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(72) Inventeurs/Inventors:
STOJDL, DAVID, CA;
BROWN, CHRISTOPHER, CA;
BELL, JOHN, CA

(73) Propriétaire/Owner:
OTTAWA HOSPITAL RESEARCH INSTITUTE, CA

(74) Agent: GOWLING WLG (CANADA) LLP

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(54) Title: ONCOLYTIC RHABDOVIRUS

(57) **Abrégé/Abstract:**

Embodiments of the invention include compositions and methods related to non- VSV rhabdoviruses and their use as anti-cancer therapeutics. Such rhabdo viruses possess tumor cell killing properties in vitro and in vivo.

Abstract

Embodiments of the invention include compositions and methods related to non-VSV rhabdoviruses and their use as anti-cancer therapeutics. Such rhabdo viruses possess tumor cell killing properties in vitro and in vivo.

DESCRIPTION

ONCOLYTIC RHABDOVIRUS

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10 I. FIELD OF THE INVENTION

This invention relates generally to virology and medicine. In certain aspects the invention relates to oncolytic viruses, particularly non-VSV oncolytic rhabdoviruses and oncolytic rhabdoviruses comprising a non-VSV glycoprotein.

II. BACKGROUND

15 A number of viruses have been shown to replicate in and kill a wide variety of tumor cells *in vitro* (Sindbis virus (Unno *et al.*, 2005); Sendai virus (Kinoh *et al.*, 2004); Coxsackie virus (Shafren *et al.*, 2004); Herpes simplex virus (Mineta *et al.*, 1995); Parvovirus (Abschuetz *et al.*, 2006); Adenovirus (Heise *et al.*, 2000); Polio virus (Gromeier *et al.*, 2000); Newcastle disease virus (Sinkovics and Horvath, 2000); Vesicular stomatitis virus (Stojdl *et al.*, 2000); Measles virus (Grote *et al.*, 2001); Reovirus (Coffey *et al.*, 1998); Retrovirus (Logg *et al.*, 2001); Vaccinia (Timiryasova *et al.*, 1999); and Influenza (Bergmann *et al.*, 2001)). In addition, such viruses have demonstrated efficacy in treating animal models of cancer.

25 Vesicular stomatitis virus (VSV), a well known and well studied rhabdovirus, has been shown to kill tumor cell lines in cell culture experiments, and has demonstrated efficacy in a variety of rodent cancer models (Stojdl *et al.*, 2000; Stojdl *et al.*, 2003). However, VSV does not kill all cancer cells.

SUMMARY OF THE INVENTION

Several newly identified rhabdoviruses are much more efficient at killing particular cancers or cancer cell lines than VSV. Also, VSV and attenuated mutants of VSV are 30 neurovirulent and cause CNS pathology in rodents and primates. Several rhabdoviruses do

not infect the CNS (*i.e.*, Muir Springs and Bahia Grande: Kerschner *et al.*, 1986), and demonstrate a more acceptable safety profile. In addition, therapies based on the novel rhabdoviruses can be used to treat cancers of the CNS, both primary and secondary. The rhabdoviruses of the invention (and/or other oncolytic agents) can be used in succession to
 5 bypass the host immune response against a particular therapeutic virus(es). This would allow prolonged therapy and improve efficacy.

Embodiments of the invention include compositions and methods related to non-VSV rhabdoviruses and their use as anti-cancer therapeutics. Such rhabdoviruses possess tumor cell killing properties *in vitro* and *in vivo*.

10 As used herein, a non-VSV rhabdovirus will include one or more of the following viruses or variants thereof: Arajas virus, Chandipura virus, Cocal virus, Isfahan virus, Maraba virus, Piry virus, Vesicular stomatitis Alagoas virus, BeAn 157575 virus, Boteke virus, Calchaqui virus, Eel virus American, Gray Lodge virus, Jurona virus, Klamath virus, Kwatta virus, La Joya virus, Malpais Spring virus, Mount Elgon bat virus, Perinet virus, Tupaia
 15 virus, Farmington, Bahia Grande virus, Muir Springs virus, Reed Ranch virus, Hart Park virus, Flanders virus, Kamese virus, Mosqueiro virus, Mossuril virus, Barur virus, Fukuoka virus, Kern Canyon virus, Nkolbisson virus, Le Dantec virus, Keuraliba virus, Connecticut virus, New Minto virus, Sawgrass virus, Chaco virus, Sena Madureira virus, Timbo virus, Almpiwar virus, Aruac virus, Bangoran virus, Bimbo virus, Bivens Arm virus, Blue crab
 20 virus, Charleville virus, Coastal Plains virus, DakArK 7292 virus, Entamoeba virus, Garba virus, Gossas virus, Humpty Doo virus, Joinjakaka virus, Kannamangalam virus, Kolongo virus, Koolpinyah virus, Kotonkon virus, Landjia virus, Manitoba virus, Marco virus, Nasoule virus, Navarro virus, Ngaingan virus, Oak-Vale virus, Obodhiang virus, Oita virus, Ouango virus, Parry Creek virus, Rio Grande cichlid virus, Sandjimba virus, Sigma virus,
 25 Sripur virus, Sweetwater Branch virus, Tibrogargan virus, Xiburema virus, Yata virus, Rhode Island, Adelaide River virus, Berrimah virus, Kimberley virus, or Bovine ephemeral fever virus. In certain aspects, non-VSV rhabdovirus can refer to the supergroup of Dimarhabdovirus (defined as rhabdovirus capable of infection both insect and mammalian cells). In specific embodiments, the rhabdovirus is not VSV. In particular aspects the non-
 30 VSV rhabdovirus is a Carajas virus, Maraba virus, Farmington, Muir Springs virus, and/or Bahia grande virus, including variants thereof.

One embodiment of the invention includes methods and compositions comprising an oncolytic non-VSV rhabdovirus or a recombinant oncolytic non-VSV rhabdovirus encoding one or more of rhabdoviral N, P, M, G and/or L protein, or variant thereof (including chimeras and fusion proteins thereof), having an amino acid identity of at least or at most 20, 30, 40, 50, 60, 65, 70, 75, 80, 85, 90, 92, 94, 96, 98, 99, 100%, including all ranges and percentages there between, to the N, P, M, G and/or L protein of Arajas virus, Chandipura virus, Cocal virus, Isfahan virus, Maraba virus, Piry virus, Vesicular stomatitis Alagoas virus, BeAn 157575 virus, Boteke virus, Calchaqui virus, Eel virus American, Gray Lodge virus, Jurona virus, Klamath virus, Kwatta virus, La Joya virus, Malpais Spring virus, Mount Elgon bat virus, Perinet virus, Tupaia virus, Farmington, Bahia Grande virus, Muir Springs virus, Reed Ranch virus, Hart Park virus, Flanders virus, Kamese virus, Mosqueiro virus, Mossuril virus, Barur virus, Fukuoka virus, Kern Canyon virus, Nkolbisson virus, Le Dantec virus, Keuraliba virus, Connecticut virus, New Minto virus, Sawgrass virus, Chaco virus, Sena Madureira virus, Timbo virus, Almpiwar virus, Aruac virus, Bangoran virus, Bimbo virus, Bivens Arm virus, Blue crab virus, Charleville virus, Coastal Plains virus, DakArK 7292 virus, Entamoeba virus, Garba virus, Gossas virus, Humpty Doo virus, Joinjakaka virus, Kannamangalam virus, Kolongo virus, Koolpinyah virus, Kotonkon virus, Landjia virus, Manitoba virus, Marco virus, Nasoule virus, Navarro virus, Ngaingan virus, Oak-Vale virus, Obodhiang virus, Oita virus, Ouango virus, Parry Creek virus, Rio Grande cichlid virus, Sandjimba virus, Sigma virus, Sripur virus, Sweetwater Branch virus, Tibrogargan virus, Xiburema virus, Yata virus, Rhode Island, Adelaide River virus, Berrimah virus, Kimberley virus, or Bovine ephemeral fever virus. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 12 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85 or more, including all integers or ranges there between, of these virus can be specifically excluded from the claim scope. VSV or any non-VSV rhabdovirus can be the background sequence into which a variant G-protein or other viral protein can be intergrated.

In another aspect of the invention, a non-VSV rhabdovirus, or a recombinant thereof, can comprise a nucleic acid segment encoding at least or at most 10, 20, 30, 40, 45, 50, 60, 65, 70, 80, 90, 100, 125, 175, 250 or more contiguous amino acids, including all value and ranges there between, of N, P, M, G or L protein of one or more non-VSV rhabdovirus, including chimeras and fusion proteins thereof. In certain embodiments a chimeric G protein will include a cytoplasmic, transmembrane, or both cytoplasmic and transmembrane portions of a VSV or non-VSV G protein.

Methods and compositions of the invention can include a second therapeutic virus, such as an oncolytic or replication defective virus. Oncolytic typically refers to an agent that is capable of killing, lysing, or halting the growth of a cancer cell. In terms of an oncolytic virus the term refers to a virus that can replicate to some degree in a cancer cell, cause the death, lysis, or cessation of cancer cell growth and typically have minimal toxic effects on non-cancer cells. A second virus includes, but is not limited to an adenovirus, a vaccinia virus, a Newcastle disease virus, an alphavirus, a parvovirus, a herpes virus, a rhabdovirus, a non-VSV rhabdovirus and the like. In other aspects, the composition is a pharmaceutically acceptable composition. The composition may also include a second anti-cancer agent, such as a chemotherapeutic, radiotherapeutic, or immunotherapeutic.

Further embodiments of the invention include methods of killing a hyperproliferative cell comprising contacting the cell with an isolated oncolytic rhabdovirus composition; or

Still further methods include the treatment of a cancer patient comprising administering an effective amount of an oncolytic rhabdovirus composition.

In certain aspects of the invention, a cell may be comprised in a patient and may be a hyperproliferative, neoplastic, pre-cancerous, cancerous, metastatic, or metastasized cell. A non-VSV rhabdovirus can be administered to a patient having a cell susceptible to killing by at least one non-VSV rhabdovirus or a therapeutic regime or composition including a non-VSV rhabdovirus. Administration of therapeutic compositions may be done 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more times with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more non-VSV rhabdovirus or recombinant non-VSV rhabdovirus, alone or in various combinations. The composition administered can have 10, 100, 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , or more viral particles or plaque forming units (pfu). Administration can be by intraperitoneal, intravenous, intra-arterial, intramuscular, intradermal, subcutaneous, or intranasal administration. In certain aspects, the compositions are administered systemically, particularly by intravascular administration, which includes injection, perfusion and the like. The methods of invention can further comprise administering a second anti-cancer therapy, such as a second therapeutic virus. In particular aspects a therapeutic virus can be an oncolytic virus, more particularly a non-VSV rhabdovirus. In other aspects, a second anti-cancer agent is a chemotherapeutic, a radiotherapeutic, an immunotherapeutic, surgery or the like.

Embodiments of the invention include compositions and methods related to a VSV rhabdoviruses comprising a heterologous G protein and their use as anti-cancer therapeutics. Such rhabdoviruses possess tumor cell killing properties *in vitro* and *in vivo*.

As used herein, a heterologous G protein includes non-VSV rhabdovirus. Non-VSV rhabdoviruses will include one or more of the following viruses or variants thereof: Arajas virus, Chandipura virus, Cocal virus, Isfahan virus, Maraba virus, Piry virus, Vesicular stomatitis Alagoas virus, BeAn 157575 virus, Boteke virus, Calchaqui virus, Eel virus American, Gray Lodge virus, Jurona virus, Klamath virus, Kwatta virus, La Joya virus, Malpais Spring virus, Mount Elgon bat virus, Perinet virus, Tupaia virus, Farmington, Bahia Grande virus, Muir Springs virus, Reed Ranch virus, Hart Park virus, Flanders virus, Kamese virus, Mosqueiro virus, Mossuril virus, Barur virus, Fukuoka virus, Kern Canyon virus, Nkolbisson virus, Le Dantec virus, Keuraliba virus, Connecticut virus, New Minto virus, Sawgrass virus, Chaco virus, Sena Madureira virus, Timbo virus, Almpiwar virus, Aruac virus, Bangoran virus, Bimbo virus, Bivens Arm virus, Blue crab virus, Charleville virus, Coastal Plains virus, DakArK 7292 virus, Entamoeba virus, Garba virus, Gossas virus, Humpty Doo virus, Joinjakaka virus, Kannamangalam virus, Kolongo virus, Koolpinyah virus, Kotonkon virus, Landjia virus, Manitoba virus, Marco virus, Nasoule virus, Navarro virus, Ngaingan virus, Oak-Vale virus, Obodhiang virus, Oita virus, Ouango virus, Parry Creek virus, Rio Grande cichlid virus, Sandjimba virus, Sigma virus, Sripur virus, Sweetwater Branch virus, Tibrogargan virus, Xiburema virus, Yata virus, Rhode Island, Adelaide River virus, Berrimah virus, Kimberley virus, or Bovine ephemeral fever virus. In certain aspects, non-VSV rhabdovirus can refer to the supergroup of Dimarhabdovirus (defined as rhabdovirus capable of infection both insect and mammalian cells). In particular aspects the non-VSV rhabdovirus is a Carajas virus, Maraba virus, Muir Springs virus, and/or Bahia grande virus, including variants thereof.

One embodiment of the invention includes methods and compositions comprising a oncolytic VSV rhabdovirus comprising a heterologous G protein or a recombinant oncolytic VSV rhabdovirus encoding one or more of non-VSV rhabdoviral N, P, M, G and/or L protein, or variant thereof (including chimeras and fusion proteins thereof), having an amino acid identity of at least or at most 20, 30, 40, 50, 60, 65, 70, 75, 80, 85, 90, 92, 94, 96, 98, 99, 100%, including all ranges and percentages there between, to the N, P, M, G, and/or L protein of a non-VSV rhabdovirus.

In another aspect of the invention, a VSV rhabdovirus comprising a heterologous G protein or recombinant thereof, can comprise a nucleic acid comprising a nucleic acid segment encoding at least or at most 10, 20, 30, 40, 45, 50, 60, 65, 70, 80, 90, 100, 125, 175, 250 or more contiguous amino acids, including all value and ranges there between, of N, P, M, G, or L protein of a non-VSV rhabdovirus, including chimeras and fusion proteins thereof. In certain aspects, a chimeric G protein may comprise a cytoplasmic, transmembrane, or both a cytoplasmic and transmembrane portion of VSV or a second non-VSV virus or non-VSV rhabdovirus.

Methods and compositions of the invention can include a second therapeutic virus, such as an oncolytic or replication defective virus. A second virus includes, but is not limited to an adenovirus, a vaccinia virus, a Newcastle disease virus, a herpes virus, a rhabdovirus, a non-VSV rhabdovirus and the like. In other aspects, the composition is a pharmaceutically acceptable composition. The composition may also include a second anti-cancer agent, such as a chemotherapeutic, radiotherapeutic, or immunotherapeutic.

Further embodiments of the invention include methods of killing a hyperproliferative cell comprising contacting the cell with an isolated oncolytic rhabdovirus, VSV comprising a heterologous G protein molecule, or a non-VSV rhabdovirus composition. Still further methods include the treatment of a cancer patient comprising administering an effective amount of such a viral composition.

In certain aspects of the invention, a cell may be comprised in a patient and may be a hyperproliferative, neoplastic, pre-cancerous, cancerous, metastatic, or metastasized cell. A virus of the invention can be administered to a patient having a cell susceptible to killing by at least one virus or a therapeutic regime or composition including a virus. Administration of therapeutic compositions may be done 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more times with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more virus, alone or in various combinations. The composition administered can have 10 , 100 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , or more viral particles or plaque forming units (pfu). Administration can be by intraperitoneal, intravenous, intra-arterial, intramuscular, intradermal, subcutaneous, or intranasal administration. In certain aspects, the compositions are administered systemically, particularly by intravascular administration, which includes injection, perfusion and the like. The methods of invention can further comprise administering a second anti-cancer therapy, such as a second therapeutic virus. In particular aspects a therapeutic virus can be an

oncolytic virus such as a VSV comprising a heterologous G protein, more particularly a non-VSV rhabdovirus. In other aspects, a second anti-cancer agent is a chemotherapeutic, a radiotherapeutic, an immunotherapeutic, surgery or the like.

Other embodiments of the invention are discussed throughout this application. Any
5 embodiment discussed with respect to one aspect of the invention applies to other aspects of the invention as well, and *vice versa*. The embodiments in the Detailed Description and Example sections are understood to be non-limiting embodiments of the invention that are applicable to all aspects of the invention.

The terms “inhibiting,” “reducing,” or “preventing,” or any variation of these terms,
10 when used in the claims and/or the specification includes any measurable decrease or complete inhibition to achieve a desired result. Desired results include but are not limited to palliation, reduction, slowing, or eradication of a cancerous or hyperproliferative condition, as well as an improved quality or extension of life.

The use of the word “a” or “an” when used in conjunction with the term “comprising”
15 in the claims and/or the specification may mean “one,” but it is also consistent with the meaning of “one or more,” “at least one,” and “one or more than one.”

Throughout this application, the term “about” is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value.

20 The use of the term “or” in the claims is used to mean “and/or” unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and “and/or.”

As used in this specification and claim(s), the words “comprising” (and any form of comprising, such as “comprise” and “comprises”), “having” (and any form of having, such as
25 “have” and “has”), “including” (and any form of including, such as “includes” and “include”) or “containing” (and any form of containing, such as “contains” and “contain”) are inclusive or open-ended and do not exclude additional, unrecited elements or method steps.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed

description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

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DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

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FIG. 1. Phylogenetic relationships between rhabdoviruses based on a GDE alignment of a relatively conserved region of the N protein (119 amino acids), and using the paramyxovirus Human parainfluenza virus 1 (HPIV-1) as the outgroup. The tree was generated by the neighbor-joining method and bootstrap values (indicated for each branch node) were estimated using 1000 tree replicas. Branch lengths are proportional to genetic distances. The scale bar corresponds to substitutions per amino acid site (Courtesy of H. Badrane and P.J. Walker).

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FIG. 2. Summary of *in vitro* tumor cell killing assay. Cells from the NCI 60 cell panel were infected for 96h with a series of dilution of various viruses. Cell viability was assayed using crystal violet staining to detect residual viable cells. The EC₅₀ was calculated from the resulting cell killing curves and summarized in table format. For clarity, the EC₅₀ values have been converted to a value from 1-7 as described in the legend. In addition, the shading has been used to indicate the EC₅₀ range (*i.e.*, darkest to lightest represents highest EC₅₀ to lowest EC₅₀ values). Viruses are abbreviated as follows: MS = Muir Springs, BG = Bahia Grande, NGG = Ngaingan, TIB = Tibrogargan, FMT = Farmington, MRB = Maraba, CRJ = Carajas, VSVHR = Vesicular Stomatitis Virus HR strain and VV = Vaccinia virus JX-963. This data demonstrates that not all rhabdoviruses are equally oncolytic, in fact closely related rhabdoviruses behave very differently on the same tumor cell lines. Thus there is currently no method to predict which rhabdoviruses have oncolytic potential. Empirical testing is required to identify good oncolytic candidate viruses.

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FIGs. 3A-3B. Rhabdovirus productivity on tumor cell lines. SNB19 human glioblastoma and NCI H226 human lung carcinoma cell lines were infected with various

rhabdoviruses (MOI=3) and monitored over time for virus production by plaque assay. The data shows that not all rhabdoviruses have the same ability to replicate in these tumor cell lines. NCIH226 cell reveal a great disparity in virus productivity with Bahia Grande not producing virus at all while Maraba virus is able to produce copious infectious virions.

5 **FIG. 4.** Schematic of rescue system to recover recombinant rhabdoviruses from plasmid DNA form. In this example, the Maraba virus has been cloned into a DNA plasmid between the T7 promoter and a rybozyme sequence from Hepatitis D virus. A549 cells are infected with T7 expressing vaccinia virus and then subsequently transfected with a Maraba genome vector engineered to express GFP. The rescued virions are purified and then used to
10 infect Vero cells for 24 hours, resulting in GFP expression in these cells when visualized by fluorescence microscopy.

FIG. 5. Bioselecting improved strains of oncolytic rhabdoviruses. Rhabdoviruses are quasi-species. Bahia Grande is not neuropathogenic but has the ability to kill human glioblastoma cells. The inventors contemplated improving its virulence while maintaining its
15 selectivity for cancer cells. To improve the virulence of a rhabdovirus for a tumor cell, the inventors selected virus mutants with increased replication capacity in a human glioblastoma cell line. Briefly, 5×10^5 SNB19 cells were infected with 2.5×10^6 viral particles, giving an MOI of 5. The initial inoculum had a volume of 200 μ l and was allowed 1 hour to infect before the cells were washed 10 times with PBS. The last wash was analyzed for viral
20 particles by plaque assay to ensure proper removal of input virus. At increasing time points, the entire supernatant was collected and replaced with fresh media. The collected media was used to infect new cells for amplification and was analyzed by plaque assay for the presence of viral particles. For the first passage, collections occurred at 4, 8, 12 and 24 hpi (hours post infection) until the initial time for viral release was determined. Viruses from the earliest
25 time point were amplified back to a population of 10^6 and then re-passed.

FIG. 6. Bioselecting improved strains of oncolytic rhabdoviruses. In this example, Bahia Grande virus underwent up to 6 iterative cycles of bioselection. The parental strain (WT) along with passages 4-6 were monitored for virus production in SNB19 cells at 4, 6 and
30 8 hours post infection. A clear and progressive improvement in speed of initial virus replication is evident during increasing rounds of bioselection. MRB = Maraba is included as an exemplar of rapid and desirable virus replication in the cancer cell line.

FIG. 7. Bahia Grande P13 underwent 13 rounds of bioselection. This virus demonstrated improved virus replication not only in the human glioblastoma used during the bioselection protocol, but on an unrelated human glioblastoma and a human ovarian carcinoma cell line. This demonstrates that rhabdoviruses can be bioselected to improve their oncolytic properties and these improvements are effective on other disparate cancers.

FIG. 8. Balb/C mice were infected intracranially with the indicated viruses and monitored for morbidity and/or mortality. Both wild type VSV (HR strain) and the delta M51 mutant strain of VSV were extremely neurotoxic, demonstrating hind limb paralysis within days of infection, while Bahia Grande and Muir Springs viruses showed no neurotoxicity. Bahia Grande P6 is a bioselected strain of Bahia Grande with improved replication in human glioblastoma cells. This strain also showed no neurotoxicity, demonstrating that rhabdoviruses can be bioselected for improved virulence on tumor cells, while maintaining their safety profile in normal healthy tissue.

FIG. 9. *In vivo* efficacy of Maraba and Carajas rhabdoviruses compared to Chandripura and WT VSV and delta 51 VSV 4T1 tumors (firefly luciferase expressing) were established in 5-8 week old Balb/C female mice by injecting 10^6 tumor cells in the left, rear mammary gland. After one week, mice were injected intravenously on day 1 & 2 (each dose = 10^7 pfu WT VSV, $\Delta 51$ GFP VSV, Maraba or Chandripura; or 10^8 pfu Carajas). Tumor responses were measured by bioluminescence imaging using an IVIS 200 (Xenogen) (measured as photons/s/cm²).

FIG. 10. Infectivity of G-less VSV pseudotyped with Isfahan G and VSV G protein.

FIG. 11. A one step growth curve of VSV WT, Isfahan and RVR IsfG1 viruses.

FIG. 12. RVR comprising an Isfahan G protein remains oncolytic. The cytotoxicity of Isfahan virus, VSV d51 and RVR IsfG1 were assessed on various cancer cell lines.

FIGs. 13A-13C. RVR comprising Isf G1 is able to escape immune response to VSV *in vivo*. *In vivo* luciferase detection was used to determine the amount of virus in mice inoculated with RVR IsfG1 or VSV. **FIG. 13A**, *in vivo* detection of recombinant virus injected into naïve mice. **FIG. 13B**, *in vivo* detection of VSV injected into mice immunized with VSV. **FIG. 13C**, *in vivo* detection of recombinant RVR IsfG1 virus injected into mice immunized with VSV.

FIG. 14. Virus yields from infected tumors. Tumors were infected with recombinant virus or VSV in the presence or absence of immunization with VSV (as indicated). Graphed data shows the amount virus resulting from the infection of the tumor.

FIG. 15. A one step growth curve of VSV WT, chandipura virus and RVR_{Cha}G¹.
5 Results show that the recombinant produces the same amount of virus as VSV.

FIG. 16. Cytotoxicity of VSV WT, chandipura virus and RVR_{Cha}G¹. Results show that the recombinant is as cytotoxic as VSV.

FIG. 17. A one step growth curve of VSV WT, Maraba virus and RVR_{Mar}G¹. Results show that recombinant virus titer was greater than VSV at 48 and 72h.

10 **FIG. 18.** Cytotoxicity of VSV WT, Maraba virus and RVR_{Mar}G¹. Results show that both maraba and the RVR_{Mar}G¹ are cytotoxic in tumor cells lines and that they are generally more cytotoxic to tumor cells than VSV WT.

DETAILED DESCRIPTION OF THE INVENTION

Aspects of the invention are based on the killing by non-VSV rhabdovirus or
15 pseudotyped rhabdovirus of several kinds or types cancer cells, which are resistant to killing by VSV. Some of the advantages of these oncolytic rhabdoviruses and recombinant rhabdoviruses include the following: (1) Antibodies to the inventive rhabdoviruses will be rare to non-existent in most populations of the world. (2) rhabdoviruses replicate more quickly than other oncolytic viruses such as adenovirus, reovirus, measles, parvovirus,
20 retrovirus, and HSV. (3) Rhabdovirus grow to high titers and are filterable through 0.2 micron filter. (4) The oncolytic rhabdoviruses and recombinants thereof have a broad host range, capable of infecting many different types of cancer cells and are not limited by receptors on a particular cell (*e.g.*, coxsackie, measles, adenovirus). (5) The rhabdovirus of the invention are amenable to genetic manipulation. (6) The rhabdovirus also has a
25 cytoplasmic life cycle and do not integrate in the genetic material a host cell, which imparts a more favorable safety profile.

Embodiments of the invention include compositions and methods related to non-VSV rhabdoviruses or pseudotyped rhabdoviruses and their use as anti-cancer therapeutics.

I. Family *Rhabdoviridae* (Rhabdovirus)

The archetypal rhabdoviruses are rabies and vesicular stomatitis virus (VSV), the most studied of this virus family. Although these viruses share similar morphologies, they are very different in their life cycle, host range, and pathology. Rhabdovirus is a family of
 5 bullet shaped viruses having non-segmented (-)sense RNA genomes. There are greater than 250 Rhabdoviruses known that infect mammals, fish, insects, and plants. The family is split into at least 5 genera: (1) Lyssavirus: including Rabies virus, other mammalian viruses, some insect viruses; (2) Vesiculovirus: including Vesicular Stomatitis Virus (VSV); (3) Ephemerovirus: including Bovine ephemeral fever virus (vertebrates); (4) Cytorhabdovirus:
 10 including Lettuce necrotic yellows virus (plants); and (5) Nucleorhabdovirus: including Potato yellow dwarf virus (plants). It has also been suggested that there is a supergroup of rhabdovirus denoted Dimarhabdovirus that include a variety of rhabdoviruses that infect both mammals and insects.

The family *Rhabdovirus* includes, but is not limited to: Arajas virus, Chandipura virus
 15 (AF128868 / gi:4583436, AJ810083 / gi:57833891, AY871800 / gi:62861470, AY871799 / gi:62861468, AY871798 / gi:62861466, AY871797 / gi:62861464, AY871796 / gi:62861462, AY871795 / gi:62861460, AY871794 / gi:62861459, AY871793 / gi:62861457, AY871792 / gi:62861455, AY871791 / gi:62861453), Cocal virus (AF045556 / gi:2865658), Isfahan virus (AJ810084 / gi:57834038), Maraba virus (SEQ ID NO:1-6),
 20 Carajas virus (SEQ ID NO:7-12, AY335185 / gi:33578037), Piry virus (D26175 / gi:442480, Z15093 / gi:61405), Vesicular stomatitis Alagoas virus, BeAn 157575 virus, Boteke virus, Calchaqui virus, Eel virus American, Gray Lodge virus, Jurona virus, Klamath virus, Kwatta virus, La Joya virus, Malpais Spring virus, Mount Elgon bat virus (DQ457103 / gi:91984805), Perinet virus (AY854652 / gi:71842381), Tupaia virus (NC_007020 /
 25 gi:66508427), Farmington, Bahia Grande virus (SEQ ID NO:13-18), Muir Springs virus, Reed Ranch virus, Hart Park virus, Flanders virus (AF523199 / gi:25140635, AF523197 / gi:25140634, AF523196 / gi:25140633, AF523195 / gi:25140632, AF523194 / gi:25140631, AH012179 / gi:25140630), Kamese virus, Mosqueiro virus, Mossuril virus, Barur virus, Fukuoka virus (AY854651 / gi:71842379), Kern Canyon virus, Nkolbisson virus, Le Dantec
 30 virus (AY854650 / gi:71842377), Keuraliba virus, Connecticut virus, New Minto virus, Sawgrass virus, Chaco virus, Sena Madureira virus, Timbo virus, Almpiwar virus (AY854645 / gi:71842367), Aruac virus, Bangoran virus, Bimbo virus, Bivens Arm virus, Blue crab virus, Charleville virus, Coastal Plains virus, DakArK 7292 virus, Entamoeba

virus, Garba virus, Gossas virus, Humpty Doo virus (AY854643 / gi:71842363), Joinjakaka virus, Kannamangalam virus, Kolongo virus (DQ457100 / gi|91984799 nucleoprotein (N) mRNA, partial cds); Koolpinyah virus, Kotonkon virus (DQ457099 / gi|91984797, AY854638 / gi:71842354); Landjia virus, Manitoba virus, Marco virus, Nasoule virus, 5 Navarro virus, Ngaingan virus (AY854649 / gi:71842375), Oak-Vale virus (AY854670 / gi:71842417), Obodhiang virus (DQ457098 / gi|91984795), Oita virus (AB116386 / gi:46020027), Ouango virus, Parry Creek virus (AY854647 / gi:71842371), Rio Grande cichlid virus, Sandjimba virus (DQ457102 / gi|91984803), Sigma virus (AH004209 / gi:1680545, AH004208 / gi:1680544, AH004206 / gi:1680542), Sripur virus, Sweetwater 10 Branch virus, Tibrogargan virus (AY854646 / gi:71842369), Xiburema virus, Yata virus, Rhode Island, Adelaide River virus (U10363 / gi:600151, AF234998 / gi:10443747, AF234534 / gi:9971785, AY854635 / gi:71842348), Berrimah virus (AY854636 / gi:71842350]), Kimberley virus (AY854637 / gi:71842352), or Bovine ephemeral fever virus (NC_002526 / gi:10086561).

15 Certain unassigned serotypes include (1) Bahia Grande group (Bahia Grande virus (BGV), Muir Springs virus (MSV), Reed Ranch virus (RRV); (2) Hart Park group (Flanders virus (FLAV), Hart Park virus (HPV), Kamese virus (KAMV), Mosqueiro virus (MQOV), Mossuril virus (MOSV); (3) Kern Canyon group (Barur virus (BARV), Fukuoka virus (FUKAV), Kern Canyon virus (KCV), Nkolbisson virus (NKOV); (4) Le Dantec group (Le 20 Dantec virus (LDV), Keuraliba virus (KEUV), (5) Sawgrass group (Connecticut virus (CNTV), New Minto virus (NMV), Sawgrass virus (SAWV); (6) Timbo group (Chaco virus (CHOV), Sena Madureira virus (SMV), Timbo virus (TIMV); and (7) other unassigned viruses (Almpiwar virus (ALMV), Aruac virus (ARUV), Bangoran virus (BGNV), Bimbo virus (BBOV), Bivens Arm virus (BAV), Blue crab virus (BCV), Charleville virus (CHVV), 25 Coastal Plains virus (CPV), DakArK 7292 virus (DAKV-7292), Entamoeba virus (ENTV), Garba virus (GARV), Gossas virus (GOSV), Humpty Doo virus (HDOOV), Joinjakaka virus (JOIV), Kannamangalam virus (KANV), Kolongo virus (KOLV), Koolpinyah virus (KOOLV), Kotonkon virus (KOTV), Landjia virus (LJAV), Manitoba virus (MNTBV), Marco virus (MCOV), Ngaingan, Nasoule virus (NASV), Navarro virus (NAVV), Ngaingan 30 virus (NGAV), Oak-Vale virus (OVRV), Obodhiang virus (OBOV), Oita virus (OITAV), Ouango virus (OUAV), Parry Creek virus (PCRV), Rio Grande cichlid virus (RGRCV), Sandjimba virus (SJAV), Sigma virus [X91062] (SIGMAV), Sripur virus (SRIV),

Sweetwater Branch virus (SWBV), Tibrogargan virus (TIBV), Xiburema virus (XIBV), Yata virus (YATAV).

Aspects of the invention may include, but is not limited to selecting non-VSV rhabdovirus or pseudotyped rhabdovirus based on growth in mammalian cell lines, lack of or
5 minimal toxicity in adult mice (animals), lack of or minimal toxicity in suckling mice (animals).

A. Rhabdoviral Genome

Typically the rhabdovirus genome is approximately 11 - 15kb with an approximately 50 nucleotide 3' leader and an approximately 60 nucleotide non-translated 5' region of a (-)
10 sense viral RNA (vRNA). Typically, rhabdovirus vRNA has 5 genes encoding 5 proteins. Rhabdoviruses have a conserved polyadenylation signal at the end of each gene and a short intergenic region between each of the 5 genes. All Rhabdoviruses contain five genes which encode the nucleocapsid protein (N), Phosphoprotein (P, also designated NS), matrix protein (M), glycoprotein (G), and large protein (L). Typically these genes are ordered on negative
15 sense vRNA as follows: 3'-N-P-M-G-(X)-L-5'. The order of the genes is important as it dictates the proportion of proteins synthesized. Any manipulations of a Rhabdovirus genome will typically include at least five transcription domains to maintain ability to infect and replicate at high levels. Rhabdoviruses have an endogenous RNA polymerase for transcription of plus sense messenger RNA (mRNA). The X gene does not occur in all
20 Rhabdoviruses. The X gene encodes a nonstructural protein found in the fish infectious hematopoietic necrosis virus (GenBank DQ164103 / gi|76262981; DQ164102 / gi|76262979; DQ164101 / gi|76262977; DQ164100 / gi|76262975; DQ164099 / gi|76262973; AB250935 / gi|112821165; AB250934 / gi|112821163; AB250933 / gi|112821161; AB250932 / gi|112821159; AB250931 / gi|112821157; AB250930 / gi|112821155; AB250929 /
25 gi|112821153; AB250928 / gi|112821151; AB250927 / gi|112821149, describing the G protein encoding nucleotide sequence), a nonstructural glycoprotein in the bovine ephemeral fever virus and a pseudogene in the rabies virus. The extra (X) gene has been found in different locations on the Rhabdovirus genome. Synthesis of the M protein in infected cells is cytopathic to the cell, and will eventually result in cell death.

30 Transmission of rhabdovirus varies depending on virus/host, but most are transmitted by direct contact - *e.g.*, transmission of rabies by animal bites or insect vector. There is a long incubation period *in vivo*, but this is not reflected in the kinetics of virus replication in

culture. The G protein spikes bind to receptors on the surface of host cells and the viruses enters the cell by endocytosis and fusion with the membrane of the vesicle, mediated by the G protein.

With no intent to be limited to a particular theory, the receptor molecules for rhabdoviruses are believed to be phospholipids rather than specific proteins. Rhabdoviral replication occurs in the cytoplasm - both the L and NS proteins are necessary for transcription - neither function alone. Five monocistronic mRNAs are produced, capped at the 5' end and polyadenylated at the 3' end and each containing the leader sequence from the 3' end of the vRNA at the 5' end of the message. These mRNAs are made by sequential transcription of the ORFs in the virus genome and it has been shown that the intergenic sequence is responsible for termination and re-initiation of transcription by the polymerase between each gene, thus producing separate transcripts.

Progeny vRNA is made from a (+)sense intermediate. The genome is replicated by the L + P polymerase complex (as in transcription), but additional host cell factors are also required. It is characteristic of Rhabdoviruses that these events all occur in a portion of the cytoplasm which acts as a virus 'factory' and appears as a characteristic cytoplasmic inclusion body.

B. Viral Protein Variants

In certain embodiments, a rhabdovirus or a non-VSV rhabdovirus will comprise a variant of one or more of the N, P, M, G, and/or L proteins. In certain aspects of the invention these viral protein variants can be comprised in a proteinaceous composition, which is further defined below. Proteinaceous compositions include viral particles and other compositions having one or more viral protein components. These polypeptide variant(s) can be engineered or selected for a modification in one or more physiological or biological characteristics, such as host cell range, host cell specificity, toxicity to non-target cells or organs, replication, cytotoxicity to a target cell, killing of cancer cells, stasis of cancer cells, infectivity, manufacturing parameters, size of virus particle, stability of viral particles, in vivo clearance, immunoreactivity, and the like. These polypeptide variant can be engineered by using a variety of methodology known in the art, including various mutagenesis techniques described see below. In certain aspects, the N, P, M, G, and/or L proteins can be heterologous to a virus (e.g., a VSV may comprise a Isfahan G protein or variant thereof).

C. Recombinant Rhabdoviruses

Recombinant rhabdovirus can be produced (1) entirely using cDNAs or (2) a combination of cDNAs transfected into a helper cell, or (3) cDNAs transfected into a cell, which is further infected with a minivirus providing in trans the remaining components or activities needed to produce either an infectious or non-infectious recombinant rhabdovirus. Using any of these methods (*e.g.*, minivirus, helper cell line, or cDNA transfection only), the minimum components required are an RNA molecule containing the cis-acting signals for (1) encapsidation of the genomic (or antigenomic) RNA by the Rhabdovirus N protein, and (2) replication of a genomic or antigenomic (replicative intermediate) RNA equivalent.

By a replicating element or replicon, the inventors mean a strand of RNA minimally containing at the 5' and 3' ends the leader sequence and the trailer sequence of a rhabdovirus. In the genomic sense, the leader is at the 3' end and the trailer is at the 5' end. Any RNA-placed between these two replication signals will in turn be replicated. The leader and trailer regions further must contain the minimal cis-acting elements for purposes of encapsidation by the N protein and for polymerase binding which are necessary to initiate transcription and replication.

For preparing engineered rhabdoviruses a minivirus containing the G gene would also contain a leader region, a trailer region and a G gene with the appropriate initiation and termination signals for producing a G protein mRNA. If the minivirus further comprises a M gene, the appropriate initiation and termination signals for producing the M protein mRNA must also present.

For any gene contained within the engineered rhabdovirus genome, the gene would be flanked by the appropriate transcription initiation and termination signals which will allow expression of those genes and production of the protein products. Particularly a heterologous gene, which is a gene that is typically not encoded by a rhabdovirus as isolated from nature or contains a rhabdovirus coding region in a position, form or context that it typically is not found, *e.g.*, a chimeric G-protein.

To produce "non-infectious" engineered Rhabdovirus, the engineered Rhabdovirus must have the minimal replicon elements and the N, P, and L proteins and it must contain the M gene (one example is the Δ G or G-less construct, which is missing the coding region for the G protein). This produces virus particles that are budded from the cell, but are non-

infectious particles. To produce “infectious” particles, the virus particles must additionally comprise proteins that can mediate virus particle binding and fusion, such as through the use of an attachment protein or receptor ligand. The native receptor ligand of rhabdoviruses is the G protein.

- 5 A “suitable cell” or “host cell” means any cell that would permit assembly of the recombinant rhabdovirus.

To prepare infectious virus particles, an appropriate cell line (*e.g.*, BHK cells) is first infected with vaccinia virus vTF7-3 (Fuerst *et al.*, 1986) or equivalent which encodes a T7 RNA polymerase or other suitable bacteriophage polymerase such as the T3 or SP6
10 polymerases (see Usdin *et al.*, 1993 or Rodriguez *et al.*, 1990). The cells are then transfected with individual cDNA containing the genes encoding the G, N, P, L and M Rhabdovirus proteins. These cDNAs will provide the proteins for building a recombinant Rhabdovirus particle. Cells can be transfected by any method known in the art (*e.g.*, liposomes, electroporation, *etc.*).

- 15 Also transfected into the cell line is a “polycistronic cDNA” containing the rhabdovirus genomic RNA equivalent. If the infectious, recombinant rhabdovirus particle is intended to be lytic in an infected cell, then the genes encoding for the N, P, M and L proteins must be present as well as any heterologous nucleic acid segment. If the infectious, recombinant rhabdovirus particle is not intended to be lytic, then the gene encoding the M
20 protein is not included in the polycistronic DNA. By “polycistronic cDNA” it is meant a cDNA comprising at least transcription units containing the genes which encode the N, P and L proteins. The recombinant rhabdovirus polycistronic DNA may also contain a gene encoding a protein variant or polypeptide fragment thereof, or a therapeutic nucleic acid. Alternatively, any protein to be initially associated with the viral particle first produced or
25 fragment thereof may be supplied in trans.

Another embodiment contemplated is a polycistronic cDNA comprising a gene encoding a reporter protein or fluorescent protein (*e.g.*, green fluorescent protein and its derivatives, β -galactosidase, alkaline phosphatase, luciferase, chloramphenicol acetyltransferase, *etc.*), the N-P-L or N-P-L-M genes, and/or a fusion protein or a therapeutic
30 nucleic acid. Another polycistronic DNA contemplated may contain a gene encoding a

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protein variant, a gene encoding a reporter, a therapeutic nucleic acid, and/or either the N-P-L genes or the N-P-L-M genes.

The first step in generating a recombinant rhabdovirus is expression of an RNA that is a genomic or antigenomic equivalent from a cDNA. Then that RNA is packaged by the N protein and then replicated by the P/L proteins. The virus thus produced can be recovered. If
5 the G protein is absent from the recombinant RNA genome, then it is typically supplied in trans. If both the G and the M proteins are absent, then both are supplied in trans.

For preparing “non-infectious rhabdovirus” particles, the procedure may be the same as above, except that the polycistronic cDNA transfected into the cells would contain the N, P
10 and L genes of the Rhabdovirus only. The polycistronic cDNA of non-infectious rhabdovirus particles may additionally contain a gene encoding a reporter protein or a therapeutic nucleic acid. For additional description regarding methods of producing a recombinant rhabdovirus lacking the gene encoding the G protein, see Takada *et al.* (1997).

1. Culturing of Cells to Produce Virus

15 Transfected cells are usually incubated for at least 24 hr at the desired temperature, usually about 37 °C. For non-infectious virus particles, the supernatant is collected and the virus particles isolated. For infectious virus particles, the supernatant containing virus is harvested and transferred to fresh cells. The fresh cells are incubated for approximately 48 hours, and the supernatant is collected.

20 2. Purification of the Recombinant Rhabdovirus

The terms “isolation” or “isolating” a Rhabdovirus means the process of culturing and purifying the virus particles such that very little cellular debris remains. One example would be to take the virion containing supernatant and pass them through a 0.1-0.2 micron pore size filter (*e.g.*, Millex-GS, Millipore) to remove the virus and cellular debris. Alternatively,
25 virions can be purified using a gradient, such as a sucrose gradient. Recombinant rhabdovirus particles can then be pelleted and resuspended in whatever excipient or carrier is desired. Titers can be determined by indirect immunofluorescence using antibodies specific for particular proteins.

3. Methods of Making Recombinant Rhabdoviruses using cDNAs and a Minivirus or a Helper Cell Line

Both “miniviruses” and “helper cells” (also known as “helper cell lines”) provide the same thing: to provide a source of rhabdovirus proteins for rhabdovirus virion assembly. One
5 example of a rhabdovirus minivirus is the VSV minivirus which expresses only the G and M protein, as reported by Stillman *et al.*, (1995). Helper viruses and miniviruses are used as methods of providing rhabdovirus proteins that are not produced from transfected DNA encoding the genes for rhabdovirus proteins.

When using a minivirus, cells are infected with vaccinia virus as described above for
10 purposes of providing T7 RNA polymerase. The desired polycistronic RNA, and plasmids containing the N, P and L genes are transfected into cells. The transfection mix is removed after approximately 3 hrs, and cells are infected with the minivirus at a multiplicity of infection (m.o.i.) of about 1. The minivirus supplies the missing G and/or M proteins. The polycistronic RNA transfected into the cell will depend on whether an infectious or non-
15 infectious recombinant rhabdovirus is wanted.

Alternatively, a minivirus could be used to provide the N, P, and L genes. The minivirus could also be used to produce the M protein in addition to N, P, and L. The minivirus also can produce the G protein.

When using a helper cell line, the genes encoding the missing rhabdovirus proteins
20 are produced by the helper cell line. The helper cell line has N, P, L, and G proteins for production of recombinant rhabdovirus particles which does not encode wild-type G protein. The proteins are expressed from genes or DNAs that are not part of the recombinant virus genome. These plasmids or other vector system is stably incorporated into the genome of the cell line. The proteins are then produced from the cell's genome and not from a replicon in
25 the cytoplasm. The helper cell line can then be transfected with a polycistronic DNA and plasmid cDNAs containing the other rhabdovirus genes not expressed by the helper virus. The polycistronic RNA used will depend on whether an infectious or non-infectious recombinant rhabdovirus is desired. Otherwise, supply of missing gene products (*e.g.*, G and/or M) would be accomplished as described above.

II. VIRAL COMPOSITIONS

The present invention concerns rhabdoviruses that are advantageous in the study and treatment of hyperproliferative or neoplastic cells (*e.g.*, cancer cells) and hyperproliferative or neoplastic conditions (*e.g.*, cancer) in a patient. It may concern, but is not limited to, rhabdoviruses with a reduced neurovirulence, *e.g.*, non-VSV rhabdoviruses. In certain aspects rhabdovirus that encode or contain one or more protein components (N, P, M, G, and/or L proteins) or a nucleic acid genome distinct from those of VSV (*i.e.*, at least or at most 10, 20, 40, 50, 60, 70, 80% identical at the amino acid or nucleotide level), and/or that have been constructed with one or more mutations or variations as compared to a wild-type virus or viral proteins such that the virus has desirable properties for use against cancer cells, while being less toxic or non-toxic to non-cancer cells than the virus as originally isolated or VSV. The teachings described below provide various examples of protocols for implementing methods and compositions of the invention. They provide background for generating mutated or variant viruses through the use of bioselection or recombinant DNA or nucleic acid technology.

A. Proteinaceous Compositions

Proteinaceous compositions of the invention include viral particles and compositions including the viral particles, as well as isolated polypeptides. In certain embodiments, the present invention concerns generating or isolating pseudotyped or non-VSV oncolytic rhabdoviruses (rhabdoviruses that lyse, kill, or retard growth of cancer cells). In certain embodiments, rhabdoviruses will be engineered to include polypeptide variants of rhabdovirus proteins (N, P, M, G, and/or L) and/or therapeutic nucleic acids that encode therapeutic polypeptides. Other aspects of the invention include the isolation of rhabdoviruses that lack one or more functional polypeptides or proteins. In other embodiments, the present invention concerns rhabdoviruses and their use in combination with or included within proteinaceous compositions as part of a pharmaceutically acceptable formulation.

As used herein, a “protein” or “polypeptide” refers to a molecule comprising polymer of amino acid residues. In some embodiments, a wild-type version of a protein or polypeptide are employed, however, in many embodiments of the invention, all or part of a viral protein or polypeptide is absent or altered so as to render the virus more useful for the treatment of a patient. The terms described above may be used interchangeably herein. A

“modified protein” or “modified polypeptide” or “variant protein” or “variant polypeptide” refers to a protein or polypeptide whose chemical structure or amino acid sequence is altered with respect to the wild-type or a reference protein or polypeptide. In some embodiments, a modified protein or polypeptide has at least one modified activity or function (recognizing
 5 that proteins or polypeptides may have multiple activities or functions). The modified activity or function may be reduced, diminished, eliminated, enhanced, improved, or altered in some other way (such as infection specificity) with respect to that activity or function in a wild-type protein or polypeptide, or the characteristics of virus containing such a polypeptide. It is contemplated that a modified protein or polypeptide may be altered with respect to one
 10 activity or function yet retain wild-type or unaltered activity or function in other respects. Alternatively, a modified protein may be completely nonfunctional or its cognate nucleic acid sequence may have been altered so that the polypeptide is no longer expressed at all, is truncated, or expresses a different amino acid sequence as a result of a frameshift or other modification.

15 In certain embodiments the size of a recombinant protein or polypeptide may comprise, but is not limited to, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96,
 20 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850, 875, 900, 925, 950, 975, 1000, 1100, 1200, 1300, 1400, 1500, 1750, 2000, 2250, 2500 or greater amino molecule residues, and any range derivable therein. It is contemplated that polypeptides may be modified by truncation, rendering them shorter
 25 than their corresponding unaltered form or by fusion or domain shuffling which may render the altered protein longer.

As used herein, an “amino molecule” refers to any amino acid, amino acid derivative, or amino acid mimic as would be known to one of ordinary skill in the art. In certain embodiments, the residues of the proteinaceous molecule are sequential, without any non-
 30 amino molecule interrupting the sequence of amino molecule residues. In other embodiments, the sequence may comprise one or more non-amino molecule moieties. In particular embodiments, the sequence of residues of the proteinaceous molecule may be

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interrupted by one or more non-amino molecule moieties. Accordingly, the term "proteinaceous composition" encompasses amino molecule sequences comprising at least one of the 20 common amino acids in naturally synthesized proteins, or at least one modified or unusual amino acid.

5 Proteinaceous compositions may be made by any technique known to those of skill in the art, including the expression of proteins, polypeptides, or peptides through standard molecular biological techniques, the isolation of proteinaceous compounds from natural sources, or the chemical synthesis of proteinaceous materials. The nucleotide and polypeptide sequences for various rhabdovirus genes or genomes have been previously
10 disclosed, and may be found at computerized databases known to those of ordinary skill in the art. One such database is the National Center for Biotechnology Information's GenBank and GenPept databases, which can be accessed via the internet at ncbi.nlm.nih.gov/. The coding regions for these known genes and viruses may be amplified and/or expressed using the techniques disclosed herein or as would be known to those of ordinary skill in the art.

15 **B. Functional Aspects**

When the present application refers to the function or activity of viral proteins or polypeptides, it is meant to refer to the activity or function of that viral protein or polypeptide under physiological conditions, unless otherwise specified. For example, the G protein is involved in specificity and efficiency of binding and infection of particular cell types.
20 Determination of which molecules possess this activity may be achieved using assays familiar to those of skill in the art, such as infectivity assays, protein binding assays, plaque assays and the like.

C. Variants of Viral Polypeptides

Amino acid sequence variants of the polypeptides of the present invention can be
25 substitutional, insertional or deletion variants. A mutation in a gene encoding a viral polypeptide may affect 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95,
30 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 or more non-contiguous or contiguous

amino acids (*i.e.*, segment) of a polypeptide, as compared to a wild-type or unaltered polypeptide or other reference polypeptide. Various polypeptides encoded by rhabdoviruses may be identified by reference to GenBank Accession Numbers and the related public database entries for each of the viruses disclosed herein.

5

Deletion variants lack one or more residues of the native, unaltered or wild-type protein. Individual residues can be deleted, or all or part of a domain (such as a catalytic or binding domain) can be deleted. A stop codon may be introduced (by substitution or insertion) into an encoding nucleic acid sequence to generate a truncated protein. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide, a specific type of insert is a chimeric polypeptide that include homologous or similar portions of a related protein in place of the related portion of a target protein. This may include the insertion of an immunoreactive epitope or simply one or more residues. Terminal additions, typically called fusion proteins, may also be generated.

15 Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, with or without the loss of other functions or properties. Substitutions may be conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of:
20 alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to
25 tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine. Alternatively, substitutions may be non-conservative such that a function or activity of the polypeptide is affected. Non-conservative changes typically involve substituting a residue with one that is chemically dissimilar, such as a polar or charged amino acid for a nonpolar or uncharged amino acid, and vice versa.

30 The term “functionally equivalent codon” is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers to codons that encode biologically equivalent amino acids (see Table 1, below).

Table 1. Codon Table

Amino Acids			Codons			
Alanine	Ala	A	GCA	GCC	GCG	GCU
Cysteine	Cys	C	UGC	UGU		
Aspartic acid	Asp	D	GAC	GAU		
Glutamic acid	Glu	E	GAA	GAG		
Phenylalanine	Phe	F	UUC	UUU		
Glycine	Gly	G	GGA	GGC	GGG	GGU
Histidine	His	H	CAC	CAU		
Isoleucine	Ile	I	AUA	AUC	AUU	
Lysine	Lys	K	AAA	AAG		
Leucine	Leu	L	UUA	UUG	CUA	CUC
					CUG	CUU
Methionine	Met	M	AUG			
Asparagine	Asn	N	AAC	AAU		
Proline	Pro	P	CCA	CCC	CCG	CCU
Glutamine	Gln	Q	CAA	CAG		
Arginine	Arg	R	AGA	AGG	CGA	CGC
					CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC
					UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU
Valine	Val	V	GUA	GUC	GUG	GUU
Tryptophan	Trp	W	UGG			
Tyrosine	Tyr	Y	UAC	UAU		

It also will be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids or 5' or 3' sequences, and yet still be essentially as set as forth herein, including having a certain biological activity. The addition of terminal sequences particularly applies to nucleic acid sequences that may, for example, include various non-coding sequences flanking either of the 5' or 3' portions of the coding region or may include various internal sequences, *i.e.*, introns, which are known to occur within genes.

The following is a discussion based upon changing of the amino acids of a N, P, L, or G protein to create an equivalent, or even an improved, molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid substitutions can be made in a protein sequence, and in its underlying DNA coding sequence, and nevertheless produce a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the DNA

sequences of rhabdovirus without appreciable loss of biological utility or activity of interest, as discussed below.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring a biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982). It is accepted that the
5 relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

It also is understood in the art that the substitution of like amino acids can be made
10 effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 $\pm$ 1); glutamate (+3.0 $\pm$ 1);
15 serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 $\pm$ 1); alanine (0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still produce a biologically equivalent and immunologically equivalent protein. In
20 such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those that are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions generally are based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity,
25 hydrophilicity, charge, size, and the like. Exemplary substitutions that take into consideration the various foregoing characteristics are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

III. NUCLEIC ACID MOLECULES

30 The present invention includes polynucleotides isolatable from cells that are capable of expressing all or part of a viral protein or polypeptide. In some embodiments of the

invention, it concerns all or parts of a viral genome that has been specifically mutated or altered to generate a virus or viral polypeptide, *e.g.*, a pseudotyped or non-VSV rhabdoviral polypeptide or virus, with certain properties and/or characteristics. The polynucleotides may encode a peptide or polypeptide containing all or part of a viral or heterologous amino acid sequence or be engineered so they do not encode such a viral polypeptide or encode a viral polypeptide having at least one function or activity added, increased, reduced, added, diminished, or absent. Recombinant proteins can be purified from expressing cells to yield active proteins. The genome of rhabdovirus members may be found in GenBank Accession Numbers in the NCBI database or similar databases;

10

A. Polynucleotides Encoding Native or Modified Proteins

As used herein, the term “RNA, DNA, or nucleic acid segment” refers to a RNA, DNA, or nucleic acid molecule that has been isolated free of total genomic DNA or other contaminants. Therefore, a nucleic acid segment encoding a polypeptide refers to a nucleic acid segment that contains wild-type, polymorphic, or mutant polypeptide-coding sequences yet is isolated away from, or purified free from, genomic nucleic acid(s). Included within the term “nucleic acid segment” are polynucleotides, nucleic acid segments smaller than a polynucleotide, and recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like.

As used in this application, the term “rhabdovirus polynucleotide” can refer to pseudotyped or non-VSV rhabdoviral nucleic acid molecule encoding at least one non-VSV rhabdovirus polypeptide. In certain embodiments the polynucleotide has been isolated free of other nucleic acids. Similarly, a “Maraba virus, Carajas virus, Muir Springs virus and/or Bahia Grande virus polynucleotide” refers to a nucleic acid molecule encoding a Maraba virus, Carajas virus, Muir Springs virus and/or Bahia Grande virus polypeptide that has been isolated from other nucleic acids. A “rhabdovirus genome” or a “Maraba virus, Carajas virus, Muir Springs virus and/or Bahia Grande virus genome” refers to a VSV or a non-VSV nucleic acid molecule that can be provided to a host cell to yield a viral particle, in the presence or absence of a helper virus or complementing coding regions supplying other factors in trans. The genome may or may have not been recombinantly mutated as compared to wild-type or an unaltered virus.

The term “cDNA” is intended to refer to DNA prepared using RNA as a template. There may be times when the full or partial genomic sequence is preferred.

It also is contemplated that a particular polypeptide from a given species may be represented by natural variants that have slightly different nucleic acid sequences but, nonetheless, encode the same protein (see Table 1 above).

Similarly, a polynucleotide encoding an isolated or purified wild-type, or modified polypeptide refers to a DNA segment including wild-type or mutant polypeptide coding sequences and, in certain aspects, regulatory sequences, isolated substantially away from other naturally occurring genes or protein encoding sequences. In this respect, the term “gene” is used for simplicity to refer to a nucleic acid unit encoding a protein, polypeptide, or peptide (including any sequences required for proper transcription, post-translational modification, or localization). As will be understood by those in the art, this functional term includes genomic sequences, cDNA sequences, and smaller engineered nucleic acid segments that express, or may be adapted to express, proteins, polypeptides, domains, peptides, fusion proteins, and mutants. A nucleic acid encoding all or part of a native or modified polypeptide may contain a contiguous nucleic acid of : 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 441, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000, 1010, 1020, 1030, 1040, 1050, 1060, 1070, 1080, 1090, 1095, 1100, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 9000, 10000, or more nucleotides, nucleosides, or base pairs.

In particular embodiments, the invention concerns isolated nucleic acid segments and recombinant vectors incorporating nucleic acid sequences that encode a wild-type or mutant rhabdovirus polypeptide(s) that includes within its amino acid sequence a contiguous amino acid sequence in accordance with, or essentially corresponding to a native polypeptide. The term “recombinant” may be used in conjunction with a polypeptide or the name of a specific polypeptide, and this generally refers to a polypeptide produced from a nucleic acid molecule that has been manipulated *in vitro* or that is the replicated product of such a molecule.

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In other embodiments, the invention concerns isolated nucleic acid segments and recombinant vectors incorporating nucleic sequences that encode a polypeptide or peptide that includes within its amino acid sequence a contiguous amino acid sequence in accordance with, or essentially corresponding to one or more rhabdovirus polypeptide.

5 The nucleic acid segments used in the present invention, regardless of the length of the coding sequence itself, may be combined with other nucleic acid sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed,
10 with the total length preferably being limited by the ease of preparation and use in the intended recombinant nucleic acid protocol.

 It is contemplated that the nucleic acid constructs of the present invention may encode full-length polypeptide(s) from any source or encode a truncated or modified version of the polypeptide(s), for example a truncated rhabdovirus polypeptide, such that the transcript of
15 the coding region represents the truncated version. The truncated transcript may then be translated into a truncated protein. Alternatively, a nucleic acid sequence may encode a full-length polypeptide sequence with additional heterologous coding sequences, for example to allow for purification of the polypeptide, transport, secretion, post-translational modification, or for therapeutic benefits such as targeting or efficacy. As discussed above, a tag or other
20 heterologous polypeptide may be added to the modified polypeptide-encoding sequence, wherein "heterologous" refers to a polypeptide or segment thereof that is not the same as the modified polypeptide or found associated with or encoded by the naturally occurring virus.

 In a non-limiting example, one or more nucleic acid construct may be prepared that include a contiguous stretch of nucleotides identical to or complementary to a particular viral
25 segment, such as a rhabdovirus N, P, M, G, or L gene. A nucleic acid construct may be at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1,000, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 15,000, 20,000, 30,000, 50,000, 100,000, 250,000, 500,000, 750,000, to at least 1,000,000 nucleotides in length, as well as constructs of greater size, up to and
30 including chromosomal sizes (including all intermediate lengths and intermediate ranges). It will be readily understood that "intermediate lengths" and "intermediate ranges," as used

herein, means any length or range including or between the quoted values (*i.e.*, all integers including and between such values).

The nucleic acid segments used in the present invention encompass modified nucleic acids that encode modified polypeptides. Such sequences may arise as a consequence of
5 codon redundancy and functional equivalency that are known to occur naturally within nucleic acid sequences and the proteins thus encoded. Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by human may be
10 introduced through the application of site-directed mutagenesis techniques, *e.g.*, to introduce improvements to the antigenicity or lack thereof of the protein, to reduce toxicity effects of the protein *in vivo* to a subject given the protein, or to increase the efficacy of any treatment involving the protein or a virus comprising such protein.

In certain other embodiments, the invention concerns isolated nucleic acid segments
15 and recombinant vectors that include within their sequence a contiguous nucleic acid sequence from that shown in sequences identified herein. Such sequences, however, may be mutated to yield a protein product whose activity is altered with respect to wild-type.

It also will be understood that this invention is not limited to the particular nucleic
20 acid and amino acid sequences of these identified sequences. Recombinant vectors and isolated nucleic acid segments may therefore variously include rhabdovirus-coding regions themselves, coding regions bearing selected alterations or modifications in the basic coding region, or they may encode larger polypeptides that nevertheless include rhabdovirus-coding regions, or may encode biologically functional equivalent proteins or peptides that have
25 variant amino acids sequences.

The nucleic acid segments of the present invention can encode rhabdovirus proteins and peptides that are the biological functional equivalent of, or variants or mutants of rhabdovirus that increase the therapeutic benefit of the virus. Such sequences may arise as a consequence of codon redundancy and functional equivalency that are known to occur
30 naturally within nucleic acid sequences and the proteins thus encoded. Alternatively, functionally equivalent proteins or peptides may be created via the application of

recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by man may be introduced through the application of site directed mutagenesis techniques, *e.g.*, to introduce improvements in cancer cell binding of a viral protein.

5 **B. Mutagenesis of Rhabdovirus Polynucleotides**

In various embodiments, the rhabdovirus polynucleotide may be altered or mutagenized. Alterations or mutations may include insertions, deletions, point mutations, inversions, and the like and may result in the modulation, activation and/or inactivation of certain proteins or molecular mechanisms, as well as altering the function, location, or
10 expression of a gene product, in particular rendering a gene product non-functional. Where employed, mutagenesis of a polynucleotide encoding all or part of a rhabdovirus may be accomplished by a variety of standard, mutagenic procedures (Sambrook *et al.*, 2001). Mutation is the process whereby changes occur in the quantity or structure of an organism. Mutation can involve modification of the nucleotide sequence of a single gene, blocks of
15 genes or whole genomes. Changes in single genes may be the consequence of point mutations which involve the removal, addition or substitution of a single nucleotide base within a DNA sequence, or they may be the consequence of changes involving the insertion or deletion of large numbers of nucleotides.

1. **Random Mutagenesis**

20 **a. Insertional Mutagenesis**

Insertional mutagenesis is based on the inactivation of a gene via insertion of a known nucleic acid fragment. Because it involves the insertion of some type of nucleic acid fragment, the mutations generated are generally loss-of-function, rather than gain-of-function mutations. However, there are several examples of insertions generating gain-of-function
25 mutations. Insertional mutagenesis may be accomplished using standard molecular biology techniques.

b. Chemical mutagenesis

Chemical mutagenesis offers certain advantages, such as the ability to find a full range of mutations with degrees of phenotypic severity, and is facile and inexpensive to
30 perform. The majority of chemical carcinogens produce mutations in DNA. Benzo[a]pyrene, N-acetoxy-2-acetyl aminofluorene and aflatoxin B1 cause GC to TA

transversions in bacteria and mammalian cells. Benzo[a]pyrene also can produce base substitutions such as AT to TA. N-nitroso compounds produce GC to AT transitions. Alkylation of the O4 position of thymine induced by exposure to n-nitrosourea results in TA to CG transitions.

5 **c. Radiation Mutagenesis**

Biological molecules are degraded by ionizing radiation. Adsorption of the incident energy leads to the formation of ions and free radicals, and breakage of some covalent bonds. Susceptibility to radiation damage appears quite variable between molecules, and between different crystalline forms of the same molecule. It depends on the total accumulated dose, and also on the dose rate (as once free radicals are present, the molecular damage they cause depends on their natural diffusion rate and thus upon real time). Damage is reduced and controlled by making the sample as cold as possible. Ionizing radiation causes DNA damage, generally proportional to the dose rate.

In the present invention, the term "ionizing radiation" means radiation comprising particles or photons that have sufficient energy or can produce sufficient energy to produce ionization (gain or loss of electrons). An exemplary and preferred ionizing radiation is an x-radiation. The amount of ionizing radiation needed in a given cell or for a particular molecule generally depends upon the nature of that cell or molecule and the nature of the mutation target. Means for determining an effective amount of radiation are well known in the art.

d. In Vitro Scanning Mutagenesis

Random mutagenesis also may be introduced using error prone PCR. The rate of mutagenesis may be increased by performing PCR in multiple tubes with dilutions of templates. One particularly useful mutagenesis technique is alanine scanning mutagenesis in which a number of residues are substituted individually with the amino acid alanine so that the effects of losing side-chain interactions can be determined, while minimizing the risk of large-scale perturbations in protein conformation (Cunningham *et al.*, 1989).

In vitro scanning saturation mutagenesis provides a rapid method for obtaining a large amount of structure-function information including: (i) identification of residues that modulate ligand binding specificity, (ii) a better understanding of ligand binding based on the identification of those amino acids that retain activity and those that abolish activity at a

given location, (iii) an evaluation of the overall plasticity of an active site or protein subdomain, (iv) identification of amino acid substitutions that result in increased binding.

2. Site-Directed Mutagenesis

Structure-guided site-specific mutagenesis represents a powerful tool for the
5 dissection and engineering of protein-ligand interactions (Wells, 1996; Braisted *et al.*, 1996). The technique provides for the preparation and testing of sequence variants by introducing one or more nucleotide sequence changes into a selected DNA.

C. Vectors

To generate mutations in a rhabdovirus genome, native and modified polypeptides
10 may be encoded by a nucleic acid molecule comprised in a vector. The term “vector” is used to refer to a carrier nucleic acid molecule into which an exogenous nucleic acid sequence can be inserted for introduction into a cell where it can be replicated. A nucleic acid sequence can be “exogenous,” which means that it is foreign to the cell into which the vector is being introduced or that the sequence is homologous to a sequence in the cell but in a position
15 within the host cell nucleic acid in which the sequence is ordinarily not found. Vectors include plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (*e.g.*, YACs). One of skill in the art would be well equipped to construct a vector through standard recombinant techniques, which are described in Sambrook *et al.* (2001) and Ausubel *et al.* (1994).

20 In addition to encoding a modified polypeptide such as modified N protein, P protein, M protein, G protein, or L protein, a vector may encode non-modified polypeptide sequences such as a tag or targeting molecule. Useful vectors encoding such fusion proteins include pIN vectors (Inouye *et al.*, 1985), vectors encoding a stretch of histidines, and pGEX vectors, for use in generating glutathione S-transferase (GST) soluble fusion proteins for later
25 purification and separation or cleavage. A targeting molecule is one that directs the modified polypeptide to a particular organ, tissue, cell, or other location in a subject’s body. Alternatively, the targeting molecule alters the tropism of an organism, such as rhabdovirus for certain cell types, *e.g.*, cancer cells.

The term “expression vector” refers to a vector containing a nucleic acid sequence
30 coding for at least part of a gene product capable of being transcribed. In some cases, RNA molecules are translated into a protein, polypeptide, or peptide. In other cases, these

sequences are not translated, for example, in the production of antisense molecules or ribozymes. Expression vectors can contain a variety of “control sequences,” which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described infra.

1. Promoters and Enhancers

A “promoter” is a control sequence that is a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements that bind regulatory proteins and molecules, such as RNA polymerase and other transcription factors. The phrases “operatively positioned,” “operatively coupled,” “operatively linked,” “under control,” and “under transcriptional control” mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and/or expression of that sequence. A promoter may or may not be used in conjunction with an “enhancer,” which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

A promoter may be one naturally associated with a gene or sequence, as may be obtained by isolating the 5’ non-coding sequences located upstream of the coding segment and/or exon. Such a promoter can be referred to as “endogenous.” Similarly, an enhancer may be one naturally associated with a nucleic acid sequence, located either downstream or upstream of that sequence. Alternatively, certain advantages will be gained by positioning the coding nucleic acid segment under the control of a recombinant or heterologous promoter, which refers to a promoter that is not normally associated with a nucleic acid sequence in its natural environment. A recombinant or heterologous enhancer refers also to an enhancer not normally associated with a nucleic acid sequence in its natural environment. Such promoters or enhancers may include promoters or enhancers of other genes, and promoters or enhancers isolated from any other prokaryotic, viral, or eukaryotic cell, and promoters or enhancers not “naturally occurring,” *i.e.*, containing different elements of different transcriptional regulatory regions, and/or mutations that alter expression.

In addition to producing nucleic acid sequences of promoters and enhancers synthetically, sequences may be produced using recombinant cloning and/or nucleic acid amplification technology, including PCR™, in connection with the compositions disclosed

herein (see U.S. Patent 4,683,202, U.S. Patent 5,928,906).

Furthermore, it is contemplated the control sequences that direct transcription and/or expression of sequences within non-nuclear organelles such as mitochondria, chloroplasts, and the like, can be employed as well.

5 Naturally, it may be important to employ a promoter and/or enhancer that effectively directs the expression of the DNA segment in the cell type, organelle, and organism chosen for expression. Those of skill in the art of molecular biology generally know the use of promoters, enhancers, and cell type combinations for protein expression, for example, see Sambrook *et al.* (2001). The promoters employed may be
10 constitutive, tissue-specific, cell selective (*i.e.*, more active in one cell type as compared to another), inducible, and/or useful under the appropriate conditions to direct high level expression of the introduced nucleic acid segment, such as is advantageous in the large-scale production of recombinant proteins and/or peptides. The promoter may be heterologous or endogenous.

15 Several elements/promoters that may be employed, in the context of the present invention, to regulate the expression of a gene. This list is not intended to be exhaustive of all the possible elements involved in the promotion of expression but, merely, to be exemplary thereof. Also provided are examples of inducible elements, which are regions of a nucleic acid sequence that can be activated in response to a specific stimulus.
20 Promoter/Enhancer (References) include: Immunoglobulin Heavy Chain (Banerji *et al.*, 1983; Gilles *et al.*, 1983; Grosschedl *et al.*, 1985; Atchinson *et al.*, 1986, 1987; Imler *et al.*, 1987; Weinberger *et al.*, 1984; Kiledjian *et al.*, 1988; Porton *et al.*, 1990); Immunoglobulin Light Chain (Queen *et al.*, 1983; Picard *et al.*, 1984); T Cell Receptor (Luria *et al.*, 1987; Winoto *et al.*, 1989; Redondo *et al.*, 1990); HLA DQ α and/or DQ β (Sullivan *et al.*, 1987); β
25 Interferon (Goodbourn *et al.*, 1986; Fujita *et al.*, 1987; Goodbourn *et al.*, 1988); Interleukin-2 (Greene *et al.*, 1989); Interleukin-2 Receptor (Greene *et al.*, 1989; Lin *et al.*, 1990); MHC Class II 5 (Koch *et al.*, 1989); MHC Class II HLA-DR α (Sherman *et al.*, 1989); β -Actin (Kawamoto *et al.*, 1988; Ng *et al.*, 1989); Muscle Creatine Kinase (MCK) (Jaynes *et al.*, 1988; Horlick *et al.*, 1989; Johnson *et al.*, 1989); Prealbumin (Transthyretin) (Costa *et al.*,
30 1988); Elastase I (Omitz *et al.*, 1987); Metallothionein (MTII) (Karin *et al.*, 1987; Culotta *et al.*, 1989); Collagenase (Pinkert *et al.*, 1987; Angel *et al.*, 1987); Albumin (Pinkert *et al.*, 1987; Tronche *et al.*, 1989, 1990); α -Fetoprotein (Godbout *et al.*, 1988; Campere *et al.*,

1989); γ -Globin (Bodine *et al.*, 1987; Percz-Stable *et al.*, 1990); β -Globin (Trudel *et al.*, 1987); c-fos (Cohen *et al.*, 1987); c-HA-ras (Triesman, 1986; Deschamps *et al.*, 1985); Insulin (Edlund *et al.*, 1985); Neural Cell Adhesion Molecule (NCAM) (Hirsh *et al.*, 1990); α 1-Antitrypsin (Latimer *et al.*, 1990); H2B (TH2B) Histone (Hwang *et al.*, 1990); Mouse
5 and/or Type I Collagen (Ripe *et al.*, 1989); Glucose-Regulated Proteins (GRP94 and GRP78) (Chang *et al.*, 1989); Rat Growth Hormone (Larsen *et al.*, 1986); Human Serum Amyloid A (SAA) (Edbrooke *et al.*, 1989); Troponin I (TN I) (Yutzey *et al.*, 1989); Platelet-Derived Growth Factor (PDGF) (Pech *et al.*, 1989); Duchenne Muscular Dystrophy (Klamut *et al.*, 1990); SV40 (Banerji *et al.*, 1981; Moreau *et al.*, 1981; Sleight *et al.*, 1985; Firak *et al.*, 1986;
10 Herr *et al.*, 1986; Imbra *et al.*, 1986; Kadesch *et al.*, 1986; Wang *et al.*, 1986; Ondek *et al.*, 1987; Kuhl *et al.*, 1987; Schaffner *et al.*, 1988); Polyoma (Swartzendruber *et al.*, 1975; Vasseur *et al.*, 1980; Katinka *et al.*, 1980, 1981; Tyndell *et al.*, 1981; Dandolo *et al.*, 1983; de Villiers *et al.*, 1984; Hen *et al.*, 1986; Satake *et al.*, 1988; Campbell *et al.*, 1988); Retroviruses (Kriegler *et al.*, 1982, 1983; Levinson *et al.*, 1982; Kriegler *et al.*, 1983, 1984a,
15 b, 1988; Bosze *et al.*, 1986; Miksicek *et al.*, 1986; Celander *et al.*, 1987; Thiesen *et al.*, 1988; Celander *et al.*, 1988; Chol *et al.*, 1988; Reisman *et al.*, 1989); Papilloma Virus (Campo *et al.*, 1983; Lusky *et al.*, 1983; Spandidos and Wilkie, 1983; Spalholz *et al.*, 1985; Lusky *et al.*, 1986; Cripe *et al.*, 1987; Gloss *et al.*, 1987; Hirochika *et al.*, 1987; Stephens *et al.*, 1987); Hepatitis B Virus (Bulla *et al.*, 1986; Jameel *et al.*, 1986; Shaul *et al.*, 1987; Spandau *et al.*,
20 1988; Vannice *et al.*, 1988); Human Immunodeficiency Virus (Muesing *et al.*, 1987; Hauber *et al.*, 1988; Jakobovits *et al.*, 1988; Feng *et al.*, 1988; Takebe *et al.*, 1988; Rosen *et al.*, 1988; Berkhout *et al.*, 1989; Laspias *et al.*, 1989; Sharp *et al.*, 1989; Braddock *et al.*, 1989); Cytomegalovirus (CMV) (Weber *et al.*, 1984; Boshart *et al.*, 1985; Foecking *et al.*, 1986); and Gibbon Ape Leukemia Virus (Holbrook *et al.*, 1987; Quinn *et al.*, 1989).

25 Inducible Elements (Element/Inducer (References)) include: MT II/Phorbol Ester (TFA), Heavy metals (Palmiter *et al.*, 1982; Haslinger *et al.*, 1985; Searle *et al.*, 1985; Stuart *et al.*, 1985; Imagawa *et al.*, 1987, Karin *et al.*, 1987; Angel *et al.*, 1987b; McNeall *et al.*, 1989); MMTV (mouse mammary tumor virus)/Glucocorticoids (Huang *et al.*, 1981; Lee *et al.*, 1981; Majors *et al.*, 1983; Chandler *et al.*, 1983; Lee *et al.*, 1984; Ponta *et al.*, 1985;
30 Sakai *et al.*, 1988); β -Interferon/poly(rI)x, poly(rc) (Tavernier *et al.*, 1983); Adenovirus 5 E2/E1A (Imperiale *et al.*, 1984); Collagenase/Phorbol Ester (TPA) (Angel *et al.*, 1987a); Stromelysin/Phorbol Ester (TPA) (Angel *et al.*, 1987b); SV40/Phorbol Ester (TPA) (Angel *et al.*, 1987b); Murine MX Gene/Interferon, Newcastle Disease Virus (Hug *et al.*, 1988);

GRP78 Gene/A23187 (Resendez *et al.*, 1988); α -2-Macroglobulin/IL-6 (Kunz *et al.*, 1989); Vimentin/Serum (Rittling *et al.*, 1989); MHC Class I Gene H-2kb/Interferon (Blonar *et al.*, 1989); HSP70/E1A, SV40 Large T Antigen (Taylor *et al.*, 1989, 1990a, 1990b); Proliferin/Phorbol Ester-TPA (Mordacq *et al.*, 1989); Tumor Necrosis Factor/PMA (Hensel
5 *et al.*, 1989); and Thyroid Stimulating Hormone α Gene/Thyroid Hormone (Chatterjee *et al.*, 1989).

The identity of tissue-specific or tissue-selective (*i.e.*, promoters that have a greater activity in one cell as compared to another) promoters or elements, as well as assays to characterize their activity, is well known to those of skill in the art. Examples of such regions
10 include the human LIMK2 gene (Nomoto *et al.* 1999), the somatostatin receptor 2 gene (Kraus *et al.*, 1998), murine epididymal retinoic acid-binding gene (Lareyre *et al.*, 1999), human CD4 (Zhao-Emonet *et al.*, 1998), mouse alpha2 (XI) collagen (Tsumaki, *et al.*, 1998), D1A dopamine receptor gene (Lee, *et al.*, 1997), insulin-like growth factor II (Wu *et al.*, 1997), human platelet endothelial cell adhesion molecule-1 (Almendo *et al.*, 1996), and the
15 SM22 α promoter.

Additional viral promoters, cellular promoters/enhancers and inducible promoters/enhancers that could be used in combination with the present invention are listed herein. Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of structural genes encoding
20 oligosaccharide processing enzymes, protein folding accessory proteins, selectable marker proteins or a heterologous protein of interest. Alternatively, a tissue-specific promoter for cancer gene therapy (Table 2) or the targeting of tumors (Table 3) may be employed with the nucleic acid molecules of the present invention.

Table 2. Candidate Tissue-Specific Promoters for Cancer Gene Therapy

Tissue-specific promoter	Cancers in which promoter is active	Normal cells in which promoter is active
Carcinoembryonic antigen (CEA)*	Most colorectal carcinomas; 50% of lung carcinomas; 40-50% of gastric carcinomas; most pancreatic carcinomas; many breast carcinomas	Colonic mucosa; gastric mucosa; lung epithelia; eccrine sweat glands; cells in testes
Prostate-specific antigen (PSA)	Most prostate carcinomas	Prostate epithelium

Tissue-specific promoter	Cancers in which promoter is active	Normal cells in which promoter is active
Vasoactive intestinal peptide (VIP)	Majority of non-small cell lung cancers	Neurons; lymphocytes; mast cells; eosinophils
Surfactant protein A (SP-A)	Many lung adenocarcinomas cells	Type II pneumocytes; Clara
Human achaete-scute homolog (hASH)	Most small cell lung cancers	Neuroendocrine cells in lung
Mucin-1 (MUC1)**	Most adenocarcinomas (originating from any tissue)	Glandular epithelial cells in breast and in respiratory, gastrointestinal, and genitourinary tracts
Alpha-fetoprotein	Most hepatocellular carcinomas; possibly many testicular cancers	Hepatocytes (under certain conditions); testis
Albumin	Most hepatocellular carcinomas	Hepatocytes
Tyrosinase	Most melanomas	Melanocytes; astrocytes; Schwann cells; some neurons
Tyrosine-binding protein (TRP)	Most melanomas	Melanocytes; astrocytes; Schwann cells; some neurons
Keratin 14	Presumably many squamous cell carcinomas (e.g.: Head and neck cancers)	Keratinocytes
EBV LD-2	Many squamous cell carcinomas of head and neck	Keratinocytes of upper digestive tract; Keratinocytes of upper digestive tract
Glial fibrillary acidic protein (GFAP)	Many astrocytomas	Astrocytes
Myelin basic protein (MBP)	Many gliomas	Oligodendrocytes
Testis-specific angiotensin-converting enzyme (Testis-specific ACE)	Possibly many testicular cancers	Spermatazoa
Osteocalcin	Possibly many osteosarcomas	Osteoblasts

Table 3. Candidate Promoters for Use with a Tissue-Specific Targeting of Tumors

Promoter	Cancers in which Promoter is active	Normal cells in which Promoter is active
E2F-regulated promoter	Almost all cancers	Proliferating cells
HLA-G	Many colorectal carcinomas; many melanomas; possibly many other cancers	Lymphocytes; monocytes; spermatocytes; trophoblast
FasL	Most melanomas; many pancreatic carcinomas; most	Activated leukocytes; neurons; endothelial cells;

Promoter	Cancers in which Promoter is active	Normal cells in which Promoter is active
	astrocytomas possibly many other cancers	keratinocytes; cells in immunoprivileged tissues; some cells in lungs, ovaries, liver, and prostate
Myc-regulated promoter	Most lung carcinomas (both small cell and non-small cell); most colorectal carcinomas	Proliferating cells (only some cell-types): mammary epithelial cells (including non-proliferating)
MAGE-1	Many melanomas; some non-small cell lung carcinomas; some breast carcinomas	Testis
VEGF	70% of all cancers (constitutive overexpression in many cancers)	Cells at sites of neovascularization (but unlike in tumors, expression is transient, less strong, and never constitutive)
bFGF	Presumably many different cancers, since bFGF expression is induced by ischemic conditions	Cells at sites of ischemia (but unlike tumors, expression is transient, less strong, and never constitutive)
COX-2	Most colorectal carcinomas; many lung carcinomas; possibly many other cancers	Cells at sites of inflammation
IL-10	Most colorectal carcinomas; many lung carcinomas; many squamous cell carcinomas of head and neck; possibly many other cancers	Leukocytes
GRP78/BiP	Presumably many different cancers, since GRP78 expression is induced by tumor-specific conditions	Cells at sites of ischemia
CarG elements from Egr-1	Induced by ionization radiation, so conceivably most tumors upon irradiation	Cells exposed to ionizing radiation; leukocytes

2. Initiation Signals and Internal Ribosome Binding Sites

A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences.

- 5 Exogenous translational control signals, including the ATG initiation codon, may need to be provided. One of ordinary skill in the art would readily be capable of determining this and providing the necessary signals. It is well known that the initiation codon must be “in-frame”

with the reading frame of the desired coding sequence to ensure translation of the entire insert. The exogenous translational control signals and initiation codons can be either natural or synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements.

5 In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent translation and begin translation at internal sites (Pelletier and Sonenberg, 1988). IRES elements from two members of the picornavirus family (polio and encephalomyocarditis) have been described
10 (Pelletier and Sonenberg, 1988), as well an IRES from a mammalian message (Macejak and Sarnow, 1991). IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed
15 using a single promoter/enhancer to transcribe a single message (see U.S. Patents 5,925,565 and 5,935,819).

3. Multiple Cloning Sites

Vectors can include a multiple cloning site (MCS), which is a nucleic acid region that contains multiple restriction enzyme sites any of which can be used in conjunction with
20 standard recombinant technology to digest the vector. (See Carbonelli *et al.*, 1999, Levenson *et al.*, 1998, and Cocea, 1997). "Restriction enzyme digestion" refers to catalytic cleavage of a nucleic acid molecule with an enzyme that functions only at specific locations in a nucleic acid molecule. Many of these restriction enzymes are commercially available. Use of such enzymes is widely understood by those of
25 skill in the art. Frequently, a vector is linearized or fragmented using a restriction enzyme that cuts within the MCS to enable exogenous sequences to be ligated to the vector. "Ligation" refers to the process of forming phosphodiester bonds between two nucleic acid fragments, which may or may not be contiguous with each other. Techniques involving restriction enzymes and ligation reactions are well known to those of skill in the art of
30 recombinant technology.

4. Termination Signals

The vectors or constructs of the present invention will generally comprise at least one termination signal. A "termination signal" or "terminator" is comprised of the RNA sequences involved in specific termination of an RNA transcript by an RNA polymerase. Thus, in certain embodiments a termination signal that ends the production of an RNA transcript is contemplated. A terminator may be necessary in vivo to achieve desirable message levels.

In negative sense RNA viruses, including rhabdoviruses, termination is defined by a RNA motif.

Terminators contemplated for use in the invention include any known terminator of transcription described herein or known to one of ordinary skill in the art, including but not limited to, for example, the termination sequences of genes, such as for example the bovine growth hormone terminator or viral termination sequences, such as for example the SV40 terminator. In certain embodiments, the termination signal may be a lack of transcribable or translatable sequence, such as due to a sequence truncation.

5. Polyadenylation Signals

In expression, particularly eukaryotic expression, one will typically include a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and/or any such sequence may be employed. Preferred embodiments include the SV40 polyadenylation signal and/or the bovine growth hormone polyadenylation signal, convenient and/or known to function well in various target cells. Polyadenylation may increase the stability of the transcript or may facilitate cytoplasmic transport.

6. Origins of Replication

In order to propagate a vector in a host cell, it may contain one or more origins of replication sites (often termed "ori"), which is a specific nucleic acid sequence at which replication is initiated. Alternatively an autonomously replicating sequence (ARS) can be employed if the host cell is yeast.

7. Selectable and Screenable Markers

In certain embodiments of the invention, cells containing a nucleic acid construct of the present invention may be identified *in vitro* or *in vivo* by including a marker in the expression vector. Such markers would confer an identifiable change to the cell permitting
5 easy identification of cells containing the expression vector. Generally, a selectable marker is one that confers a property that allows for selection. A positive selectable marker is one in which the presence of the marker allows for its selection, while a negative selectable marker is one in which its presence prevents its selection. An example of a positive selectable marker is a drug resistance marker.

10 Usually the inclusion of a drug selection marker aids in the cloning and identification of transformants, for example, genes that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin and histidinol are useful selectable markers. In addition to markers conferring a phenotype that allows for the discrimination of transformants based on the implementation of conditions, other types of markers including screenable markers such
15 as GFP, whose basis is colorimetric analysis, are also contemplated. Alternatively, screenable enzymes such as herpes simplex virus thymidine kinase (tk) or chloramphenicol acetyltransferase (CAT) may be utilized. One of skill in the art would also know how to employ immunologic markers, possibly in conjunction with FACS analysis. The marker used is not believed to be important, so long as it is capable of being expressed simultaneously
20 with the nucleic acid encoding a gene product. Further examples of selectable and screenable markers are well known to one of skill in the art.

D. Host Cells

As used herein, the terms "cell," "cell line," and "cell culture" may be used interchangeably. All of these terms also include their progeny, which is any and all
25 subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, "host cell" refers to a prokaryotic or eukaryotic cell, and it includes any transformable organisms that is capable of replicating a vector and/or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for
30 vectors or viruses (which does not qualify as a vector if it expresses no exogenous polypeptides). A host cell may be "transfected" or "transformed," which refers to a process by which exogenous nucleic acid, such as a modified protein-encoding sequence, is

transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

Host cells may be derived from prokaryotes or eukaryotes, including yeast cells, insect cells, and mammalian cells, depending upon whether the desired result is replication of the vector or expression of part or all of the vector-encoded nucleic acid sequences. Numerous cell lines and cultures are available for use as a host cell, and they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials (www.atcc.org). An appropriate host can be determined by one of skill in the art based on the vector backbone and the desired result. A plasmid or cosmid, for example, can be introduced into a prokaryote host cell for replication of many vectors. Bacterial cells used as host cells for vector replication and/or expression include DH5 α , JM109, and KC8, as well as a number of commercially available bacterial hosts such as SURE[®] Competent Cells and SOLOPACK[™] Gold Cells (STRATAGENE[®], La Jolla, CA). Alternatively, bacterial cells such as E. coli LE392 could be used as host cells for phage viruses. Appropriate yeast cells include *Saccharomyces cerevisiae*, *Saccharomyces pombe*, and *Pichia pastoris*.

Examples of eukaryotic host cells for replication and/or expression of a vector include HeLa, NIH3T3, Jurkat, 293, Cos, CHO, Saos, and PC12. Many host cells from various cell types and organisms are available and would be known to one of skill in the art. Similarly, a viral vector may be used in conjunction with either a eukaryotic or prokaryotic host cell, particularly one that is permissive for replication or expression of the vector.

Some vectors may employ control sequences that allow it to be replicated and/or expressed in both prokaryotic and eukaryotic cells. One of skill in the art would further understand the conditions under which to incubate all of the above described host cells to maintain them and to permit replication of a vector. Also understood and known are techniques and conditions that would allow large-scale production of vectors, as well as production of the nucleic acids encoded by vectors and their cognate polypeptides, proteins, or peptides.

E. Expression Systems

Numerous expression systems exist that comprise at least all or part of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed

for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

The insect cell/baculovirus system can produce a high level of protein expression of a
5 heterologous nucleic acid segment, such as described in U.S. Patents 5,871,986 and
4,879,236, and which can be bought, for example,
under the name MAXBAC® 2.0 from INVITROGEN® and BACPACK™ BACULOVIRUS
EXPRESSION SYSTEM FROM CLONTECH®.

In addition to the disclosed expression systems of the invention, other examples of
10 expression systems include STRATAGENE®'s COMPLETE CONTROL™ Inducible
Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or
its pET Expression System, an *E. coli* expression system. Another example of an inducible
expression system is available from INVITROGEN®, which carries the T-REX™
(tetracycline-regulated expression) System, an inducible mammalian expression system that
15 uses the full-length CMV promoter. INVITROGEN® also provides a yeast expression
system called the Pichia methanolica Expression System, which is designed for high-level
production of recombinant proteins in the methylotrophic yeast Pichia methanolica. One of
skill in the art would know how to express a vector, such as an expression construct, to
produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

20 F. Nucleic Acid Detection

In addition to their use in directing the expression of poxvirus proteins, polypeptides
and/or peptides, the nucleic acid sequences disclosed herein have a variety of other uses. For
example, they have utility as probes or primers for embodiments involving nucleic acid
hybridization. They may be used in diagnostic or screening methods of the present invention.
25 Detection of nucleic acids encoding rhabdovirus or rhabdovirus polypeptide modulators are
encompassed by the invention.

1. Hybridization

The use of a probe or primer of between 13 and 100 nucleotides, preferably between
17 and 100 nucleotides in length, or in some aspects of the invention up to 1-2 kilobases or
30 more in length, allows the formation of a duplex molecule that is both stable and selective.
Molecules having complementary sequences over contiguous stretches greater than 20 bases

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in length are generally preferred, to increase stability and/or selectivity of the hybrid molecules obtained. One will generally prefer to design nucleic acid molecules for hybridization having one or more complementary sequences of 20 to 30 nucleotides, or even longer where desired. Such fragments may be readily prepared, for example, by directly synthesizing the fragment by chemical means or by introducing selected sequences into recombinant vectors for recombinant production.

Accordingly, the nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of DNAs and/or RNAs or to provide primers for amplification of DNA or RNA from samples. Depending on the application envisioned, one would desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of the probe or primers for the target sequence.

For applications requiring high selectivity, one will typically desire to employ relatively high stringency conditions to form the hybrids. For example, relatively low salt and/or high temperature conditions, such as provided by about 0.02 M to about 0.10 M NaCl at temperatures of about 50°C to about 70°C. Such high stringency conditions tolerate little, if any, mismatch between the probe or primers and the template or target strand and would be particularly suitable for isolating specific genes or for detecting specific mRNA transcripts. It is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide.

For certain applications, for example, site-directed mutagenesis, it is appreciated that lower stringency conditions are preferred. Under these conditions, hybridization may occur even though the sequences of the hybridizing strands are not perfectly complementary, but are mismatched at one or more positions. Conditions may be rendered less stringent by increasing salt concentration and/or decreasing temperature. For example, a medium stringency condition could be provided by about 0.1 to 0.25 M NaCl at temperatures of about 37°C to about 55°C, while a low stringency condition could be provided by about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Hybridization conditions can be readily manipulated depending on the desired results.

In other embodiments, hybridization may be achieved under conditions of, for example, 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM MgCl₂, 1.0 mM dithiothreitol, at temperatures between approximately 20°C to about 37°C. Other hybridization conditions

utilized could include approximately 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, at temperatures ranging from approximately 40°C to about 72°C.

In certain embodiments, it will be advantageous to employ nucleic acids of defined sequences of the present invention in combination with an appropriate means, such as a label, for determining hybridization. A wide variety of appropriate indicator means are known in the art, including fluorescent, radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of being detected. In preferred embodiments, one may desire to employ a fluorescent label or an enzyme tag such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmentally undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known that can be employed to provide a detection means that is visibly or spectrophotometrically detectable, to identify specific hybridization with complementary nucleic acid containing samples.

In general, it is envisioned that the probes or primers described herein will be useful as reagents in solution hybridization, as in PCR™, for detection of expression of corresponding genes, as well as in embodiments employing a solid phase. In embodiments involving a solid phase, the test DNA (or RNA) is adsorbed or otherwise affixed to a selected matrix or surface. This fixed, single-stranded nucleic acid is then subjected to hybridization with selected probes under desired conditions. The conditions selected will depend on the particular circumstances (depending, for example, on the G+C content, type of target nucleic acid, source of nucleic acid, size of hybridization probe, *etc.*). Optimization of hybridization conditions for the particular application of interest is well known to those of skill in the art. After washing of the hybridized molecules to remove non-specifically bound probe molecules, hybridization is detected, and/or quantified, by determining the amount of bound label. Representative solid phase hybridization methods are disclosed in U.S. Patents 5,843,663, 5,900,481 and 5,919,626. Other methods of hybridization that may be used in the practice of the present invention are disclosed in U.S. Patents 5,849,481, 5,849,486 and 5,851,772.

2. Amplification of Nucleic Acids

Nucleic acids used as a template for amplification may be isolated from cells, tissues or other samples according to standard methodologies (Sambrook *et al.*, 2001). In certain

embodiments, analysis is performed on whole cell or tissue homogenates or biological fluid samples without substantial purification of the template nucleic acid. The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to first convert the RNA to a complementary DNA.

5 The term "primer," as used herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process. Typically, primers are oligonucleotides from ten to twenty and/or thirty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded and/or single-stranded form, although the single-stranded form is preferred.

10 Pairs of primers designed to selectively hybridize to nucleic acids corresponding to sequences of genes identified herein are contacted with the template nucleic acid under conditions that permit selective hybridization. Depending upon the desired application, high stringency hybridization conditions may be selected that will only allow hybridization to sequences that are completely complementary to the primers. In other embodiments,
15 hybridization may occur under reduced stringency to allow for amplification of nucleic acids contain one or more mismatches with the primer sequences. Once hybridized, the template-primer complex is contacted with one or more enzymes that facilitate template-dependent nucleic acid synthesis. Multiple rounds of amplification, also referred to as "cycles," are conducted until a sufficient amount of amplification product is produced.

20 A number of template dependent processes are available to amplify the oligonucleotide sequences present in a given template sample. One of the best known amplification methods is the polymerase chain reaction (referred to as PCRTM) which is described in detail in U.S. Patents 4,683,195, 4,683,202 and 4,800,159, and in Innis *et al.*, 1988.

25 A reverse transcriptase PCRTM amplification procedure may be performed to quantify the amount of mRNA amplified and are well known (see Sambrook *et al.*, 2001; WO 90/07641; and U.S. Patent 5,882,864).

 Another method for amplification is ligase chain reaction ("LCR"), disclosed in European Application No. 320 308. U.S.

30 Patent 4,883,750 describes a method similar to LCR for binding probe pairs to a target sequence. A method based on PCRTM and oligonucleotide ligase assay (OLA), disclosed in

U.S. Patent 5,912,148, may also be used. Alternative methods for amplification of target nucleic acid sequences that may be used in the practice of the present invention are disclosed in U.S. Patents 5,843,650, 5,846,709, 5,846,783, 5,849,546, 5,849,497, 5,849,547, 5,858,652, 5,866,366, 5,916,776, 5,922,574, 5,928,905, 5,928,906, 5,932,451, 5,935,825, 5,939,291 and 5,942,391, GB Application No. 2 202 328, and in PCT Application No. PCT/US89/01025, Qbeta Replicase, described in PCT Application No. PCT/US87/00880, may also be used as an amplification method in the present invention. Isothermal amplification as described by Walker *et al.* (1992) can also be used. As well as Strand Displacement Amplification (SDA), disclosed in U.S. Patent 5,916,779.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS), including nucleic acid sequence based amplification (NASBA) and 3SR (Kwoh *et al.*, 1989; PCT Application WO 88/10315).

European Application No. 329 822 disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention.

PCT Application WO 89/06700 disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter region/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods include "RACE" and "one-sided PCR" (Frohman, 1990; Ohara *et al.*, 1989).

3. Detection of Nucleic Acids

Following any amplification, it may be desirable to separate and/or isolate the amplification product from the template and/or the excess primer. In one embodiment, amplification products are separated by agarose, agarose-acrylamide, or polyacrylamide gel electrophoresis using standard methods (Sambrook *et al.*, 2001).

Separation of nucleic acids may also be effected by chromatographic techniques known in art. There are many kinds of chromatography which may be used in the practice of the present invention, including adsorption, partition, ion-exchange, hydroxylapatite, molecular sieve, reverse-phase, column, paper, thin-layer, and gas chromatography as well as HPLC.

Typical visualization methods includes staining of a gel with ethidium bromide and visualization of bands under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the separated amplification products can be exposed to x-ray film or visualized under the appropriate
5 excitatory spectra.

In particular embodiments, detection is by Southern blotting and hybridization with a labeled probe. The techniques involved in Southern blotting are well known to those of skill in the art (see Sambrook *et al.*, 2001). One example of the foregoing is described in U.S. Patent 5,279,721, which discloses an apparatus and method
10 for the automated electrophoresis and transfer of nucleic acids.

Other methods of nucleic acid detection that may be used in the practice of the instant invention are disclosed in U.S. Patents 5,840,873, 5,843,640, 5,843,651, 5,846,708, 5,846,717, 5,846,726, 5,846,729, 5,849,487, 5,853,990, 5,853,992, 5,853,993, 5,856,092, 5,861,244, 5,863,732, 5,863,753, 5,866,331, 5,905,024, 5,910,407, 5,912,124, 5,912,145,
15 5,919,630, 5,925,517, 5,928,862, 5,928,869, 5,929,227, 5,932,413 and 5,935,791.

4. Other Assays

Other methods for genetic screening may be used within the scope of the present invention, for example, to detect mutations in genomic nucleic acids, cDNA and/or RNA
20 samples. Methods used to detect point mutations include denaturing gradient gel electrophoresis ("DGGE"), restriction fragment length polymorphism analysis ("RFLP"), chemical or enzymatic cleavage methods, direct sequencing of target regions amplified by PCRTM (see above), single-strand conformation polymorphism analysis ("SSCP") and other methods well known in the art. One method of screening for point mutations is based on
25 RNase cleavage of base pair mismatches in RNA/DNA or RNA/RNA heteroduplexes. As used herein, the term "mismatch" is defined as a region of one or more unpaired or mispaired nucleotides in a double-stranded RNA/RNA, RNA/DNA or DNA/DNA molecule. This definition thus includes mismatches due to insertion/deletion mutations, as well as single or multiple base point mutations (for example see U.S. Patent 4,946,773. Alternative methods
30 for detection of deletion, insertion or substitution mutations that may be used in the practice of the present invention are disclosed in U.S. Patents 5,849,483, 5,851,770, 5,866,337, 5,925,525 and 5,928,870.

G. Methods of Gene Transfer

Suitable methods for nucleic acid delivery to effect expression of compositions of the present invention are believed to include virtually any method by which a nucleic acid (*e.g.*, DNA or RNA, including viral and nonviral vectors) can be introduced into an organelle, a cell, a tissue or an organism, as described herein or as would be known to one of ordinary skill in the art. Such methods include, but are not limited to, direct delivery of nucleic acid such as by injection (U.S. Patents 5,994,624, 5,981,274, 5,945,100, 5,780,448, 5,736,524, 5,702,932, 5,656,610, 5,589,466 and 5,580,859), including microinjection (Harland and Weintraub, 1985; U.S. Patent 5,789,215,); by electroporation (U.S. Patent 5,384,253, incorporated herein by reference); by calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990); by using DEAE dextran followed by polyethylene glycol (Gopal, 1985); by direct sonic loading (Fechheimer *et al.*, 1987); by liposome mediated transfection (Nicolau and Sene, 1982; Fraley *et al.*, 1979; Nicolau *et al.*, 1987; Wong *et al.*, 1980; Kaneda *et al.*, 1989; Kato *et al.*, 1991); by microprojectile bombardment (PCT Application Nos. WO 94/09699 and 95/06128; U.S. Patents 5,610,042; 5,322,783 5,563,055, 5,550,318, 5,538,877 and 5,538,880); by agitation with silicon carbide fibers (Kaepler *et al.*, 1990; U.S. Patents 5,302,523 and 5,464,765, each incorporated herein by reference); by *Agrobacterium* mediated transformation (U.S. Patents 5,591,616 and 5,563,055,); or by PEG mediated transformation of protoplasts (Omirulleh *et al.*, 1993; U.S. Patents 4,684,611 and 4,952,500); by desiccation/inhibition mediated DNA uptake (Potrykus *et al.*, 1985). Through the application of techniques such as these, organelle(s), cell(s), tissue(s) or organism(s) may be stably or transiently transformed.

H. Lipid Components and Moieties

In certain embodiments, the present invention concerns compositions comprising one or more lipids associated with a nucleic acid, an amino acid molecule, such as a peptide, or another small molecule compound. In any of the embodiments discussed herein, the molecule may be either a rhabdovirus polypeptide or a rhabdovirus polypeptide modulator, for example a nucleic acid encoding all or part of either a rhabdovirus polypeptide, or alternatively, an amino acid molecule encoding all or part of rhabdovirus polypeptide

modulator. A lipid is a substance that is characteristically insoluble in water and extractable with an organic solvent. Compounds other than those specifically described herein are understood by one of skill in the art as lipids, and are encompassed by the compositions and methods of the present invention. A lipid component and a non-lipid may be attached to one
5 another, either covalently or non-covalently.

A lipid may be naturally occurring or synthetic (*i.e.*, designed or produced by man). However, a lipid is usually a biological substance. Biological lipids are well known in the art, and include for example, neutral fats, phospholipids, phosphoglycerides, steroids, terpenes, lysolipids, glycosphingolipids, glucolipids, sulphatides, lipids with ether and ester-
10 linked fatty acids and polymerizable lipids, and combinations thereof.

A nucleic acid molecule or amino acid molecule, such as a peptide, associated with a lipid may be dispersed in a solution containing a lipid, dissolved with a lipid, emulsified with a lipid, mixed with a lipid, combined with a lipid, covalently bonded to a lipid, contained as a suspension in a lipid or otherwise associated with a lipid. A lipid or lipid/virus-associated
15 composition of the present invention is not limited to any particular structure. For example, they may also simply be interspersed in a solution, possibly forming aggregates which are not uniform in either size or shape. In another example, they may be present in a bilayer structure, as micelles, or with a "collapsed" structure. In another non-limiting example, a lipofectamine (Gibco BRL)-poxvirus or Superfect (Qiagen)-virus complex is also
20 contemplated.

In certain embodiments, a lipid composition may comprise about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, about 20%, about 21%, about 22%, about 23%, about 24%, about 25%, about
25 26%, about 27%, about 28%, about 29%, about 30%, about 31%, about 32%, about 33%, about 34%, about 35%, about 36%, about 37%, about 38%, about 39%, about 40%, about 41%, about 42%, about 43%, about 44%, about 45%, about 46%, about 47%, about 48%, about 49%, about 50%, about 51%, about 52%, about 53%, about 54%, about 55%, about 56%, about 57%, about 58%, about 59%, about 60%, about 61%, about 62%, about 63%,
30 about 64%, about 65%, about 66%, about 67%, about 68%, about 69%, about 70%, about 71%, about 72%, about 73%, about 74%, about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about

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86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, about 100%, or any range derivable therein, of a particular lipid, lipid type, or non-lipid component such as a drug, protein, sugar, nucleic acids or other material disclosed herein or as would be known to one of skill in the art. In a non-limiting example, a lipid composition may comprise about 10% to about 20% neutral lipids, and about 33% to about 34% of a cerebroside, and about 1% cholesterol. Thus, it is contemplated that lipid compositions of the present invention may comprise any of the lipids, lipid types, or other components in any combination or percentage range.

10 IV. PHARMACEUTICAL FORMULATIONS AND TREATMENT REGIMENS

In an embodiment of the present invention, a method of treatment for a hyperproliferative or neoplastic disease, such as cancer, by the delivery of a non-VSV rhabdovirus, such as Maraba virus, Carajas virus, Muir Springs virus, and/or Bahia Grande virus, is contemplated. Examples of cancer contemplated for treatment include lung cancer, head and neck cancer, breast cancer, pancreatic cancer, prostate cancer, renal cancer, bone cancer, testicular cancer, cervical cancer, gastrointestinal cancer, lymphomas, pre-neoplastic lesions, pre-neoplastic lesions in the lung, colon cancer, melanoma, bladder cancer and any other cancers or tumors that may be treated, including metastatic or systemically distributed cancers.

20 An effective amount of the pharmaceutical composition, generally, is defined as that amount sufficient to detectably and repeatedly to slow, ameliorate, reduce, minimize, or limit the extent of the disease or its symptoms. More rigorous definitions may apply, including elimination, eradication, or cure of disease.

Preferably, patients will have adequate bone marrow function (defined as a peripheral absolute granulocyte count of $> 2,000 / \text{mm}^3$ and a platelet count of $100,000 / \text{mm}^3$), adequate liver function (bilirubin $< 1.5 \text{ mg / dl}$) and adequate renal function (creatinine $< 1.5 \text{ mg / dl}$).

A. Administration

To kill cells, inhibit cell growth, inhibit metastasis, decrease tumor or tissue size, and otherwise reverse, stay, or reduce the malignant phenotype of tumor cells, using the methods and compositions of the present invention, one would generally contact a hyperproliferative or neoplastic cell with a therapeutic composition such as a virus or an expression construct

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encoding a polypeptide. The routes of administration will vary, naturally, with the location and nature of the lesion, and include, *e.g.*, intradermal, transdermal, parenteral, intravascular, intravenous, intramuscular, intranasal, subcutaneous, regional, percutaneous, intratracheal, intraperitoneal, intraarterial, intravesical, intratumoral, inhalation, perfusion, lavage, direct
5 injection, alimentary, and oral administration and formulation.

To effect a therapeutic benefit with respect to a vascular condition or disease, one would contact a vascular cell with the therapeutic compound. Any of the formulations and routes of administration discussed with respect to the treatment or diagnosis of cancer may also be employed with respect to vascular diseases and conditions.

10 Intratumoral injection, or injection into the tumor vasculature is contemplated for discrete, solid, accessible tumors. Local, regional or systemic administration is also contemplated, particularly for those cancers that are disseminated or are likely to disseminated systemically. The viral particles may be administering by at least or at most 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 injections.

15 In the case of surgical intervention, the present invention may be used preoperatively, to render an inoperable tumor subject to resection. Alternatively, the present invention may be used at the time of surgery, and/or thereafter, to treat residual or metastatic disease. For example, a resected tumor bed may be injected or perfused with a formulation comprising a rhabdovirus polypeptide or a rhabdovirus, which may or may not harbor a mutation, that is
20 advantageous for treatment of cancer or cancer cells. The perfusion may be continued post-resection, for example, by leaving a catheter implanted at the site of the surgery. Periodic post-surgical treatment also is envisioned.

Continuous administration also may be applied where appropriate, for example, where a tumor is excised and the tumor bed is treated to eliminate residual, microscopic disease.
25 Delivery via syringe or catheterization is preferred. Such continuous perfusion may take place for a period from about 1-2 hours, to about 2-6 hours, to about 6-12 hours, to about 12-24 hours, to about 1-2 days, to about 1-2 wk or longer following the initiation of treatment. Generally, the dose of the therapeutic composition via continuous perfusion will be equivalent to that given by a single or multiple injections, adjusted over a period of time
30 during which the perfusion occurs. It is further contemplated that limb perfusion may be

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used to administer therapeutic compositions of the present invention, particularly in the treatment of melanomas and sarcomas.

Treatment regimens may vary as well, and often depend on tumor type, tumor location, disease progression, and health and age of the patient. Obviously, certain types of tumor will require more aggressive treatment, while at the same time, certain patients cannot tolerate more taxing protocols. The clinician will be best suited to make such decisions based on the known efficacy and toxicity (if any) of the therapeutic formulations.

In certain embodiments, the tumor being treated may not, at least initially, be resectable. Treatments with therapeutic viral constructs may increase the resectability of the tumor due to shrinkage at the margins or by elimination of certain particularly invasive portions. Following treatments, resection may be possible. Additional treatments subsequent to resection will serve to eliminate microscopic residual disease at the tumor site.

A typical course of treatment, for a primary tumor or a post-excision tumor bed, will involve multiple doses. Typical primary tumor treatment involves a 1, 2, 3, 4, 5, 6 or more dose application over a 1, 2, 3, 4, 5, 6-week period or more. A two-week regimen may be repeated one, two, three, four, five, six or more times. During a course of treatment, the need to complete the planned dosings may be re-evaluated.

The treatments may include various "unit doses." Unit dose is defined as containing a predetermined quantity of the therapeutic composition. The quantity to be administered, and the particular route and formulation, are within the skill of those in the clinical arts. A unit dose need not be administered as a single injection but may comprise continuous infusion over a set period of time. Unit dose of the present invention may conveniently be described in terms of plaque forming units (pfu) or viral particles for viral constructs. Unit doses range from 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} pfu or vp and higher. Alternatively, depending on the kind of virus and the titer attainable, one will deliver 1 to 100, 10 to 50, 100-1000, or up to about 1×10^4 , 1×10^5 , 1×10^6 , 1×10^7 , 1×10^8 , 1×10^9 , 1×10^{10} , 1×10^{11} , 1×10^{12} , 1×10^{13} , 1×10^{14} , or 1×10^{15} or higher infectious viral particles (vp) to the patient or to the patient's cells.

B. Injectable Compositions and Formulations

The preferred method for the delivery of an expression construct or virus encoding all or part of a rhabdovirus genome to cancer or tumor cells in the present invention is via intravascular injection. However, the pharmaceutical compositions disclosed herein may
5 alternatively be administered intratumorally, parenterally, intravenously, intrarterially, intradermally, intramuscularly, transdermally or even intraperitoneally as described in U.S. Patents 5,543,158, 5,641,515 and 5,399,363.

Injection of nucleic acid constructs may be delivered by syringe or any other method
10 used for injection of a solution, as long as the expression construct can pass through the particular gauge of needle required for injection (for examples see U.S. Patents 5,846,233 and 5,846,225).

Solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose.
15 Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms. The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (U.S. Patent
20 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof,
25 and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be
30 preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged

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absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous, intratumoral, and intraperitoneal administration. In this connection, sterile aqueous media that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards required by governments of the countries in which the compositions are being used.

The compositions disclosed herein may be formulated in a neutral or salt form. Pharmaceutically-acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug release capsules and the like.

As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the

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therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The phrase “pharmaceutically-acceptable” or “pharmacologically-acceptable” refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a protein as an active ingredient is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared.

C. Combination Treatments

The compounds and methods of the present invention may be used in the context of hyperproliferative or neoplastic diseases/conditions including cancer and atherosclerosis. In order to increase the effectiveness of a treatment with the compositions of the present invention, such as rhabdoviruses, it may be desirable to combine these compositions with other agents effective in the treatment of those diseases and conditions. For example, the treatment of a cancer may be implemented with therapeutic compounds of the present invention and other anti-cancer therapies, such as anti-cancer agents or surgery.

Various combinations may be employed; for example, a non-VSV rhabdovirus, such as Maraba virus, Carajas virus, Muir Springs virus, and/or Bahia Grande virus, is “A” and the secondary anti-cancer therapy is “B”, which may include a second rhabdovirus:

A/B/A B/A/B B/B/A A/A/B A/B/B B/A/A A/B/B/B B/A/B/B
 B/B/B/A B/B/A/B A/A/B/B A/B/A/B A/B/B/A B/B/A/A
 B/A/B/A B/A/A/B A/A/A/B B/A/A/A A/B/A/A A/A/B/A

Administration of the therapeutic virus or viral constructs of the present invention to a patient will follow general protocols for the administration of that particular secondary therapy, taking into account the toxicity, if any, of the virus treatment. It is expected that the treatment cycles would be repeated as necessary. It also is contemplated that various standard therapies, as well as surgical intervention, may be applied in combination with the described cancer or tumor cell therapy.

1. Anti-Cancer Therapy

An “anti-cancer” agent is capable of negatively affecting cancer in a subject, for example, by killing cancer cells, inducing apoptosis in cancer cells, reducing the growth rate of cancer cells, reducing the incidence or number of metastases, reducing tumor size, inhibiting tumor growth, reducing the blood supply to a tumor or cancer cells, promoting an immune response against cancer cells or a tumor, preventing or inhibiting the progression of cancer, or increasing the lifespan of a subject with cancer. Anti-cancer agents include biological agents (biotherapy), chemotherapy agents, and radiotherapy agents. More generally, these other compositions would be provided in a combined amount effective to kill or inhibit proliferation of the cell. This process may involve contacting the cells with virus or viral construct and the agent(s) or multiple factor(s) at the same time. This may be achieved by contacting the cell with a single composition or pharmacological formulation that includes both agents, or by contacting the cell with two distinct compositions or formulations, at the same time, wherein one composition includes the virus and the other includes the second agent(s).

Tumor cell resistance to chemotherapy and radiotherapy agents represents a major problem in clinical oncology. One goal of current cancer research is to find ways to improve the efficacy of chemo- and radiotherapy by combining it with gene therapy. For example, the herpes simplex-thymidine kinase (HS-tK) gene, when delivered to brain tumors by a retroviral vector system, successfully induced susceptibility to the antiviral agent ganciclovir (Culver *et al.*, 1992). In the context of the present invention, it is contemplated that poxvirus therapy could be used similarly in conjunction with chemotherapeutic, radiotherapeutic, immunotherapeutic, or other biological intervention, in addition to other pro-apoptotic or cell cycle regulating agents.

Alternatively, a viral therapy may precede or follow the other treatment by intervals ranging from minutes to weeks. In embodiments where the other agent and virus are applied separately to the cell, one would generally ensure that a significant period of time did not expire between the time of each delivery, such that the agent and virus would still be able to exert an advantageously combined effect on the cell. In such instances, it is contemplated that one may contact the cell with both modalities within about 12-24 h of each other and, more preferably, within about 6-12 h of each other. In some situations, it may be desirable to

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extend the time period for treatment significantly, however, where several days (2, 3, 4, 5, 6 or 7) to several weeks (1, 2, 3, 4, 5, 6, 7 or 8) lapse between the respective administrations.

a. Chemotherapy

Cancer therapies also include a variety of combination therapies with both chemical
 5 and radiation based treatments. Combination chemotherapies include, for example, cisplatin (CDDP), carboplatin, procarbazine, mechlorethamine, cyclophosphamide, camptothecin, ifosfamide, melphalan, chlorambucil, busulfan, nitrosurea, dactinomycin, daunorubicin, doxorubicin, bleomycin, plicomycin, mitomycin, etoposide (VP16), tamoxifen, raloxifene, estrogen receptor binding agents, taxol, gemcitabine, navelbine, farnesyl-protein transferase
 10 inhibitors, transplatinum, 5-fluorouracil, vincristine, vinblastine and methotrexate, Temazolomide (an aqueous form of DTIC), or any analog or derivative variant of the foregoing. The combination of chemotherapy with biological therapy is known as biochemotherapy.

b. Radiotherapy

15 Other factors that cause DNA damage and have been used extensively include what are commonly known as γ -rays, X-rays, proton beams, and/or the directed delivery of radioisotopes to tumor cells. Other forms of DNA damaging factors are also contemplated such as microwaves and UV-irradiation. It is most likely that all of these factors effect a broad range of damage on DNA, on the precursors of DNA, on the replication and repair of
 20 DNA, and on the assembly and maintenance of chromosomes. Dosage ranges for X-rays range from daily doses of 50 to 200 roentgens for prolonged periods of time (3 to 4 wk), to single doses of 2000 to 6000 roentgens. Dosage ranges for radioisotopes vary widely, and depend on the half-life of the isotope, the strength and type of radiation emitted, and the uptake by the neoplastic cells.

25 The terms "contacted" and "exposed," when applied to a cell, are used herein to describe the process by which a therapeutic construct and a chemotherapeutic or radiotherapeutic agent are delivered to a target cell or are placed in direct juxtaposition with the target cell. To achieve cell killing or stasis, both agents are delivered to a cell in a combined amount effective to kill the cell or prevent it from dividing.

c. Immunotherapy

Immunotherapeutics, generally, rely on the use of immune effector cells and molecules to target and destroy cancer cells. The immune effector may be, for example, an antibody specific for some marker on the surface of a tumor cell. The antibody alone may
5 serve as an effector of therapy or it may recruit other cells to actually effect cell killing. The antibody also may be conjugated to a drug or toxin (chemotherapeutic, radionuclide, ricin A chain, cholera toxin, pertussis toxin, *etc.*) and serve merely as a targeting agent. Alternatively, the effector may be a lymphocyte carrying a surface molecule that interacts, either directly or indirectly, with a tumor cell target. Various effector cells include cytotoxic
10 T cells and NK cells. The combination of therapeutic modalities, *i.e.*, direct cytotoxic activity and inhibition or reduction of certain rhabdovirus or rhabdovirus polypeptides would provide therapeutic benefit in the treatment of cancer.

Immunotherapy could also be used as part of a combined therapy. The general approach for combined therapy is discussed below. In one aspect of immunotherapy, the
15 tumor cell must bear some marker that is amenable to targeting, *i.e.*, is not present on the majority of other cells. Many tumor markers exist and any of these may be suitable for targeting in the context of the present invention. Common tumor markers include carcinoembryonic antigen, prostate specific antigen, urinary tumor associated antigen, fetal antigen, tyrosinase (p97), gp68, TAG-72, HMFG, Sialyl Lewis Antigen, MucA, MucB,
20 PLAP, estrogen receptor, laminin receptor, erb B and p155. Tumor cell lysates may also be used in an antigenic composition.

An alternative aspect of immunotherapy is to combine anticancer effects with immune stimulatory effects. Immune stimulating molecules include: cytokines such as IL-2, IL-4, IL-12, GM-CSF, IFN γ , chemokines such as MIP-1, MCP-1, IL-8 and growth factors such as
25 FLT3 ligand. Combining immune stimulating molecules, either as proteins or using gene delivery in combination with a tumor suppressor has been shown to enhance anti-tumor effects (Ju *et al.*, 2000).

As discussed earlier, examples of immunotherapies currently under investigation or in use are immune adjuvants (*e.g.*, *Mycobacterium bovis*, *Plasmodium falciparum*,
30 dinitrochlorobenzene and aromatic compounds) (U.S. Patents 5,801,005 and 5,739,169; Hui and Hashimoto, 1998; Christodoulides *et al.*, 1998), cytokine therapy (*e.g.*, interferons α , β

and γ , IL-1, GM-CSF and TNF) (Bukowski *et al.*, 1998; Davidson *et al.*, 1998; Hellstrand *et al.*, 1998) gene therapy (*e.g.*, TNF, IL-1, IL-2, p53) (Qin *et al.*, 1998; Austin-Ward and Villaseca, 1998; U.S. Patents 5,830,880 and 5,846,945) and monoclonal antibodies (*e.g.*, anti-ganglioside GM2, anti-HER-2, anti-p185) (Pietras *et al.*, 1998; Hanibuchi *et al.*, 1998; U.S. Patent 5,824,311). Herceptin (trastuzumab) is a chimeric (mouse-human) monoclonal antibody that blocks the HER2-neu receptor (Dillman, 1999). Combination therapy of cancer with herceptin and chemotherapy has been shown to be more effective than the individual therapies. Thus, it is contemplated that one or more anti-cancer therapies may be employed with the rhabdovirus-related therapies described herein.

10 (1) Passive Immunotherapy

A number of different approaches for passive immunotherapy of cancer exist. They may be broadly categorized into the following: injection of antibodies alone; injection of antibodies coupled to toxins or chemotherapeutic agents; injection of antibodies coupled to radioactive isotopes; injection of anti-idiotypic antibodies; and finally, purging of tumor cells
15 in bone marrow.

Preferably, human monoclonal antibodies are employed in passive immunotherapy, as they produce few or no side effects in the patient. However, their application is somewhat limited by their scarcity and have so far only been administered intralesionally. Human monoclonal antibodies to ganglioside antigens have been administered intralesionally to
20 patients suffering from cutaneous recurrent melanoma (Irie and Morton, 1986). Regression was observed in six out of ten patients, following, daily or weekly, intralesional injections. In another study, moderate success was achieved from intralesional injections of two human monoclonal antibodies (Irie *et al.*, 1989).

It may be favorable to administer more than one monoclonal antibody directed against
25 two different antigens or even antibodies with multiple antigen specificity. Treatment protocols also may include administration of lymphokines or other immune enhancers as described by Bajorin *et al.* (1988). The development of human monoclonal antibodies is described in further detail elsewhere in the specification.

(2) Active Immunotherapy

30 In active immunotherapy, an antigenic peptide, polypeptide or protein, or an autologous or allogenic tumor cell composition or "vaccine" is administered, generally with a

distinct bacterial adjuvant (Ravindranath and Morton, 1991; Morton *et al.*, 1992; Mitchell *et al.*, 1990; Mitchell *et al.*, 1993). In melanoma immunotherapy, those patients who elicit high IgM response often survive better than those who elicit no or low IgM antibodies (Morton *et al.*, 1992). IgM antibodies are often transient antibodies and the exception to the rule appears
5 to be anti ganglioside or anticarbohydrate antibodies.

(3) Adoptive Immunotherapy

In adoptive immunotherapy, the patient's circulating lymphocytes, or tumor infiltrated lymphocytes, are isolated *in vitro*, activated by lymphokines such as IL 2 or transduced with genes for tumor necrosis, and readministered (Rosenberg *et al.*, 1988; 1989). To achieve this,
10 one would administer to an animal, or human patient, an immunologically effective amount of activated lymphocytes in combination with an adjuvant incorporated antigenic peptide composition as described herein. The activated lymphocytes will most preferably be the patient's own cells that were earlier isolated from a blood or tumor sample and activated (or "expanded") *in vitro*. This form of immunotherapy has produced several cases of regression
15 of melanoma and renal carcinoma, but the percentage of responders were few compared to those who did not respond.

d. Genes

In yet another embodiment, the secondary treatment is a gene therapy in which a therapeutic polynucleotide is administered before, after, or at the same time as a rhabdovirus
20 is administered. Delivery of a rhabdovirus in conjunction with a vector encoding one of the following gene products will have a combined anti-cancer effect on target tissues. Alternatively, the rhabdovirus may be engineered as a viral vector to include the therapeutic polynucleotide. A variety of proteins are encompassed within the invention, some of which are described below. Table 4 lists various genes that may be targeted for gene therapy of
25 some form in combination with the present invention.

(1) Inducers of Cellular Proliferation

The proteins that induce cellular proliferation further fall into various categories dependent on function. The commonality of all of these proteins is their ability to regulate cellular proliferation. For example, a form of PDGF, the sis oncogene, is a secreted growth
30 factor. Oncogenes rarely arise from genes encoding growth factors, and at the present, sis is the only known naturally-occurring oncogenic growth factor. In one embodiment of the

present invention, it is contemplated that anti-sense mRNA directed to a particular inducer of cellular proliferation is used to prevent expression of the inducer of cellular proliferation.

(2) Inhibitors of Cellular Proliferation

The tumor suppressor oncogenes function to inhibit excessive cellular proliferation. The inactivation of these genes destroys their inhibitory activity, resulting in unregulated proliferation. Tumor suppressors include p53, p16 and C-CAM. Other genes that may be employed according to the present invention include Rb, APC, DCC, NF-1, NF-2, WT-1, MEN-I, MEN-II, *zac1*, p73, VHL, MMAC1 / PTEN, DBCCR-1, FCC, *rsk-3*, p27, p27/p16 fusions, p21/p27 fusions, anti-thrombotic genes (*e.g.*, COX-1, TFPI), PGS, Dp, E2F, *ras*, myc, *neu*, *raf*, *erb*, *fms*, *trk*, *ret*, *gsp*, *hst*, *abl*, E1A, p300, genes involved in angiogenesis (*e.g.*, VEGF, FGF, thrombospondin, BAI-1, GDAIF, or their receptors) and MCC.

(3) Regulators of Programmed Cell Death

Apoptosis, or programmed cell death, is an essential process for normal embryonic development, maintaining homeostasis in adult tissues, and suppressing carcinogenesis (Kerr *et al.*, 1972). The Bcl-2 family of proteins and ICE-like proteases have been demonstrated to be important regulators and effectors of apoptosis in other systems. The Bcl 2 protein, discovered in association with follicular lymphoma, plays a prominent role in controlling apoptosis and enhancing cell survival in response to diverse apoptotic stimuli (Bakhshi *et al.*, 1985; Cleary and Sklar, 1985; Cleary *et al.*, 1986; Tsujimoto *et al.*, 1985; Tsujimoto and Croce, 1986). The evolutionarily conserved Bcl-2 protein now is recognized to be a member of a family of related proteins, which can be categorized as death agonists or death antagonists.

Subsequent to its discovery, it was shown that Bcl 2 acts to suppress cell death triggered by a variety of stimuli. Also, it now is apparent that there is a family of Bcl-2 cell death regulatory proteins which share in common structural and sequence homologies. These different family members have been shown to either possess similar functions to Bcl 2 (*e.g.*, BclXL, BclW, BclS, Mcl-1, A1, Bfl-1) or counteract Bcl 2 function and promote cell death (*e.g.*, Bax, Bak, Bik, Bim, Bid, Bad, Harakiri).

e. Surgery

Approximately 60% of persons with cancer will undergo surgery of some type, which includes preventative, diagnostic or staging, curative and palliative surgery. Curative surgery is a cancer treatment that may be used in conjunction with other therapies, such as the treatment of the present invention, chemotherapy, radiotherapy, hormonal therapy, gene therapy, immunotherapy and/or alternative therapies.

Curative surgery includes resection in which all or part of cancerous tissue is physically removed, excised, and/or destroyed. Tumor resection refers to physical removal of at least part of a tumor. In addition to tumor resection, treatment by surgery includes laser surgery, cryosurgery, electrosurgery, and microscopically controlled surgery (Mohs' surgery). It is further contemplated that the present invention may be used in conjunction with removal of superficial cancers, pre-cancers, or incidental amounts of normal tissue.

Upon excision of part of all of cancerous cells, tissue, or tumor, a cavity may be formed in the body. Treatment may be accomplished by perfusion, direct injection or local application of the area with an additional anti-cancer therapy. Such treatment may be repeated, for example, every 1, 2, 3, 4, 5, 6, or 7 days, or every 1, 2, 3, 4, and 5 weeks or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 months. These treatments may be of varying dosages as well.

f. Other agents

It is contemplated that other agents may be used in combination with the present invention to improve the therapeutic efficacy of treatment. These additional agents include immunomodulatory agents, agents that affect the upregulation of cell surface receptors and GAP junctions, cytostatic and differentiation agents, inhibitors of cell adhesion, agents that increase the sensitivity of the hyperproliferative cells to apoptotic inducers, or other biological agents. Immunomodulatory agents include tumor necrosis factor; interferon α , β , and γ ; IL-2 and other cytokines; F42K and other cytokine analogs; or MIP-1, MIP-1 β , MCP-1, RANTES, and other chemokines. It is further contemplated that the upregulation of cell surface receptors or their ligands such as Fas/Fas ligand, DR4 or DR5/TRAIL (Apo-2 ligand) would potentiate the apoptotic inducing ability of the present invention by establishment of an autocrine or paracrine effect on hyperproliferative cells. Increases intercellular signaling by elevating the number of GAP junctions would increase the anti-hyperproliferative effects

on the neighboring hyperproliferative cell population. In other embodiments, cytostatic or differentiation agents can be used in combination with the present invention to improve the anti-hyperproliferative efficacy of the treatments. Inhibitors of cell adhesion are contemplated to improve the efficacy of the present invention. Examples of cell adhesion inhibitors are focal adhesion kinase (FAKs) inhibitors and Lovastatin. It is further contemplated that other agents that increase the sensitivity of a hyperproliferative cell to apoptosis, such as the antibody c225, could be used in combination with the present invention to improve the treatment efficacy.

There have been many advances in the therapy of cancer following the introduction of cytotoxic chemotherapeutic drugs. However, one of the consequences of chemotherapy is the development/acquisition of drug-resistant phenotypes and the development of multiple drug resistance. The development of drug resistance remains a major obstacle in the treatment of such tumors and therefore, there is an obvious need for alternative approaches such as viral therapy.

Another form of therapy for use in conjunction with chemotherapy, radiation therapy or biological therapy includes hyperthermia, which is a procedure in which a patient's tissue is exposed to high temperatures (up to 106°F). External or internal heating devices may be involved in the application of local, regional, or whole-body hyperthermia. Local hyperthermia involves the application of heat to a small area, such as a tumor. Heat may be generated externally with high-frequency waves targeting a tumor from a device outside the body. Internal heat may involve a sterile probe, including thin, heated wires or hollow tubes filled with warm water, implanted microwave antennae, or radiofrequency electrodes.

A patient's organ or a limb is heated for regional therapy, which is accomplished using devices that produce high energy, such as magnets. Alternatively, some of the patient's blood may be removed and heated before being perfused into an area that will be internally heated. Whole-body heating may also be implemented in cases where cancer has spread throughout the body. Warm-water blankets, hot wax, inductive coils, and thermal chambers may be used for this purpose.

Hormonal therapy may also be used in conjunction with the present invention or in combination with any other cancer therapy previously described. The use of hormones may be employed in the treatment of certain cancers such as breast, prostate, ovarian, or cervical

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cancer to lower the level or block the effects of certain hormones such as testosterone or estrogen. This treatment is often used in combination with at least one other cancer therapy as a treatment

V. EXAMPLES

5 The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. One skilled in the art will appreciate readily that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those objects, ends and advantages inherent herein. The present examples, along with the methods described herein
10 are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses which are encompassed within the spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

EXAMPLE 1

15 SCREENING FOR NOVEL ONCOLYTIC CANDIDATE RHABDOVIRUSES

In vitro screens. As an initial screen to identify novel oncolytic viruses, rhabdovirus field isolates were assessed for their ability to kill human tumor cells from the NCI 60 cell panel. This has been a fruitful strategy for the inventors in the past to determine the relative effectiveness of a series of VSV mutants as oncolytic (cancer cell lysing) candidates.
20 Initially, the inventors have examined 13 novel rhabdoviruses that have been previously determined to replicate in mammalian cells. It is contemplated that this procedure will be extended to study rhabdoviruses for which there is less experience in cell culture. In an effort to rapidly and efficiently screen through a matrix of 60 cells infected with 13 different viruses, the inventors use a rapid and inexpensive assay in 96 well format using MTS
25 reduction to formazan, or crystal violet staining of residual cells, to measure cell number and viability. The inventors grow cell lines to 80% confluence in 96 well plates and then expose them in parallel to our rhabdovirus field isolates at increasing MOIs (MOI = 0.0001 - 10 PFUs/cell). At 48 and 96 hours post infection, cells are stained with aqueous MTS reagent (Promega USA) and incubated for 3 hours to allow sufficient formazan formation.
30 Alternatively, the plates of infected cells are washed with buffer to remove dead cells, stained with crystal violet dye, washed to remove residual dye, after which time the dye is solubilized using detergent. These plates are then read using the integrated multiwell plate reader

(Biotek SyncrasyHT; USA), the data curve fitted, and the EC_{50} determined from this curve. Typically, assays are performed in sextuplet, with the highest and lowest EC_{50} values removed, and averaging the remaining four EC_{50} to ultimately determine a value and confidence interval. (For example see FIG. 2)

5 As a counter screen to assess whether a particular virus infects/kills normal human cells *in vitro*, cultures of normal human fibroblasts, epithelium and endothelium and neuronal cultures from the inventors collection and those commercially available (Cambrex, USA) will be screened. Cultures will be infected with candidate viruses (0.1 to 20 pfu/cell) for 48 and 96 hours. Cell viability will be detected by MTS assay, or crystal violet assay, and further
10 characterized by labeling with activated caspase 3 antibody D175 (Cell Signaling Technologies, USA) and detected using a FITC-conjugated secondary antibody. Studies will be done in parallel with known susceptible/resistant human and mouse tumor cell lines. A combination of untreated cells and cells treated with TRAIL and cyclohexamide has been used to establish the dynamic range of the assay, with preliminary z-factor determinations
15 significantly above 0.5.

 Another contingency is that viruses may replicate and spread efficiently within cultures without rapidly killing these cells. These are also potentially interesting viruses, provided their replication is tumor selective in nature, as their lytic capacity could subsequently be increased through recombinant engineering. To detect these viruses, the
20 inventors will infect cells of the NCI 60 cell panel with field isolates at a low MOI (0.1 pfu/cell) in duplicate wells of a 24 well plate. After 1 hour, wells will be washed thoroughly to remove free input virus, medium added and the cultures incubated for a further 72 hours. These culture supernatants will subsequently be titered on a permissive cell line (Vero cells) to detect and quantify productive infection. The final wash from each of these will be titered
25 to control for residual input virus. Candidate virus hits in this assay will be confirmed in tissue culture cells using virus-specific antisera and standard immunofluorescence microscopy.

Rank based on all parameters. Several properties contribute to oncolytic killing of tumor cells including: ability to induce apoptosis, rate of virus production, quantity of virus
30 produced, as well as special functions such as syncytia formation. Promising candidates from the initial screen will be characterized further with respect to apoptosis induction (as determined by TUNEL assay and immunofluorescence staining for activated caspase-3), and

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one step growth curves to compare kinetics and to quantify virus production. These studies will serve as a guide to improving these strains. For example: (1) if a virus kills tumor cells well but shows unacceptable toxicity to normal cells, the inventors will attenuate this virus using one or more of the strategies outline below; (2) alternatively, if a virus shows slower
 5 killing kinetics while maintaining a high replication rate, then the inventors may add a toxic or therapeutic transgene; (3) If a candidate virus replicates slowly yet is an effective killer, the inventor will select a variant with increased growth kinetics to boost its potency.

From the inventors experience with VSV and other oncolytic viruses, they have identified three key *in vitro* gating criteria to narrow the list of candidates: (1) selective tumor
 10 cell killing, (2) productive replication within tumor cells (independent of killing), and (3) efficacy on VSV resistant tumor lines (UACC-62 melanoma, A431 and NCI-H226 lung, DU-145 prostate, HL60 leukemia). Based on these criteria, results from the screening assays described above will be integrated to pare the list for further evaluate in preliminary *in vivo* testing.

15 ***In vivo* Toxicity and Biodistribution.** The two routes of administration related to a clinical setting are intravenous (IV) and intracranial (IC) injections. Lead candidates identified during *in vitro* screening for toxicity and biodistribution in mice following infection will be assessed by these routes. Groups of 3 mice will be infected either by IV at doses of 1×10^5 to 1×10^9 pfu, or by IC at 1×10^2 to 1×10^6 pfu. In addition to mortality,
 20 morbidity will be monitored daily for signs of lethargy, dehydration, weight loss and limb paralysis. Histopathology will be performed on 2 mice from the minimum lethal dose group (highest dose if no lethal dose is achieved) from each candidate virus infection. WT VSV and mock infection will serve as appropriate positive and negative controls respectively. Organs will be harvested from the remaining mouse in this group, homogenized and titered as
 25 a preliminary assessment of virus biodistribution.

For viruses that display an acceptable lethal dose range, the inventors will subsequently assess biodistribution in tumor bearing mice to identify viruses compatible with systemic administration. The inventor will employ three of our existing cancer models representing very different organ targets of critical clinical relevance: (1) CT-26 mouse colon
 30 carcinoma (1×10^5 cells) injected intravenously to form disseminated lungs tumors in syngeneic Balb/C mice (2), 4T1 mouse breast carcinoma (4×10^5 cells) injected into the fat pad of syngeneic Balb/C mice to form a single primary tumor with spontaneous metastases,

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and (3) U87 human glioblastoma cells (1×10^5 cells) stereotactically implanted in the cortex of nude mice. A maximum tolerable dose for each virus and route (IV or IC) will be determined from the preliminary *in vivo* toxicity experiments. This value will serve as an initial therapeutic dose for biodistribution studies in tumor bearing mice. In groups of 3 mice, tumors will be established for 1 week and then treated IV or IC with a single dose of each candidate virus at their respective MTD. Forty-eight hours post treatment, animals will be perfused with saline to flush any free virus from the circulation, and tumors and organs will be harvested, homogenized and titered to quantify infectious virus. In this fashion, the inventors will determine which viruses can be delivered to tumor sites by systemic injection, as well as the relative tumor selectivity of virus replication *in vivo*.

Re-Rank. Based on the toxicity, biodistribution, systemic delivery and tumor selectivity profiles in *in vivo* studies, the inventors will select the best candidates to proceed with detailed characterization and further development.

EXAMPLE 2

BUILDING RECOMBINANTS

Sequencing and Recombinant System. In order to facilitate rapid research and development, subsequent production of clinical material and to ensure the safety and stability of therapeutic viruses, the inventors will clone and rescue recombinant forms selected viruses.

Many negative strand ssRNA viruses have been cloned and rescued using standard recombinant techniques. The inventors will employ similar strategies that have been adopted successfully for reported recombinant -ssRNA viruses. Briefly, the genome of a candidate virus will be isolated by RNA extraction (Qiagen Corp) from 1×10^9 virus purified particles. The purified genomic RNA is then primed with random hexamers and reverse transcribed to cDNA, subsequently rendered double-stranded and cloned by ligating EcoRI adapters, size fractionated and finally ligating into an EcoRI digested bacterial plasmid (pT7Blue ; Novagen). The result is a library of genomic fragments that can be easily sequenced by standard techniques. Because of the random primed nature of this library, this strategy will not "capture" the extreme 3' and 5' ends. To do this the inventors ligate oligos to the 3' or 5' ends of the purified genomic RNA using T4 RNA ligase. Using primers complementary to the newly ligated oligo flanking the genome, the inventors PCR amplify and clone the ends of

the genome for subsequent sequencing. This sequence information is then used to design end-specific primers for amplifying the entire genome, which is then cloned into a specialized plasmid. This plasmid flanks the genome with a T7 promoter on one end and a hepatitis delta self-cleaving ribozyme and T7 terminator sequence on the opposite flank. When transfected
 5 into T7 RNA polymerase expressing (previously infected with a T7 expressing vaccinia virus) A549 cells, this plasmid generates viral genomes in the cytoplasm. In parallel, the viruses' coding sequences for N, P and L genes are cloned into CMV promoter driven expression plasmids. Co-transfection of the genome construct with the N, P and L plasmids into these A549 cells reconstitutes the viral replication complex on the viral genome and
 10 results in rescue of infectious virus. As a proof of principle the inventors have cloned, genetically manipulated, and rescued Maraba virus using this method. See FIG. 17 and FIG. 18 for examples of Maraba related viruses.

EXAMPLE 3

OPTIMIZATION/AUGMENTATION

15 The non-VSV rhabdoviruses are feral viruses; and as with all oncolytic viruses reported thus far, including VSV, the inventors predict that these field isolates will benefit from further optimization through *in vitro* selection and/or recombinant engineering strategies. Some candidates may require attenuation (*e.g.*, Maraba virus) while some may require augmentation of their replication and/or tumor killing kinetics (*e.g.*, Muir Springs
 20 virus). The following is a summary of several strategies the inventors will employ to maximize the effectiveness of newly identified therapeutic viruses.

Engineered Mutations. VSV blocks nuclear/cytoplasmic mRNA transport as a means to defeat host cell innate immunity. The inventors have previously described engineering mutations into the M protein of VSV to disable this activity and thereby
 25 selectively attenuate this virus in normal cells. Given that other members of the vesiculoviruses genus have also demonstrated this ability (Chandipura, and spring viremia of carp) and that most vesiculoviruses sequenced thus far (VSV, Chandipura, Piry, Cocal, spring viremia of carp, Maraba) have the critical sequence motif required by VSV for this function, the inventors contemplate attenuate of non-VSV rhabdovirus in an analogous
 30 fashion to that used for VSV. However, other rhabdoviruses such as rabies and bovine ephemeral fever virus do not have this motif and do not block nuclear cytoplasmic mRNA transport and perhaps will not be amenable to this strategy of attenuation. As more

information becomes available regarding rhabdovirus/host interaction from consortium labs and others, additional structure/functioned-guided manipulations to attenuate theses viruses will be possible.

Transgenes. There are now several reports of “arming” oncolytic viruses with suicide genes or immune mediators to increase their potency. The inventors will focus on adding transgenes to increase the cytotoxicity of candidate viruses that show efficient replication, but insufficient tumor killing. The inventors have a priority-weighted list of transgenes that are currently being engineered into Maraba virus. At present the ranking consists of: (1) Apoptosis Inducing Factor (AIF) – an oxido-reductase homolog responsible for chromatin collapse and degradation in a caspase-independent manner. (2) HaraKiri - the most potent of the BH3-only pro-apoptotic member of the Bcl-2 family responsible for induction of conventional caspase-dependent apoptosis (Type I PCD). (3) XAF1 – a potent tumor suppressor gene and direct inhibitor of the IAP family. (4) Atg4B – the key protease responsible for initiating autophagy (Type II PCD).

Ultimately, members of the intrinsic or extrinsic pathways of cell death could be engineered with Tat or other protein transduction domains to be secreted from virus infected cells to induce bystander killing within the tumor mass. The inventors remain cognizant that other bystander killing effects maybe mediated through components of the host immunity to virus and/or tumor. Thus an alternative strategy would be to engineer a transgene(s) to draw immune cells to sites of infection. Evidence indicates that virus infection of CT26 lung tumors induces neutrophils to infiltrate the tumor and cause a massive apoptotic bystander killing effect.

Directed evolution to improve oncolytic Rhabdoviruses. Many examples of directed evolution have been described where the replication fitness of a parental virus strain was either increased or decreased by serial passage in mammalian cell culture. Rhabdoviruses are particularly amenable to this type of procedure as they exist not as a single entity, but as a population of strains called a quasi-species. The members of the quasi-species represent point mutants of the dominant genome. When an appropriate selection pressure is applied, the fittest member of the population is selected for, and becomes the dominant genome. This has tremendous utility in efforts to build a better oncolytic virus because it provides one with a ready-made collection of mutants from which to select a variant with better oncolytic capabilities. Thus, to attenuate a given candidate, the inventors will select

small plaque mutants on primary fibroblasts and subsequently amplify this cloned virus on tumor cells to back-select against non-productive mutations (*i.e.*, mutations which uniformly debilitate, such as polymerase mutations, as opposed to specific disabilities in normal cells/tissues). By performing this in iterative cycles at high MOI (10 pfu/cell), the inventors expect to isolate a mutant that maintains robust replication in tumor cells, yet has lost the ability to productively infect healthy normal cells. Alternatively, the inventors may augment the potency of non-VSV rhabdoviruses, either by selecting faster replicators, or more lethal killers. To speed up the replication rate of a candidate virus the inventors will perform iterative rounds of infection/replication in tumor cell lines, but at each subsequent round will decrease the post infection harvest time. This selection pressure will force viruses to evolve towards rapid replication. If enhanced cytotoxicity is desirable, the inventors will infect resistant or recalcitrant tumor cell lines (1×10^6 cells) with candidate viruses (MOI=1). Live cells will subsequently be stained with JC1 vital dye to detect early apoptosis events by dual color flow cytometry. Cells undergoing apoptosis will be sorted onto monolayers of Vero cells to recover the virus replicating within them. Iterative rounds of this assay, again with decreasing harvest times, will select for a more rapidly lethal phenotype. Viruses improved in this way will be sequenced to map the genetic alterations and contribute to our structure/function analysis efforts toward better understanding of the biology of rhabdoviruses and oncolysis. The reverse genetic screen allows for an unbiased approach to improving rhabdoviruses, and represents a good complement to efforts to make improvements through recombinant engineering of transgenes or rational mutations based on structure/function studies.

EXAMPLE 4

IN VIVO TESTING OF NOVEL RECOMBINANT ONCOLYTIC RHABDOVIRUS(ES)

The inventors have chosen to use orthotopic models of cancer as they more accurately recapitulate the human clinical disease. However, unlike subcutaneous tumor models, orthotopic tumors are not readily accessible and therefore difficult to assess without sacrificing the experimental animal. To solve this problem, a multimodal optical imaging technology is adopted that allows non-invasive imaging, and repeated measure the growth or regression of the implanted tumors, as well as the development or regression of distal metastatic lesions. The inventors have a highly sensitive fully integrated whole animal imaging platform (IVIS 200; Xenogen Corp) that can detect photons emitted even from

within deep tissue. It can measure fluorescent light emitted by recombinant fluorescent proteins such as GFP as well as detect luciferase-generated bioluminescence. By using substrate-specific luciferase reporter genes, one expressed from the virus and the other expressed from tumor cells, the inventors can measure the bioluminescence resulting from virus replication concurrently with tumor measurements. To do this the inventors have cloned either YFP or a novel monomeric RFP in frame with either firefly luciferase or a novel renilla-like luciferase from the marine copepod *Gaussia princeps*. Between these two coding sequences the inventors have engineered a translation "stop-restart" sequence of 30 amino acids. This small motif comes from the foot and mouth disease virus and allows for the stoichiometric expression of two proteins from a single mRNA, is very small and does not suffer from cell to cell variability as do IRES motifs. These dual reporter constructs were cloned into lentivirus vectors, packaged into virus, and used to establish stable reporter tagged 4T1, CT26 and U87 human glioblastoma cells. These cells lines are used in three orthotopic mouse tumor models: U87 human gliomas implanted intracranially into CD-1 nude mice; 4T1 mouse breast carcinoma cells implanted into the fat pad of Balb/C females (spontaneous, aggressive metastatic disease model); CT-26 colon carcinoma injected into the tail vein of Balb/C mice (disseminated tumors in the lung). The choice of orthotopic model was predicated on the following criteria: aggressive, rapidly developing tumor, and therefore challenging to treat; represent very different organ targets; span both immune competent and immunocompromised host systems.

The first studies will be to evaluate dose response characteristics in our models to identify an optimal dose. From preliminary toxicity experiments, the inventors will have defined an MTD for each of our candidate strains in non-tumor bearing Balb/C animals. Therefore the inventors will test doses from the MTD, decreasing in half log intervals down to 1×10^3 pfu. Using the IVIS to image replication in the established tumors, kinetics of initial virus delivery and duration of subsequent replication will be studied as a function of dose. In parallel studies, mice will be sacrificed during this time course and examined using fluorescence microscopy to determine how dose affects the ability to reach all portions of the tumor and distal metastatic lesions. Healthy tissue will be examined to assess tumor specific replication. Finally, safety at each dose will be determined by monitoring mice for any signs of morbidity such as weight loss, dehydration, and behavioral changes. Tumor responses to the viruses in head-to-head comparisons will be assessed following single dose IV treatment. The sensitivity and quantitative nature of optical imaging technology make it ideally suited

for this purpose. Thus tumors will be established as described above and monitor tumor growth or regression following virus dosing and compare these results to UV inactivated virus controls. Based on previous work with VSV, it is contemplated that a single dose may not be sufficient for complete and durable tumor regressions. This necessitates a series of experiments to determine the most efficacious number and timing of doses. In a strategy similar to that described above, the inventors will use tumor models to develop maximally effective dosing strategies. This will be done while monitoring for virus deliver to the tumor, replication, duration of replication at the tumor bed and spread to distant tumor sites, in concert with tumor growth/regression. In addition, the inventors will examine immune cell infiltration and activation in tumor beds and surrounding lymph nodes using flow cytometry and immunohistochemistry as another parameter of oncolytic activity. Ultimately, efficacy will be confirmed by monitoring these mice for overall survival, and/or time to progression; comparing virus treated groups with those treated with UV-inactivated virus as controls. An example of the animal model can be found in FIG. 13.

Cycle back to Optimization/Augmentation. It may be that several cycles of optimization and then re-testing will be required to ultimately develop a maximally effective therapeutic virus. Therefore, the inventors will use the results from *in vivo* testing to guide additional rounds of biological and/or recombinant optimization and then re-test in tumor models.

Table 4. Rhabdovirus mediated cell killing on the NCI 60 cell panel. Cells from the NCI 60 cell panel were plated in 6 well plates to a confluency of 90%. These cells were infected at log dilutions with various rhabdoviruses, as indicated. After 48 hours, the monolayers were washed, fixed and stained with crystal violet to score for viable cells. Values represent the pfu required to kill 50% of cells within 48h.

Malignancy	Cell Line	Chandipura	Maraba	Carajas	Isfahan	Klamath	Sawgrass	VSV HR
NSC LUNG	A549-ATCC	$\leq 10^2$	$\leq 10^2$	10^4	10^5	$\geq 10^6$	NE	$\geq 10^6$
NSC LUNG	EKVX	$\leq 10^2$	10^3		$\geq 10^6$			10^3
NSC LUNG	HOP92	10^3	10^3		10^5			$\leq 10^2$
NSC LUNG	NCI-H226	$\geq 10^6$	$\geq 10^6$	10^4				
NSC LUNG	NCI-H23	$\leq 10^2$	$\leq 10^2$		$\leq 10^2$	10^4		$\leq 10^2$
MELANOMA	LOX IMVI	$\leq 10^2$	10^3	10^3				$\leq 10^2$
MELANOMA	M 14	10^3	$\leq 10^2$	10^3		$\geq 10^6$		10^5
MELANOMA	SK-MEL-2	$\leq 10^2$	10^3					$\leq 10^2$
MELANOMA	MALME 3M	10^3	10^5	10^5	10^3			10^5
MELANOMA	UACC-257	$\leq 10^2$	$\leq 10^2$	$\leq 10^2$	10^3			$\leq 10^2$
MELANOMA	UACC-62		$\leq 10^2$	10^3				$\geq 10^6$
LEUKEMIA	MOLT-4		10^3					$\leq 10^2$
LEUKEMIA	K-562		10^5					
OVARIAN	OVCAR-3		10^3					$\leq 10^2$

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Malignancy	Cell Line	Chandipura	Maraba	Carajas	Isfahan	Klamath	Sawgrass	VSV HR
OVARIAN	OVCAR-4	10^3	$\leq 10^2$	10^5	10^4	$\geq 10^6$	10^4	10^3
OVARIAN	OVCAR-8	NE	$\geq 10^6$	$\geq 10^6$	NE		NE	10^3
OVARIAN	SK-OV-3	$\leq 10^2$	10^5	10^5	$\geq 10^6$		$\geq 10^6$	10^4
CNS	SF-268		$\leq 10^2$	10^4				10^4
CNS	SF-539	$\leq 10^2$	$\leq 10^2$	10^3	10^4			10^5
CNS	SNB-19	10^3	10^4	$\leq 10^2$				$\leq 10^2$
CNS	SNB-75	10^3	10^3	NE	10^5	$\geq 10^6$		$\leq 10^2$
COLON	HT29	10^4	$\geq 10^6$	NE	NE		NE	10^5
COLON	COLO 205	$\leq 10^2$	$\leq 10^2$		$\geq 10^6$			10^3
COLON	HCT-15	10^5	10^4	10^5	$\geq 10^6$			10^3
COLON	SW-620	$\leq 10^2$	$\leq 10^2$	10^3	10^5			$\leq 10^2$
BREAST	HS 578T	$\geq 10^6$	$\geq 10^6$				$\geq 10^6$	10^4
BREAST	MDA-MB-435	$\leq 10^2$	$\leq 10^2$	$\leq 10^2$	10^3			$\leq 10^2$
RENAL	TK-10	$\leq 10^2$	10^3		10^4			10^4
RENAL	786-O	10^4	$\leq 10^2$	10^5	10^5			10^5
RENAL	ACHN	10^5	10^3	10^5	$\geq 10^6$		NE	$\leq 10^2$
RENAL	A498	10^5	10^5	$\geq 10^6$				10^4
PROSTATE	DU-145		$\leq 10^2$		$\geq 10^6$			$\geq 10^6$
PROSTATE	PC-3		$\geq 10^6$		NE			$\leq 10^2$
MOUSE COLON	CT26	$\leq 10^2$	$\leq 10^2$	$\geq 10^6$	NE			$\leq 10^2$

Table 5. Focused comparison between four rhabdoviruses. Cells from the NCI 60 cell panel were plated in 6 well plates to a confluency of 90%. These cells were infected at log dilutions with various rhabdoviruses, as indicated. After 48 hours, the monolayers were washed, fixed and stained with crystal violet to score for viable cells. Values represent the pfu required to kill 50% of cells within 48h.

		Chandipura	Maraba	Carajas	WT VSV
Lung	A549	$\leq 10^2$	$\leq 10^2$	10^4	$\geq 10^6$
	H226	$\geq 10^6$	$\geq 10^6$	10^4	$\leq 10^2$
melanoma	M14	10^3	$\leq 10^2$	10^3	10^5
	Malme 3M	10^3	10^5	10^5	10^5
	UACC-62		$\leq 10^2$	10^3	$\geq 10^6$
leukemia	K562		10^5		10^3
Ovarian	OVCAR4	10^3	$\leq 10^2$	10^5	10^3
	OVCAR8		$\geq 10^6$	$\geq 10^6$	10^3
	SK-OV-3	$\leq 10^2$	10^5	10^5	10^4
CNS	SF268		$\leq 10^2$	10^4	10^4
	SF539	$\leq 10^2$	$\leq 10^2$	10^3	10^5
Colon	HCT-15	10^5	10^4	10^5	10^3
Breast	HS578T	$\geq 10^6$	$\geq 10^6$		10^4
Renal	786-O	10^4	$\leq 10^2$	10^5	10^5
	ACHN	10^5	10^3	10^5	$\leq 10^2$
Prostate	DU-145		$\leq 10^2$		$\geq 10^6$
	PC-3		$\geq 10^6$		$\leq 10^2$

Differences between VSV and other rhabdoviruses on the NCI 60 cell panel include:

- (1) preferential killing by Maraba virus compared to VSV of A549 lung, M14 melanoma, UACC-62 melanoma, SF268 CNS, SF539 CNS, 786-O renal, DU-145 prostate; (2)
- preferential killing by Carajas virus compared to VSV for M14 melanoma, UACC-62

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melanoma, SF539 CNS; preferential killing by VSV for H226 lung, K562 leukemia, OVCAR-8 ovarian, HCT-15, HS578T breast, and PC-3 prostate. All other cell lines of the 60 cell panel show similar susceptibilities to VSV, Maraba and Carajas and Chandipura

- 5 **Table 6.** *In vitro* killing of selected transformed and immortalized cells by novel rhabdoviruses. Cells were plated in 6 well dishes and allowed reach 75% confluency. These cells were subsequently infected with each virus at a fixed titer. Cultures were scored visually for cell death after 96h. 4+ = 100% obliterated, 3+ = 75-90% dead, 2+ = 50% dead, 1+ = <30% dead, -- = no death.

		Farmington	Muir Springs	Rio Grande	Ngaingan	Tibrogargan	Le Dantec	Kwatta
Human	293T	++++	++++	+++	++	+		
Mouse	4T1	+	+	++	+			
Human	SW620	+++	+++	+++	+			
Hamster	BHKT7	+	+++	+++	+++	+++		
Human	U2OS	++++	++	++++	++++			
monkey	Vero	+++	++++	+++	++++			

10

EXAMPLE 5

CHIMERIC RHABDOVIRUSES

- One potential problem with oncolytic viral compositions is the potential for an immune response in a patient. Such an immune response may blunt the effectiveness of further applications of oncolytic virus since a significant portion of the applied virus may be neutralized by the patient's immune system. To avoid this problem it would be preferable to have a plurality of oncolytic viral compositions that are immunologically distinct. In this case a different oncolytic virus may be applied to a patient for each subsequent therapy thereby providing sustained oncolytic activity that is minimally effected by a host immune response. To this end a number of pseudotyped viral compositions were constructed and tested for their ability to infect cells.

- To study the possibility of using oncolytic Rhabdoviruses that comprises various G proteins from a number of Rhabdoviruses various recombinant viruses were constructed. Each recombinant included the VSV Indiana wild type backbone (N, P, M and L genes) unless otherwise specified. Furthermore, recombinants included a luciferase reporter gene, either Firefly (FL) or Renilla (RL) between the G and the L gene. The general nomenclature used to refer to the recombinants is RVR_aG^x , wherein RVR stands for Rhabdovirus recombinant, (a) denotes the origin to the G-protein or G-protein-like gene and (x) denotes the version number.

RVR with Isfahan G protein. A RVR genome was cloned into the pXN2VSV vector such that XhoI and NheI restriction sites flanked the G or G-like genes. The viral stop start sequence was added to the 3' end of all G or G-like genes which encoded the following sequence: CTCGAGGGTATGAAAAAACTAACAGATATCACGGCTAG (SEQ ID NO:25). Recombinant virus was pseudotyped with the Isfahan G protein which has a protein sequence identity of 37% compared to VSV G Ind. The RVR comprising the FL reporter gene was designated RVR_{Isf} G¹ (wherein version 1 indicates the presence of the FL reporter gene).

Furthermore antibody neutralization studies showed that serum comprising antibodies from mice immunized with VSV WT did not significantly neutralize the activity of RVR Isf G¹ *in vitro*.

Furthermore, when mice immunized with VSV-WT were injected with RVR_{Isf}G¹ the virus with the Isf G polypeptide is able to evade the immune system. As shown in FIG. 6C, RVR_{Isf}G¹ was detectable at various locations in immunized mice following viral inoculation. The level of RVR_{Isf}G¹ detect in the immunized mice was similar to the level detected in naive controls animals (FIG. 6A). On the other hand, no virus was detected in immunized mice that were inoculated with VSV (FIG. 6B). Thus, oncolytic viruses comprising the Isf G polypeptide escape host immune response to previously administered VSV *in vivo*.

These results were further confirmed by injecting tumors in immunized naïve mice with VSV or recombinant virus and determined the virus yield from the infections. As shown in FIG. 7, recombinant virus injected into tumors of immunized or naïve mice yielded large amounts of progeny virus. On the other hand, propagation of VSV injected in immunized mice was barely detectable.

Two additional RVRs comprising the Isf were also constructed. RVR_{Isf}G² comprises an RL reporter gene in place of the FL reporter gene from RVR_{Isf}G¹. Also, RVR_{Isf}G³ comprises a chimeric VSV-Isf G protein. The chimeric protein (SEQ ID NO:19) comprises the Isfahan G ectodomain with VSV G transmembrane domain and cytoplasmic tail.

RVR with Chandipura G protein. Chandipura G has a protein sequence homology of 42% with VSV G (Indiana). The same cloning strategy described above was used to construct RVR_{Cha}G¹. A one step growth curve with RVR_{Cha}G¹ showed that it produces

similar amounts of virus compared to VSV (FIG. 8). Furthermore, the RVR had similar cytotoxicity as compared to VSV (FIG. 9).

RVR with Maraba G protein. Maraba G has a protein sequence homology 83% to VSV G (Indiana). This is the first report of the sequence of the Maraba G protein provided as a DNA sequence in SEQ ID NO:20. The same cloning strategy described above was used to construct RVR_{Mar}G¹. A one step growth curve with RVR_{Mar}G¹ showed that recombinant virus titer was greater than VSV at 48 and 72h. Thus, switching the G protein may stabilize the virus and thereby enhance yield (FIG. 10). Furthermore, the RVR_{Mar}G¹ was shown to be cytotoxic (FIG. 11). Furthermore, antibody neutralization assays showed that serum from mice immunized with VSV WT did not neutralize the activity of RVR_{Mar}G¹ indicating the RVR is capable of immune evasion.

RVR with Muir Springs G protein. Muir Springs G has 25.4% protein sequence homology to VSV G (Indiana). The Muir Springs G sequence is provided in SEQ ID NO:21 (amino acid) and SEQ ID NO:22 (DNA). The same cloning strategy described above was used to construct RVR_{Mur}G¹.

RVR with Klamath virus G protein. Pseudotyping experiments confirmed that the Klamath G protein is functional at in a low pH (6.8) environment, unlike VSV G. This of great importance since it is known that the tumor core is hypoxic and acidic. Thus, it may be an advantage to have a virus which can replicate in such an environment. VSV HRGFP-Klamath pseudotyped were generated such that the virions contained the genome of one virus but the envelope proteins of both viruses by co infection into CT26 Cells. 24 hours after co infection the supernatant was collected and the pseudotyped particles tittered. Pseudotyped virus was then used (along with control virus to infect target cells in media of two different acidity. Results show that the Klamath G protein was responsible for the ability of the virus to infect at low pH.

Essentially the same cloning strategy described above was used to construct RVR_{Kla}G². However, unlike previous strategies, this recombinant includes the Klamath G in addition to the original VSV G (Indiana).

RVR with Farmington (Far) virus G protein. Farmington virus is a non-vesiculovirus that is non-neurotropic and demonstrates formation of large syncytia.

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RVR with Bahia Grande (Bah) virus G protein. Bahia Grande virus is a non-vesiculovirus that is non-neurotropic.

RVR with JSR retroviral Env protein. Since VSV has a known neurotoxicity, a strategy whereby a VSV recombinant would not infect neurons would be advantageous. JSR
5 Env is originally from the JSRV retrovirus (a non-neurotropic virus) envelope (Env) gene non-neurotropic. A chimera comprising JSRV Env ectodomain with VSV G transmembrane domain and cytoplasmic tail is generated (DNA sequence provided as SEQ ID NO:23).

RVR with Ebola G protein. Ebola is a non-neurotropic virus with a glycoprotein that functions to bind receptor and mediate membrane fusion. The G protein contains a furin
10 Cleavage site at amino acid position 497-501. The products of cleavage (GP1 & GP2) are linked by disulfide bonds and thought to act as a possible decoy for neutralizing antibodies or immunomodulator. However, the furin cleavage site not required for infection or tropism. The Ebola G protein DNA sequence is provided as SEQ ID NO:24.

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U.S. Patent 5,846,233
20 U.S. Patent 5,846,708
U.S. Patent 5,846,709
U.S. Patent 5,846,717
U.S. Patent 5,846,726
U.S. Patent 5,846,729
25 U.S. Patent 5,846,783
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U.S. Patent 5,849,481
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30 U.S. Patent 5,849,487
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5 U.S. Patent 5,853,993
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15 U.S. Patent 5,882,864
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U.S. Patent 5,905,024
U.S. Patent 5,910,407
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25 U.S. Patent 5,919,630
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U.S. Patent 5,925,517
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U.S. Patent 5,925,565
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We claim:

1. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and an oncolytic recombinant rhabdovirus encoding a G protein sequence that is:

(i) the Isfahan virus G protein sequence as set forth in SEQ ID NO: 26;

(ii) the Maraba virus G protein sequence as set forth in SEQ ID NO: 5;

(iii) the Muir Springs virus G protein sequence as set forth in SEQ ID NO: 21;

(iv) a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 26;

(v) a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 5; or,

(vi) a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 21;
the rhabdovirus further encoding M, P, N and L proteins from vesicular stomatitis virus (VSV).

2. The pharmaceutical composition of claim 1, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the Isfahan virus G protein sequence as set forth in SEQ ID NO: 26.

3. The pharmaceutical composition of claim 1, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the Maraba virus G protein sequence as set forth in SEQ ID NO: 5.

4. The pharmaceutical composition of claim 1, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the Muir Springs virus G protein sequence as set forth in SEQ ID NO: 21.

5. The pharmaceutical composition of claim 1, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the amino acid sequence at least 96% identical to SEQ ID NO: 26.

6. The pharmaceutical composition of claim 1, wherein the isolated oncolytic recombinant rhabdovirus encodes a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 5.
7. The pharmaceutical composition of claim 1, wherein the isolated oncolytic recombinant rhabdovirus encodes the a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 21.
8. The pharmaceutical composition of any one of claims 1 to 7, wherein said composition comprises 10^3 to 10^{13} plaque forming units (pfu) of the isolated oncolytic recombinant rhabdovirus.
9. An isolated oncolytic recombinant rhabdovirus encoding a G protein sequence that is:
 - (i) the Isfahan virus G protein sequence as set forth in SEQ ID NO: 26,
 - (ii) the Maraba virus G protein sequence as set forth in SEQ ID NO: 5,
 - (iii) the Muir Springs virus G protein sequence as set forth in SEQ ID NO: 21,
 - (iv) a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 26,
 - (v) a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 5 and
 - (vi) a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 21;the rhabdovirus further encoding M, P, N and L proteins from vesicular stomatitis virus (VSV).
10. The isolated oncolytic recombinant rhabdovirus of claim 9, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the Isfahan virus G protein sequence as set forth in SEQ ID NO: 26.
11. The isolated oncolytic recombinant rhabdovirus of claim 9, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the Maraba virus G protein sequence as set forth in SEQ ID NO: 5.

12. The isolated oncolytic recombinant rhabdovirus of claim 9, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the Muir Springs virus G protein sequence as set forth in SEQ ID NO: 21.
13. The isolated oncolytic recombinant rhabdovirus of claim 9, wherein the isolated oncolytic recombinant rhabdovirus encodes the G protein having the amino acid sequence at least 96% identical to SEQ ID NO: 26.
14. The isolated oncolytic recombinant rhabdovirus of claim 9, wherein the isolated oncolytic recombinant rhabdovirus encodes a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 5.
15. The isolated oncolytic recombinant rhabdovirus of claim 9, wherein the isolated oncolytic recombinant rhabdovirus encodes the a G protein having an amino acid sequence at least 96% identical to SEQ ID NO: 21.
16. The oncolytic recombinant rhabdovirus of any one of claims 9 to 15, wherein the virus is provided in a composition further comprising a carrier, and said composition comprises 10^3 to 10^{13} plaque forming units (pfu) of the isolated oncolytic recombinant rhabdovirus.
17. Use of an effective amount of the pharmaceutical composition of any one of claims 1 to 8 for treating cancer in a subject.
18. Use of the pharmaceutical composition of any one of claims 1 to 8, in the preparation of a medicament for treating cancer in a subject.
19. The use according to claim 17 or 18, wherein the cancer is, in the alternative, lung cancer, head and neck cancer, breast cancer, cancer of the central nervous system, pancreatic cancer, prostate cancer, renal cancer, bone cancer, testicular cancer, cervical cancer, ovarian cancer, gastrointestinal cancer, lymphoma, liver cancer, colon cancer, melanoma, or bladder cancer.
20. The use according to any one of claims 17 to 19, wherein the cancer is metastatic.
21. The use according to any one of claims 17 to 20, wherein the subject is a human.

22. The use according to any one of claims 17 to 21, wherein the composition is for intraperitoneal, intravascular, intramuscular, intratumoral, subcutaneous or intranasal use.
23. The use according to any one of claims 17 to 22, wherein the composition is for use multiple times.
24. The use according to any one of claims 17 to 23, wherein the pharmaceutical composition is for use in combination with an additional anti-cancer therapy that is, in the alternative, chemotherapy, radiotherapy, or immunotherapy.
25. The pharmaceutical composition of any one of claims 1 to 8, for use in treating cancer in a subject.
26. The pharmaceutical composition of any one of claims 1 to 8, for use in the preparation of a medicament for treating cancer in a subject.
27. The pharmaceutical composition of claim 25 or 26, wherein the cancer is, in the alternative, lung cancer, head and neck cancer, breast cancer, cancer of the central nervous system, pancreatic cancer, prostate cancer, renal cancer, bone cancer, testicular cancer, cervical cancer, ovarian cancer, gastrointestinal cancer, lymphoma, liver cancer, colon cancer, melanoma, or bladder cancer.
28. The pharmaceutical composition of any one of claims 25 to 27, wherein the cancer is metastatic.
29. The pharmaceutical composition of any one of claims 25 to 28, wherein the subject is a human.
30. The pharmaceutical composition of any one of claims 25 to 29, wherein the composition is for intraperitoneal, intravascular, intramuscular, intratumoral, subcutaneous or intranasal use.
31. The pharmaceutical composition of any one of claims 25 to 30, wherein the composition is for use multiple times.

32. The pharmaceutical composition of any one of claims 25 to 31, wherein the pharmaceutical composition is for use in combination with an additional anti-cancer therapy that is, in the alternative, chemotherapy, radiotherapy, or immunotherapy.

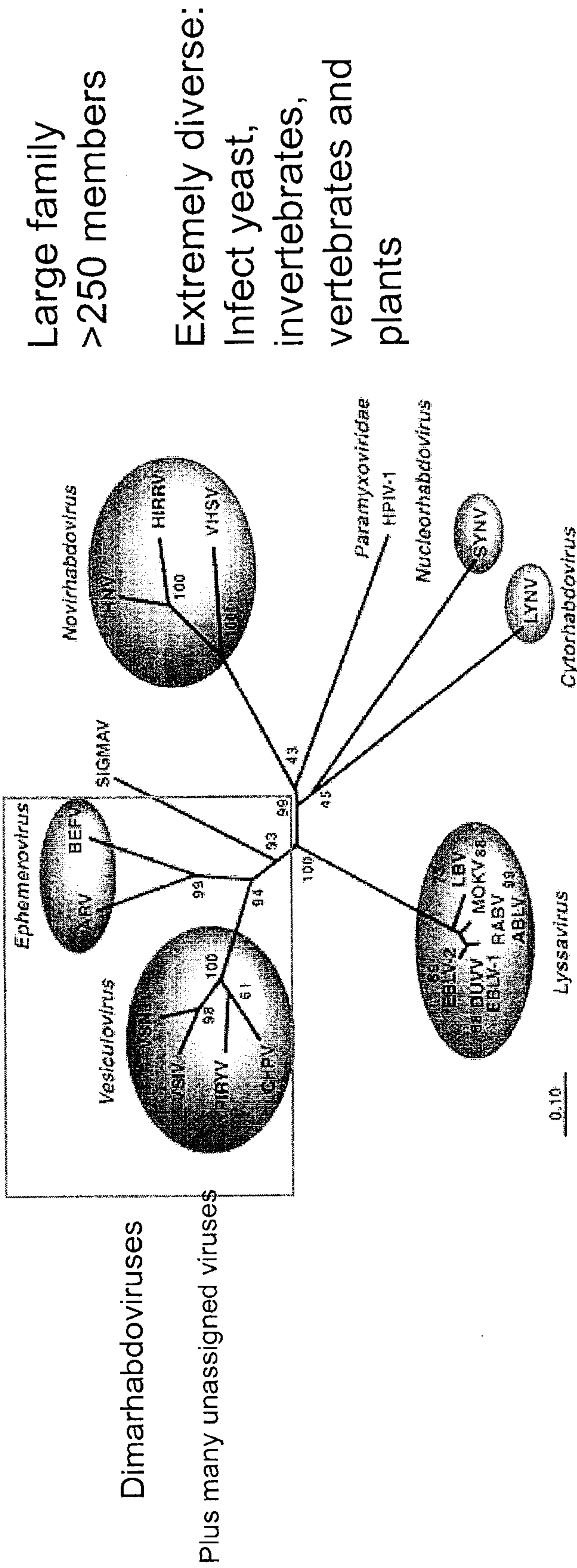


FIG. 1

Cytotoxicity
NCI60 panel
96h

Legend

EC₅₀

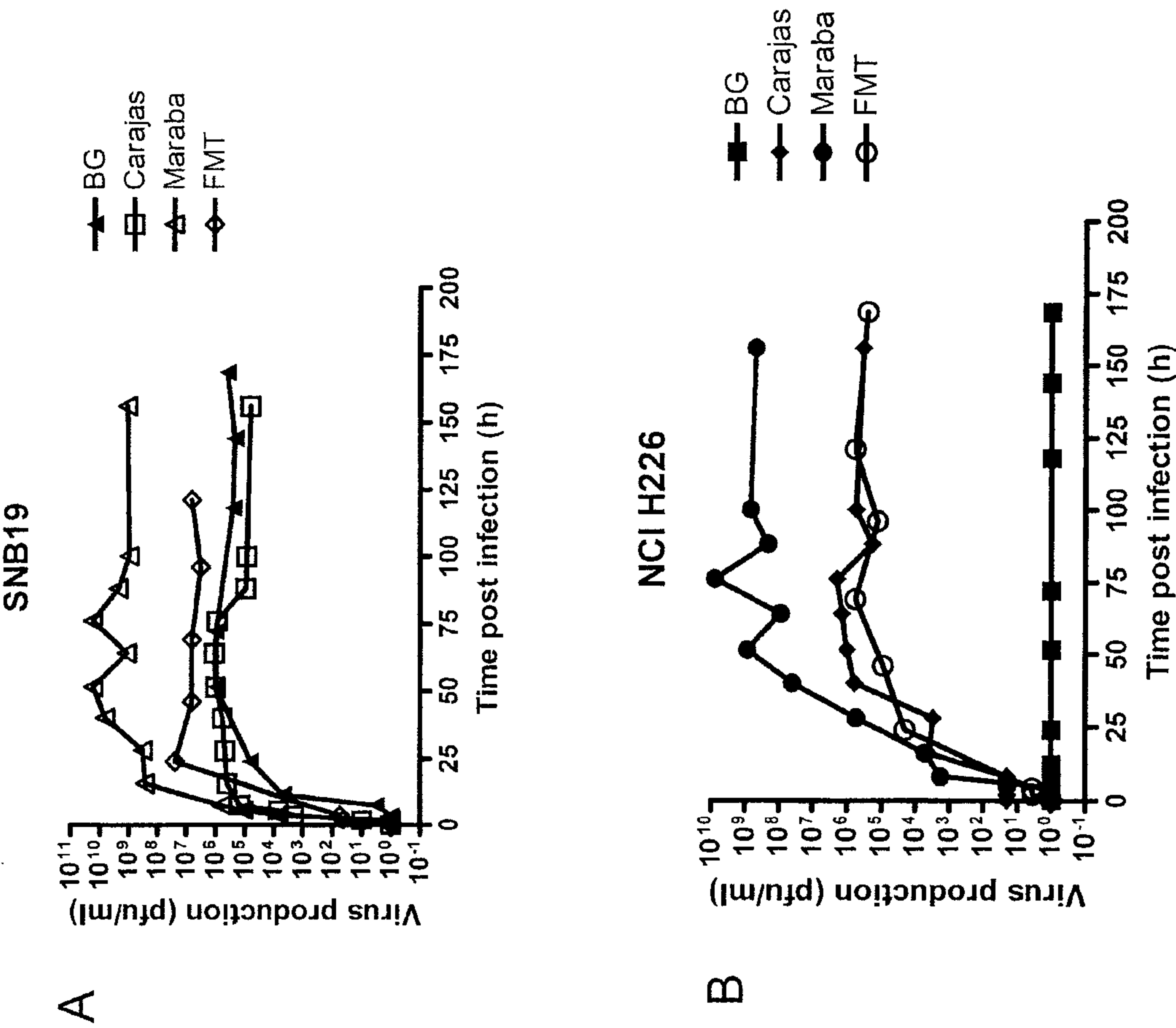
- 1= <0.001
- 2= <0.01
- 3= <0.1
- 4= <1
- 5= <10
- 6= >10
- 7= >>10

Closely related strains behave very differently on the same cells

Same virus behaves differently on different cells

Organism	Source	Cell Line	Day	MS	BG	NGG	TIB	FMT	MRB	CRJ	VSU	WV
Human Osteosarcoma	U2OS	Day 4	3	3	3	4	1	1	1	1	2	2
Human Breast	MCF7(2nd)	Day 4	5	5	5	5	2	2	1	2	2	2
Human Breast	MDA-MB-231	Day 4	4	4	4	4	2	1	1	1	2	2
Human Breast	MDA-MB-435	Day 4	5	5	5	5	2	2	1	2	3	3
Human Breast	NCIADR-RE	Day 4	5	5	5	5	3	2	4	2	2	2
Human Breast	T47D	Day 4	5	5	5	5	2	2	2	3	2	2
Human CNS	SF268	Day 4	4	4	4	4	1	2	1	2	3	3
Human CNS	SF205	Day 4	5	5	5	5	3	2	2	2	3	3
Human CNS	SF530	Day 4	5	5	5	5	1	1	1	1	2	2
Human CNS	SNB19	Day 4	2	1	4	1	1	1	1	1	3	3
Human CNS	SNB75	Day 4	5	5	5	5	1	2	5	1	1	1
Human CNS	U118	Day 4	5	5	5	5	4	1	2	1	2	1
Human CNS	U343	Day 4	4	3	4	1	1	1	1	1	2	2
Human CNS	U373	Day 4	2	1	3	1	1	1	1	1	2	2
Human Colon	COLO 205	Day 4	5	5	5	5	3	5	3	3	3	3
Human Colon	HCT116	Day 4	5	5	5	5	1	2	1	2	2	2
Human Colon	HCT15	Day 4	5	5	5	5	2	3	3	3	3	3
Human Colon	HT29	Day 4	5	5	5	5	2	1	2	2	3	3
Human Colon	SW620	Day 4	3	3	3	3	2	2	1	1	4	4
Human Melanoma	M14	Day 4	5	5	5	5	3	3	1	3	1	1
Human Melanoma	MALME3M	Day 4	5	5	5	5	2	3	5	3	1	1
Human Melanoma	SKMEL28	Day 4	4	4	4	4	1	3	1	2	1	1
Human Melanoma	UACC257	Day 4	5	5	5	5	2	2	1	2	1	1
Human Melanoma	UACC62	Day 4	5	5	5	5	2	3	4	2	1	1
Human Lung	A549	Day 4	5	5	5	5	1	2	3	1	3	3
Human Lung	HOP62	Day 4	5	5	5	5	1	2	3	2	1	1
Human Lung	HOP92	Day 4	5	5	5	5	2	3	3	2	2	2
Human Lung	NCI-H226	Day 4	5	5	5	5	3	2	4	4	3	3
Human Lung	NCI-H23	Day 4	5	5	5	5	3	2	1	1	2	2
Human Ovarian	OVCAR3	Day 4	5	5	5	5	3	3	2	2	2	2
Human Ovarian	OVCAR4	Day 4	5	5	5	5	5	2	3	1	3	3
Human Ovarian	OVCAR8	Day 4	2	1	3	1	1	1	1	1	1	1
Human Pancreas	PANC-1	Day 4	2	1	5	4	1	1	1	1	1	1
Human Prostate	DU145	Day 4	5	5	5	5	3	2	5	3	2	2
Human Prostate	PC3	Day 4	5	5	5	5	3	2	5	3	2	2
Human Renal	786-O	Day 4	5	5	5	5	4	1	5	1	3	3
Human Renal	ACHN	Day 4	5	5	5	5	1	2	1	1	3	3
Human Renal	SN12C	Day 4	5	5	5	5	2	3	4	2	2	2
Human Renal	TK10	Day 4	5	5	5	5	1	2	1	1	2	2
Human Skin Carcinoma	A431	Day 4	5	5	5	5	4	3	5	4	2	2
Monkey Kidney, Normal	CV-1	Day 4	4	3	4	1	1	1	1	1	2	2
Monkey Kidney, Normal	VERO	Day 4	4	4	4	4	4	1	1	1	3	3
Mouse Breast	EMT6	Day 4	4	4	4	4	4	3	1	4	1	4
Mouse Breast	4T1	Day 4	3	4	1	4	2	2	3	2	3	3
Mouse Colon	CT26	Day 4	4	4	4	4	3	1	1	1	4	4
Mouse Glioma	GL 281	Day 4	5	5	5	5	5	2	2	2	2	2

FIG. 2



FIGS. 3A-3B

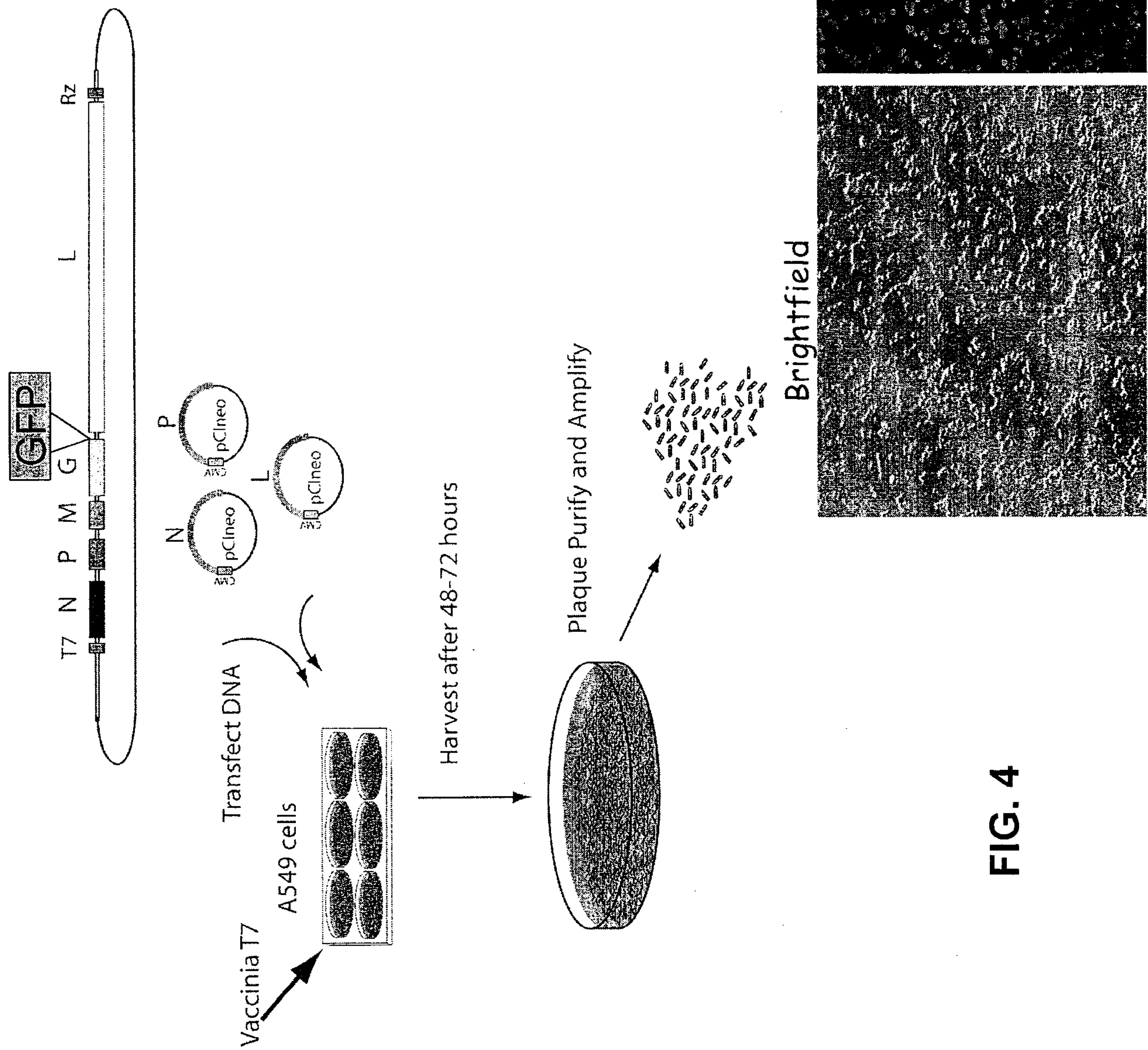


FIG. 4

Directed evolution of Bahia Grande

Goal: Select for variants with faster replication in human GBM

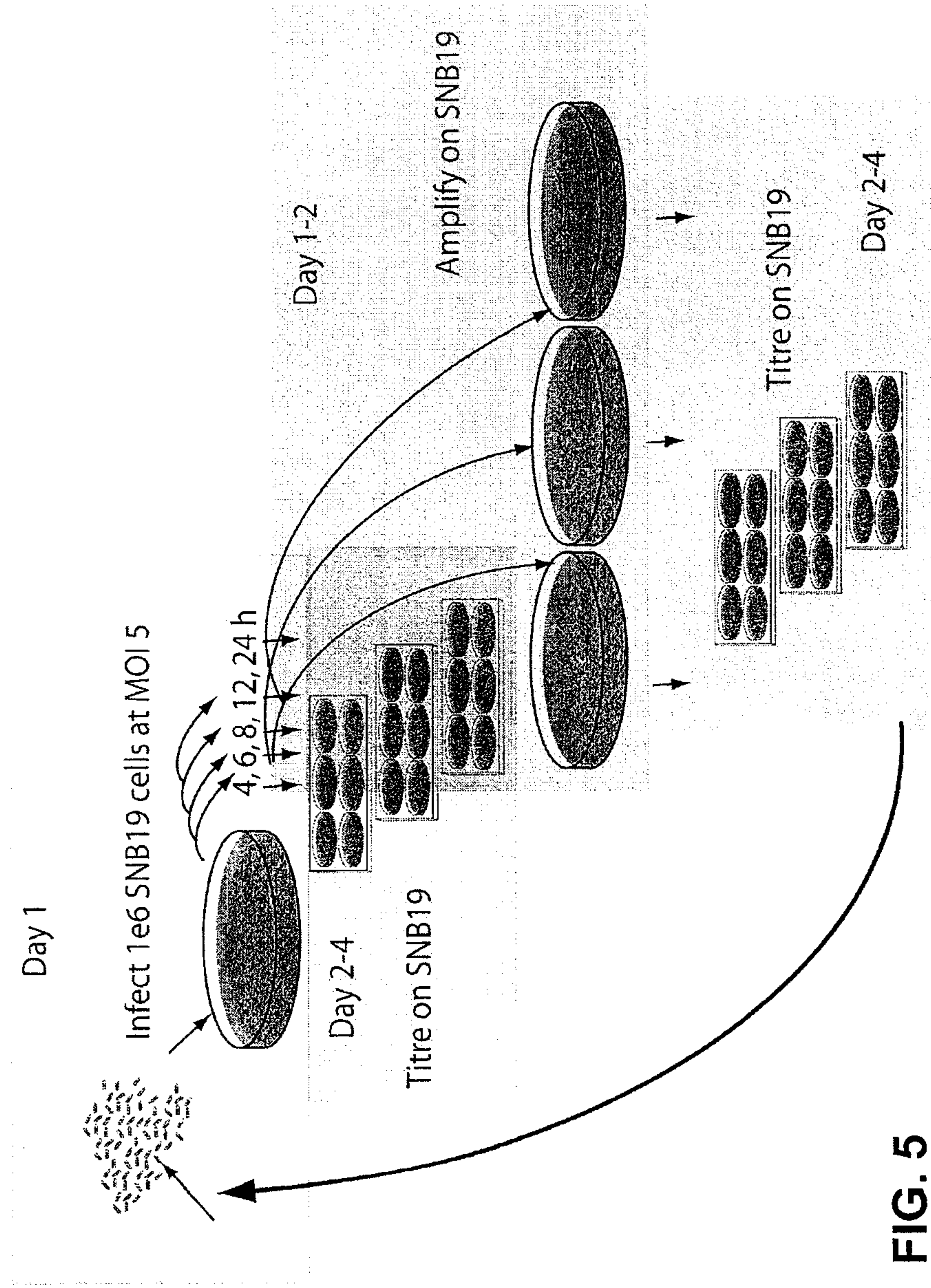


FIG. 5

Directed Evolution

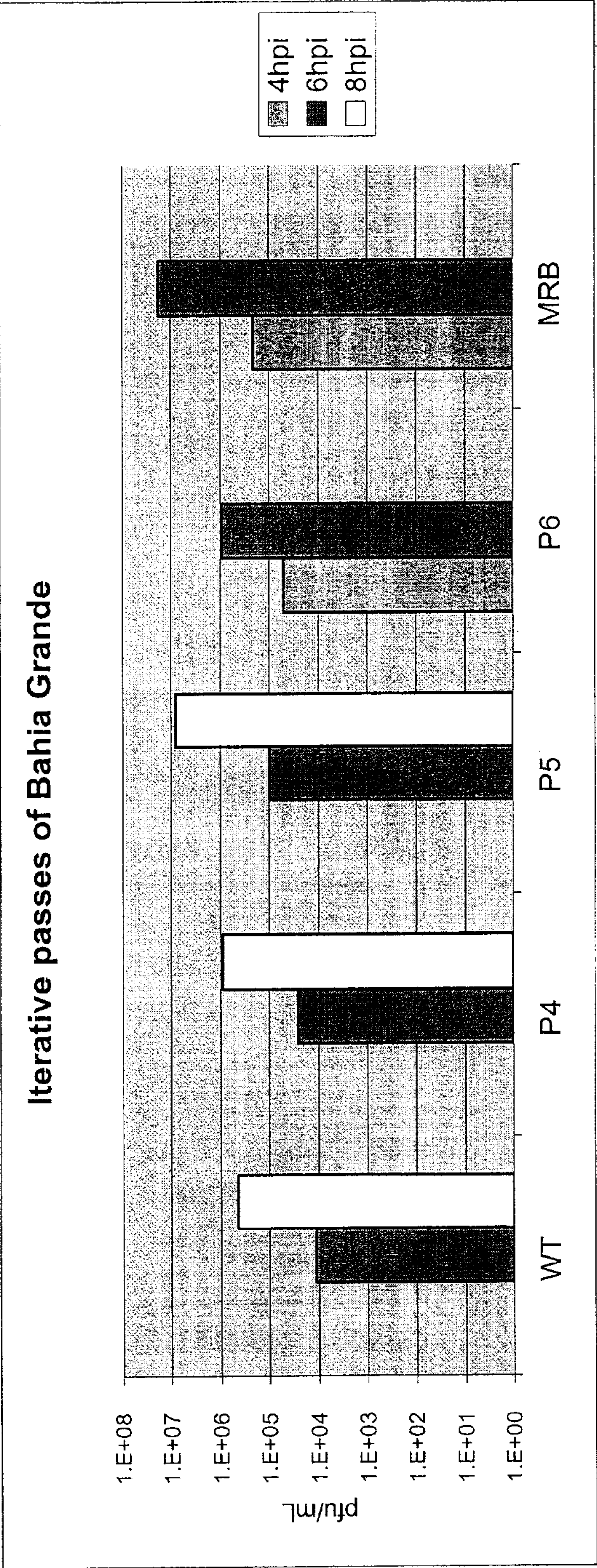


FIG. 6

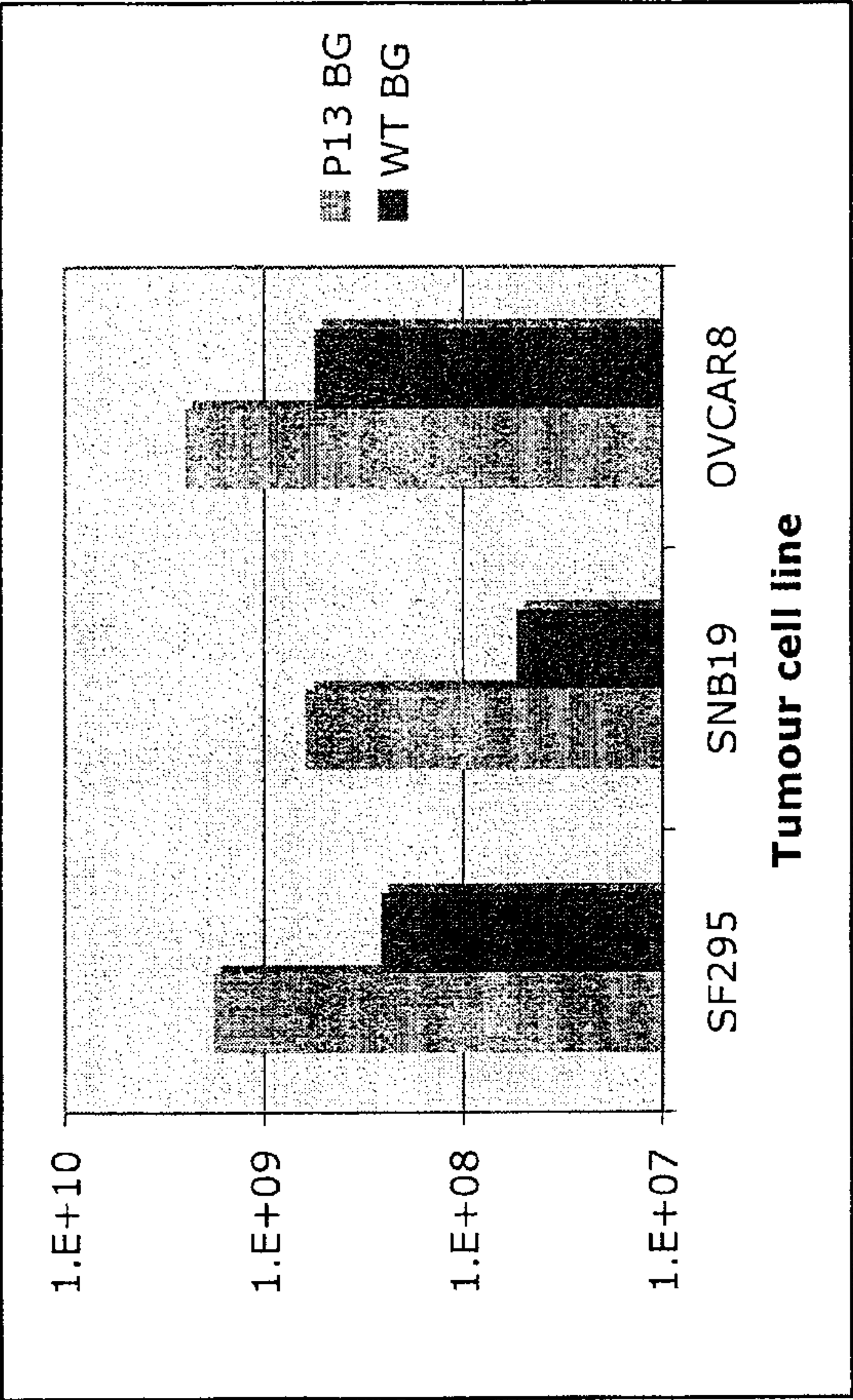


FIG. 7

Bahia Grande and Muir Springs show no
neurotoxicity

Intracranial Toxicity	
	I.C (LD, pfu)
WT VSV	<10
VSV delta M51	<10
Bahia Grande	>1e ⁷
Muir Springs	>1e ⁷
Bahia Grande P6	>1e ⁷

FIG. 8

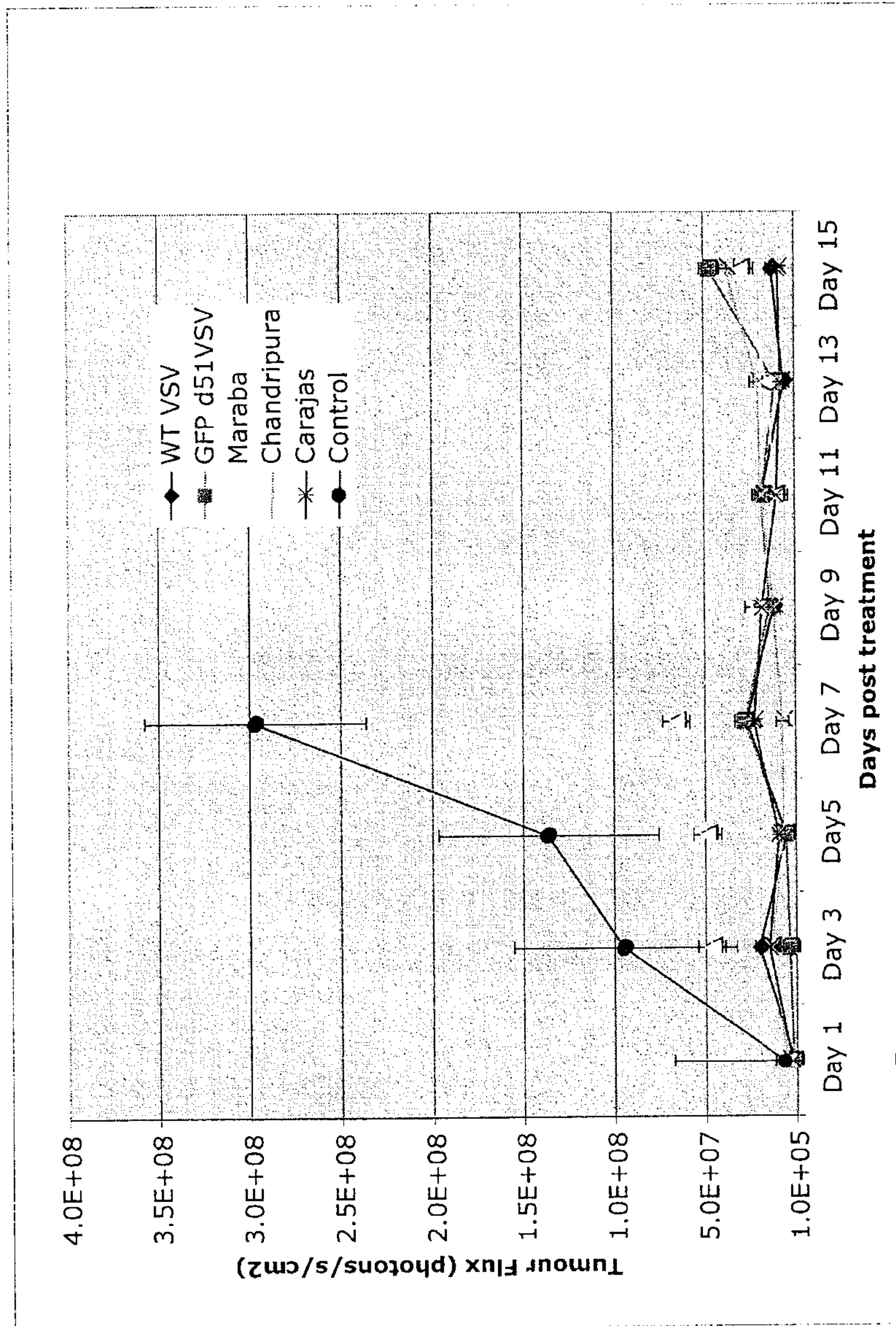


FIG. 9

Infectivity of G-less VSV WT Pseudotyped with Various G's

24h MOI 1

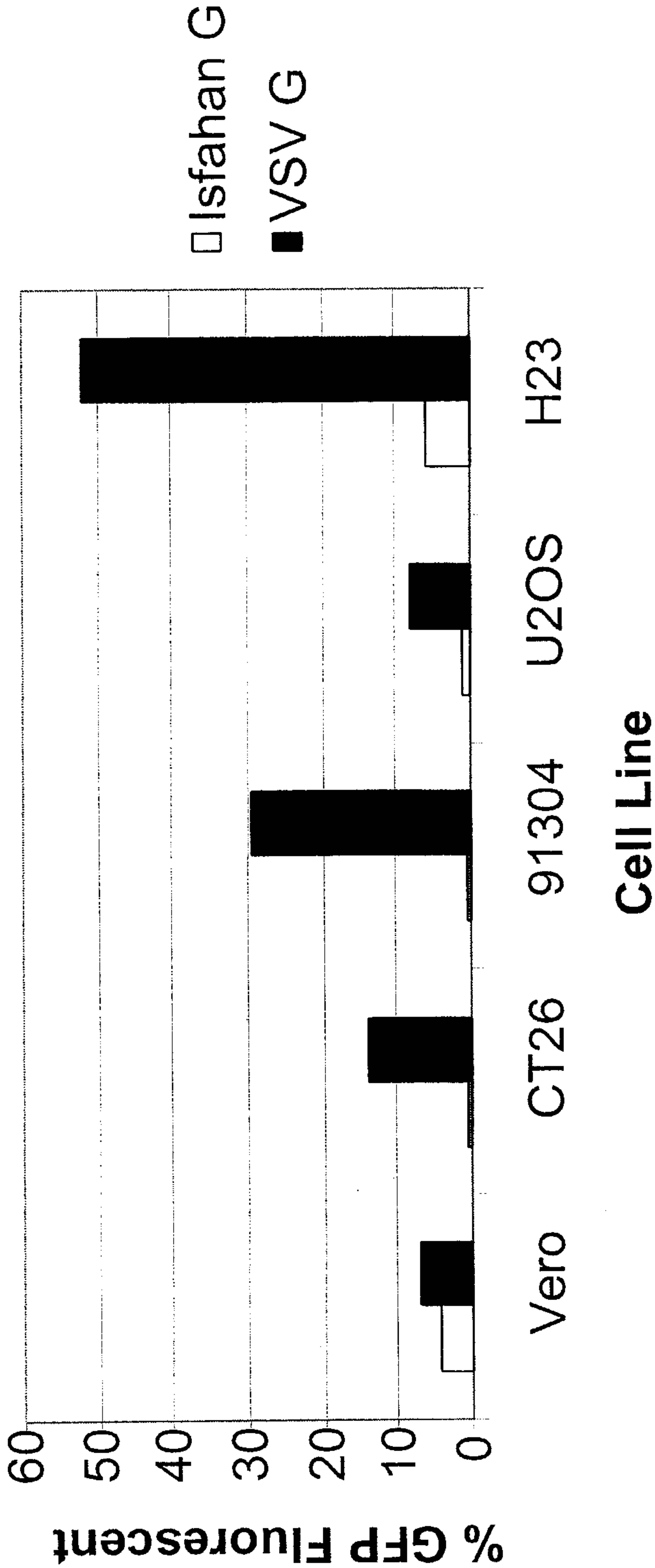


FIG. 10

One Step Growth Curve with VSV WT, Isfahan and RVR IsfG1

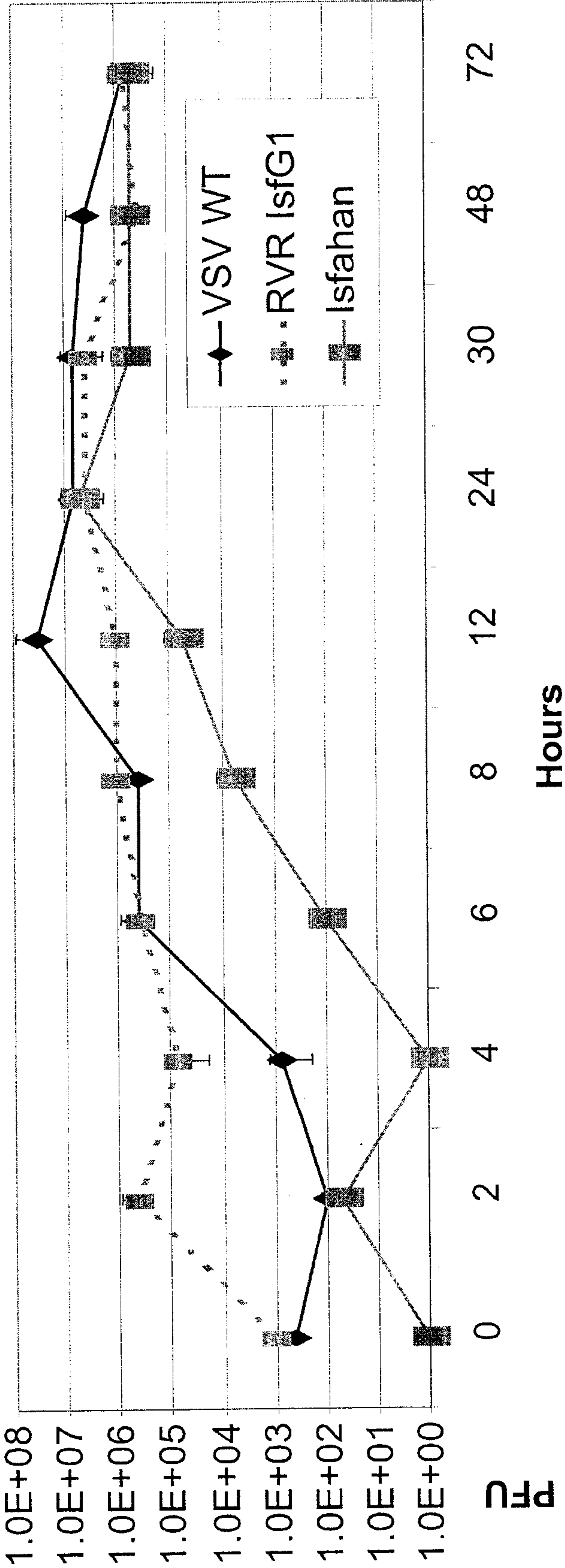


FIG. 11

MTS Assay
48h MOI 0.01

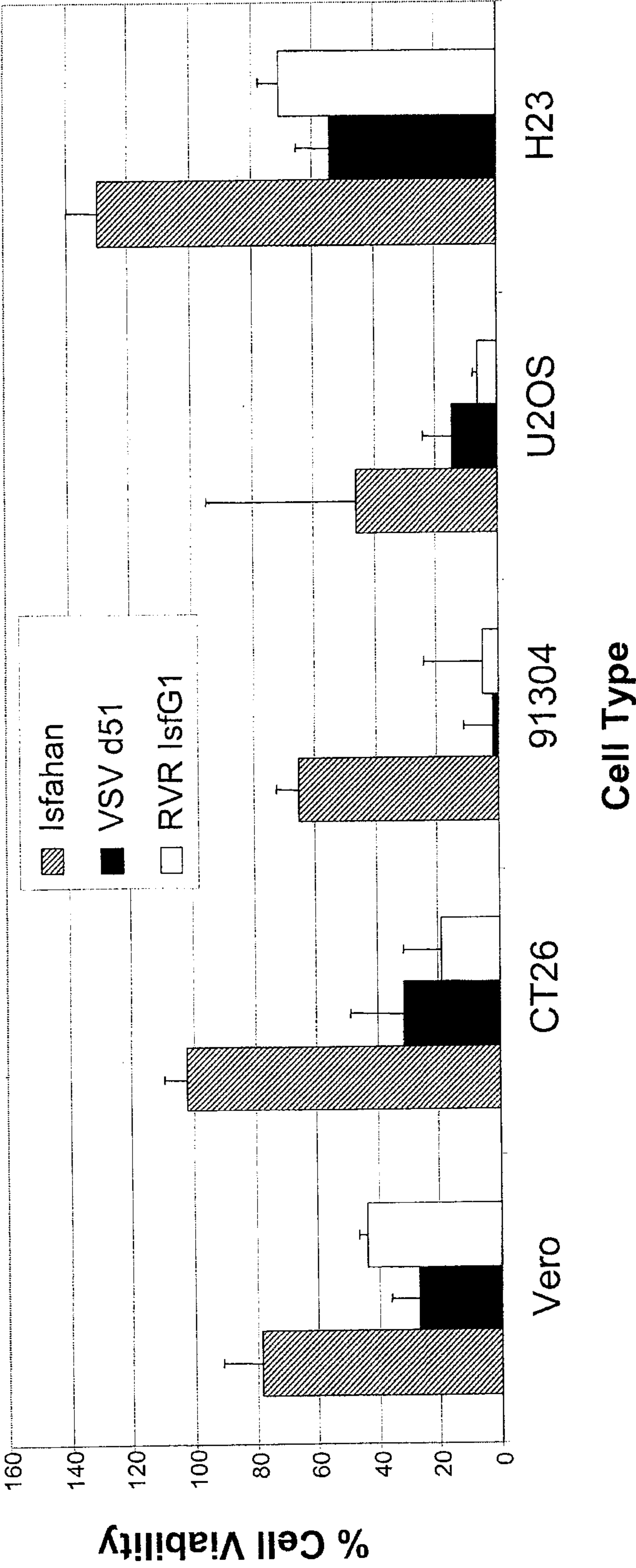
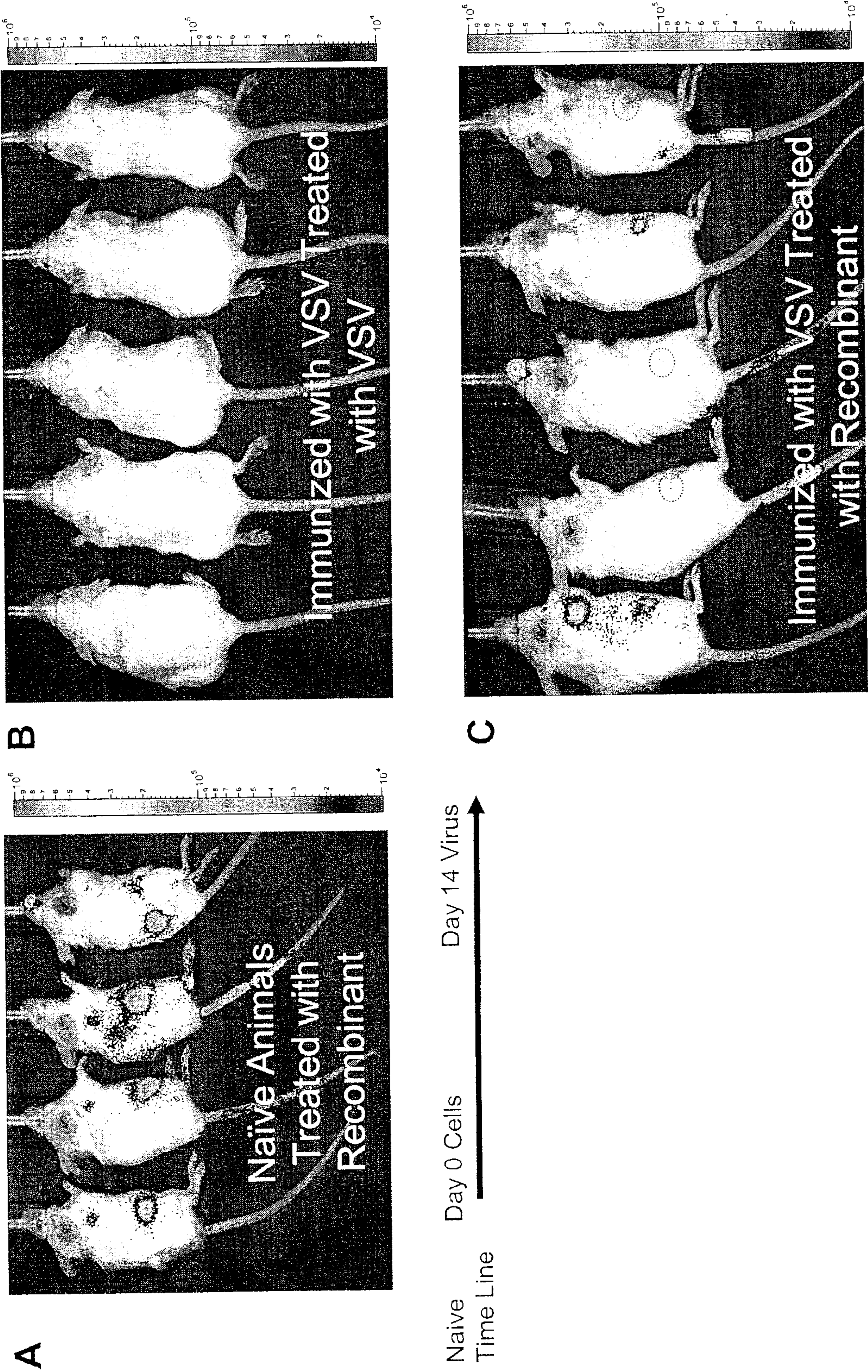


FIG. 12



FIGs. 13A-13C

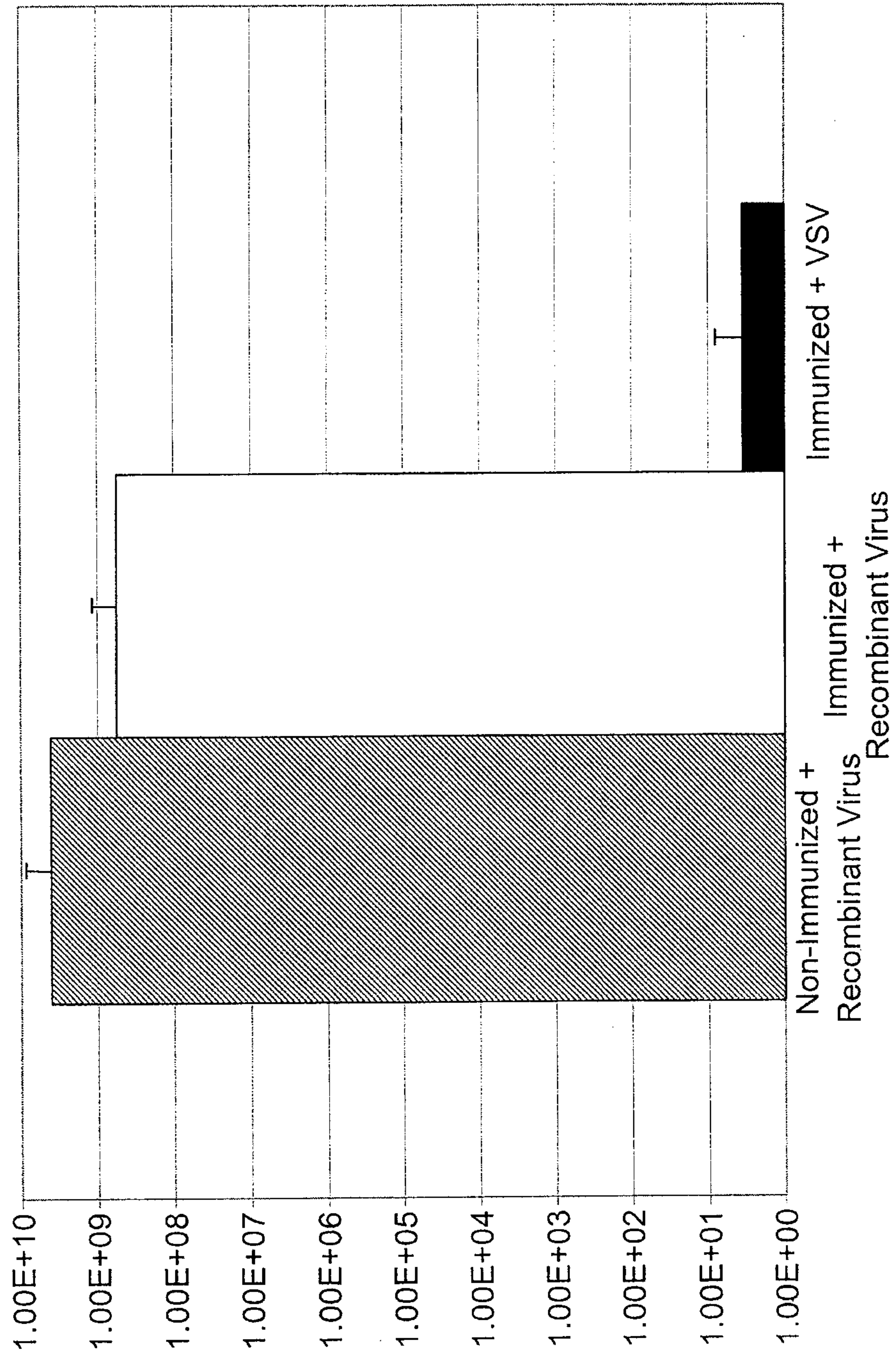


FIG. 14

One Step Growth Curve with WT VSV, Chandipura and RVR Cha G1

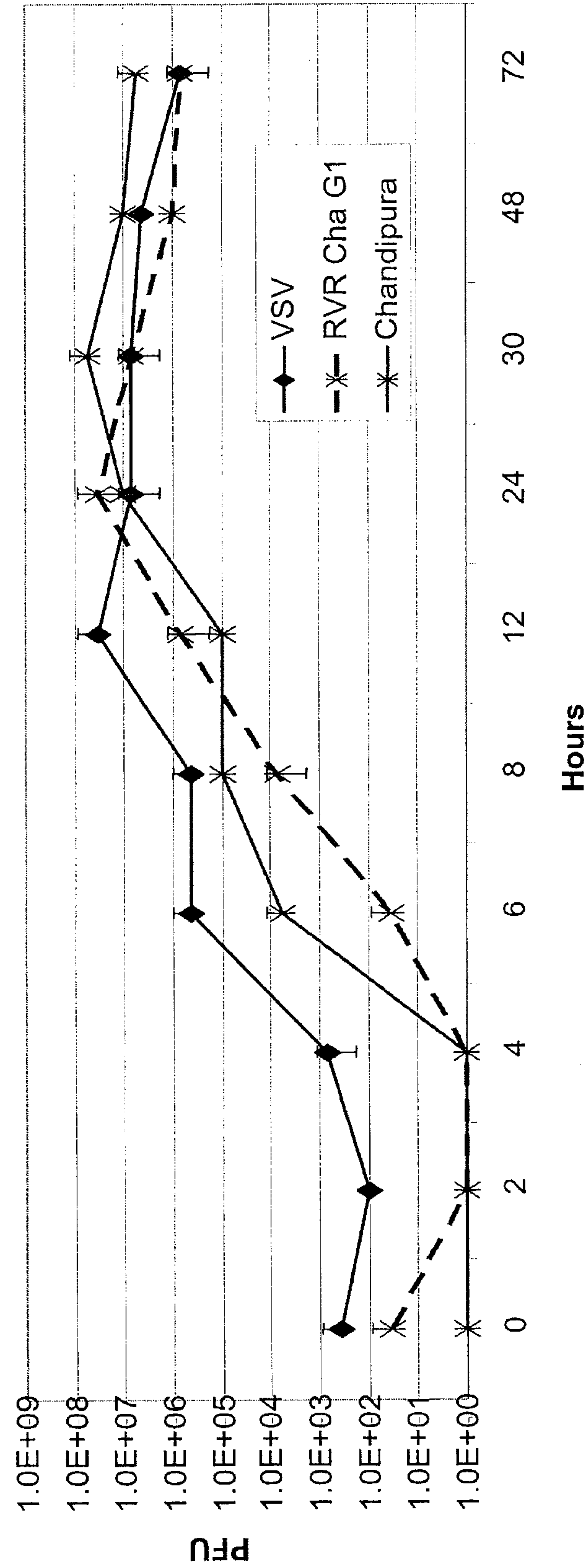


FIG. 15

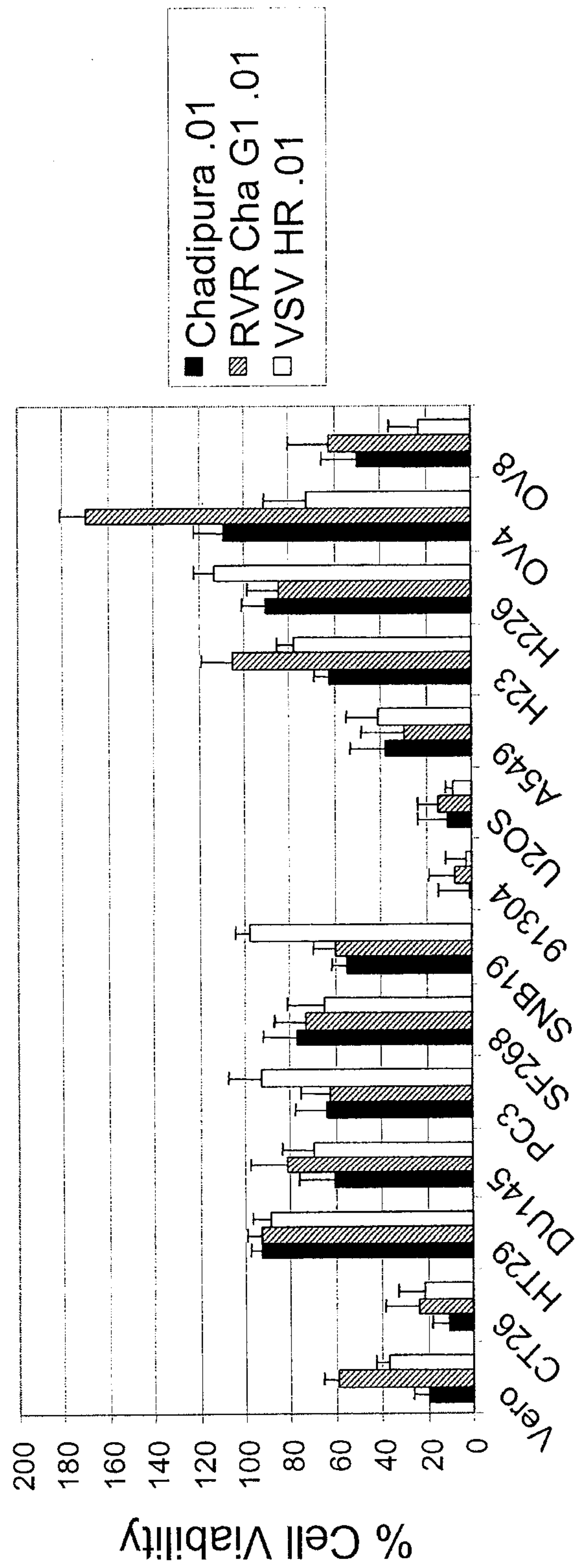


FIG. 16

One Step Growth Curve with VSV WT, Maraba and RVR Mar G1

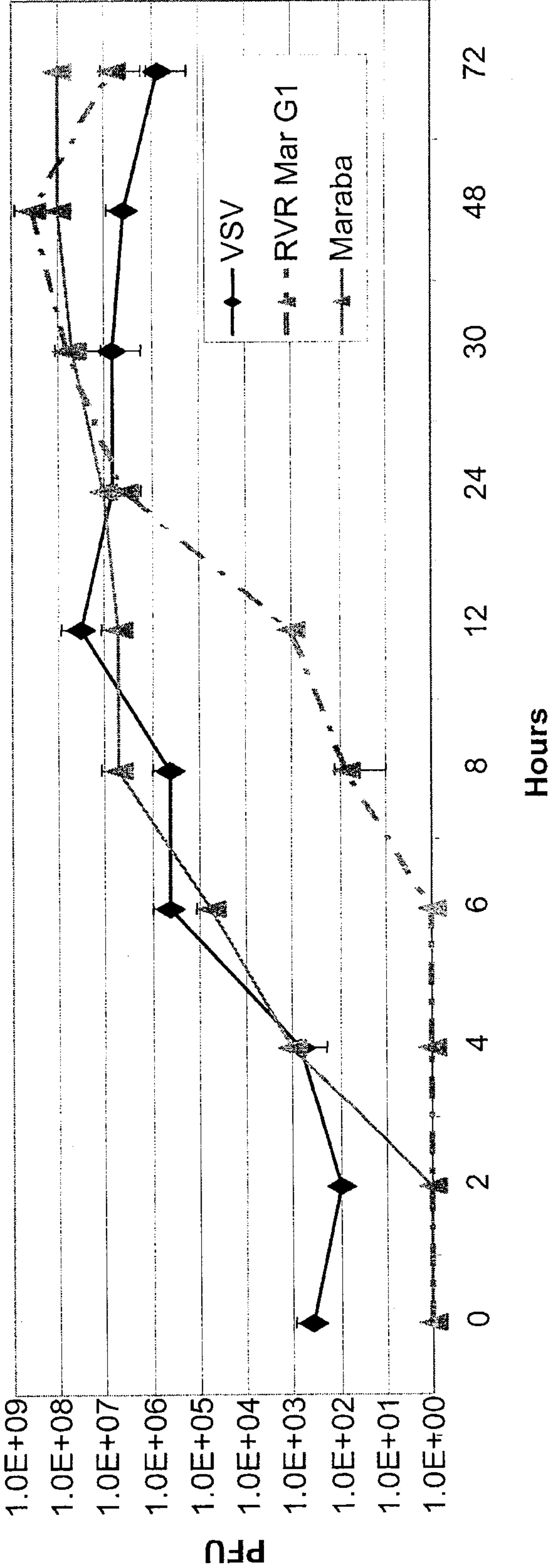


FIG. 17

RVR Mar G1

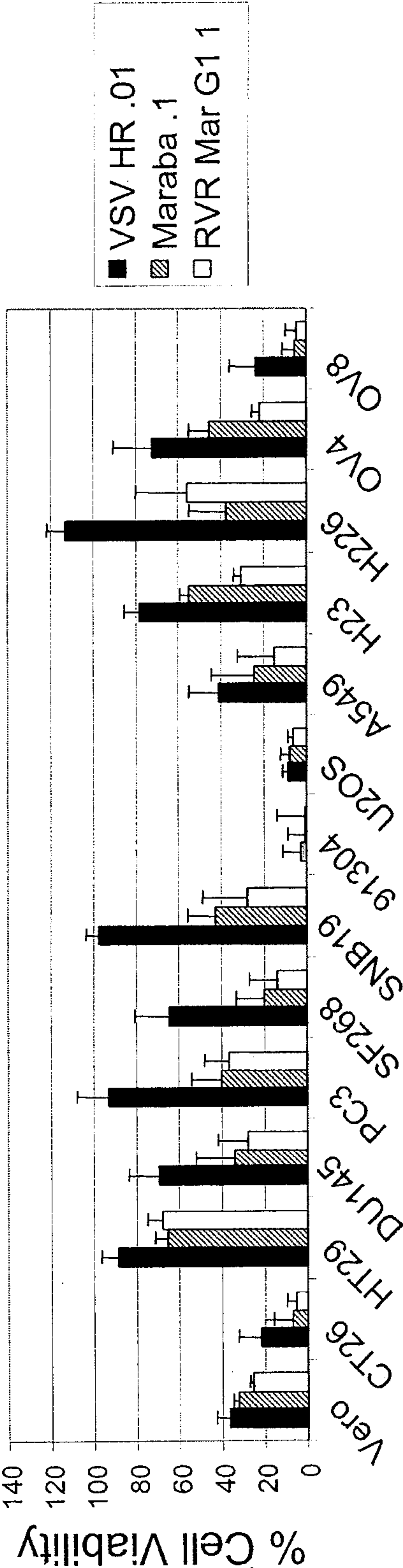


FIG. 18