGAAAGTACATGAAGAGAA ATGGCATGGAATCTCCAATTACAATCTCAAGATAGTCTCATCTCTTACTAACA TGATCAATACAGAGAACTCTCAGAATAGGGATTAGTTAGTTCAGGCCACTCTGTTACTC CTCTTCTCATCTCAATTATGTCGGGACTAAGCACAACTCACTGGTCAATGAATTAAAG ATTATATAACCAAAAGTGTGCTTAAAGGCTCTGAATTAAAGTTACATGAATGCAACA TAAGTTGCTGATCCTAAAGGAAATTAGCCTAAGTCAAGCAGCAGGCTATGCGG AGCTTGGCTGCTCAGCTTAAGGTTAGTCAAGGTTCTGAAAGCCCCGACTTTAGAC TGAAAGCAGATAGTTAGTAACTCAGTCAGCAAGATCGGTCTATTGTTAGAACAACC CTTATTGGATATTCTGATGGGTTTTACCTACATACATTATGAAGGAATAATAGCT GTAAGGAACTTAAAGTGTGCTGTCACATGGTAAAGTGTGACAGGGGTG ATTATCGACCATTATATCTTAACTGTTACTGTTACTGCTTCAATTGAGGTAA TAAACTGTGACTGTGACTGTAACCGTCATCTTGTATTGTCATATCTCCAA ACACTAAACATTGACAATTCAAGATTACTCGTCAGACGAGTACTACATAACATATTCA ATGGCATGAGATCGTCCAAAACCAAGAAGATTCCCATTAACAAATATGACAGCAGAACATC GTTATATCATTACATTCTCAGGTGGGGAGGTGTATGTTAGGTGAGAAATTATT TTCTCTGTTACACAGTCATCAACTACTGATGTTACCGTCATGTTAGGAGTTCA ACTGTCAGTCCAAACCGTAAAGGCTAAAGGAGATATGCTCTGAGTCATTAAGATCTC CAACGAACTCTCGCAATCAATTAAACGGAACTGATTATAAGTCAAACAAACATGA CAGGTTAAAGATCAGTGTGAACTGTTAACTTAAACAAACTGTCATTGGAAAGCTCTG GAAGACTGAGCAAGACACTGGGCCAGGTCCTTATTACCAATCTTCATGAGTTGGGATA CTTATCTAAAGGCAGGATTGTCAGGAAATGGAAACCCCTTACCCGAATTGGATGAA ATACTGTGATATCCAGACCTAACCAAGGTAATTGCTCAAGGTATCATAAAATGCCCGAGA TATGTTATGGGACATACAATGATTTGCTCTTGTGACTGTTAGGAAAAGACATGTTAG TTAGCGTTATTCTAGATTCACTGAGTCAGCTGAGGAGATCCAGAGGATTACAGTATTAACT CTACTACTATACCTTATAAGGAGAGTATCCAAGAGTAACAAACACAAGAAGTACTA CAACGAGCTGTTCTCTCTAGATGAACCTGGGTGATATCAGTATTGAGAAACAAACA GATTAAACGCAATTCTTACATTGGGGAGATTATCTACATACAAATCTTCAAGTATTGTT AAATTGAGTGGCTTATTCTCATCTCAATTAACTTAACTAATAACTAACTCAATTG TGCACACTGCTATTATTTAACTGGATCATCAGACAATAAAAGATGTTACAAAGATATAT CGAAGAGGGTATTAAGAAAATTAGGATCCAGATCTTAACTAAGGCAGAGCCTTGAT TGTATCAGCGTATTACATTAACCTGAACTTAAACACACTGATTAATAACTTAAAGCAG AAACTCTTACAGTGTATTGACTTAATTGACTTAATTGAGGATTATTGAGGTTATACTCTATA ATTGGAGCAGATCTAACCTCACCAGATTGCTTAATCTTATTAACTAAAGAACAA ATTCTAAATAATGGATGAGCTCACAGGAGCAAGCTGGAAACAATTAGTTAGAAGGAA GAAACCTTTACAGGAGATGGAAGTGAATTGATATCTGTTAGCGACGCTACTGTAC CAGAATGTCATTGGACAGTCTTACAGTGTGAGCTATTACTCTTGTGAGTATG CGAATTGACTCATACCAACCTCATGAAGTACAGCAGATTGCTGACTAATAAAATGTC ATAAAAAGAAGAATAAAAGTCTCTTAATATCCCACAACTCTTATTGAGGAAATGAGG TTAATAAGGAGATTTCGATCTTAAACATTACCATGTCCTCATCCAGAATGTAACA GAGATTATTCTTAATCTGATGACAAAATGCAATTCAAACACTCAGTAAACATGGATA ATTCTAAATAACCTGTTGATGGTTAGAGAGGAAACTGAGTCGCTTAAATTGCAATGAG	

TABLE 9-continued

CedV Genome and rCedV Genome incorporating modification that add or remove restriction enzyme sites		
Virus	SEQ ID NO:	Sequence
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<212> TYPE: DNA
<213> ORGANISM: Henipavirus nipahense

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 <212> TYPE: DNA  
 <213> ORGANISM: Henipavirus nipahense

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<210> SEQ ID NO 5  
<211> LENGTH: 1641  
<212> TYPE: DNA  
<213> ORGANISM: Henipavirus hendraense

<400> SEQUENCE: 5

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<210> SEQ\_ID NO 6

<211> LENGTH: 1641

<212> TYPE: DNA

<213> ORGANISM: Henipavirus hendraense

<400> SEQUENCE: 6

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tcttagtatga atcaatcaact acaacaatct aaggattaca ttaaagaagc tcaaaaagatc	1440
ttggacactg tgaatccgtc gttgataagt atgctatcaa tgatcatcct ttatgttttgc	1500
tccattgcag cactgtgcatttggtctgatc actttcataa gctttgtaat agttgagaaa	1560
aagagagggaa attacagcgag gctagatgtat aggcaagtgc gaccggtcag taatggtgat	1620
ctgttattata ttggaacata a	1641

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<210> SEQ_ID NO 7
<211> LENGTH: 1815
<212> TYPE: DNA
<213> ORGANISM: Henipavirus hendraense
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<400> SEQUENCE: 7	
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caaggttaag ttatcaagaa ttattacggc acaatggaca tcaagaaaat taacgatggg	120
ttatttagata gtaagataact tggggcggtt aacacagtga tagctttgtt gggatcaatc	180
atcatcatttgc tcatgaaatat catgataatt caaaattaca ccagaacgac tgataatcag	240
gcactaatca aagagtcaact ccagagtgtt cagcaacaaa tcaaagctt aacagacaaa	300
atcggggacac agataggccc caaagtctca ctgattgaca catccagcac catcacaatt	360
cctgctaaca tagggttact gggatccaag ataagtcatgtt ctaccagcag tattaatgag	420
aatgttaacg ataaatgcaatattactt ctcctttaa agattcatga gtgtatc	480
tcttgtccga atcccttgcc tttcagagaa taccgaccaa tctcacaagg ggtgatgtat	540
cttggtaggac tgccaaacca gatctgtcta cagaagacaa catcaacaaat cttaaagccc	600
aggctgatcatctt accaattaat accagagaag gggtttgcacactgacccca	660
cttttggctg ttgataatgg ctcttcgc tatagccatc ttgaaaagat cgatcatgt	720
actagaggaa ttgcaaaaca aaggataataa ggggtgggtt aggtatttgc taggggtgat	780
aagggtccat caatgttttat gaccaatgtt tggacaccac ccaatccaag caccatccat	840
cattgcagct caacttacca tgaagatTTT tattacacat tgcgcgtt gtccatgt	900
ggagatcccttc ttcttaacag tacttcttgg acagagtcaatc tgcgttgc	960
gttccatcataaa aaagtgtatg tggagactac aatcagaaat acatcgatcat aactaaatgtt	1020
gaaaggagggaa agtacgatataa ggtaatgcct tacggccatc caggtatcaaa gcaagggat	1080
acattgtact ttccggccgt cggtttcttgc ccaaggaccc aatttcaataa taatgactct	1140
aattgtccca taatttcatgtt caagtacago aaagcagaaa actgttaggtt ttcaatgggt	1200
gtcaactcca aaagtcatca tattttgaga tcaggactat tgaagtataa tctgtcttt	1260
ggaggagaca tcataactcca atttatcgat attgctgaca atagattgac catcggttct	1320
ccttagtaaga tatacaatttccatc ccttagtcaa cccgttttgc accaggcatc atattcttgg	1380
gatacgatga ttaaatttggat cgtatgttgc accgttgcacc ctctaaagatc acagtggaga	1440
aataacagtg tgatattcttag acctggacac tcaacgtgtc tgcgtttaa tgcgttgc	1500
gaggtatgttggat gggaaaggac atataatgtt gctttctaa tagatcggtt aaactgggtt	1560
agtgcgttggat ttttatttttttcaaa cagtaaccaa actgcagaga accctgtgtt tgcgttattc	1620

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aaggataacg agatccttta ccaagttcca ctggctgagg atgacacaaa tgcacaaaaa	1680
accatcacag attgcttctt gctggagaat gtcatatggt gtatatcact agtagaaata	1740
tacgataccg gagacagtgt gataagacca aaactgtttg cagtcagat acctgccaa	1800
tgttcagaga gttga	1815

<210> SEQ ID NO 8  
<211> LENGTH: 1815  
<212> TYPE: DNA  
<213> ORGANISM: Henipavirus hendraense

<400> SEQUENCE: 8	
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ttatttagata gtaagatact tggggcggtt aacacagtga tagctttgtt gggatcaatc	180
atcatcattg tgatgaatat catgataatt caaaattaca ccagaacgac tgataatcag	240
gcactaatca aagagtcact ccagagtgt a cagcaacaaa tcaaagctt aacagacaaa	300
atcgggacag agataggccc caaagtctca ctaattgaca catccagcac catcacaatt	360
cctgctaaca tagggttact gggatccaag ataagtcaatc ctaccagcag tattaatgag	420
aatgttaacg ataaatgcaatc atttactctt cctccctttaa agattcatga gtgttatc	480
tcttgtccga atcccttgcc tttcagagaa taccgaccaa tctcacaagg ggtgagtgtat	540
ctttaggac tgccgaacca gatctgtcta cagaagacaa catcaacaat cttaagccc	600
aggctgatcatcataactt accaattaat accagagaag ggggtttgcac cactgaccca	660
ctttggctg ttgataatgg cttcttcgca tatagccatc ttgaaaagat cgatcatgt	720
actagaggaa ttgcaaaaca aaggataataa ggggtgggtt aggtattgga taggggtgtat	780
aagggtccat caatgtttat gaccaatgtt tggacaccac ccaatccaag caccatccat	840
cattgcacgt caacttacca tgaagatttt tattacacat tgcgcacgt gtcccatgt	900
ggagatccta tccttaacag tacttcctgg acagagtcaac tgcgtctgtat tcgtcttgct	960
gtaaagaccaa aaagtatgtatc tggagactac aatcagaaat acatcgctat aactaaagtt	1020
gaaagagggaa agtacgataa ggtgatgcct tacggccat caggtatcaa gcaagggat	1080
acattgtact ttccggccgt cggttttttgcac ccaaggaccc aatttcaata taatgactct	1140
aattgtccca taattcatttgc acgtacagc aaagcagaaa actgttaggtt ttcaatgggt	1200
gtcaactcca aaagtccatc tattttgaga tcaggactat tgaagtataa tctatcttt	1260
ggaggagaca tcatactcca atttatcgat attgctgaca atagattgac catcggtct	1320
ccttagtaaga tatacaattc ccttagtcaa cccgttttccat accaggccat atattctgg	1380
gatacgtga ttaaatttgc acgtgttgc accgttgcacc ctctaaagat acagtggaga	1440
aataacagtgc tggatcttagt acctggacac tgcacgtgtc tgcgtttaa tgcgttccc	1500
gaggtatgtt gggaaaggac atataatgtatc tttttctaa tagaccggct aaactgggtt	1560
agtgcgtgggtt tttatataa cagtaacca actgcagaga accctgtgtt tgcgttcc	1620
aaggataacg agatccttta ccaagttcca ctggctgagg atgacacaaa tgcacaaaaa	1680
accatcacag attgcttctt gctggagaat gtcatatggt gtatatcact agtagaaata	1740
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tgttcagaga gttga	1815
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<210> SEQ ID NO 9	
<211> LENGTH: 1638	
<212> TYPE: DNA	
<213> ORGANISM: Mojiang virus	
<400> SEQUENCE: 9	
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ctgacataaca actataagat caagggttcg ccatctacaaa agctaatttgt ggtcaaattg	180
atacctaaca ttgatagtgt taaaaactgt actcagaaac agtatgtga atacaagaac	240
ttagtaagga aagccttaga accggtaaaa atggcttattt acaccatgtc caataatgtt	300
aagtccggta ataacaagta cagatttgcg ggtgcaatta tggctggagt tgcccctcggt	360
gttgcaacag cagccactgt tacagcaggg atagctctcc atagatcaaa tgaaaatgca	420
caggcaattt caaacatgaa gagtgcttattt caaaatacaa atgaggcagt aaagcaattt	480
caatttggcca ataaacaaac actagctgtt attgacacca taagaggaga gatcaataac	540
aatataatac ccgttataaa tcaatttgacg tggcacacaa ttgggctcag tggtaggtata	600
agactcactc agtactactc tggaaataata actgcattt ggccagctt gcagaatcca	660
gttggccaaatggatttccat tcaagcaata tcttagtgtt ttaatggcaa ctttgcatttt	720
ctgctgaaga ttatgggta tacaagtggt gatctttatg aaattctaca tagtgaatta	780
attagaggca acattataga cggttgcattt gatgcaggat acatagctt agaaatagaa	840
ttcccccaatc taacatttgtt acctaattgtc gtgtacagg agttaatgcc tatcgttat	900
aacatagacg gggatggatg ggtcacactt gtgcacagg ttgtacttac aaggactaca	960
ctgttatcaa atattgatac gagtagatgt acaatcacag atagtagtgtt catatgtgac	1020
aacgactacg ctttgcctat gtcacacag cttattggct gcttacagg agatacatct	1080
aagtgtgtca gagagaaggt agtctcaagt tatgtcccta aatttgcgtt gtctgtatgg	1140
tttagtgcattt caaattgcctt caataactatc tgccgatgtt tggatcaga tactccatc	1200
tcacaaatgc tcggagccac tttatcattt ctagacaaca agaggtgtt agtataatc	1260
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aatgttagatc ttggcccacc tatagttata gataagattt acatagggaa tcagctggca	1380
ggtttataatc aaacccatcata agaggcagaa gattacattt agaagtcaaa agagtttta	1440
aaagggggtt accccatcattt tatcactt ggttccatgg ttgtcccttataatgtt	1500
atattatgtt ccattgtgtc agtaatagca ctgttatttgtt caatattttttt aacagttttt	1560
ggtaacgtgg taaggcagca gttcacgtt actcagcatg ttccatgtt ggagaatatc	1620
aattatgttaa gtcattaa	1638

<210> SEQ ID NO 10	
<211> LENGTH: 1878	
<212> TYPE: DNA	
<213> ORGANISM: Mojiang virus	
<400> SEQUENCE: 10	
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aaaaaaatatt atggagtggaa aactgctgag aagggtgccg acagcataag tggtataag	120
gtattcatat tcatgtataac acttctgata ctgcacagggtg ctattattac aataacacta	180
aatatccca acctgacagc ggctaaaagt caacagaata tgctgaaaat aatccaagat	240
gacgtgaatg ccaaatttaga aatgttcgtg aatcttgcatt aattgggtgaa ggggtgaaatt	300
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aacctccaga ccaaattccct gcaaaaatatt gtttacttag aagaatctat tactaagcag	420
tgcacttgca accctttatc tgggatattt ccaacatcg gcccaaccta ccctccaact	480
gataaaaccag acgatgatac cacagatgtat gacaaagtgg acaccacgt taaggctatt	540
gagtaccccca agccggatgg gtgcaataga actggcgacc atttcacgtat ggagcccgga	600
gctaactttt atactgtccc taaccttagga ccggcaagttt ctaattctga cgagtgttac	660
acaacccctt cttttcaat tgggtccctcc atctatatgt tttctcaaga gattagaaaa	720
acggactgca cagcaggaga gatattatca attcagatcg ttctaggccg aatagtagac	780
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ctataactttc agatgtatgg attgtccaga aataggcaaa gtttaaggc actgtgtgaa	1140
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gcaaggtggaa aacctgtgtat aataggacag acattccgc cctcagatcc ttataaaggc	1320
tcaaatggtc ggatgtacac tataatggtc tggatcttc tccgtcatcc	1380
tggAACAGAT atcttagatt tgggataaca ccagatattt ctgttaagatc aacaacctgg	1440
ttgaaaagtc aagatccgtat aatgaagatt ttgtcaacat gcacgaacac tgatagagat	1500
atgtgtcctg aaatttgca tactagaggt tatcaagata tttttccatt gtcggaggat	1560
tcagagtatt atacatacat aggcataact cctaataatg gtggaaactaa aaactttgt	1620
gccgtacgtg actcagatgg tcataatgcata tccattgata ttttacaaa ttattatgt	1680
atcacctcag ctactataag ctgtttcatg tacaaatgt agatgggtg tattgcaatc	1740
acagaaggaa aaaaacagaa agacaatcct caacggatat atgcacatcc ttacaaaatt	1800
aggcaaatgt gttataatataa gaagtctgc acagtgtactg tgggtatgc caaaaatatc	1860
acaatcagga ggtattaa	1878

<210> SEQ ID NO 11  
<211> LENGTH: 1989  
<212> TYPE: DNA  
<213> ORGANISM: Ghana virus

<400> SEQUENCE: 11

atgaagaaaa agacggacaa tcccacaata tcaaagaggg gtcacaacca ttctcgagga	60
atcaaaatcta gagcgtact cagagagaca gataattttt ccaatgggt aatagttgag	120
aatttagtta gaaactgtca tcatccaatg aagaacaatc taaactatac taagacacaa	180

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aaaagagatt ctacaatccc ttatcggtg gaagagagaa aaggacatta tccaaagatt	240
aaacatctta ttgataaaatc ttacaagcat ataaaaagag ggaagagaag aaatggtcat	300
aatgggaaca ttataactat aattctgtg ttgattttaa ttttgaagac acagatgagt	360
gaaggtgcta tccattacga gactctaagt aagatcggt taataaaggg aatcaccaga	420
gagtacaag tcaaaggaac tccgtcaagt aaagacatag tcatcaaatt gattccgaat	480
gtcaccggtc ttaacaagtg cacgaacata tcaatggaaa actataaaga acaacttgac	540
aaaatactaa ttcctattaa caacataatt gaattgtatg caaactcaac taaatcagcc	600
cctgggatg cacgtttgc tggcgttata attgcaggag tggcattagg tggtgcagcg	660
gcagccccaa taactgccgg cattgcactg catgaagctc gacagaatgc agagagaatt	720
aatctcttaa aggatagcat ttctgccact aacaacgcag tagcagaact ccaggaagca	780
actgggtggaa tagtaaatgt cattacagga atgcaagatt acatcaatac aaatctagtc	840
ccgcagattg acaaactgca atgttagtcg atcaaaaacgg cattagacat atctctcc	900
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ggcagtgaat gggtatctct tgcctactcg tatatattga ttagaaactc atatctctca	1260
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ggcagccaa cattgtatgat gatcgataat caaacatgtt caatagtaag aattgaagaa	1560
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gtcggcaatc ctgtttcac tgacaagctg gacataacaa gtcaaatttc caacatcaac	1680
caatccattt aacaatccaa attttatcta gataagtcta aggctatact tgacaagata	1740
aatctcaact taattggctc tgcattccata tcaataacttt tcataattgc gatcttatca	1800
ttgattctct ctattataac ttttgcattt gtgtatgataa ttgtcagaag atataacaaa	1860
taacactcctc ttataaaatc tgatccatcc agtagggagga gtactataca ggacgtatata	1920
atcatccoga accccggaga acattcgatt agatcgatcg ctgcgtcaat tgacagagat	1980
cgagattga	1989

<210> SEQ ID NO 12  
<211> LENGTH: 1899  
<212> TYPE: DNA  
<213> ORGANISM: Ghana virus

<400> SEQUENCE: 12

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actctttcg ataagaagac cctcaatcaa tctaaaatca ccaagcagggtt gatattttggg	120
tttagatccc acagtgagag aaatttggaa aagcagaaga atcaaaatga tcattacatg	180

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actgtttcaa ccatgattct tgagatatta gttgtctgg gcatcatgtt taatctcata	240
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agcaatatca cagtctgaa tttaaatctt aatcaattga caaacaaaat tcaaagagaa	360
attatttccta ggatcactct tattgacaca gcaaccacca ttacaattcc tagtgccatt	420
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aagtgtgagt tcaagacacc gacacttgc ctgaatgact gcagaataaa ctgtacccc	540
ccactaaacc cgtctgtatgg agtggaaatg agttcttgc ccactaactt gggtgcacat	600
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ggattataca atagaacagc attggacgaa agatgtatac taaacccgag attgacaata	720
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atgtttcta ggtcattttta ttgcggcaca aatgctgtga actatcatc ttgtacggc	900
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gatgatgaat cttgcctgaa aagtttattac aatcaagggt cgccctcagca ccaagtagtc	1260
aactgtctga taaggatcag aaatgcacag agagataatc caacctggaa tgttatcaca	1320
gttgcatttgc ctaatacata cccaggatca aggacgag tctttggaa cttctccaaa	1380
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cttgcatttgc ggataaggcag tgcacgaact acgacaatat cgtgcatttgc gttcaacaat	1740
gaaaatttggt gtatagctgc attagagatc acaagattga atgatgcata agacca	1800
attttattact ctttcggct gcctactgtat tgcggacac catatccccca caccggtaag	1860
atgaccagggg ttcccttgcg ctccacatata aactactaa	1899

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<210> SEQ_ID NO 13
<211> LENGTH: 1638
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

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<400> SEQUENCE: 13
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ggaataacaa gaaaataacaa gatcaaaagc aatcctctca caaaagacat tgttatataa	180

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actcatgacc ttgtcggtga tgtaagactg gccggagtttaaatggcagg agttgctatt	360
ggaattgcaa ccgcagctca aattactgca ggttagcat tatatgaggc aataaaaat	420
gctgacaaca tcaacaaact caaaagcago atagaatcaa ctaatgaagc tggtttaag	480
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ttaacaatg acaattcaga atggatcago attgtcccaa atttcatatt ggtaaggAAC	960
acattaatat caaatataga gattggattt tgcttaattt caaagaggag tgtagtgc	1020
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gagaagtgtc ctcgagagct ggtggttca tcacacgttc ccagattgc actatcta	1140
ggggttttgt ttgctaattt cataagcgctc acatgccagt gtcaaacaac aggttagggca	1200
atctcacagt caggagaaca aactctgctg atgattgata acaccacctg tcctacagcc	1260
gtactcggtt atgtgtatcat cagttggaa aaatatctt ggtcagtaaa ttataactct	1320
gaaggcatttgc tattggtcc tcctgtcttt actgataaag ttgacatatac aagtcaata	1380
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cttgataactg ttaacccgtc attaataago atgttgtctt tgatcataact gtatgtacta	1500
tcaatttgcattt cattgtgtat aggattgattt acatttcatat gttttatcat tggtgagaaa	1560
aaaagaaaca cctatagcag attagaggac aggagagtca gacctacaag tagtgggat	1620
ctctattaca ttgggttag	1638

<210> SEQ ID NO 14  
 <211> LENGTH: 1644  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 14

atggctacac aagaggtcag gctaaagtgt ttgtctgtg ggatcatagt tctggtttg	60
tcattagaag ggctagggat actacattat gagaacttta gtaagatagg gctggtaaa	120
ggtattacaa gaaagtacaa gattaagagt aacccttgc ccaaggatata tgcgtatcaa	180
atgatcccta atgtctcgaa tgtctcaaag tgcacccggaa ctgttatggaa gaattacaaa	240
agcagactca caggattct ctcaccaatc aaaggcgcca tgcactgtca caataataac	300
acgcattaccat tagttgtga tgtcaagttt gcaggtgtgg tgcgttgcagg gattgcattc	360
gggatagcta ctgctgcaca aatcacagca ggtgttgcct tatatgaggc aatgaagaac	420
gcagacaata tcaataaaact caagagcago atagacttca caaatgaggc tggttgcata	480

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ttacaggaaa cagctgagaa aacagtctac gtccctactg ctcttcaaga ttacatcaac	540
actaaccttg ttcctacaat agatcaaatt agctgcaagc aaacagagct cgcatcagac	600
ttggcggtgt ctaagtatct gtcgtatctg ctctttgtt tcggaccta cttacaggat	660
ccagtctcta attccatgac tateccaagca atatctcaag cattttgggg caattacgaa	720
accttactga gaacgcttgg ttacgcgacc gaggacttcg acgacctttt agaaagtgtat	780
agcataacag gccagatgt ctatgttagat ctcagtagct attacataat agtaagggtg	840
tatTTcccA tactaacaga gatccaacag gcttatgtgc aggagttgt tccagtgtat	900
tttaataacg ataattcaga atggatcagc attgtccccgaa atttcgtgtt gatttaggaaac	960
acgctgattt caaatataga agtcaagtac tgcttaatca ccaagaaaag tgtgatttgt	1020
aatcaggact atgctacacc catgacggct acgctgagag aatgcttgac aggtccaca	1080
gataagtgcc caagggagtt agtagtctca tcccatgttc caagatttc cctctcagga	1140
ggagtcttgg ttgcaaattt tataagtgtg acatgtcagt gtcagactac tgggaggggca	1200
atatctcaat caggggaaaca gacactactg atgattgaca atactacctg cacaacagtt	1260
gttcttaggaa acataatcat aagccttggaa aaatattttg gatcaataaa ttacaattct	1320
gagagcattt ctgtttggcc accagtctat acagacaaag ttgatctc aagtcagata	1380
tcttagtata atcaatcaact acaacaatct aaggattaca ttaaaagaac tc当地agatc	1440
ttggacactg tgaatccgtc gttgataagt atgctatcaa tgatcatcct ttatgtttt	1500
tccattgcag cactgtgcat tggctgtatc actttcataa gctttgtat agttgagaaa	1560
aagagagggaa attacagcag gctagatgtt aggcaggatgc gaccgggtcag taatggtgat	1620
ctgtattata ttggAACATA ataa	1644

<210> SEQ ID NO 15  
 <211> LENGTH: 1815  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 15

atgatggctg attccaaatt ggtaagcctg aacaataatc tatctggtaa aatcaaggat	60
caaggttaag ttatcaagaa ttattacggc acaatggaca tcaagaaaat taacgtatgg	120
ttattagata gtaagatact tggggcggtt aacacagtga tagctttgtt gggatcaatc	180
atcatcattt tcatgtatcat catgataatt caaaattaca ccagaacgc tgataatcag	240
gcactaatca aagagtcaact ccagagtgtt cagcaacaaa tcaaagctt aacagacaaa	300
atcggggacag agataggccc caaagtctca ctaattgaca catccagcac catcacaatt	360
cctgctaaca tagggttact gggatccaag ataagtcaatc ctaccaggcag tattatgtat	420
aatgttaacg ataaatgca atttactt ctcctttaa agattcatgtatcgtatc	480
tcttgcgttccaa atcctttgcc tttcagagaa taccgacca tctcacaagg ggtgagtgat	540
cttgcgttccaa atcctttgcc tttcagagaa taccgacca tctcacaagg ggtgagtgat	600
aggctgtat cctataactt accaattaat accagagaag gggtttgcattactgaccca	660
cttttggctg ttgataatgg cttcttcgc tataggccatc ttgaaaagat cgatcatgt	720

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actagaggaa	ttgc当地	aaggataata	gggggtgggtg	aggtatttggat	780	
aaagggtccat	caatgtttat	gaccaatgtt	tggacaccac	ccaatccaag	caccatccat	840
cattgc当地	caacttacca	tgaagatttt	tattacat	tgtgc当地	gtcccatgtg	900
ggagatctta	tccttaacag	tacttcctgg	acagagtcac	tgtctctgat	tcgtcttgc当地	960
gtaagaccaa	aaagtgtat	tggagactac	aatcagaat	acatcgctat	aactaaagtt	1020
gaaagaggaa	agtacgataa	ggtgatgcct	tacggccat	caggtatcaa	gcaagggat	1080
acattgtact	ttccggccgt	cggtttttg	ccaaggacgg	aatttcaata	taatgactct	1140
aattgtcccc	taattcatgt	caagtacagc	aaagcagaaa	actgtaggct	ttcaatgggt	1200
gtcaactcca	aaagtcatta	tatttgaga	tcaggactat	tgaagtataa	tctatctctt	1260
ggaggagaca	tcataactcca	atttatcgag	attgctgaca	atagattgac	catcggttct	1320
ccttagtaaga	tataacaatc	ccttaggtcaa	cccgtttct	accaggcata	atattcttgg	1380
gatacgtat	ttaaatttagg	cgtatgtat	accgttgacc	ctctaagagt	acagtggaga	1440
aataacagtg	tgatttctag	acctggacag	tcacagtgtc	ctcgattaa	tgtctgtccc	1500
gagggtatgt	gggaaggggac	atataatgt	gctttctaa	tagaccggct	aaactgggtt	1560
agtgc当地	tttatttaaa	cagtaaccaa	acagcagaga	accctgtgtt	tgccgttattc	1620
aaaggataacg	agatccttta	ccaagttcca	ctggctgaaag	atgacacaaa	tgcacaaaaaa	1680
accatcacag	attgcttctt	gctggagaat	gtcatatgtt	gtatatcaact	agtagaaata	1740
tacgatacag	gagacagtgt	gataaggcca	aaactatttgc	cagtcaagat	acctgccc当地	1800
tgttcagaga	gttga					1815

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<210> SEQ ID NO 16
<211> LENGTH: 1641
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide
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ttccccaaatc taacatttgt acctaattgt gtagtacagg agttaatgcc tatacggttat	900
aacatagacg gggatgagt ggttaacactt gtgcacagg ttgtacttac aaggactaca	960
ctgttatcaa atattgatac gagtagatgt acaatcacag atagtagtgtt catatgtgac	1020
aacgactacg ctttgcctat gtcacacagc cttattggct gtttacaggg agatacatct	1080
aagtgtgcta gagagaaggt agtctcaagt tatgtcccta aatttgctt gtctgatgg	1140
ttagtgtatg caaattgcct caatactatc tgccgatgtt tggatacaga tactccaatc	1200
tcacaaagtc tcggagccac tgtatcatta cttagacaaca agagggttc agtataatcag	1260
gttaggatgatg tcttgatttc tgtaggatca tatcttaggg atggagaata taatgctgat	1320
aatgttaggc ttggcccacc tatagttata gataagattt acataggaaa tcagctggca	1380
ggttataatc aaaccttaca agaggcagaa gattacattt agaagtcaga agagttctta	1440
aaagggggta acccttcaat tatactctt ggttccatgg ttgtccctta tatattttag	1500
atattaatag ccattgtgtc agtaatagca ctatgttcaat aacagtaaaa	1560
ggtaacgtgg taaggcagca gttcacgtat actcagcatg ttccctagcat ggagaatatc	1620
aattatgtaa gtcattaata a	1641

<210> SEQ ID NO 17  
<211> LENGTH: 1992  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 17

atgaagaaaa agacggacaa tcccacaata tcaaagagggt gtcacaacca ttctcgagga	60
atcaaatcta gaggcgctact cagagagaca gataattttt ccaatggct aatagtttag	120
aattttagtta gaaactgtca tcatccaatg aagaacaatc taaactatac taagacacaa	180
aaaagagattt ctacaatccc ttatcggttgaagagatg aaggacatattt tccaaagatt	240
aaacatctta ttgataatc ttacaaggat ataaaaagag ggaagagaag aaatggtcat	300
aatgggaaca ttataactat aattctgtt gttgatttaa ttttgaagac acagatgagt	360
gaaggtgtca tccattacga gactctaagt aagatcggtt taataaaggaa aatcaccaga	420
gagtacaaag tcaaaggaac tccgtcaatg aaagacatag tcatcaaattt gattccgaat	480
gtcacccggtc ttaacaatgt cacgaacata tcaatggaaa actataaaga acaacttgac	540
aaaatactaa ttccttattaa caacataattt gaattgtatg caaaactcaac taaatcagcc	600
cctggaaatg cacgtttgc tggcgttata attgcaggag tggcattagg tggcagcg	660
gcagccccaa taactgcggg cattgcactg catgaagctc gacagaatgc agagagaatt	720
aatctttaa aggatagcat ttctgccact aacaacgcag tagcagaactt ccaggaagca	780
actgggtggaa tagtaatgtt cattacagga atgcaagattt acatcaatc aatcttagtc	840
ccgcagattt acaaactgca atgttagtcaatg atcaaaacgg cattagacat atctctcc	900
caataactattt cagaaatattt aacagtgttc ggtccaaacc ttcaaaatcc agtaactact	960
tccatgtcaa tacaagccat atcacaatcc ttgggggaa atatagatttt gctcttaaac	1020
ctacttaggtt acactgc当地 cgacttattt gatttgc当地 aaagtaaaag tataacaggg	1080

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caaaaacat acataaatct tgaacattac ttcatggtaa tcagagtata ttatcctata	1140
atgacaaca tcagcaatgc ttatgtccag gaattgtatca aaatttagctt caatgtcgat	1200
ggcagtgaat gggtatctct tgcaccctcg tatatatattga ttagaaactc atatctctca	1260
aacatagaca ttcagaatg ttcataacc aaaaattcag tgatatgtcg tcatgacttt	1320
gcaatgcca ttagttacac cttaaaggaa tgcctaactg gagacactga aaagtgtccg	1380
agagaggctg ttgtaacctc atatgtccca agatttgcta ttcgggggg agtgatttat	1440
gctaattgtc taagtacaac atgtcaatgc tatcaaactg gcaaaggtaat tgctcaagac	1500
ggcagccaa cattgtatgtat gatcgataat caaacatgtt caatagtaag aattgaagaa	1560
atcctcatat caacaggaa atatctggga agtcaggagt acaatacgat gcatgtgtca	1620
gtcggcaatc ctgttccac tgacaagctg gacataacaa gtcaaatttc caacatcaac	1680
caatccattg aacaatccaa attttatcta gataagtcta aggctatact tgacaagata	1740
aatctcaact taattggctc tgcaccata tcaataacttt tcataattgc gatcttatca	1800
ttgattctct ctattataac ttttgtgatt gtgtatgataa ttgtcagaag atataacaaa	1860
tacactctc ttataaactc tgatocatcc agtaggagga gtactataca ggacgtatata	1920
atcatcccga accccggaga acattcgatt agatcagctg ctgcgtcaat tgacagagat	1980
cgagattgtat ga	1992

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<210> SEQ ID NO 18
<211> LENGTH: 1899
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

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<400> SEQUENCE: 18
atgccgcaga agactgtgga attcattaac atgaattccc ctctagaaag aggggtcagc      60
actcttttag ataagaagac cctcaatcaa tctaaaaatca ccaaggcaggg gtatTTGGG     120
ttaggatccc acagttagagaa aatggaaag aagcagaaga atcaaaaatga tcattacatg    180
actgtttcaa ccatgattct tgagatatta gttgtcctgg gcatcatgtt taatctcata    240
gttttaacta tgggttattaa tcagaatgac aacatcaatc aaaggatggc agaacttaca   300
agcaatatca cagtctgaa cttaaatctt aatcaattga caaacaaaat tcaaagagaa   360
attattccta ggatcactct tattgacaca gcaaccacca ttacaattcc tagtgccatt   420
acttacatat tagcaactct gacaaccaga atctcggaaat tattggcgtc aatcaaccaa  480
aagtgtgagt tcaagacacc gacacttgcc ctgaatgact gcagaataaa ctgtacccc  540
ccactaaacc cgtctgtatgg agtggaaatg agttcttgc ccactaactt gggtgcacat  600
ggccctctc cctgttagaaa ctttccatcc gtacctacaa tttactatata tcggattcca  660
ggattataca atagaacgc attggacgaa agatgtatata taaacccgag attgacaata  720
agcagtgacaa aatggctt tgcactctt gatatgataaaaatgcac cagaggattc  780
aaatactatg aattgtatgac atttggagaa atactggagg gtccggaaaa agaaccacaa  840
atgtttcttta ggtcatatcc ttcccccaca aatgtgtga actatcatcc ttgtacccg  900
atcgtgactg tcaatgaagg atatccctt tgccttgaat gcacccctc agatccctt  960
tacaaagcaa atctatctaa tagcacatcc catttggta tactgaggca taacaaggat 1020

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gagaaaatag tttcaatgcc tagcttaac ctttctactg atcaagagta tgttcagata	1080
atccctgcag aagggtggcg cacagcagag agtggcaatc tttactccc ttgtatttggaa	1140
aggctcttac acaaaccgagt caccatcct ttatgcaaaa agtcaaattg ttgcgaact	1200
gatgatgaat cttgcctgaa aagttattac aatcaagggtt cgcctcagca ccaagtagtc	1260
aactgtctga taaggatcag aaatgcacag agagataatc caacctggaa tgttatcaca	1320
gttgatctga ctaatacata cccaggatca aggagcagga tcttttggaaag ctctccaaa	1380
ccgatgtttt atcaatcatc agtatcatgg catactttc ttcaaggtagc agagataaca	1440
gacccatata agtatcaatt ggactgggtt gatacaccctt atatatctcg tcctggagga	1500
tctgagtgcc cttecgaaaa ttattgtcca acggatgtctt gggaaaggac atataatgt	1560
gtctatacgta taactccaaa taacgatctt ttgtcactg tgtatggaa gagtgaacaa	1620
gttgcagaga acccttattt cgcaatcttc tcacgggatc aaatcttggaa agaattccct	1680
cttgatgcattt ggataaggcag tgcacgaact acgacaatattt cgtgcttcat gttcaacaat	1740
gaaatttttgtt gtatagctgc attagagatc acaagattga atgatgacat cataagacca	1800
atttattact cttecggtt gcctactgtat tgccggacac catatccccca caccggtaag	1860
atgaccagggtt cccttgcgtt cttccatata aactactaa	1899

<210> SEQ\_ID NO 19  
<211> LENGTH: 1566  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 19	
atgggtggta tcctggacaa gaggtgtcac tgcaacctgc tgatcctgtat cctgtatgtc	60
agcgagtgca gcgtggcat cctgcactac gagaagctgtt ccaagatcgg cctgggttggaa	120
ggcgtgacca ggaagtacaa gatcaagago aaccccttgc ccaaggacat cgtatcaag	180
atgatccccca acgtgagcga catgagccag tgcacccggca gcgtgtatggaa gaactacaag	240
accaggctga acggcatcct gaccccttgc aaggccgecc tggagatcta caagaacaac	300
acccacgacc tgggtggcga cgtgagactg gcccggcgttgc tcatggccgg cgtggccatc	360
ggcatcgcta cagccgccccca gatcacagcc ggagtggccc tgcgtggggc catgaagaac	420
gccgacaaca tcaacaagctt gaagagcago atcgagagca ccaacgaggc cgtgggttggaa	480
ctgcaggaga cccggaaaaa gaccgtgtac gtgtgttgcaccat ccctgcaggatcaatcaac	540
accaacctgg tggccaccat cgacaagatc agctgcaagc agaccgagctt gtccctggac	600
ctggcccttgc gcaagtacctt gagcgacccgtt ctgttgcgttgc tggcccccacatccatc	660
cccggtggca acagcatgac catccaggcc atcagccagg cttccggccgg caactacgag	720
acccctgtgtt ggaccctggg ctacgcccaccat gaggacttgc acgaccgttgc ggagagcgc	780
agcatcaccg gccagatcat ctacgtggac ctgagcagctt actacatcat cgtgggggttgc	840
tacttccccca tcctgaccga gatccagcag gcctacatcc agggactgttgc gcccgttgc	900
ttcaacaacg acgacagcga gtggatcago atcgatccccca acttcatcctt ggtgcggaaac	960
acccctgtatca gcaacatcga gatcggtttt tgcgtatca ccaagagaag cgtgtatgtc	1020

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aaccaggact acgccacccc catgaccaac aacatgagag agtgcctgac cggcagcacc	1080
gagaagtgcc ctggaaact ggtgggtcc agccacgtgc ccaggttcgc cctgtccaac	1140
ggcgtgtgt tcgccaactg catcagcgtg acctgccagt gccagaccac cggcagggcc	1200
atctcccaga gcggcgagca gacactgctg atgatcgaca acaccacctg cccccccgccc	1260
gtgctggca acgtgtatcat cagcctggaa aagtacctgg gcagcgtgaa ctacaacagc	1320
gagggcatcg ccatacgcccc tccctgttcc accgacaagg tggacatcag cagccagatc	1380
agcagcatga accagagcct gcagcagagc aaggattaca tcaaggaggc ccagaggctg	1440
ctggacacccg tgaaccccaag catgaagcag atcgaggaca agatcgagga gatcctgagc	1500
aagatctacc acatcgagaa cgagatcgcc aggatcaaga agctgatcgg cgaggccct	1560
ggggc	1566

<210> SEQ ID NO 20  
 <211> LENGTH: 1566  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 20	
atggccaccc aggagggtgcg gctgaagtgc ctgctgtgcg gcatcatcgt gctgggtctg	60
tccctggagg gcctgggcat cctgcactac gagaagctgt ccaagatcgg cctggtaag	120
ggcatcacca ggaagtacaa gatcaagagc aacccctga ccaaggacat cgtgtatcaag	180
atgatccccca acgtgagcaa cgtgtccaaag tgccacggca ccgtgtatggaa gaactacaag	240
agcaggctga ccggcatctt gagcccatc aaggcgccca tcgagctgtaa caacaacaac	300
acccacgacc tgggtggcga cgtgaagctg gccggcgtgg tggatggccgg catcgccatc	360
ggaatcgcca cagccgccccca gatcacagcc ggcgtggccc tgtacgaggc catgaagaac	420
gccgacaaca tcaacaagct gaagagcagc atcgagacca ccaacgaggc cgtggtaag	480
ctgcaggaga ccggcggaaaa gaccgtgtac gtgctgaccg ccctgcagga ctacatcaac	540
accaacctgg tgcccaccat cgaccagatc agctgcaagc agaccgagct ggccctggac	600
ctggccctga gcaagtacctt gagcgacccgt ctgttcgtgt tggcccccac cctgcaggac	660
cccggtgagca acagcatgac catccagggc atcagccagg ccttcggccg caactacgag	720
acccctgtga ggaccctggg ctacgcccacc gaggacttcg acggcctgtc ggagagcgac	780
agcatcaccg gccagatcgt gtacgtggac ctgagcgtact acatcatcat cgtgagggtg	840
tacttccccca ttctgaccga gatccagcag gcctacgtgc aggagctgtc gcccgtcagc	900
ttcaacaacg cacaacacgca gtggatcago atcgatccccaa acttcgtgtc gatcggaaac	960
accctgtatca gcaacatcga ggtgaagtc tgccctgtatca ccaagaaaag cgtgtatcgtc	1020
aaccaggact acgccacccc catgacccgcg acgtgtgagag agtgcctgac cggcagcacc	1080
gacaagtgcc ctggaaact ggtgggtcc agccacgtgc ccagggtcgc cctgagcggc	1140
ggagtgtgt tcgccaactg catcagcgtg acctgccagt gccagaccac cggcagggcc	1200
atctcccaga gcggcgagca gacactgctg atgatcgaca acaccacctg caccacgtg	1260
gtgctggca acatcatcat cagcctggaa aagtacctgg gcagcatcaa ctacaactcc	1320
gagagcatcg ccgtgggacc ccccgatgtac accgacaagg tggacatcag cagccagatc	1380

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agcagcatga accagagcct gcagcagago aaggattaca tcaaggaggc ccagaaaatc	1440
ctggacaccg tgaaccccg catgaagcag atcgaggaca agatcgagga gatcctgagc	1500
aagatctacc acatcgagaa cgagatcgcc aggatcaaga agctgatcg ggaggcccct	1560
ggcgcc	1566

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 1656

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Henipavirus nipahense

&lt;400&gt; SEQUENCE: 21

atggaaaaccg acactctgct gctgtgggc ctgctgctgt gggtcctgg ctcaactggc	60
gacgcagcat caacagataa tcaggccatg atcaaagatg cattgcagag tatccagcag	120
cagatcaagg ggcttgccga caaaaattggc acagagatag ggccgaaagt atcactgatt	180
gatacatcca gtactatcac tattccagct aatattggc tgtaggttc aaagatcagc	240
cagtcaactg caagtataaa tgagaatgtg aatgaaaaat gcaaatttac actgcctccc	300
ttgaaaatcc acgaatgtaa catttcttgt cctaaccac tcccttttag agagtataag	360
ccgcagacag aaggagttag caatctggta ggattaccta ataatatctg tctgcaaaag	420
acatctaatac agatactgaa accaaagctg atttcataca ccttaccctg agtcggtaa	480
agtggcacct gtatcacaga cccactgctg gctatggatg agggctactt tgcataatgc	540
cacctggaaa aaatcggtac atgttcaaga ggggtctcca aacaaagaat aataggagtt	600
ggagaggtac tagacagagg tgacgaagta cttctttgtt ttagactaa cgtctggacc	660
ccatcaaatac caaacaccgt ttaccattgc agtgcgtgt acaacaatga attctattat	720
gtgctttgtg cagtgtcagt tggggagac cttattctga atagcaccta ctggccgga	780
tcaactaatga tgactcgtct agctgtaaaa cctaagaata atggtagag ttacaatcaa	840
catcaatttg ctttacggaa tattgagaaa gggaaatgtat aaaaatgttat gccatatgg	900
ccctcaggca tcaaacaagg tgacaccctg tacttccctg ctgttaggatt tttggtcagg	960
acagagttca catacaatga ttcaaattgt cccatcgca agtgcataa cagcaaacct	1020
gaaaactgca ggctatctat ggggattaga ccaaacagtc attatatctc tcgatctgaa	1080
ctactaaat acaatctatc ggtgaggag aactctaaaa ttgtattcat tgaaatatct	1140
gatcaaagac tatctattgg atctccttagc aaaatctatg attctttggg tcaacctgtt	1200
ttctaccaag catcttttc atgggacact atgattaaat ttggagatgt ccaaacagtt	1260
aaccctttag ttgtaaattg gcgtgacaac acggtaatct caagacctgg gcaatcacaa	1320
tgccttagat tcaacaagtg cccagaggtt tgctggaa gggttataaa tgatgcttc	1380
ctgattgata gaatcaattg gataagcgcg ggtgtattcc ttgacacgca ccagaccgca	1440
gagaatcctg tttttactgt attcaaaatg aatgaagtagt ttacagagc acaactagct	1500
tccgaggaca ccaatgcaca aaaaacaata actaattgct tcctttgaa gaataagatc	1560
tgggtatatacactgggtga gatatacgc acaggagaca atgttataag acctaaacta	1620
ttcgcagtttta agataccaga gcaatgtaca taataa	1656

&lt;210&gt; SEQ ID NO 22

&lt;211&gt; LENGTH: 1662

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<212> TYPE: DNA
<213> ORGANISM: Henipavirus hendraense

<400> SEQUENCE: 22

atggaaaccg acactctgct gctgtggc ctgctgctgt gggtcctgg ctcaactggc      60
gacgcagcaa gaacgactga taatcaggca ctaatcaaag agtcaactcca gagtgtacag    120
caacaaaatca aagcttaac agacaaaatc gggacagaga taggccccaa agtctacta    180
attgacacat ccagcaccat cacaattcct gctaacatag ggttactggg atccaagata    240
agtcagtcta ccagcagtat taatgagaat gttaacgata aatgcaaatt tactttct     300
cctttaaga ttcatgagtg taatatctct tgccgaaatc cttgcctt cagagaatac    360
cgaccaatct cacaaggggt gagtgatctt gttagactgc cgaaccagat ctgtctacag    420
aagacaacat caacaatctt aaagcccagg ctgatatcct atacttacc aattaatacc    480
agagaagggg tttgcacatc tgaccactt ttggctgtt ataatggctt cttcgcctat    540
agccatettg aaaagatcgg atcatgtact agaggaattt caaaacaaag gataataggg    600
gtgggtgagg tattggatag gggtgataag gtgccatcaa tgtttatgac caatgtttgg    660
acaccaccca atccaagcac catccatcat tgcaatcctt cttaccatga agattttat    720
tacacattgt ggcgcgtgtc ccatgtgggaa gatcctatcc ttaacagtac ttccctggaca    780
gagtcaactgt ctctgattcg tcttgctgtt agacaaaaaa gtgatagttt agactacaat    840
cagaaataca tcgctataac taaagttgaa agagggaaat acgataaggt gatgccttac    900
ggtccatcag gtatcaagca aggggataca ttgtactttc cggccgtcgg tttttggcca    960
aggaccgaat ttcaatataa tgactctaat tgcccataa ttcatgttca gtacagcaaa    1020
gcagaaaact gttaggcttca aatgggtgtc aactccaaaa gtcattatat ttttagatca   1080
ggactattgtt agtataatct atctttggaa ggagacatca tactccaatt tatcgagatt   1140
gctgacaata gattgaccat cggttctcct agtaagatata acaatccctt aggtcaaccc   1200
gttttctacc aggcatacata ttcttggat acgtgatca aattaggcga tggtgatacc   1260
gttgaccctc taagagtaca gtggagaaat aacagtgttca tttcttagacc tggacagtca   1320
cagtgtcctc gatttaatgt ctgtcccgag gtatgctggg aagggacata taatgtatgt   1380
tttctaatac accggctaaa ctgggttagt gctgggtttt atttaaacag taaccaaaaca   1440
gcagagaacc ctgtgtttgc cgtattcaag gataacgaga tcctttacca agttccactg   1500
gctgaagatg acacaaaatgc acaaaaaacc atcacagatt gtttcttgc ggagaatgtc   1560
atatgggtgttatacacttagt agaaaatatac gatacaggag acagtgtgtt aaggccaaaa   1620
ctatggcag tcaagatacc tgcccaatgt tcagagatgtt ga                                1662

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<210> SEQ ID NO 23
<211> LENGTH: 1668
<212> TYPE: DNA
<213> ORGANISM: Mojiang virus

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<400> SEQUENCE: 23

atggcactaa ataaaaatata gttcagttca ctgttccttg gttatctatt agtgtacgct      60
acgactgttc agtcttagtat acactatgac tccttatcta aggtcggtgt cattaagggt    120
ctgacataca actataagat caagggttcg ccatctacaa agctaattgtt ggtcaatattg    180
atacctaaca ttgatagtgtt taaaaactgtt actcagaaac agtatgtatca aacaagaac    240

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ttagtaagga aaggcttaga accggtaaaa atggctattt acaccatgtt caataatgtt 300  
aagtccggta ataacaagta cagatttgc ggtgcaatta tggctggagt tgccctcggt 360  
gttgcaacag cagccactgt tacagcaggat atagctctcc atagatcaaa tgaaaatgca 420  
caggcaattt caaacatgaa gagtgctattt caaaatacaa atgaggcgtt aaagcaattt 480  
caatttggcca ataaacaaac actagctgtt attgacacca taagaggaga gatcaataac 540  
aatataatac ccgttataaa tcaatttgago tgtgacacaa ttggctcag tgtaggtata 600  
agactcactc agtactactc tgaataata actgcattt ggccagctt gcagaatcca 660  
gtaaatacaa ggattaccat tcaagcaata tctatgtgtt ttaatggcaaa ctgtatgaa 720  
ctgctgaaga ttatgggtt tacaagtggat gatctttatg aaatttcata tagtgaatta 780  
attagaggca acattataga cggtgatgtt gatgcaggat acatagctt agaaatagaa 840  
ttccccaaatc taacatttgtt acctaattgtt gtagtacagg agttaatgcc tatcagtttat 900  
aacatagacg gggatgagtg ggtaacactt gtgccaaggat ttgtacttac aaggactaca 960  
ctgttatcaa atattgtatc gagtagatgtt acaatcacatg atagtagtgtt catatgtgac 1020  
aacgactacg ctttgccat gtcacacgat cttatttgtt gcttacaggat agatacatct 1080  
aagtgtgttaa gagagaaggtt agtctcaatgtt tatgtccata aatttgcgtt gtctgttgg 1140  
ttatgttatgtaa caaattgcctt caatactatc tgccatgtt tggatcacata tactccaatc 1200  
tcacaaatgc tcggagccac tgtatcatta cttagacaaca agaggtgttc agtataatcgt 1260  
gttaggagatg tcttgatttc tgctcgatca tatcttaggatg atggagaataataatgtgtat 1320  
aatgttagacg ttggcccacc tatagttata gataagatgg acataggaaa tcagctggca 1380  
ggttataatc aaacccatca aagggcagaa gattacatttgg agaagtccaga agagttctt 1440  
aaagggggttta accccatcaat tatcaatc tttttccatgg ttgtccatgat tataatgttat 1500  
atattaatag ccatttgttc agtaatagca ctgtattgtt caattaaattt aacagtaaaa 1560  
aaatataaca aatttataaga tgatcctgtt tattacaatg attacaaaag agaacgtatt 1620  
aatggcaaaatc ccactgttcaatgtt gtttccatgg ttgtccatgat tataatgttat 1668

<210> SEQ ID NO 24

<211> LENGTH: 1953

<212> TYPE: DNA

<213> ORGANISM: Ghana virus

<400> SEQUENCE: 24

atgaagaaaa agacggacaa tcccacaata tcaaagaggg gtcacaacca ttctcgagga 60  
atcaaatctt gaggctactt cagagagaca gataattttt ccaatgggtt aatagttgg 120  
aattttatgtt gaaactgtca tcatccaaatgtt aagaacaatc taaactatatac taagacacaaa 180  
aaaagagattt ctacaatccc ttatcgtgtt gaagagagaaa aaggacatattt tccaaagattt 240  
aaacatctta ttgataatcc ttacaaggat ataaaaaggg ggaagagaag aatgggttttcat 300  
aatggaaaca ttataactat aatttgcgtt ttgtatccat ttttgaagac acagatgttt 360  
gaaggtgtttcaatcc ttatcgtgtt gaagagagaaa aaggacatattt tccaaagattt 420  
gaggatcatgtt gaaactgtca tcatccaaatgtt aagaacaatc taaactatatac taagacacaaa 480  
gtcaccggtc ttacaactgtt cacgaacata tcaatggaaa actataaaga acaacttgac 540  
aaaataactaa ttccatattaa caacataattt gatatgttatg caaaactcaac taaatcagcc 600

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cctggaaatg cacgtttgc tggegttata attgcaggag tggcattagg tggcagcg	660
gcagccaaa taactgccgg cattgcactg catgaagctc gacagaatgc agagagaatt	720
aatctcttaa aggatagcat ttctgccact aacaacgcag tagcagaact ccaggaagca	780
actggtgaa tagtaaatgt cattacagga atgcaagatt acatcaatac aaatcttagtc	840
ccgcagattg acaaactgca atgttagtcag atcaaaccgg cattagacat atctctcc	900
caatactatt cagaaatatt aacagtgttc ggtccaaacc ttcaaaatcc agtaactact	960
tccatgtcaa tacaagccat atcacaatcc ttgggggaa atatagattt gctcttaaac	1020
ctacttaggtt acactgcaaa cgacttattt gatttgcgaa agagaaaaag tataacaggc	1080
caaataacat acataaatct tgaacattac ttcatggtaa tcagagtata ttatcctata	1140
atgacaacaa tcagcaatgc ttatgtccag gaattgtatca aaattagctt caatgtcgat	1200
ggcagtgaat gggtatctct tgcaccctcg tatatatgtt ttagaaactc atatctctca	1260
aacatagaca tatacgttatacc tctcataacc aaaaatttcg tgatatgtcg tcatgacttt	1320
gcaatgccaatg tgagttacac cttaaaggaa tgcctaactg gagacactga aaagtgtccg	1380
agagaggctg ttgtAACCTC atatgtcccc agatttgctt tctccgggg agtgatttat	1440
gctaattgtc taagtacaac atgtcaatgc tatcaaactg gcaaagtaat tgctcaagac	1500
ggcagccaaa cattgtatgtt gatcgataat caaacatgtt caatagtaag aattgaagaa	1560
atccctcatat caacaggaa atatctggaa agtcaggagt acaatacgat gcatgtgtca	1620
gtcggcaatc ctgtcttcac tgacaagctg gacataacaa gtcaaatttc caacatcaac	1680
caatccattt gaaatccaa attttatcta gataagtcttta aggctataact tgacaagata	1740
aatctcaact taattggctc tgcaccatac tcaataacttt tcataattgc gatcttatca	1800
ttgatttctt ctattataac ttttgtgatt gtgtatgataa ttaaatataaa caaatttata	1860
gtatgtccg attattacaa tgattacaaa agagaacgtt ttaatggcaa agccagtaag	1920
agtaacaata tatattatgtt aggtgattga tga	1953

<210> SEQ ID NO 25  
<211> LENGTH: 1959  
<212> TYPE: DNA  
<213> ORGANISM: Mojiang virus

<400> SEQUENCE: 25

atgctttctc agctccaaaa aaattactta gacaactcaa accaacaagg tgataaaatg	60
aacaacccag ataagaattt aagtgtcaac ttcaaccctt tagaattttaga taaagggtcaa	120
aaagatctca ataagtctta ttatgttaaa aacaagaattt ataacgtttc aaatcttatta	180
aatgaaatgtt gttgttataa ggttatttata ttgtatgtata cacttctgtt actgacaggt	240
gcttatttttta caataacactt aaatatcacc aacctgacag cggctaaag tcaacagaat	300
atgctgaaaa taatccaaga tgacgtgaat gccaaattttt aatgttcgtt gaatcttgc	360
caatttggtaa aggggtttaat taaaggccaaa gtgtcactca taaatacagc agtgagcgctc	420
agcataacccg gtcagatctc aaacccctccag accaaattcc tgcaaaaata tgtttactta	480
gaagaatctta ttactaagca gtgcacttgc aaccctttat ctgggatatt tccaaatcatca	540
ggcccaacctt accctccaaac tgataaaacca gacgtatgtt ccacagatgt tgacaaatgt	600
gacaccacgta ttaaggcttat tgagtacccc aagccggatg ggtgcaatag aactggcgac	660

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catttcacga tggagccgg agctaacttt tatactgtcc ctaacctagg accggcaagt	720
tctaattctg acgagtgtta cacaaccccc tcttttcaa ttgggtcctc catctatatg	780
ttttctcaag agatttagaaa aacggactgc acagcaggag agatattatc aattcagatc	840
gtcttaggcc gaatagtaga caagggctcg cagggtcctc aagcatcacc cttattagta	900
tgggccgtcc caaatccaaa gatcataaac tcgtgtgtcg tcgcagctgg agacgagatg	960
ggatgggtgt tatgctcagt gacattaact gcagcatcg gggagccat acctcacatg	1020
tttgcgttgt tctgggtgtaa taagttagaa cctgacaccg aagttgtatc ctatagaatc	1080
acaggctatg cttatctctt agataaacaac tatgactctg tctttatagg taagggcggt	1140
ggtattcaga aaggtaacga tctatacttt cagatgtatg gattgtccag aaataggcaa	1200
agtttaagg cactgtgtga acatggatca tgccctggca ctggagggtgg agggtatcaa	1260
gtgttgtgtg acagggtctgt gatgtcttc gggaggtgaag aatcactaat tacaatgca	1320
tatctgaagg tgaatgatct ggcaagtggg aaacctgtga taataggaca gacatttccg	1380
ccctcagatt cttataaagg ctcaaatggt cgatgtaca ctataggta taaatatggt	1440
ctgtatcttg ctccgtcatc ctggAACAGA tatcttagat ttgggataac accagatatt	1500
tctgttaagat caacaacctg gttgaaaagt caagatccga taatgaagat tttgtcaaca	1560
tgcacgaaca ctgatagaga tatgtgtctt gaaatttgcg atactagagg ttatcaagat	1620
atttttccat tgcggagga ttcaagat tatcacataca taggcataac tcctaataat	1680
ggtggaaacta aaaactttgt ggccgtacgt gactcagatg gtcatatagc atccattgtat	1740
attttacaaa attattatag tatcacctca gctactataa gctgcttcat gtacaaagat	1800
gagatttgggt gtattgcaat cacagaaggg aaaaaacaga aagacaatcc tcaacggata	1860
tatgcacatt cttacaaaat taggcaaatg tggataata tgaagtctgc cacagtgact	1920
gtgggtaatg ccaaaaatat cacaatcagg aggtattaa	1959

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 1926

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Ghana virus

&lt;400&gt; SEQUENCE: 26

atgctttctc agctccaaaa aaattactta gacaactcaa accaacaagg tgataaaaatg	60
aacaacccag ataagaaatt aagtgtcaac ttcaaccctt tagaattaga taaaggtcaa	120
aaagatctca ataagtctta ttatgttaaa aacaagaatt ataacgtttc aaatcttatta	180
aatgaaagtc aaaatgatca ttacatgact gttcaacca tgattctga gatattagtt	240
gtccctggcga tcatgtttaa tctcatagtt ttaactatgg tggattatca gaatgacaac	300
atcaatcaa ggtggcaga acttacaago aatatcacag tcctgaacct aaatcttataat	360
caattgacaa acaaattca aagagaaatt attccttagga tcactttat tgacacagca	420
accaccattt caattccttag tgccattact tacatattag caactctgac aaccagaatc	480
tcggaattat tgccgtcaat caacccaaag tgtgagttca agacaccgac acttgcctg	540
aatgactgca gaataaaactg taccaccca ctaaaccctg ctgatggagt gaaaatgagt	600
tctcttgcca ctaacttgggt tgcacatggg ccctctcccgt gtagaaactt ttcatccgt	660
cctacaattt actattatcg gattccagga ttatacaata gaacagcatt ggacgaaaga	720

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tgtataactaa acccgagatt gacaataago agtacaaaat ttgcttatgt ccactctgaa	780
tatgataaaa attgcaccag aggattcaaa tactatgaat tcatgacatt tggagaata	840
ctggagggtc cggaaaaaga acccagaatg tttcttaggt cattttatc gcccacaaat	900
gtgtgtact atcattcttg tacgccgatc gtgactgtca atgaaggata tttctttgc	960
cttgaatgca ctccttcaga tcccttgtac aaagcaaatac tatctaatacg cacattccat	1020
ttggtgatac tgaggcataa caaggatgag aaaatagttt caatgcctag cttaacctt	1080
tctactgatc aagagtatgt tcagataatc cctgcagaag gtggcggcac agcagagagt	1140
ggcaatctt acttcccttg tatttggaaagg ctcttacaca aacgagtcac ccattctta	1200
tgcaaaaagt caaattgttc gcgaaactgtat gatgaatctt gcctgaaaag ttattacaat	1260
caagggtcgc ctcagcacca agtagtcaac tgtctgataa ggatcagaaa tgacacagaga	1320
gataatccaa cttggatgtt tattcacatgat gatctgacta atacataccg aggatcaagg	1380
agcaggatct ttggaaagctt ctccaaaccg atgctttatc aatcatcagt atcatggcat	1440
actcttcttc aggttagcaga gataacagac cttagataagt atcaatttggc ctgggtggat	1500
acaccctata tatctcgcc tggaggatct gagtgccctt tcggaaatata ttgtccaacg	1560
gtatgctggg aagggacata taatgtatgtc tatagcttaa ctccaaataa cgatctttt	1620
gtcactgtgtt atttgaagag tgaacaagtt gcagagaacc cttatttcgc aatcttc	1680
cgggatcaaat tcttggaaaga attcccttctt gatgcatggta taaggcgtgc acgaaactacg	1740
acaatatcgatgtt caacaatgaa atttgggtgtat tagctgcatt agagatcaca	1800
agattgtatg atgacatcat aagaccaattt tattactctt tctggctgcc tactgtatgc	1860
cggacaccat atccccacac cggtaagatg accagggttc ctttgcgcac cacatataac	1920
tactaa	1926

<210> SEQ ID NO 27  
 <211> LENGTH: 6  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 27

acgcgt

6

<210> SEQ ID NO 28  
 <211> LENGTH: 1674  
 <212> TYPE: DNA  
 <213> ORGANISM: Cedar virus

<400> SEQUENCE: 28

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aatgcagcaat ttgttaggtt tgatgttgcattt aaatttgcataa aaataggtgtt ggtgcacagg	120
agagtcctaa attataaaaat taaaggagat ccaatgacaa aagaccttgc ttttgcattt	180
atcccttataca tagtgaatat cactgtatgtt gtggatgtgc ctttgcgttgc ttacaatgtt	240
accgtgagga gattgtttt accttatac aacatgtttt ggttataactt gaataacaca	300
aatgctaaaa tggatgtttt gatgtatgtt ggtgtgtatca tgggtggat agcaataggt	360

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atagccacag cagctcagat cacagcagg tttgctttt atgaggcaaa aaagaacaca	420
gaaaatattc agaaattaac agacagcatc atgaaaacac aggactcgat tgataaactt	480
actgacagtg tggggacaag catacttata ttgaataagc tacagacata catcaacaat	540
caactggtagtac caaatctaga gcttctatcc tgccgacaaa acaaattga gtttgatcta	600
atgttaaccac agtatttgtt ggtatctatg actgttattg gtcctaatat caataatcct	660
gttataaaag atatgactat tcaatcttt tcacttctt ttgatggcaa ttatgatata	720
atgtatgtcag aacttggta tacacctcgat gatttcttag atttgcata gatgtatgt	780
ataacagggc aaataattta tggttatgt gaaaacttgt acgttgtat caggacat	840
ctacacctcc taattgaagt acctgtatcc caaatatatg agttcaacaa aataactatg	900
atgtatgtatg gaggagaata ctgtcaacc atacctaatt tcataatata aagaggtat	960
tatataatgtc atatagatgt tgcaatgt tatatgacca aagcaagcgt aatttgcata	1020
caagattatt cactcccgat gagccaaac ttaagaagct gttatcaagg tgagacagaa	1080
tactgtctcg ttgaggcagt catcgctca cactctccaa gatttgcata tacaatgg	1140
gttattttcg ccaattgtat aaatacaatt tggatgttc aagacaatgg taagactatc	1200
actcaaaaca taaaccaatt cgtaagcatg atcgacaaca gtacttgcata tgatgtcatg	1260
gttagataagt ttactatcaa ggttagaaaa tatatggggaa gaaaagatata caataatatt	1320
aatatccaga taggaccgca gatcataatt gataagggtt acttgcataa tgaaataaac	1380
aagatgaatc aatctttaaa agatagtatt ttctacctga gagaagccaa gagaatttt	1440
gactcgtatc atatcgtct tatatctcca agcgttcaat tgtttctat aataatatca	1500
gtcctctcat ttattatattt attgattatc atagatatact tgatgttata atcaaaacat	1560
tcataataat ataacaattt tatagatgtat cctgattattt acaatgatca caaaagagaa	1620
cgttataatg gcaaaaggccat taagatgtatc aatataatattt atgtatgtatc ttat	1674

&lt;210&gt; SEQ ID NO 29

&lt;211&gt; LENGTH: 1869

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Cedar virus

&lt;400&gt; SEQUENCE: 29

atgctttctc agctccaaaa aaattactta gacaactcaa accaacaagg tgataaaatg	60
aacaacccag ataagaaattt aagtgtcaac ttcaaccctt tagaatttgcataaaatgtca	120
aaagatctca ataagtctta ttatgttataa aacaagaattt ataacgttcaatcttata	180
aatgaaatgc tgcacgatattt caagttttgtt atttattgttata tattctact gctaatttgc	240
attacaataat tcaatataat cacaatataca attgttataa ctcgtctgaa agtacatgaa	300
gagaataatg gcatggatc tcctaatttta caatcttcc aagatagtct ctcatcttt	360
actaacatga tcaatacaga gataactcctt agaataaggaa ttttagttac agccacttct	420
gttactctctt cttcatctat caattatgtc gggactaaga caaatcaact ggtcaatgaa	480
ttaaaagattt atataaccaa aagttgtggc tttaagggtcc ctgtatgttataa gttacatgaa	540
tgcaacataat gttgtgtatc tccaaaaattt agcaaatctg caatgtacag caccaatgcc	600
tatgcccggc ttgctggatcc acctaagata tttgtatccaa agaccccgac	660
tttagactga agcagataga ttatgtatca ccagtgcggc aagatcggtc tatttgcata	720

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aacaaccctt	tattggatat	ttctgatggg	tttttacct	acatacatta	tgaaggata	780
aatagctgta	aaaaatcaga	ttcatttaaa	gtgctgctgt	cacatggta	aatagttgac	840
aggggtgatt	atcgaccatc	attatatcta	ttatcaagt	attaccatcc	ttattcaatg	900
caggtataaa	actgtgtacc	tgtgacttgt	aaccagtcat	ccttgtatt	ctgtcatatc	960
tccaacaaca	ctaaaacatt	ggacaattca	gattactcg	cagacgagta	ctacataaca	1020
tatttcaatg	gcatacatcg	tccaaaacc	aagaagattc	ccattaacaa	tatgacagca	1080
gacaatcggtt	atatccattt	tacattctca	ggggggggag	gtgtatgtt	aggtgaagaa	1140
tttatttattc	ctgttaccac	agtcatcaat	actgatgtat	tcacgcatga	ttattgtgag	1200
agtttcaact	gttcagtcca	aaccggtaaa	agtctaaagg	agatatgctc	tgagtcatta	1260
agatctccaa	cgaactcatc	gcgatacaat	ttaaacggaa	tcatgattat	aagtcaaaac	1320
acatgacag	attttaagat	tcagttgaat	ggtataactt	ataacaaact	gtcattcgga	1380
agtcctggaa	gactgagcaa	gacactgggc	caggtcctt	attaccaatc	ttcaatgagt	1440
tgggataactt	atctaaaggc	aggatttgtc	gagaaatgg	aacccttac	cccgaattgg	1500
atgaacaata	ctgtgatatac	cagaccta	caaggtatt	gtccaaggta	tcataaatgc	1560
cccgagat	gttatggagg	gacatacaat	gatattgctc	cttttagatct	aggaaaagac	1620
atgtatgtta	gcgttattct	agattcagat	cagttgcag	agaatccaga	gattacagta	1680
tttaactcta	ctactatact	ttataaggag	agagtatcca	aaagtaact	aaacacaaga	1740
agtactacaa	cgagctgttt	tctttccta	gatgaacctt	ggtgtatatc	agtattagaa	1800
acaaacagat	ttaacggcaa	atctattagg	cccgagattt	attcatacaa	aattcctaag	1860
tattgttaa						1869

<210> SEQ ID NO 30  
 <211> LENGTH: 1566  
 <212> TYPE: DNA  
 <213> ORGANISM: Henipavirus nipahense

<400> SEQUENCE: 30						
atggcagtt	tacttaacaa	gagatattat	tctaattct	taatactgtat	tttgatgtac	60
tcggagtgca	gtgtcggat	tttcattat	gagaaattga	gtaagattgg	gcttgtcaaa	120
ggaataacaa	gaaaatacaa	gatcaaaagc	aatcctctca	caaaagacat	tgttattaaa	180
atgattccga	atgtgtcaaa	catgtctcaa	tgcacgggaa	gtgtcatgga	aaactataaa	240
acacgattaa	acggtatcc	aacgcctata	aagggggcatt	tagagattta	caagaacaac	300
actcatgacc	ttgtcggtga	tgtaagactg	gccggagtt	taatggcagg	agttgttatt	360
ggaattgcaa	ccgcagctca	aattactgca	ggtgttagcat	tatatgaggc	aatgaaaaat	420
gctgacaaca	tcaacaaact	caaaagcago	atagaatcaa	ctaatgaagc	tgttgttaag	480
cttcaagaga	ctgcagaaaa	gacagtctat	gtactgaccg	ctttgcagga	ttacattaaat	540
actaacttgg	taccgacaat	tgacaagata	agctgcacaa	agacggaaact	ctcatttagat	600
ctagcactat	caaagtacct	ctctgatttg	ctttttgtat	ttggtcccaa	ccttcaagac	660
ccagtttcta	attcaatgac	tatacaggct	atatctcagg	cattcggtgg	aaattatgaa	720
acactgctaa	gaacggtggg	ttacgctaca	gaagactttg	atgatcttct	agaaagtgac	780
agcataacgg	gtcaaattat	ctacggttat	ttaagtggct	actacataat	tgtcagggtt	840

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tattttccta	tcctgactga	aatccaacag	gcctataatcc	aagaattgtt	gccagtgagc	900
tttaacaatg	acaattcaga	atggatcago	attgtcccaa	atttcatatt	ggtaaggAAC	960
acattaatat	caaatataga	gattggattt	tgcttaatta	caaagaggag	tgtgatctgc	1020
aaccaagatt	atgcaacacc	catgacaaac	aatatgaggg	aatgtttgac	ggggtcgact	1080
gagaagtgtc	ctcgagagct	ggtgtttca	tcacacgttc	ccagatttc	actatctaac	1140
ggggttttgt	ttgctaattt	cataaggcgtc	acatgccagt	gtcaaacaac	aggtagggca	1200
atctcacagt	caggagaaca	aactctgctg	atgattgata	acaccacctg	tcctacagcc	1260
gtactcggtt	atgtgatcat	cagttggga	aaatatctt	ggtcagtaaa	ttataactct	1320
gaaggccattt	ctattggtcc	tcctgtctt	actgataaa	ttgacatatac	aagtcaaaata	1380
tctagcatga	atcagtcctt	acaacaatct	aaggactata	tcaaagaagc	tcaacgactc	1440
cttgatactg	ttaacccgtc	aatgaagcag	atcgaggaca	agatcgagga	gatcctgagc	1500
aagatctacc	acatcgagaa	cgagatcgcc	aggatcaaga	agctgatcgg	cgaggcccct	1560
ggccgc						1566

<210> SEQ ID NO 31  
<211> LENGTH: 1746  
<212> TYPE: DNA  
<213> ORGANISM: Henipavirus nipahense

<400> SEQUENCE: 31

atggaaaccg	acactctgct	gctgtgggtc	ctgctgctgt	gggtccctgg	ctcaactggc	60
gacgtcgaca	tgaagcagat	cgaggacaag	ctggaggaga	tgcagagcaa	gctgaagaag	120
atcgagaacg	agctggccag	gatcaagaag	gtcgactaca	cctcaacaga	taatcaggcc	180
atgatcaaag	atgcattgca	gagtatccag	cagcagatca	aggggcttgc	cgacaaaatt	240
ggcacagaga	tagggccgaa	agtatcactg	attgatacat	ccagactat	cactattcca	300
gctaatttgc	ggctgttagg	ttcaaagato	agccagtcaa	ctgcaagtat	aatgagaat	360
gtgaatgaaa	aatgcaaatt	tacactgcct	cccttgaaaa	tccacgaatg	taacatttct	420
tgtcctaacc	cactccctt	tagagagtat	aagccgcaga	cagaaggagt	gagcaatctg	480
gtaggattac	ctaataatat	ctgtctgcaa	aagacatcta	atcagatact	gaaaccaaag	540
ctgatttcat	acaccttacc	cgtagtcggt	caaagtggc	cctgtatcac	agacccactg	600
ctggctatgg	atgaggggcta	ctttgcata	agccacctgg	aaaaaatcgg	atcatgttca	660
agaggggtct	ccaaacaaag	aataatagga	gttggagagg	tactagacag	aggtgacgaa	720
gtacccctt	tgtttatgac	taacgtctgg	accccatcaa	atccaaacac	cgtttaccat	780
tgcagtgcgc	tgtacaacaa	tgaattctat	tatgtgtt	gtgcagtgtc	agttgttgg	840
gaccctattt	tgaatagcac	ctactggcc	ggatcactaa	tgtatgactg	tctagctgt	900
aaacctaaga	ataatggtga	gagttacaat	caacatcaat	ttgccttacg	gaatatttag	960
aaagggaaagt	atgataaagt	tatgocatata	ggaccctca	gcatcaaaca	aggtgacacc	1020
ctgtacttcc	ctgctgttagg	atttttggtc	aggacagagt	tcacatacaa	tgattcaat	1080
tgtccccatcg	cagagtgtca	atacagcaaa	cctgaaaact	gcaggctatc	tatggggatt	1140
agaccaaaca	gtcattatata	ccttcgatct	ggactactaa	aatacaatct	atcggatgag	1200
gagaactcta	aaattgtattt	cattgaaata	tctgatcaa	gactatctat	tggatctcct	1260

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agcaaaaatct atgattcttt gggtaaacct gtttctacc aagcatctt ttcatggac	1320
actatgatta aatttgaga tgtccaaaca gttaccctt tagttgtaaa ttggcgtgac	1380
aacacggtaa tctcaagacc tggcaatca caatgccta gattcaacaa gtggccagag	1440
gtttgctggg aagggttta taatgatgct ttctgattt atagaatcaa ttggataagc	1500
gcgggtgtat tccttgacag caaccagacc gcagagaatc ctgttttac tgtattcaaa	1560
gataatgaag tactttacag agcacaacta gttccgagg acaccaatgc aaaaaaaca	1620
ataactaatt gttcccttt gaagaataag atctggtgta tatcacttgt tgagatatac	1680
gacacaggag acaatgttat aagacctaaa ctattcgca gttaaagatacc agagcaatgt	1740
acataa	1746

<210> SEQ ID NO 32  
 <211> LENGTH: 1758  
 <212> TYPE: DNA  
 <213> ORGANISM: Henipavirus hendraense

<400> SEQUENCE: 32	
atggaaaaccg acactctgct gctgtggtc ctgctgtgt gggtcctgg ctcaactggc	60
gacgtcgaca tgaagcagat cgaggacaag ctggaggaga tgcagagacaa gctgaagaag	120
atcgagaacg agctggccag gatcaagaag gtgcactaca cccggaccac cgacaaccag	180
gcctgtatca aagagtccct gcagagcgtc cagcagcaga tcaaggccct gaccgacaag	240
atcggcaccg agatcggccc caaagtgtcc ctgatcgaca ccagcagcac catcaccatc	300
cccgccaaca tcgggtgtct gggctccaag atcagccaga gcaccagctc catcaacgg	360
aacgtgaacg acaagtgc当地 gttaccctg cccccctga agatccacga gtgcaacatc	420
agctgccccca accccctgcc ctteccggag taccggccca tcagccagg cgtagcgc当地	480
ctgggtggcc tgc当地 accca gatctgc当地 cagaaaaacc cctccaccat cctgaaggcc	540
cggctgtatca gtc当地 accccct gccatcaac accccggagg gctgtgc当地 caccgaccct	600
ctgctggccg tggacaacgg cttttc当地 tacagccacc tggaaaagat cggcagctgc	660
accggggc当地 ttgccaagca gccc当地 cttt当地 gggcc当地 gggcc当地 gagccacgtg	720
aagggtgc当地 gcatgttcat gaccaacgtg tggacccccc ccaacccca cacaatccac	780
cactgc当地 gagca caccctacca cgaggactt tactacacc tgc当地 cctgtgc当地 gagccacgtg	840
ggcgacccca tcctgaacag caccagctgg accgagagcc tgagcctgat cccgctggcc	900
gtgc当地 cccca agagc当地 gagc当地 cggc当地 actac aaccagaatg atatcgccat caccaagg	960
gagc当地 gggc当地 agtacgacaa agtgc当地 gccc当地 tacggcc当地 gccc当地 gagccac	1020
acactgtact tccccccgt gggctccctg cccggaccg agttccagta caacgc当地 ac	1080
aactgc当地 cccca tcatccactg caagtacago aaggccgaga actgc当地 gagcatggc	1140
gtgaacagca agagccacta catcctgc当地 agcggccctgc tgaagtacaa cctgtccctg	1200
ggc当地 ggccaca tcatc当地 tgc当地 gttcatcgag atcgc当地 gacaaccatgac catcgcc	1260
cccaaggcaaga tctacaacag cctggccag cccgtgttct accaggccag ctacagctgg	1320
gacaccatga tcaagctggg ggacgtggac accgtggacc ccctgc当地 gggt gca	1380
aacaacagcg tgatcagcag accccggccag agccagtgcc cccgg	1440
gaaatgtgct gggagggcac ctacaacgc gccc当地 tgc当地 accggct gaaatgg	1500

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tccgcggag	tgtacctgaa	ctccaaccag	accggcggaga	accccgtgtt	cgcgtgttc	1560
aaggacaacg	agatcctgta	ccaggtgccc	ctggccgagg	acgacaccaa	cggccagaaa	1620
accatcaccg	actgctttct	gctggaaaac	gtgatctggt	gcatcagcct	ggtggagatc	1680
tacgacacccg	gcgactccgt	gatccggccc	aagctgtttg	ccgtgaagat	ccccgcccag	1740
tgcagcgaga	gctgatga					1758

<210> SEQ ID NO 33  
<211> LENGTH: 1677  
<212> TYPE: DNA  
<213> ORGANISM: Mojiang virus

<400> SEQUENCE: 33						
atggcactaa	ataaaaatat	gttcagttca	ctgttccttg	gttatctatt	agtgtacgct	60
acgactgttc	agtcttagtat	acactatgac	tccttatcta	aggtcggtgt	cattaagggt	120
ctgacataca	actataagat	caagggttcg	ccatctacaa	agctaatttgt	ggtcaaattg	180
atacctaaca	ttgatagtgt	taaaaaactgt	actcagaaac	agtatgtat	atacaagaac	240
tttagtaagga	aaggcttaga	accggtcaaa	atggctattt	acaccatgt	caataatgtt	300
aagtccggta	ataacaagta	cagatttgc	ggtgcattt	tggctggagt	tgccctcggt	360
gttgcaacag	cagccactgt	tacagcaggg	atagctctcc	atagatcaa	tgaaaatgca	420
caggcaattt	caaacatgaa	gagtgcattt	caaataacaa	atgaggcagt	aaagcaattt	480
caatttggcca	ataaaacaaac	actagctgt	attgacacca	taagaggaga	gatcaataac	540
aatataatac	ccgttataaa	tcaatttgc	tgtacacaa	ttgggctcag	tgttaggtata	600
agactcactc	agtactactc	tgaaataata	actgcattt	ggccagctt	gcagaatcca	660
gttaataacaa	ggattaccat	tcaagcaata	tcttagtgt	ttaatggcaa	ctttgtatgaa	720
ctgctgaaga	ttatgggta	tacaagtgtt	gatctttatg	aaatttctaca	tagtgaatta	780
attaggaggca	acatttata	cgttgatgt	gatgcaggat	acatagctt	agaaatagaa	840
ttccccaaatc	taacatttgt	acctaattgt	gtagtagcagg	agttaatgcc	tatcagttat	900
aacatagacg	gggatgagtg	ggtaacactt	gtgccaagg	ttgtacttac	aaggactaca	960
ctgttatcaa	atattgatac	gagtagatgt	acaatcacag	atagtagtgt	catatgtgac	1020
aacgactacg	ccttgcctat	gtcacacgg	cttattggct	gcttacaggg	agatacatct	1080
aagtgtgcta	gagagaaggt	agtctcaagt	tatgtcccta	aatttgcgtt	gtctgtatgg	1140
ttagtgtatg	caaattgcct	caatactatc	tgccgatgt	tggatacaga	tactccaatc	1200
tcacaaaatc	tcggagccac	tgtatcatta	ctagacaaca	agaggtgtc	agtatatacg	1260
gttaggagatg	tcttgattt	tgtcgatca	tatcttaggg	atggagaata	taatgctgat	1320
aatgttagagc	ttggcccccacc	tatagttata	gataaggattt	acataggaaa	tcaagtggca	1380
ggtattaaatc	aaaccttaca	agaggcagaa	gattacattt	agaagtca	agagttctta	1440
aaagggggtta	acccttcaat	tatcaacttca	agcggttcaat	tgtttctaa	aataatatac	1500
gtcctctcat	ttattatatt	attgatttac	atagtagata	tgtactgtt	atcaaaacat	1560
tcatataat	ataacaattt	tatagatgt	cctgatttt	acaatgat	caaaagagaa	1620
cgttattatg	gcaaaagccag	taagagtaac	aatatataatt	atgttaggt	ttaataaa	1677

<210> SEQ ID NO 34

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<211> LENGTH: 1962
<212> TYPE: DNA
<213> ORGANISM: Mojiang virus

<400> SEQUENCE: 34

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aacaacccag ataagaattt aagtgtcaac ttcaaccott tagaattttaga taaaggtcaa     120
aaagatctca ataagtctta ttatgttaaa aacaagaattt ataaacgtttc aaatcttatta   180
aatgaaagtgc tgcacgatat caagtttgc atttattgtt tattctcaact gctaatttac    240
attacaataa tcaatataat cacaatatac attgttataa ctcgtctgaa agtacaacag    300
aatatgtga aaataatcca agatgacgtg aatgccaat tagaaatgtt cgtgaatctt    360
gatcaattgg tgaagggtaa aattaagcca aaagtgtcac tcataaatac agcagtgagc    420
gtcagcatac ccggcatacgat ctcaaaccctc cagaccaat ttcgtcaaaa atatgtttac  480
ttagaagaat ctattactaa gcagtgcact tgcaaccott tatctggat atttccaaca    540
tcaggcccaa cctaccctcc aactgataaa ccagacgtg ataccacaga ttagtacaaa    600
gtggacacca cgatggatcc tattgatgtt cccaaaggcg atgggtgc aa tagaactggc    660
gaccatttca cgatggagcc cggagctaac ttatctactg tccctaaacctt aggaccggca  720
agttcttaattt ctgacgatgtt ttacacaaac ccctctttt caattgggtc ctccatctat  780
atgttttctc aagagattt aaaaacggac tgcacagcgag gagatattt atcaatttgc    840
atcgtcttag gccgaatagt agacaagggtt cagcagggtc ctcaagcatc acccttattt  900
gtatggcccg tcccaatcc aaagatcata aactcgtgtt ctgtcgacg tggagacgag    960
atgggatggg tggatgttgc agtacatca actgcacat caggggagcc catacctcac 1020
atgtttatgtt ggttctgggtt gtataatgtt gaaatgttgc cccaaagggtt atcctataga 1080
atcacaggctt atgcttatctt cttatgttca caatatgtt ctgtctttt aggttacggc 1140
gggttatttca agaaaggtaa cgatctatac ttatgttgc atggattgtc cagaaatagg 1200
caaagtttta aggcactgtt tgaatgttgc tcatgcctcg gcactggagg tggagggat 1260
caagtgttgc tgcacaggcc tttatgttgc tttatgttgc aagaatgttca aatttacaaat 1320
gcataatgttca aggttacatgtt tttatgttgc tttatgttgc tttatgttgc aacatgttca 1380
ccggcccttgc attttatgttca aggttacatgtt tttatgttgc tttatgttgc tttatgttca 1440
gggttatttca tttatgttgc tttatgttgc tttatgttgc tttatgttgc tttatgttca 1500
atgtttatgttca gatcaacaaac ctgggttgc agtcaagatgc cgataatgttca gatgttgc 1560
acatgttgc acactgttgc agatatgttgc cttgttgc gcaatgttca aggttacatgttca 1620
gatatgttgc tttatgttgc tttatgttgc tttatgttgc tttatgttgc tttatgttca 1680
aatgggttgc cttttatgttca tttatgttgc tttatgttgc tttatgttca gatgttgc 1740
gatatgttgc tttatgttca tttatgttgc tttatgttgc tttatgttca gatgttgc 1800
gatgttgc tttatgttca tttatgttgc tttatgttca gatgttgc tttatgttca gatgttgc 1860
atataatgttca tttatgttca tttatgttca tttatgttca gatgttgc tttatgttca gatgttgc 1920
actgtgggttca tttatgttca tttatgttca tttatgttca gatgttgc tttatgttca gatgttgc 1962

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<210> SEQ ID NO 35  
<211> LENGTH: 1962  
<212> TYPE: DNA

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&lt;213&gt; ORGANISM: Ghana virus

&lt;400&gt; SEQUENCE: 35

atgaagaaaa agacggacaa tcccacaata tcaaagaggg gtcacaacca ttctcgagga	60
atcaaatcta gagcgctact cagagagaca gataattattt ccaatgggct aatagtttag	120
aattttagta gaaactgtca tcataccaggta aagaacaatc taaactatac taagacacaa	180
aaaagagatt ctacaatccc ttatcggttg gaagagagaa aaggacatta tccaaagatt	240
aaacatctta ttgataaatc ttacaaggcat ataaaaaagag ggaagagaag aaatggtcat	300
aatgggaaca ttataactat aattctgttg ttgatTTAA ttttgaagac acagatgagt	360
gaaggggtcta tccattacga gactctaagt aagatcggtt taataaaggg aatcaccaga	420
gagttacaaag tcaaaggaac tccgtcaagt aaagacatag tcataccattt gattccgaat	480
gtcacccggc ttaacaagtgc cacgaacata tcaatggaaa actataaaga acaacttgac	540
aaaatactaa ttccctattaa caacataattt gaattgtatg caaactcaac taaatcagcc	600
cctgggaatg cacgtttgc tggcgTTATA attgcaggag tggcattagg tgTTGcagcg	660
gcagccccaa taactgccgg cattgcactg catgaagctc gacagaatgc agagagaatt	720
aatctcttaa aggatagcat ttctgccaact aacaacgcg tagcagaact ccaggaagca	780
actgggtggaa tagtaaatgt cattacagga atgcaagattt acatcaatac aaatctagtc	840
ccgcagattt acaaactgca atgtatgcg atcaaaacgg cattagacat atctctcc	900
caataactattt cagaatattt aacagtgttc ggtccaaacc ttcaaaatcc agtaactact	960
tccatgtcaa tacaagccat atcacaatcc ttggggggaa atatagattt gctcttaaac	1020
ctactaggtt acactgcaaa cgacttattt gattgtctcg aaagtaaaag tataacaggc	1080
caaataacat acataaaatct tgaacattac ttcatggtaa tcaagatata ttatcctata	1140
atgacaacaa tcagcaatgc ttatgtccag gaattgtatca aaattagctt caatgtcgat	1200
ggcagtgaat gggtatctct tgcgtccctcg tatatatttga tttagaaactc atatctctca	1260
aacatagaca tatcagaatg tctcataacc aaaaattttagt tgatatgtcg tcatgacttt	1320
gcaatgecaa ttagtttacac cttaaaggaa tgcgttactg gagacactga aaagtgtccg	1380
agagaggctg ttgttacccat atatgtccca agatttgcata tctccgggggg agtgatttat	1440
gtaattgttc taatgtacaac atgtcaatgc tatcaactg gcaatgttataat tgcgtcaagac	1500
ggcagccaaa cattgtatgtt gatcgataat caaacatgtt caatgttataat aattgttataa	1560
atcctcatat caacaggaa atatctggaa agtcaaggat acaatgttataat gcatgttca	1620
gtcggcaatc ctgttccac tgacaaggctg gacataacaa gtcaatgttataat caacatcaac	1680
caatccattt aacaatccaa attttatcta gataatgttataat aggcttataat tgacaaggata	1740
aatctcaact taattggccc aagcggttcaa ttgttctaa taataatatac agtctctca	1800
tttatttat tattgtattt catgttataat ttgttactgttataat aatcaaaaaca ttcatataaa	1860
tataacaat ttatagatga tcctgatttataat tacaatgttataat acaaaaagaga acgttataat	1920
ggcaaaagcca gtaaggttataat tatgttaggtt attgtatgttataat	1968

&lt;210&gt; SEQ ID NO 36

&lt;211&gt; LENGTH: 1929

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Ghana virus

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<400> SEQUENCE: 36

atgctttctc	agctccaaaa	aaattactta	gacaactcaa	accaacaagg	tgataaaaatg	60
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aaagatctca	ataagtctta	ttatgttaaa	aacaagaattt	ataacgtttc	aaatcttatta	180
aatgaaagtc	tgcacgatat	caagtttgt	atttattgtt	tattctca	gctaatttac	240
attacaataa	tcaatataat	cacaatatac	attgttataa	ctcgctgaa	agtaaatgac	300
aacatcaatc	aaaggatggc	agaacttaca	agcaatatac	cagtcctgaa	ctttaatctt	360
aatcaattga	caaacaaaat	tcaaagagaa	attattccta	ggatcactt	tattgacaca	420
gcaaccacca	ttacaattcc	tagtgcatt	acttacat	tagcaactt	gacaaccaga	480
atctcggaat	tattgccgtc	aatcaaccaa	aagtgtgagt	tcaagacacc	gacacttgtc	540
ctgaatgact	gcagaataaa	ctgtacccc	ccactaaacc	cgtctgtatgg	agtggaaaatg	600
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gtacctacaa	tttactatta	tcggattcca	ggattataca	atagaacagc	attggacgaa	720
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 41

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1				5					10				15		

Lys	Ile	Glu	Asn	Glu	Leu	Ala	Arg	Ile	Lys	Lys
		20						25		

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**1.** A replication-competent recombinant Cedar virus (rCedV) chimera wherein one or both of the F and G envelope glycoprotein genes of CedV are replaced with one or both of the F and G envelope glycoprotein genes, respectively, of a non-CedV henipavirus.

**2.** The rCedV chimera of claim **1**, wherein the non-CedV henipavirus is selected from the group consisting of Hendra virus (HeV), Nipah virus (NiV), Ghana virus (GhV), and Mojiang virus (MojV).

**3.** The rCedV chimera of claim **1**, wherein the non-CedV henipavirus is selected from the Malaysian strain of NiV (NiV-M) and the Bangladesh strain of NiV (NiV-B).

**4.** The rCedV chimera of claim **2**, comprising the F and G envelope glycoprotein genes of HeV (rCedV-HeV).

**5.** The rCedV chimera of claim **2**, comprising the F and G envelope glycoprotein genes of NiV (rCedV-NiV).

**6.** The rCedV chimera of claim **3**, comprising the F and G envelope glycoprotein genes of NiV-M (rCedV-NiV-M).

**7.** The rCedV chimera of claim **3**, comprising the F and G envelope glycoprotein genes of NiV-B (rCedV-NiV-B).

**8.** The rCedV chimera of claim **1**, further comprising a reporter sequence.

**9.** The rCedV of claim **8**, wherein the reporter sequence encodes green fluorescent protein (GFP) or luciferase protein (Luc).

**10.** (canceled)

**11.** A replication-competent recombinant Cedar virus (rCedV) chimera, comprising the F and G envelope glycoprotein genes of CedV, further comprising a coding sequence for one or both of (i) a soluble F envelope glycoprotein (sF) of a non-CedV henipavirus, (ii) a soluble G envelope glycoprotein (sG) of a non-CedV henipavirus.

**12.** The rCedV chimera of claim **11**, wherein the sF coding sequence, the sG coding sequence, or both, are from NiV.

**13.** The rCedV chimera of claim **11**, wherein the sF coding sequence, the sG coding sequence, or both, are from HeV.

**14.** A replication-competent recombinant Cedar virus (rCedV) chimera, comprising one or both of (i) a gene

encoding a henipavirus F envelope protein fusion protein, and (ii) a gene encoding a henipavirus G envelope protein fusion protein, wherein the fusion protein comprises the ectodomain and transmembrane domain of a non-CedV henipavirus F envelope protein or G envelope protein, respectively, fused to the cytoplasmic tail domain of CedV F envelope protein or G envelope protein, respectively, or the fusion protein comprises the ectodomain of a non-CedV henipavirus F envelope protein or G envelope protein, respectively, fused to the transmembrane domain and cytoplasmic tail domain of CedV F envelope protein or G envelope protein, respectively.

**15.** The rCedV chimera of claim **14**, wherein the non-CedV henipavirus is selected from the group consisting of HeV, NiV, GhV, and MojV.

**16.** (canceled)

**17.** The rCedV chimera of claim **14**, wherein the non-CedV henipavirus is the Malaysian strain of NiV (NiV-M) or the Bangladesh strain of NiV (NiV-B).

**18.** A vaccine composition, comprising a rCedV chimera according to claim **1** and a pharmaceutically acceptable carrier.

**19.** The vaccine composition of claim **18**, further comprising an adjuvant.

**20.** The vaccine composition of claim **18**, further comprising one or both of (i) a soluble F envelope glycoprotein (sF) of a non-CedV henipavirus, (ii) a soluble G envelope glycoprotein (sG) of a non-CedV henipavirus.

**21.** The vaccine composition of claim **20**, wherein the non-CedV henipavirus sG and sF comprise NiV sG and sF or HeV sG and sF.

**22.** (canceled)

**23.** A method of treating, reducing the risk of, or preventing henipavirus infection in a subject in need thereof, comprising administering to the subject an effective amount of the vaccine composition of claim **18**.

**24-30.** (canceled)

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