

that can be used to direct VSV/CDV hybrids include, without limitation, urokinase plasminogen activator uPA polypeptides, cytokines such as IL-13 or IL-6, single chain T cell receptors (scTCRs), echistatin polypeptides, stem cell factor (SCF), EGF and integrin binding polypeptides.

5 In some cases, a VSV/CDV hybrid provided herein can have a nucleic acid molecule that includes a sequence encoding an interferon (IFN) polypeptide (e.g., a human IFN- β polypeptide), a sodium iodide symporter (NIS) polypeptide (e.g., a human NIS polypeptide), a fluorescent polypeptide (e.g., a GFP polypeptide), any appropriate therapeutic transgene (e.g., HSV-TK or cytosine deaminase), polypeptide that antagonizes
10 host immunity (e.g., influenza NS1, HSV γ 34.5, or SOCS1), or tumor antigen (e.g., cancer vaccine components). The nucleic acid encoding the IFN polypeptide can be positioned between the nucleic acid encoding the VSV M polypeptide and the nucleic acid encoding the VSV L polypeptide. Such a position can allow the viruses to express an amount of the IFN polypeptide that is effective to activate anti-viral innate immune responses in non-
15 cancerous tissues, and thus alleviate potential viral toxicity, without impeding efficient viral replication in cancer cells. The nucleic acid encoding the NIS polypeptide can be positioned between the nucleic acid encoding the VSV M polypeptide and the VSV L polypeptide. Such a position of can allow the viruses to express an amount of the NIS polypeptide that (a) is effective to allow selective accumulation of iodide in infected cells,
20 thereby allowing both imaging of viral distribution using radioisotopes and radiotherapy targeted to infected cancer cells, and (b) is not so high as to be toxic to infected cells. Positioning the nucleic acid encoding an IFN polypeptide between the nucleic acid encoding the VSV M polypeptide and the nucleic acid encoding the VSV L polypeptide and positioning the nucleic acid encoding a NIS polypeptide between the nucleic acid
25 encoding the VSV M polypeptide and the VSV L polypeptide within the genome of a VSV can result in VSVs that are viable, that have the ability to replicate and spread, that express appropriate levels of functional IFN polypeptides, and that expression appropriate levels of functional NIS polypeptides to take up radio-iodine for both imaging and radio-virotherapy.

30 In ~~general, one aspect, the present disclosure refers to of this document features a~~ CDV F polypeptide having signal peptide sequence that is less than 75 amino acid residues in length. The signal

peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide.

In another embodimentexample, this document features a nucleic acid molecule encoding a CDV F polypeptide. In one aspect, the present disclosure refers to a nucleic acid molecule encoding a CDV F polypeptide disclosed herein. The CDV F polypeptide can have a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide.

In another embodimentexample, this document features a recombinant virus comprising a CDV F polypeptide. In one aspect, the present disclosure refers to a recombinant virus comprising a CDV F polypeptide disclosed herein. The CDV F polypeptide can have a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide.

In another embodimentexample, this document features a recombinant virus comprising a nucleic acid molecule. In one aspect, the present disclosure refers to a recombinant virus comprising a nucleic acid molecule disclosed herein. The nucleic acid molecule can encode a CDV F polypeptide. The CDV F polypeptide can have a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at

least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide.

5 In another ~~embodiment~~aspect, ~~this document features~~the present disclosure refers
to a CDV H polypeptide comprising 454A, 464A, 479A, 494A, 510A, 520A, 525A,
526A, 527S, 528A, 529A, 537A, 539A, 547A, 548A, or a combination thereof according
to the amino acid numbering of SEQ ID NO:2. The CDV H polypeptide can comprise a
combination of two, three, four, five, or six of 454A, 464A, 479A, 494A, 510A, 520A,
10 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A. The CDV H polypeptide
can comprise a combination of seven, eight, nine, ten, or eleven of 454A, 464A, 479A,
494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A. The
CDV H polypeptide can comprise a combination of 12, 13, or 14 of 454A, 464A, 479A,
494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A. The
15 CDV H polypeptide can comprise 454A, 464A, 479A, 494A, 510A, 520A, 525A, 526A,
527S, 528A, 529A, 537A, 539A, 547A, and 548A. The CDV H polypeptide can
comprise M437 according to the amino acid numbering of SEQ ID NO:5.

In another ~~embodiment~~aspect, ~~this document features~~the present disclosure refers
to a CDV H polypeptide comprising the sequence set forth in Figure 11 except that ~~the~~
20 ~~said~~ sequence comprises a mutation of a presented amino acid residue selected from the
group consisting of P454, V/L/F460, L/F/W479, I494, I/L/V510, Y520, Y/N525, D/G526,
I/V527, S/T528, R529, Y/D537, Y539, Y/F547, and T/M548 according to the amino acid
numbering of SEQ ID NO:5. The CDV H polypeptide can comprise a mutation of two,
three, four, five, or six presented amino acid residues selected from the group. The CDV
25 H polypeptide can comprise a mutation of seven, eight, nine, ten, or eleven presented
amino acid residues selected from the group. The CDV H polypeptide can comprise a
mutation of 12, 13, or 14 presented amino acid residues selected from the group. The
CDV H polypeptide can comprise a mutation of the presented amino acid residues of the
group. The CDV H polypeptide can comprise M437 according to the amino acid
30 numbering of SEQ ID NO:5.

In another ~~embodiment~~example, this document features a nucleic acid molecule
encoding a CDV H polypeptide. In one aspect, the present disclosure refers to a nucleic
acid molecule encoding a CDV H polypeptide as disclosed herein. The CDV H
polypeptide can comprise the sequence set forth in

Figure 11 except that the sequence comprises a mutation of a presented amino acid residue selected from the group consisting of P454, V/L/F460, L/F/W479, I494, I/L/V510, Y520, Y/N525, D/G526, I/V527, S/T528, R529, Y/D537, Y539, Y/F547, and T/M548 according to the amino acid numbering of SEQ ID NO:5. The CDV H polypeptide can comprise a mutation of two, three, four, five, or six presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of seven, eight, nine, ten, or eleven presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of 12, 13, or 14 presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of the presented amino acid residues of the group. The CDV H polypeptide can comprise M437 according to the amino acid numbering of SEQ ID NO:5.

In another embodiment example, this document features a recombinant virus comprising a CDV H polypeptide. In one aspect, the present disclosure refers to a recombinant virus comprising a CDV H polypeptide disclosed herein. The CDV H polypeptide comprising the sequence set forth in Figure 11 except that the sequence comprises a mutation of a presented amino acid residue selected from the group consisting of P454, V/L/F460, L/F/W479, I494, I/L/V510, Y520, Y/N525, D/G526, I/V527, S/T528, R529, Y/D537, Y539, Y/F547, and T/M548 according to the amino acid numbering of SEQ ID NO:5. The CDV H polypeptide can comprise a mutation of two, three, four, five, or six presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of seven, eight, nine, ten, or eleven presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of 12, 13, or 14 presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of the presented amino acid residues of the group. The CDV H polypeptide can comprise M437 according to the amino acid numbering of SEQ ID NO:5. The virus can comprise a CDV F polypeptide, wherein the CDV F polypeptide comprises a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide

can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide.

In another embodimentexample, this document features a recombinant virus comprising a nucleic acid molecule encoding a CDV H polypeptide. The CDV H polypeptide can comprise the sequence set forth in Figure 11 except that the sequence comprises a mutation of a presented amino acid residue selected from the group consisting of P454, V/L/F460, L/F/W479, I494, I/L/V510, Y520, Y/N525, D/G526, I/V527, S/T528, R529, Y/D537, Y539, Y/F547, and T/M548 according to the amino acid numbering of SEQ ID NO:5. The CDV H polypeptide can comprise a mutation of two, three, four, five, or six presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of seven, eight, nine, ten, or eleven presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of 12, 13, or 14 presented amino acid residues selected from the group. The CDV H polypeptide can comprise a mutation of the presented amino acid residues of the group. The CDV H polypeptide can comprise M437 according to the amino acid numbering of SEQ ID NO:5. The virus can comprise a nucleic acid molecule encoding a CDV F polypeptide. The CDV F polypeptide can have a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide.

In another embodimentexample, this document features a recombinant virus described herein that is a hybrid virus of (a) CDV and (b) VSV, MeV, or Adenovirus.

In another embodimentaspect, ~~this document features~~ the present disclosure refers to a replication-competent vesicular stomatitis virus comprising an RNA molecule, wherein ~~the said~~ RNA molecule comprises a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive

sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide, and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein ~~the said~~ RNA molecule lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a functional VSV G polypeptide. The CDV F polypeptide can have a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide. The CDV H polypeptide can be a CDV H polypeptide described in one of the preceding paragraphs. The CDV H polypeptide can comprises an amino acid sequence of a single chain antibody. The single chain antibody can be a single chain antibody directed to CD19, CD20, CD38, CD46, EGFR, α FR, HER2/neu, or PSMA. The RNA molecule can comprise a nucleic acid sequence that is a template for a positive sense transcript encoding a NIS polypeptide.

In another ~~embodiment~~example, this document features a composition comprising a virus of any of the preceding paragraphs. In one aspect, the present disclosure refers to a composition comprising any of the viruses disclosed herein.

In another ~~embodiment~~aspect, ~~this document features~~the present disclosure refers to a nucleic acid molecule comprising a nucleic acid strand comprising a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide, and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein ~~the said~~ nucleic acid strand lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a

functional VSV G polypeptide. The CDV F polypeptide can have a signal peptide sequence that is less than 75 amino acid residues in length. The signal peptide sequence can comprise no more than 75 amino acid residues of SEQ ID NO:6. The CDV F polypeptide can comprise SEQ ID NO:4 with the proviso that the CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4. A recombinant virus comprising the CDV F polypeptide and a CDV H polypeptide can exhibit increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and the CDV H polypeptide. The CDV H polypeptide can be a CDV H polypeptide described in one of the preceding paragraphs. The CDV H polypeptide can comprises an amino acid sequence of a single chain antibody. The single chain antibody can be a single chain antibody directed to CD19, CD20, CD38, CD46, EGFR, α FR, HER2/neu, or PSMA. The RNA molecule can comprise a nucleic acid sequence that is a template for a positive sense transcript encoding a NIS polypeptide.

In another embodiment example, this document features a composition comprising a nucleic acid molecule of any of the preceding paragraphs. In one aspect, the present disclosure refers to a composition comprising any of the nucleic acid molecules disclosed herein.

In another embodiment example, this document features a method for treating cancer. The method comprises administering a composition described herein (e.g., a composition containing a virus described herein) to a mammal comprising cancer cells, wherein the number of cancer cells within the mammal is reduced following the administration. In one aspect, the present disclosure refers to use of a composition disclosed herein in the manufacture of a medicament for treating cancer, wherein the medicament is to be administered to a mammal comprising cancer cells, wherein the number of cancer cells within said mammal is reduced following said administration. The mammal can be a human. The cancer can be myeloma, melanoma, glioma, lymphoma, mesothelioma, lung cancer, brain cancer, stomach cancer, colon cancer, rectum cancer, kidney cancer, prostate cancer, ovary cancer, breast cancer, pancreas cancer, liver cancer, or head and neck cancer.

In another embodiment example, this document features a method for inducing tumor regression in a mammal. The method comprises administering a composition described herein (e.g., a composition containing a virus described herein) to a mammal comprising a tumor, wherein the size of the tumor is reduced following the administration. In one aspect, the present disclosure refers to use of a composition disclosed herein in the manufacture of a medicament for inducing tumor regression in a mammal comprising a tumor, wherein the size of said tumor is reduced following said administration. The mammal can be a human. The cancer can be myeloma, melanoma, glioma, lymphoma, mesothelioma, lung cancer, brain cancer, stomach cancer, colon cancer, rectum cancer,

kidney cancer, prostate cancer, ovary cancer, breast cancer, pancreas cancer, liver cancer, or head and neck cancer.

In another ~~embodiment~~example, this document features a method for rescuing replication-competent vesicular stomatitis viruses from cells. The vesicular stomatitis viruses comprise an RNA molecule comprising a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide, and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein the RNA molecule lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a functional VSV G polypeptide. The method comprises (a) inserting nucleic acid encoding the RNA molecule into the cells under conditions wherein replication-competent vesicular stomatitis viruses are produced, and (b) harvesting the replication-competent vesicular stomatitis viruses.

In one aspect, the present disclosure refers to a method for rescuing replication-competent vesicular stomatitis viruses from cells, wherein said vesicular stomatitis viruses comprise an RNA molecule comprising a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide, and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein said RNA molecule lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a functional VSV G polypeptide, wherein said method comprises:

(a) inserting nucleic acid encoding said RNA molecule into said cells under conditions wherein replication-competent vesicular stomatitis viruses are produced, and (b) harvesting said replication-competent vesicular stomatitis viruses.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this ~~invention~~disclosure pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the ~~invention~~disclosure, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more ~~embodiments~~examples of the ~~invention~~disclosure are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the ~~invention~~disclosure will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF DRAWINGS

WHAT IS CLAIMED IS:

1. A CDV F polypeptide having signal peptide sequence that is less than 75 amino acid residues in length.
2. The CDV F polypeptide of claim 1, wherein said signal peptide sequence comprises no more than 75 amino acid residues of SEQ ID NO:6.
3. The CDV F polypeptide of any one of claims 1-2, wherein said CDV F polypeptide comprises SEQ ID NO:4 with the proviso that said CDV F polypeptide lacks at least amino acid residues 1 to 60 or lacks at least amino acid residues 1 to 105 of SEQ ID NO:4.
4. The CDV F polypeptide of any one of claims 1-3, wherein a recombinant virus comprising said CDV F polypeptide and a CDV H polypeptide exhibits increased fusogenic activity as compared to a comparable control recombinant virus comprising a full length, wild-type CDV F polypeptide and said CDV H polypeptide.
5. A nucleic acid molecule encoding a CDV F polypeptide of any one of claims 1-4.
6. A recombinant virus comprising a CDV F polypeptide of any one of claims 1-4.
7. A recombinant virus comprising a nucleic acid molecule of claim 5.
8. A CDV H polypeptide comprising 454A, 464A, 479A, 494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, 548A, or a combination thereof according to the amino acid numbering of SEQ ID NO:2.
9. The CDV H polypeptide of claim 8, wherein said CDV H polypeptide comprises a combination of two, three, four, five, or six of 454A, 464A, 479A, 494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A.

10. The CDV H polypeptide of claim 8, wherein said CDV H polypeptide comprises a combination of seven, eight, nine, ten, or eleven of 454A, 464A, 479A, 494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A.

11. The CDV H polypeptide of claim 8, wherein said CDV H polypeptide comprises a combination of 12, 13, or 14 of 454A, 464A, 479A, 494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A.

12. The CDV H polypeptide of claim 8, wherein said CDV H polypeptide comprises 454A, 464A, 479A, 494A, 510A, 520A, 525A, 526A, 527S, 528A, 529A, 537A, 539A, 547A, and 548A.

13. The CDV H polypeptide of claim 8, wherein said CDV H polypeptide comprises M437 according to the amino acid numbering of SEQ ID NO:5.

14. A CDV H polypeptide comprising the sequence set forth in Figure 11 except that said sequence comprises a mutation of a presented amino acid residue selected from the group consisting of P454, V/L/F460, L/F/W479, I494, I/L/V510, Y520, Y/N525, D/G526, I/V527, S/T528, R529, Y/D537, Y539, Y/F547, and T/M548 according to the amino acid numbering of SEQ ID NO:5.

15. The CDV H polypeptide of claim 14, wherein said CDV H polypeptide comprises a mutation of two, three, four, five, or six presented amino acid residues selected from said group.

16. The CDV H polypeptide of claim 14, wherein said CDV H polypeptide comprises a mutation of seven, eight, nine, ten, or eleven presented amino acid residues selected from said group.

17. The CDV H polypeptide of claim 14, wherein said CDV H polypeptide comprises a mutation of 12, 13, or 14 presented amino acid residues selected from said group.
18. The CDV H polypeptide of claim 14, wherein said CDV H polypeptide comprises a mutation of the presented amino acid residues of said group.
19. The CDV H polypeptide of claim 14, wherein said CDV H polypeptide comprises M437 according to the amino acid numbering of SEQ ID NO:5.
20. A nucleic acid molecule encoding a CDV H polypeptide of any one of claims 8-19.
21. A recombinant virus comprising a CDV H polypeptide of any one of claims 8-19.
22. The recombinant virus of claim 21, wherein said virus comprises a CDV F polypeptide of any one of claims 1-4.
23. A recombinant virus comprising a nucleic acid molecule of claim 20.
24. The recombinant virus of claim 23, wherein said virus comprises a nucleic acid molecule of claim 5.
25. The recombinant virus of any one of claims 6, 7, and 21-24, wherein said recombinant virus is hybrid virus of (a) CDV and (b) VSV, MeV, or Adenovirus.
26. A replication-competent vesicular stomatitis virus comprising an RNA molecule, wherein said RNA molecule comprises a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV

F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide, and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein said RNA molecule lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a functional VSV G polypeptide.

27. The virus of claim 26, wherein said CDV F polypeptide is a CDV F polypeptide of any one of claims 1-4.

28. The virus of any one of claims 26-27, wherein said CDV H polypeptide is a CDV H polypeptide of any one of claims 8-19.

29. The virus of any one of claims 26-28, wherein said CDV H polypeptide comprises an amino acid sequence of a single chain antibody.

30. The virus of claim 29, wherein said single chain antibody is a single chain antibody directed to CD19, CD20, CD38, CD46, EGFR, α FR, HER2/neu, or PSMA.

31. The virus of any one of claims 26-30, wherein said RNA molecule comprises a nucleic acid sequence that is a template for a positive sense transcript encoding a NIS polypeptide.

32. A composition comprising a virus of any one of claims 6, 7, and 21-31.

33. A nucleic acid molecule comprising a nucleic acid strand comprising a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide,

and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein said nucleic acid strand lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a functional VSV G polypeptide.

34. The nucleic acid molecule of claim 33, wherein said CDV F polypeptide is a CDV F polypeptide of any one of claims 1-4.

35. The nucleic acid molecule of any one of claims 33-34, wherein said CDV H polypeptide is a CDV H polypeptide of any one of claims 8-19.

36. The nucleic acid molecule of any one of claims 33-35, wherein said CDV H polypeptide comprises an amino acid sequence of a single chain antibody.

37. The nucleic acid molecule of claim 36, wherein said single chain antibody is a single chain antibody directed to CD19, CD20, CD38, CD46, EGFR, α FR, HER2/neu, or PSMA.

38. The nucleic acid molecule of any one of claims 33-37, wherein said RNA molecule comprises a nucleic acid sequence that is a template for a positive sense transcript encoding a NIS polypeptide.

39. A composition comprising a nucleic acid molecule of any one of claims 5, 20, and 33-38.

40. ~~A method for treating cancer, wherein said method comprises administering~~Use of a composition of any one of claims 32 and 39 in the manufacture of a medicament for treating cancer, wherein the medicament is to be administered to a mammal comprising cancer cells, wherein the number of cancer cells within said mammal is reduced following said administration.

41. The use~~method~~ of claim 40, wherein said mammal is a human.

42. The ~~use~~method of any one of claims 40-41, wherein said cancer is myeloma, melanoma, glioma, lymphoma, mesothelioma, lung cancer, brain cancer, stomach cancer, colon cancer, rectum cancer, kidney cancer, prostate cancer, ovary cancer, breast cancer, pancreas cancer, liver cancer, or head and neck cancer.

43. ~~A method for inducing tumor regression in a mammal, wherein said method comprises administering~~Use of a composition of any one of claims 32 and 39 ~~in the manufacture of a medicament for inducing tumor regression in a mammal to a mammal~~ comprising a tumor, wherein the size of said tumor is reduced following said administration.

44. The ~~use~~method of claim 43, wherein said mammal is a human.

45. The ~~use~~method of any one of claims 43-44, wherein said cancer is myeloma, melanoma, glioma, lymphoma, mesothelioma, lung cancer, brain cancer, stomach cancer, colon cancer, rectum cancer, kidney cancer, prostate cancer, ovary cancer, breast cancer, pancreas cancer, liver cancer, or head and neck cancer.

46. A method for rescuing replication-competent vesicular stomatitis viruses from cells, wherein said vesicular stomatitis viruses comprise an RNA molecule comprising a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV N polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV P polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV M polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV F polypeptide, a nucleic acid sequence that is a template for a positive sense transcript encoding a CDV H polypeptide, and a nucleic acid sequence that is a template for a positive sense transcript encoding a VSV L polypeptide, wherein said RNA molecule lacks a nucleic acid sequence that is a template for a positive sense transcript encoding a functional VSV G polypeptide, wherein said method comprises:

- (a) inserting nucleic acid encoding said RNA molecule into said cells under conditions wherein replication-competent vesicular stomatitis viruses are produced, and
- (b) harvesting said replication-competent vesicular stomatitis viruses.