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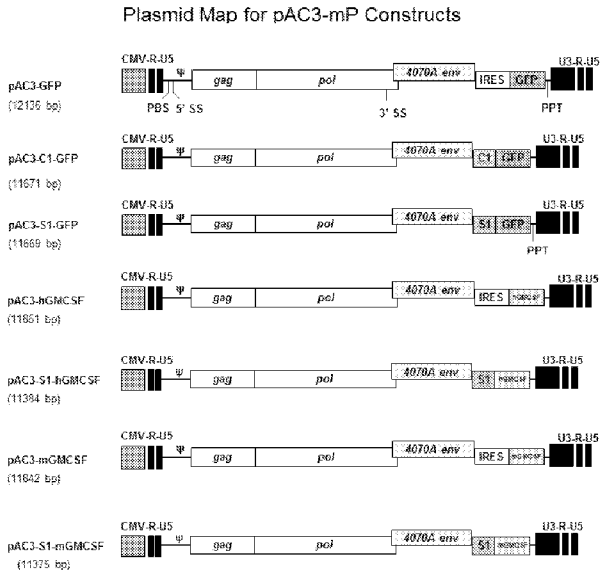

FIGURE 8A

(57) Abstract: This disclosure provides a retroviral replicating vector for gene delivery comprising a therapeutic cassette containing at least one mini-promoter linked to a gene to be expressed.

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RETROVIRAL VECTOR WITH MINI-PROMOTER CASSETTE

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application Serial No. 61/718,610, filed October 25, 2012, the disclosure of which is incorporated herein by reference.

TECHNICAL FIELD

[0002] This disclosure relates to retroviral replicating vectors (RRV) for treating cell proliferative. The disclosure further relates to the use of such retroviral replicating vectors for delivery and expression of heterologous nucleic acids.

BACKGROUND

[0003] The development of effective methods of delivering genes and heterologous nucleic acids to cells and subjects has been a goal for possible treatments of diseases and disorders.

[0004] Replicating retroviral vectors (RRV; a.k.a. replication competent retroviruses) have been used to selectively infect tumors in animal models (Wang *et al.*, Hum. Gene. Ther., 14:117-127, 2003, Tai *et al.*, Mol Ther, 12:842-851, 2005), where replication occurs through the tumor. The conventional strategy for transgene expression has been to use an IRES component to allow internal initiation of translation from the internal ribosome binding site. The IRES component is about 600bp leaving approximately 900 bp for coding sequence in size-limited vectors. If the vector is equipped with a prodrug-activating gene such as cytosine deaminase or purine nucleotide phosphorylase expressed from an internal IRES sequence, then the tumor can be eliminated or growth/spreading inhibited by subsequent treatment with prodrugs (*e.g.*, 5-fluorocytosine, which is converted *in situ* by cytosine deaminase to the anti-cancer drug 5-fluorouracil (Tai *et al.*, Mol Ther., 12:117-127, 2005, Ostertag *et al.*, Neuro Oncol., 2012)). Such vectors are now in the clinic for experimental treatment of primary brain cancer (see the World Wide Web at clinicaltrials.gov, NCT01156584). However the genetic stability of such an RRV is significantly reduced when the total insert size exceeds approximately 1.5 kb, so that a number of potentially useful genes or gene combinations are not guaranteed to be stable enough for easy and reliable therapeutic use. A

particular example is the commonly used prodrug activating gene from herpes thymidine kinase (HSVtk)(SEQ ID NO:35) that can activate common anti-herpetic drugs such as ganciclovir, acyclovir, valacyclovir (Valtrex™) or other analogues by phosphorylation *in situ* leading to cell killing. The HSVtk gene has a coding sequence of just over 1.1kb and when combined with with an IRES used in some expression constructs results in an insert of greater than about 1.6kb. This size is not sufficiently stable for clinical use. Another example is the combination of the cytosine deamine gene (SEQ ID NO:1 or 3) with the UPRT gene (SEQ ID NO:7) or OPRT gene (WO2010036986, Perez *et al.*, Mol. Ther., 2005), where these fusion genes are about 1200bp. When combined with an IRES the size exceeds about 1.8kb and showed undesirable instability although expression, before deletions occurred, was satisfactory.

[0005] Logg *et al.* (PNAS, 105(12):4733-4738, 2008) tried various shorter sequences of IRES constructs to improve the size of the heterologous gene incorporated into the RRV with limited success. Specifically, Logg *et al.* demonstrated the expression could be obtained, however, stability was reduced due to the nature of the smaller IRES's having a splice donor/acceptor role.

SUMMARY

[0006] This disclosure provides methods and compositions that allow the stable expression *in vivo* of a gene or multiple genes exceeding a total size of about 0.9 kb in a replicating vector. The disclosure provides vectors comprising at least one mini-promoter cassette capable of expressing heterologous gene(s) that can be greater than 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, or 1.9 kb. If one considers a therapeutic cassette to be a plurality of mini-promoter cassettes or a single mini-promoter cassette and a second cassette comprising a polIII promoter or IRES operably linked to a second therapeutic molecule then the overall therapeutic cassette can comprise about 1.2-2.0 kb. For example, where two mini-promoter cassettes are present in a therapeutic cassette, a first mini-cassette can express a first gene or therapeutic molecule, while the second cassette can express a second gene or therapeutic molecule.

[0007] Also disclosed are novel minipromoters contructs in a recombinant replication competent retrovirus (RRV) for driving expression of genes that are about 1.2 kb. With the foregoing general concept in mind, the disclosure provides a recombinant replication competent retrovirus (RRV) comprising: a retroviral GAG protein; a retroviral POL protein; a retroviral envelope (ENV); a retroviral polynucleotide comprising Long-Terminal Repeat (LTR) sequences at the 3' end of the retroviral polynucleotide sequence, a promoter sequence at the 5' end of the retroviral polynucleotide, said promoter being suitable for expression in a mammalian cell, a *gag* nucleic acid domain, a *pol* nucleic acid domain and an *env* nucleic acid domain; a therapeutic cassette comprising at least one mini-promoter operably linked to a heterologous polynucleotide, wherein the cassette is positioned 5' to the 3' LTR and 3' to the *env* nucleic acid domain encoding the retroviral envelope; and cis-acting sequences necessary for reverse transcription, packaging and integration in a target cell. In one embodiment, the therapeutic cassette comprises a least one core- or mini-promoter and enhancer operably linked to a heterologous polynucleotide. In one embodiment, the retroviral polynucleotide sequence is derived from a gamma retrovirus, such as murine leukemia virus (MLV), Moloney murine leukemia virus (MoMLV), Feline leukemia virus (FeLV), Baboon endogenous retrovirus (BEV), porcine endogenous virus (PERV), the cat derived retrovirus RD114, squirrel monkey retrovirus, Xenotropic murine leukemia virus-related virus (XMRV), avian reticuloendotheliosis virus (REV), or Gibbon ape leukemia virus (GALV). In another embodiment, the MLV is an amphotropic MLV or an ecotropic MLV with an amphotropic or GALV envelope gene. In yet another embodiment, the retrovirus is an oncoretrovirus or gamma retrovirus. In yet another embodiment, the vector comprises the mini-promoter cassette can infect a mammalian target cell. In another embodiment, the target cell is a cell having having aberrant proliferative capactity such as those associated with a cell proliferative disorder. The cell proliferative disorder can be selected from the group consisting of, but is not limited to, neoplasias and autoimmune diseases. In one embodiment, the promoter for transcription of the RRV genome comprises a CMV

promoter. In a further embodiment, the promoter comprises a CMV-R-U5 domain polynucleotide. In one embodiment, the CMV-R-U5 domain comprises the immediately early promoter from human cytomegalovirus linked to an MLV R-U5 region. In another embodiment, the *gag* and *pol* of the polynucleotide are derived from an oncoretrovirus or gamma retrovirus. In one embodiment, the *env* domain encodes an amphotropic ENV protein. In yet a further embodiment of any of the foregoing, the therapeutic cassette comprises at least one mini-promoter cassette and can also include an enhancer and which comprises a therapeutic (heterologous) polynucleotide sequence that upon expression codes for a therapeutic protein or a therapeutic nucleic acid (*e.g.*, an siRNA, shRNA, microRNA or the like). In one embodiment, the mini-promoter cassette is a promoter for RNA polymerase II. In another embodiment, the mini-promoter cassette is a promoter for RNA polymerase III (*e.g.*, a U6 promoter). In one embodiment, the therapeutic cassette comprises a single mini-promoter cassette comprising a mini-promoter and enhancer operably linked to a coding sequence for a therapeutic molecule or molecules. In another embodiment, the therapeutic cassette comprises at least one mini-promoter cassette and a second cassette. The second cassette may be a second mini-promoter cassette, an IRES cassette or a polIII promoter cassette. The mini-promoter promotes transcription of an operably linked gene or coding nucleic acid sequence.

[0008] A mini-promoter, as the name refers, includes the minimal amount of elements necessary for effective transcription and/or translation of an operably linked coding sequence and has better expression than a core promoter. A mini-promoter can include a core promoter, but also includes additional regulatory domains that promote transcription. A mini-promoter is about 100-600 bp in length while a core promoter is typically less than about 100bp (*e.g.*, about 70-80 bp). Where a therapeutic cassette comprises a core promoter, a second cassette (*e.g.*, a second mini-promoter cassette, polIII promoter cassette or IRES cassette) will be present or the core promoter will be accompanied by an enhancer. Furthermore, where a core promoter is present, the cassette will typically comprise an enhancer element or another element either

upstream or downstream of the core promoter sequence that facilitates expression of an operably linked coding sequence above the expression levels of the core promoter alone.

[0009] Accordingly, the disclosure provides small regulatory promoter domains (*e.g.*, modified core promoters) derived from either cellular elements as determined for "core promoter" elements (<100, < 200, < 400 or < 600 bp) that allow ubiquitous expression at significant levels in target cells and are useful for stable incorporation into vectors, in general, and replicating retroviral vectors, in particular, to allow efficient expression of transgenes. Also provided are core promoters plus minimal enhancer sequences to allow better gene expression, that are still under 200, 400 or 600bp. Such enhanced promoters include modified core promoters, naturally occurring tissue specific promoters, small viral promoters such as the Rous Sarcoma virus derived promoters. In yet other embodiments, the therapeutic cassette comprising at least one mini-promoter cassette will have expression levels that are greater than or about equal to or about 1 fold to 2 fold less than the expression levels of an IRES cassette with the same gene.

[0010] The vector can comprise any number of different heterologous polynucleotides operably lnked to a core- or mini-promoter. For example, the heterologous polynucleotide can comprise a cytokine gene, an siRNA, microRNA or RNAi molecules, a targeting sequence, a binding domain, a cytotoxic gene, a single chain antibody or any combination thereof. When the heterologous polynucleotide is a non—translated RNA such as siRNA, microRNA or RNAi then no mini-promoter may be necessary, but may be included in combination with a transcribed gene. In yet a further embodiment, the heterologous polynucleotide comprises a polynucleotide having a sequence as set forth in SEQ ID NO: 3 (CDopt-3pt), 5 (CDopt), 11 (CDopt-UPRT), 13 (CDopt-linker-UPRT), 15 (CDopt3-OPRT), 17 (CDopt3-linker-OPRT), or 75 (HSVtkopt). In a further embodiment, the heterologous sequence encodes a polypeptide comprising a sequence as set forth in SEQ ID NO: 4 or 76. In one embodiment, the heterologous nucleic acid is human codon optimized and encodes a polypeptide as set forth in SEQ ID NO:4 or 76.

[0011] The disclosure provides an isolated polynucleotide comprising from 5′ to 3′: a CMV-R-U5 fusion of the immediate early promoter from human cytomegalovirus to an MLV R-U5 region; a PBS, primer binding site for reverse transcriptase; a 5′ splice site; ψ packaging signal; a *gag* coding sequence for MLV group specific antigen; a *pol* coding sequence for MLV polymerase polyprotein; a 3′ splice site; a 4070A *env* coding sequence for envelope protein of MLV strain 4070A; at least one mini-promoter cassettes operably linked to a therapeutic gene; a polypurine tract; and a U3-R-U5 MLV long terminal repeat. In one embodiment, the 3′ LTR is derived from an oncoretrovirus or gamma-retrovirus. In a further embodiment, the 3′ LTR comprises a U3-R-U5 domain.

[0012] The disclosure provides a method of treating a cell proliferative disorder in a subject comprising contacting the subject or cell with a retrovirus of the disclosure, wherein the heterologous nucleic acid sequence encodes a therapeutic protein that inhibits proliferation of a neoplastic cell. In one embodiment, the retrovirus comprises a polynucleotide encoding a polypeptide having a sequence as set forth in SEQ ID NO: 4, 12, 14, 16, 18 or 76, wherein the polynucleotide is operably linked to a mini-promoter.

[0013] The disclosure provides the sequences of certain RRVs having promoter cassettes operably linked to a cytotoxic gene. For example, SEQ ID NO:19 depicts a pAC3-C1.yCD2 vector wherein the vector comprises a *gag*, *pol* and *env* sequence, the *env* sequence immediately followed by a promoter CMV core promoter and a humanized cytosine deaminase with 3 heat stabilized mutation, which is then followed by the 3′ LTR. SEQ ID NO:20 depicts a similar structure however, the cassette comprises an S1 promoter followed by the transgene of human GMCSF. SEQ ID NO:21 shows the sequence of a an RRV vector "pACE-CD". SEQ ID NO:22 shows a sequence similar to SEQ ID NO:19 and 20 except the promoter cassette comprises an S1 promoter operably linked to murine GMCSF. SEQ ID NO:39 shows the sequence of an RRV having an S1-yCD2 cassette. SEQ ID NO:40 shows the sequence of an RRV having a C1-GFP cassette. SEQ ID NO:41 shows the sequence of an RRV having an S1-GFP cassette. Other vectors of the disclosure comprising mini-promoters linked to

heterologous nucleic acids are set forth in SEQ ID NOs:77-85 and 86.

[0014] The disclosure provides a vector comprising a recombinant replication competent retrovirus (RRV) and having a mini-promoter cassette, wherein the vector infects a target cell multiple times leading to a mean of 3 or more copies of the retrovirus genome per target cell. The multiple copies provide a "super" infection useful for gene delivery and protein production *in vivo* and *in vitro*. In one embodiment, the RRV comprises: a retroviral GAG protein; a retroviral POL protein; a retroviral envelope; a retroviral polynucleotide comprising Long-Terminal Repeat (LTR) sequences at the 3' end of the retroviral polynucleotide sequence, a promoter sequence at the 5' end of the retroviral polynucleotide, said promoter being suitable for expression in a mammalian cell, a *gag* nucleic acid domain, a *pol* nucleic acid domain and an *env* nucleic acid domain; a cassette comprising at least one mini-promoter or core-promoter and enhancer operably linked to a heterologous polynucleotide, wherein the cassette is positioned 5' to the 3' LTR and 3' to the *env* nucleic acid domain encoding the retroviral envelope; and cis-acting sequences necessary for reverse transcription, packaging and integration in a target cell, wherein the RRV maintains higher replication competency after 6 passages compared to a pACE vector (SEQ ID NO:21, *i.e.*, the vector of Logg *et al.*, Hum Gene Ther. 2001 May 20;12(8):921-32). In one embodiment, the retroviral polynucleotide sequence is derived from murine leukemia virus (MLV), Moloney murine leukemia virus (MoMLV),Feline leukemia virus (FeLV), Baboon endogenous retrovirus (BEV), porcine endogenous virus (PERV), the cat derived retrovirus RD114, squirrel monkey retrovirus, Xenotropic murine leukemia virus-related virus (XMRV), avian reticuloendotheliosis virus (REV), or Gibbon ape leukemia virus (GALV). In another embodiment, the MLV is an amphotropic MLV. In yet another embodiment, the retrovirus is an oncoretrovirus or gamma retrovirus. In yet another embodiment, the target cell is a cell having aberrant cell proliferative capacity such as those associated with a cell proliferative disorder (*e.g.*, a cancer cell). The cell proliferative disorder can be selected from the group consisting

of, but is not limited to, lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer, brain cancer, head and neck cancer, pancreatic cancer, melanoma, stomach cancer and ovarian cancer, lymphoma, leukemia, rheumatoid arthritis and other autoimmune diseases. In one embodiment, the vector can comprise a promoter to drive transcription of the *gag*, *pol* and *env* such as a CMV promoter having a sequence as set forth in SEQ ID NO:19, 20 or 22 from nucleotide 1 to about nucleotide 582 and may include modification to one or more nucleic acid bases and which is capable of directing and initiating transcription. In yet a further embodiment, the promoter comprises a sequence as set forth in SEQ ID NO: 19, 20 or 22 from nucleotide 1 to about nucleotide 582. In a further embodiment, the promoter comprises a CMV-R-U5 domain polynucleotide. In one embodiment, the CMV-R-U5 domain comprises the immediately early promoter from human cytomegalovirus linked to an MLV R-U5 region. In yet another embodiment, the CMV-R-U5 domain polynucleotide comprises a sequence as set forth in SEQ ID NO: 19, 20 or 22 from about nucleotide 1 to about nucleotide 1202 or sequences that are at least 95% identical to a sequence as set forth in SEQ ID NO: 19, 20 or 22, wherein the polynucleotide promotes transcription of a nucleic acid molecule operably linked thereto. In another embodiment, the *gag* and *pol* of the polynucleotide are derived from an oncoretrovirus or gamma retrovirus. The *gag* nucleic acid domain can comprise a sequence from about nucleotide number 1203 to about nucleotide 2819 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, 99% or 99.8% identity thereto. The *pol* domain can comprise a sequence from about nucleotide number 2820 to about nucleotide 6358 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, 99% or 99.9% identity thereto. In one embodiment, the *env* domain encodes an amphotropic env protein. The *env* domain can comprise a sequence from about nucleotide number 6359 to about nucleotide 8323 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, 99% or 99.8% identity thereto. The mini-promoter of the vector can be any regulatory domain that is smaller than 600 bp (*e.g.*, about 600 bp, 550 bp, 500 bp, 450 bp, 400 bp, 350 bp, 300 bp, 250 bp, 200 bp, 150 bp, 100 bp, about 90 bp, about 80 bp, about 76 bp, about 74 bp or

smaller) and allows for transcription of an operably linked coding sequence or non-coding sequence. In one embodiment the mini-promoter comprises a sequence from about nucleotide number 8330 to about nucleotide 8406 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, or 99% identity thereto. In another embodiment, the mini-promoter comprises a sequence selected from the group consisting of SEQ ID NO:56, 57, 59, 65, 67, 68, 69, 71, 72, 73, and 74.

[0015] The details of one or more embodiments of the disclosure are set forth in the accompanying drawings and the description below. Other features, objects, and advantages will be apparent from the description and drawings, and from the claims.

BRIEF DESCRIPTION OF DRAWINGS

[0016] **Figure 1** shows a general structural motif of a core promoter and various elements that can be present (Juven-Gershon & Kadonaga, Developmental Biology 339: 225-229 2010). Typically a core promoter stretches from about -40bp upstream of the transcription start site to about 40bp down stream of the start site to initiating translation codon. Abbreviations have the following meanings:, BREu - upstream TFII*B* *R*ecognition *E*lement;TATA "the tata box"; BREd - downstream TFII*B* *R*ecognition *E*lement; Inr - initiator site for transcription; MTE - motif ten element; DPE - downstream promoter element; DCE - downstream core element; XCPE1 - X core promoter element 1.

[0017] **Figure 2A-B** shows vector stability of RRV in pAC backbone containing C1 and S1 core promoter driving transgene (A) GFP and (B) CD expression. The numbers above each lane indicates the number of infection cycle. Arrows indicate expected fragment size.

[0018] **Figure 3** shows vector stability of RRV in pAC backbone containing IRES element or S1 core promoter driving transgene (human and mouse GM-CSF) expression. The numbers above each lane indicates the number of infection cycle. Arrows indicate expected fragment size.

[0019] **Figure 4A-H** shows (A) GFP protein expression measured by Fluorescent Activated Cell Sorting (FACS) of pAC3-GFP, pAC3.C1-GFP and pAC3.S1-GFP vector in fully infected human tumor cell lines U87, 1306-MG and T98s. MFI - Mean Fluorscent Intensity. (B)

Protein expression (Western Blot) of pAC3-yCD2, pAC3.C1-yCD2 and pAC3.S1-yCD2 vector in transiently transfected 293T cells. (C) Protein expression (Western Blot) of pAC3-yCD2, pAC3.C1-yCD2 and pAC3.S1-yCD2 vector in fully infected U87 cells. (D)-(F) GM-CSF protein expression of pAC3-hGMCSF and pAC3.S1-hGMCSF: (D) in transiently transfected 293T; (E) in fully infected U87; (F) in fully infected and PC3 cells. (G)-(H) GM-CSF protein expression of pAC3-mGMCSF and pAC3.S1-mGMCSF: (G) in transiently transfected 293T; (H) in fully infected EMT6 cells.

[0020] **Figure 5A-B** shows (A) Viral replication kinetics of pAC3-emd, pAC3-hGMCSF and pAC3S1-hGMCSF vectors in U87 cells. (B) Viral replication kinetics of pAC3-emd, pAC3-mGMCSF and pAC3.S1-mGMCSF vectors in EMT6 cells.

[0021] **Figure 6** shows the cell killing curve in U87 cells treated with PALA from two different sources with nearly identical results.

[0022] **Figure 7** shows GFP expression from an IRES-cassette, S1 cassette and SV40 cassette.

[0023] **Figure 8A-B** show diagrams of constructs used in the disclosure.

[0024] **Figure 9** shows gene expression mediated by mini- and synthetic-promoters in transiently transfected cells (293T, left side; Hela cells right side).

DETAILED DESCRIPTION

[0025] As used herein and in the appended claims, the singular forms "a," "and," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a cell" includes a plurality of such cells and reference to "the vector" includes reference to one or more vectors and so forth.

[0026] Also, the use of "or" means "and/or" unless stated otherwise. Similarly, "comprise," "comprises," "comprising" "include," "includes," and "including" are interchangeable and not intended to be limiting.

[0027] It is to be further understood that where descriptions of various embodiments use the term "comprising," those skilled in the art would understand that in some specific instances, an

embodiment can be alternatively described using language "consisting essentially of" or "consisting of."

[0028] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice of the disclosed methods and compositions, the exemplary methods, devices and materials are described herein.

[0029] General texts and serial volumes, which describe molecular biological techniques useful herein, including the use of vectors, promoters and many other relevant topics, include Methods in Molecular Biology, Series Ed. John M. Walker,Humana Press, ISSN: 1064-3745; Methods in Enzymology, Elsevier Press; company reagent fact sheets and method support publications; scientific networking sites such as Researchgate (world wide web at researchgate.net) and labtests online (*e.g.*, [http://] labtestonline.org/understanding/features/methods/) and individual laboratory sites such as [http://www]cshl.edu.

[0030] The publications discussed throughout the text are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior disclosure.

[0031] The disclosure provides methods and compositions useful for gene or protein delivery to a cell or subject. Such methods and compositions can be used to treat various diseases and disorders in a subject including cancer and other cell proliferative diseases and disorders. The disclosure provides retroviral replicating vectors for gene delivery utilizing core-promoter and/or mini-promoter cassettes operably linked to a heterologous polynucleotide to be expressed.

[0032] Above a size of about 1.5kb stability of transgenes in RRV vectors can be variable. The conventional strategy for transgene expression following the successful cloning of an IRES cassette into MLV (Logg *et al.*, *supra*) has been to use an IRES component to allow internal initiation of translation from the

internal ribosome binding site. The IRES component is about 600bp leaving approximately 900 bp for coding sequence. Accordingly, the size of the polynucleotide linked to the IRES cassette is limited by stability. One alternative to increase the size of the polynucleotide to be expressed or delivered is to use a smaller regulatory sequence that promotes transcription such as a promoter, promoter/enhancer, or other regulatory domains.

[0033] Most promoters are rather large; typically over 600bp for full functionality and the full size of a promoter can be many kilobases. Smaller promoters can be generated that allow reliable expression of transgenes in mammalian cells from vectors such as replicating retroviral vectors (RRVs). For example, one possible solution is to use the "core" promoters described by Kadanaga and collaborators (Juven-Gershon *et al.*, Nature Methods, 11:917-922, 2006). These core promoters are based on the adenovirus major late (AdML) and cytomegalovirus (CMV) major immediate early genes, and the synthetic "super core promoter" SCP1. Other cellular core promoters include, but are not limited to, the human heme oxygenase proximal promoter (121 bp; Tyrrell *et al.*, Carcinogenesis, 14: 761-765, 1993), the CTP:phosphocholine cytidylyltransferase (CCT) promoter (240bp; Zhou *et al.*, Am. J. Respir. Cell Mol. Biol., 30: 61-68, 2004); the Human ASK (for Activator of S phase Kinase, also known as HsDbf4 gene, 63bp; Yamada *et al.* J.Biol.Chem., 277: 27668-27681, 2002); and the HSVTK intragenic core (Al-Shawi *et al.*, Mol. Cell. Biol., 11: 4207, 1991; Salamon *et al.*, Mol. Cell. Biol., 15:5322, 1995). Furthermore, these "core" promoters can be used as a starting point for further modifications to improve the activity of the promoter. For example, such modifications including the additional of other domains and sequences to the "core" promoter to improve functionality (*e.g.*, enhancers, Kozak sequences and the like). In one embodiment, such further modifications can includes the addition of enhancers.

[0034] The length of these core promoters are approximately 70-80 bp each, thus leaving approximately 1.4 kb of capacity for transgene sequence. The use of such promoters can give useful expression of genes such as the HSVtk gene which is >1.1kb long. However, such promoters are not always reliable for obtaining

levels of expression equivalent to or better than those from the IRES driven expression vectors. Furthermore, there is variability in expression levels from cell to cell and in some cases the levels of expression of the transgene is undetectable. The two CMV and Adenovirus derived core-promoters are even less reliable than the synthetic SCP1 promoter.

[0035] The use of core promoters (Juven-Gershon *et al.*, Nat. Methods, 2006; Juven-Gershon and Kadonaga Dev. Biol. 339:225-229, 2010), as described herein, although not as effective as an IRES, allow expression of longer genes, which have therapeutic benefit. Furthermore, using rational design techniques various promoter-components can be used to optimize expression and stability of the RRV. Such optimized core promoters provide a more effective expression and stability of the viral polynucleotide. For example, "designer" promoters can comprise a core promoter that has been further modified to include one or more additional elements suitable for stability and expression.

[0036] As described herein, the use of such core promoters either alone or including additional elements for expression can be used in various vectors including replication competent retroviral vectors. The disclosure provides a RRV comprising a therapeutic cassette 3' to the env coding sequence and 5' to the 3' LTR. By "therapeutic cassette" is meant a domain within the RRV that comprises at least one mini-promoter cassette or a core-promoter cassette and one additional cassette (*e.g.*, an IRES, polIII or minipromoter cassette), wherein a therapeutic polynucleotide sequence that upon expression codes for a therapeutic protein (*e.g.*, cytosine deaminse, thymidine kinase and the like) or a therapeutic nucleic acid (*e.g.*, an siRNA, shRNA, microRNA or the like). Accordingly, a "therapeutic cassette" can comprise a single mini-promoter cassette comprising a mini-promoter operably linked to a coding sequence for a therapeutic molecule or molecules, or may include at least one mini-promoter cassette and a second cassette. The second cassette may be a second mini-promoter cassette, a core-promoter cassette, an IRES cassette or a polIII promoter cassette.

[0037] As used herein, a "core promoter" refers to a minimal promoter comprising about 50-100 bp and lacks enhancer elements. Such core promoters include, but are not limited to, SCP1, AdML and CMV core promoters. More particularly, where a core-promoter cassette is present a second cassette (*e.g.*, a second mini-promoter cassette, a polIII promoter cassette or IRES cassette) will be present. In some embodiments, a vector comprising a cassette with a core promoter specifically excludes the use of SCP1, AdML and CMV core promoters, but rather utilize designer core promoters as described further herein and below.

[0038] Core promoters include certain viral promoters. Viral promoters, as used herein, are promoters that have a core sequence but also usually some further accessory elements. For example, the early promoter for SV40 contains three types of elements: a TATA box, an initiation site and a GC repeat (Barrera-Saldana *et al.*, EMBO J, 4:3839-3849, 1985; Yaniv, Virology, 384:369-374, 2009). The TATA box is located approximately 20 base-pairs upstream from the transcriptional start site. The GC repeat regions is a 21 base-pair repeat containing six GC boxes and is the site that determines the direction of transcription. This core promoter sequence is around 100 bp. Adding an additional 72 base-pair repeats, thus making it a "mini-promoter," is useful as a transcriptional enhancer that increase the functionality of the promoter by a factor of about 10. When the SP1 protein interacts with the 21 bp repeats it binds either the first or the last three GC boxes. Binding of the first three initiates early expression, and binding of the last three initiates late expression. The function of the 72 bp repeats is to enhance the amount of stable RNA and increase the rate of synthesis. This is done by binding (dimerization) with the AP1 (activator protein 1) to give a primary transcript that is 3' polyadenylated and 5' capped. Other viral promoters, such as the Rous Sarcom Virus (RSV), the HBV X gene promoter, and the Herpes Thymidine kinase core promoter can also be used as the basis for selection desired function.

[0039] A core promoter typically encompasses -40 to +40 relative to the +1 transcription start site (Juven-Gershon and Kadonaga, Dev. Biol. 339:225-229, 2010), which defines the location

at which the RNA polymerase II machinery initiates transcription. Typically, RNA polymerase II interacts with a number of transcription factors that bind to DNA motifs in the promoter. These factors are commonly known as "general" or "basal" transcriptions factors and include, but are not limited to, TFIIA (transcription factor for RNA polymerase IIA), TFIIB, TFIID, TFIIE, TFIIF, and TFIIH. These factors act in a "general" manner with all core promoters; hence they are often referred to as the "basal" transcription factors.

[0040] Juven-Gershon *et al.*, 2006 (*supra*), describe elements of core promoters. For example, the pRC/CMV core promoter consists of a TATA box and is 81 bp in length; the CMV core promoter consists of a TATA box and a initiator site; while the SCP synthetic core promoters (SCP1 and SCP2) consist of a TATA box, an Inr (initiator), an MTE site (Motif Ten Element), and a DPE site (Down stream promoter element) and is about 81 bp in length. The SCP synthetic promoter has improved expression compared to the simple pRC/CMV core promoter.

[0041] As used herein a "mini-promoter" or "small promoter" refers to a regulatory domain that promotes transcription of an operably linked gene or coding nucleic acid sequence. The mini-promoter, as the name implies, includes the minimal amount of elements necessary for effective transcription and/or translation of an operably linked coding sequence. A mini-promoter can comprise a "core promoter" in combination with additional regulatory elements or a "modified core promoter". Typically, the mini-promoter or modified core promoter will be about 100-600 bp in length while a core promoter is typically less than about 100bp (*e.g.*, about 70-80 bp). In other embodiments, where a core promoter is present, the cassette will typically comprise an enhancer element or another element either upstream or downstream of the core promoter sequence that facilitates expression of an operably linked coding sequence above the expression levels of the core promoter alone.

[0042] Accordingly, the disclosure provides mini-promoters (*e.g.*, modified core promoters) derived from cellular elements as determined for "core promoter" elements (<100, <200, <400 or <600

bp) that allow ubiquitous expression at significant levels in target cells and are useful for stable incorporation into vectors, in general, and replicating retroviral vectors, in particular, to allow efficient expression of transgenes. Also provided are mini-promoters comprising core promoters plus minimal enhancer sequences and/or Kozak sequences to allow better gene expression compared to a core-promoter lacking such sequences that are still under 200, 400 or 600bp. Such mini-promoters include modified core promoters and naturally occurring tissue specific promoters such as the elastin promoter (specific for pancreatic acinar cells, (204 bp; Hammer *et al.*, Mol Cell Biol., 7:2956-2967, 1987) and the promoter from the cell cycle dependent ASK gene from mouse and man (63-380 bp; Yamada *et al.*, J. Biol. Chem., 277: 27668-27681, 2002). Ubiquitously expressed small promoters also include viral promoters such as the SV40 early and late promoters (about 340 bp), the RSV LTR promoter (about 270 bp) and the HBV X gene promoter (about 180 bp) (*e.g.*, R Anish *et al.*, PLoS One, 4: 5103, 2009) that has no canonical "TATTAA box" and has a 13 bp core sequence of 5'-CCCCGTTGCCCGG-3' (SEQ ID NO:42). In yet other embodiments, the therapeutic cassette comprising at least one mini-promoter cassette will have expression levels that exceed, are about equal to, or about about 1 fold to 2.5 fold less than the expression levels of an IRES cassette present in an RRV.

[0043] Transcription from a core- or mini-promoter occurs through the interaction of various elements. In focused transcription, for example, there is either a single major transcription start site or several start sites within a narrow region of several nucleotides. Focused transcription is the predominant mode of transcription in simpler organisms. In dispersed transcription, there are several weak transcription start sites over a broad region of about 50 to 100 nucleotides. Dispersed transcription is the most common mode of transcription in vertebrates. For instance, dispersed transcription is observed in about two-thirds of human genes. In vertebrates, focused transcription tends to be associated with regulated promoters, whereas dispersed transcription is typically observed in constitutive promoters in CpG islands.

[0044] A listing and description of some core promoter elements that may be shuffled into a core promoter sequence for both focused and disperse promoter elements is given in Table 1. As mentioned previously, a mini-promoter used in the compositions of the disclosure can comprise a core promoter that is further modified. Such modifications can include the incorporation of one or more additional elments as set forth in Table 1.

[0045] Table 1: Binding sites that can contribute to a focused core promoter (almost always with a "TATA box and a single transcription start site (TSS)), or a dispersed promoter without a TATA box, usually with a DPE element (see R. Dickstein, Trasncription, 2(5):201-206, 2011; Juven-Gershon *et al.*, Nat. Methods, 2006, supra). Symbols for nucleotides follow the international convention (world wide web: chem.qmul.ac.uk/iubmb/misc/naseq.html).

Transcription factor	Full name	Binding site wrt to transcription start site (TSS +1)
BREu	TFIIB recognition element, upstream	Upstream of TATA Box, SSRCGCC
TATA box	TATA box	T at -31/-30 TATAWAAR, key focused promoter element
BREd	TFIIB recognition element, downstream	-23 to -17 RTDKKKK
XCPE1	HBV X core promoter element 1	-8 to +2 DSGYGGRASM from HBV Xgene
XCPE2	HBV X core promoter element 2	VCYCRTTRCMY from HBV Xgene
Inr	initiator	-2 to +4 YYANWYY
DCE SI	Downstream core element site 1	+6 to +11 CTTC
DCE SII	Downstream core element site II	+16 to +21 CTGT
DCE SIII	Downstream core element site III	+30 to +34 AGC
MTE	Motif ten element	+18 to +27 CSARCSSAAC mostly in Drosophila
DPE	Downstream promoter element	+28 to +33 RGWYVT common in Drosophila, key dispersed promoter element

[0046] Table 2 sets forth oligonucleotides that can be used to construct and clone enhancer elements into core promoter regions. As mentioned above, the modified/optimized core promoters of the disclosure can include a core sequence with the addition of elements from Table 1 and may further include enhancers cloned as

set forth in Table 2. In doing so, the size of the core-promoter is increased and can be described as a "mini-promoter". However, the final mini-promoter should not exceed 600 bp and will typically be about 100 bp, 200 bp, 300 bp, 400 bp, 500 bp and any integer there between.

[0047] **Table 2.** Oligonucleotides used for constructing enhancer segments.

No.	Oligonucleotide	Motif Sequence (SEQ ID NOs in	Reference
1	AP-1	5'-TGTCTCAG-3' (43)	Hallahan*et al.* Int. J. Radiat. Oncol. Biol. Phys. 36:355-360, 1996
2	CArG	5'-CCATATAAGG-3' (44)	Datta *et al.* Proc. Natl. Acad. Sci. USA 89:10149-10153, 1992
3	NF-κB1	5'-GGAAATCCCC-3' (45)	Ueda *et al.* FEBS Lett. 491:40-44, 2001
4	NF-κB2	5'-GGAAAGTCCCC-3' (46)	Kanno *et al.* EMBO J. 8:4205-4214, 1989
5	NF-κB3	5'-GGAGTTCCC-3' (47)	Hong *et al.* J. Biol.Chem. 275:18022-18028 2000.
6	NF-Y	5'-CATTGGG-3' (48)	Hu *et al.* J. Biol. Chem. 275:2979-2985, 2000.
7	CRE1	5'- TTACGTAA-3' (49)	Theil *et al.*, BMC Mol. Biol., 6:2 1-14, 2005
8	CRE2	5'- TTGCATCA-3' (50)	Theil *et al.*, BMC Mol. Biol. 6:2 1-14, 2005

AP-1, activating protein-1; NF-κB, nuclear factor κB; CRE, cAMP response elements.

[0048] In addition, most eukaryotic mRNAs contain a short recognition sequence called Kozak sequence (RCCATGG; (SEQ ID NO:51)), where ATG is the translational start site. The presence of a Kozak sequence can greatly facilitates the binding of mRNA to ribosome in the translation machinery. To improve gene expression level, it is advantageous to incorporate Kozak sequence downstream of the core promoter. Although the core promoter has demonstrated useful transcription, efficient protein translation is equally important to confer gene expression. Thus, in one embodiment, the mini-promoter includes regulatory elements (*e.g.*, Kozak sequences) that can improve translation of transcript mRNA. Other "Kozak-like" sequences that can promote efficient translation are known in the art. For example, sequences derived from the 5'-UTR of tobacco

mosaic virus mRNA as well as from the lobster tropomyosin gene are able to function in eukaryotic cells to enhance protein translation (Gallei *et al.*, 1989, Gallei *et al.*, 1992 and Gallei *et al.*, 2002; Sano *et al.*, 2002). The length of these sequences varies from 7 to 68 nucleotides (see, *e.g.*, Table 3).

[0049] **Table 3:** Known translational enhancer found in 5' UTR of coding genes.

Enhancer element	**Origin**	**Length**	**Sequence**
Kozak	eukaryotes	7 nt	RCCATGG (SEQ ID NO:51)
Omega	tobacco mosaic virus	68 nt	m'pppTTATTTTTACAAAATTACCAA CAACAACAAACAACAAACAATTACA ATTACTATTTACAATTACAATG (SEQ ID NO:52)
L21	eukaryotes	21 nt	AACTCCTAAAAAACCGCCACC (SEQ ID NO:53)

Particularly, the 5' UTR immediately upstream of the ATG initiation codon have been shown to influence the level of translation initiation. Thus, in one embodiment, the mini-promoter includes regulatory elements (*e.g.*, Kozak sequences) that can improve translation of transcript mRNA. In addition, analysis of the sequence to be expressed and translated (*i.e.*, the sequence to which the mini-promoter is operably linked) can provide insight on modifications useful for better expression. For example, a heat-stabilized, humanized, yeast cytosine deaminase (yCD2) coding sequence (see, *e.g.*, SEQ ID NO:3) has 3 in-frame ATG within the first 15 amino acids in the coding region. The spacing in the 5'UTR and the lack of Kozak sequence flanking the initiation codon in yCD2 mRNA is suboptimal for efficient protein translation initiation. Thus, incorporation of Kozak sequence and/or other translational enhancer element may greatly improve the translation initiation and thus protein production of transgenes.

[0050] As mentioned above, the mini-promoters can comprise optimized or modified core promoters that include one or more additional elements that facilitate expression of an operably linked coding sequence. One way of selecting for functional mixtures of these elements is to simply synthesize the various elements or variations of these elements, ligate them together and select functionally for mini-promoters that are able to express in the desired situation. Juven-Gershon *et al.* describes assays which

can be used to determine the expression levels of operably linked genes (*e.g.*, using luciferase report constructs and the like). Using these techniques in combination with elements that bind the transcription factors AP-1, nuclear factor κB (NF-κB), CArG binding factor A (CBF-A) and nuclear factor Y (NF-Y) (see Table 2) one can obtain functional enhancers (Ogawa *et al.*, Biotechniques, 42:628-633, 2007) combined with a cellular core promoter (for example, from the hemoxygenase core) to yield an overall active promoter of approximately 165 bp total. However, other core promoters such as the SCP1 core, optimized core sequences as described here, the TK intragenic core (Al-shawi *et al.*, Mol. Cell. Biol., 11: 4207, 1991; Salamon *et al.*, Mol. Cell. Biol., 15:5322 1995); or the human ASK gene core (Yamada *et al.*) can be used. Various other genes can be used as positive selectable markers. These include: dyhdrofolate reductase (DHFR; Simonsen *et al.*, Nuc Acid Res., 16:2235-2246, 1988) with methotrexate in conjunction with a nucleotide transport inhibitor such as dipyridamole (Warlick *et al.*, Biochemical Pharmacology, 59: 141–151, 2000) or nitrobenzylmercaptopurine riboside phosphate (Allay*et al.*, Stem Cells, 16(suppl 1):223-233, 1998); Cytosine deaminase using N-(phosphonacetyl)-L-aspartate (PALA) to block *de novo* synthesis of uracil and anabolically downstream bases and cytosine to supply these through pyrimidine salvage pathways (Wahl *et al.*, J. Biol. Chem., 254:8679; Unger *et al.*, Can. Gene Ther., 14:30-38); and various other selectable markers known to those skilled in the art. In general, higher levels of expression of the selectable marker is indicative of better expression.

[0051] In addition, modified or optimized promoters may be obtained through "directed evolution", error prone PCR and the like. For example, rounds of expression and selection can provide for the introduction of errors in a mini-promoter (*e.g.*, a core promoter or modified core promoter) and selection of positive expression profiles using selectable systems such as the DHFR and CD selection schemes described above. In another embodiment, transgenes that are not sufficiently expressed using mini-promoters can be selected for increased expression in the context of an RRV by including a metabolically selectable gene in the RRV and passing

the RRV through multiple rounds of replication and selection. The relatively high error rate of the viral reverse transcriptase enzyme allows the incorporation of mutations and advantageous mutations are then selected and become the dominant sequence. Such improved mini-promoters can then be amplified, cloned and used as a more efficient minipromoter. Advantageously, for the use of RRV as anticancer agents, the selection can be performed in tumor cell lines of a desired cell type, such as colon, brain, lung, breast or prostate cancers. For example, sequential passage of the RRV encoding the selectable marker driven by a putative minimal promoter in the presence of the selective agent leads to selection for the best expressing minimal promoter. Passage of the RRV in tumor cell lines of the proposed target type can be used if there are tissue specificity issues with a particular combination. In one embodiment, the mini-promoter is synthesized as a single entity and the rate of error accumulation of the RRV reverse transcriptase is relied on to introduce diversity on which selection can be made. In a separate embodiment, the initial promoter is synthesized with programmed random inhomogeneities in the sequence so that when incorporated into the RRV as the promoter for the selectable marker, there is a larger landscape of possible sequences to to select from. In another embodiment, the initial viral vector can be supplied with random variants in the promoter sequence and the same type of selection can be used to identify optimal mini-promoter sequences. In another embodiment, Kozak sequence RCCATGG (SEQ ID NO:51) can be incorporated downstream of the mini promoters to facilitate the initial binding of the mRNA to the small subunit of the ribosome, thus improve translation.

[0052] Optimized mini-promoters with sufficient expression can be used in any situation where nucleic acid size is limiting (*e.g.*, viral vectors). In one embodiment the optimized mini-promoter is used in a replicating RRV to express one or more genes with an anticancer effect. In one embodiment the mini-promoter is used to express two genes, either as a fusion, a fusion gene separated by a protease cleavage site such as the furin endogenous protease target, or separated by a self-processing sequence like the 2A family (de Felipe *et al.*, Trends Biotech, 24:68-75, 2006) or by the

inclusion of two mini-promoters, one for each gene. In another embodiment, the mini-promoter can be used to express a first gene or coding sequence and then a second cassette comprising a polIII promoter can be used to express an siRNA, shRNA or microRNA. Because the mini-promoter cassette is smaller, it can be effectively combined to incorporate other therapeutic coding sequences.

[0053] The mini-promoters described herein that are operably linked to a gene or coding sequence to be expressed can be used to drive transcription in a vector. In one embodiment, the disclosure provides vectors comprising from 5' to 3': a CMV-R-U5 fusion of the immediate early promoter from human cytomegalovirus to an MLV R-U5 region; a PBS, primer binding site for reverse transcriptase; a 5' splice site; ψ packaging signal; a *gag* coding sequence for MLV group specific antigen; a *pol* coding sequence for MLV polymerase polyprotein; a 3' splice site; a 4070A *env* coding sequence for envelope protein of MLV strain 4070A; a therapeutic cassette comprising (a) at least one mini-promoter cassettes operably linked to a therapeutic gene or (b) a core-promoter and at least one other cassette selected from the group consisting of a polIII promoter cassette, a second core-promoter cassette, a mini-promoter cassette and an IRES cassette; a polypurine tract; and a U3-R-U5 MLV long terminal repeat. In a further embodiment, each of these various "portion" of the vector (*e.g.*, the *gag*, *pol*, *env* and the like) can comprise well known sequences in the art derived from various gamma retroviral vectors (*e.g.*, MLV, GALV and the like). In some embodiments, the vector is derived from or engineered from an MLV viral sequence. Figure 8A and 8B depict various vectors of the disclosure as described in more detail elsewhere herein. For example, the promoter at the 5' end of the vector can comprise a CMV promoter having a sequence as set forth in SEQ ID NO:19, 20 or 22 from nucleotide 1 to about nucleotide 582 and may include modification to one or more nucleic acid bases and which is capable of directing and initiating transcription. In yet a further embodiment, the vector promoter comprises a sequence as set forth in SEQ ID NO: 19, 20 or 22 from nucleotide 1 to about nucleotide 582. In a further embodiment, the promoter comprises a CMV-R-U5

domain polynucleotide. In one embodiment, the CMV-R-U5 domain comprises the immediately early promoter from human cytomegalovirus linked to an MLV R-U5 region. In yet another embodiment, the CMV-R-U5 domain polynucleotide comprises a sequence as set forth in SEQ ID NO: 19, 20 or 22 from about nucleotide 1 to about nucleotide 1202 or sequences that are at least 95% identical to a sequence as set forth in SEQ ID NO: 19, 20 or 22 from about nucleotide 1 to about 1202, wherein the polynucleotide promotes transcription of a nucleic acid molecule operably linked thereto. In another embodiment, the *gag* and *pol* genes of the vector are derived from an oncoretrovirus or gamma retrovirus. The *gag* nucleic acid domain can comprise, for example, a sequence from about nucleotide number 1203 to about nucleotide 2819 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, 99% or 99.8% identity thereto. The *pol* domain can comprise a sequence from about nucleotide number 2820 to about nucleotide 6358 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, 99% or 99.9% identity thereto. In one embodiment, the *env* domain encodes an amphotropic env protein. The *env* domain can comprise a sequence from about nucleotide number 6359 to about nucleotide 8323 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, 99% or 99.8% identity thereto.

[0054] A therapeutic cassette is located just downstream of the *env* termination codon. Typically the therapeutic cassette starts immediately after or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or about 100 basepairs downstream of the *env* stop codon. The beginning of the therapeutic cassette will typically have a minimal distance from the *env* stop codon so as to optimize the size of the heterologous gene in the cassette. As mentioned above, the therapeutic cassette can comprise one or more mini-promoters each operably linked to a therapeutic coding sequences, or a mini-promoter and a polIII promoter each operably linked to a therapeutic coding sequences, or a mini-promoter and an IRES each operably linked to a therapeutic coding sequences. The mini-promoter of the vector can be any regulatory domain that is smaller than 600 bp (*e.g.*, about 599 bp, 550 bp, 500 bp, 450 bp, 400 bp, 350 bp, 300 bp, 250 bp, 200 bp, 150 bp, 100 bp, about 90 bp, about 80 bp, about 76 bp, about 74 bp or smaller) and allows for

transcription of an operably linked coding sequence or non-coding sequence. In one embodiment the cassette comprises a core-promoter such as from about nucleotide number 8330 to about nucleotide 8406 of SEQ ID NO: 19 or 22 or a sequence having at least 95%, 98%, or 99% identity thereto. In another embodiment, the core-promoter set forth in SEQ ID NO:19 or 22 from about 8328 to 8404 can be substituted with any number of other core- or mini-promoters including the promoters having the sequences as set forth in SEQ ID NO:56, 57, 59, 65, 66, 67, 68, 69, 71, 72, 73, and 74 and may further include additional sequences such as enhancer (*e.g.*, SEQ ID NO:58 and 70).

[0055] The disclosure provides the sequences of certain RRVs having promoter cassettes operably linked to a cytotoxic gene. For example, SEQ ID NO:19 depicts a pAC3-C1.yCD2 vector wherein the vector comprises a *gag*, *pol* and *env* sequence, the *env* sequence immediately followed by a CMV core promoter and a humanized cytosine deaminase with 3 heat stabilized mutation, which is then followed by the 3' LTR. SEQ ID NO:20 depicts a similar structure however, the cassette comprises an S1 promoter followed by the transgene of human GMCSF. SEQ ID NO:21 shows the sequence of a prior art RRV vector "pACE-CD". SEQ ID NO:22 shows a sequence similar to SEQ ID NO:19 and 20 expect the promoter cassette comprises an S1 promoter operably linked to murine GMCSF. SEQ ID NO:39 shows the sequence of an RRV having an S1-yCD2 cassette. SEQ ID NO:40 shows the sequence of an RRV having a C1-GFP cassette. SEQ ID NO:41 shows the sequence of an RRV having an S1-GFP cassette.

[0056] The terms "express" and "expression" mean allowing or causing the information in a gene or DNA sequence to become manifest, for example producing a protein by activating the cellular functions involved in transcription and translation of a corresponding gene or DNA sequence. A DNA sequence is expressed in or by a cell to form an "expression product" such as a protein. The expression product itself, *e.g.* the resulting protein, may also be said to be "expressed" by the cell. A polynucleotide or polypeptide is expressed recombinantly, for example, when it is expressed or produced in a foreign host cell under the control of a foreign or

native promoter, or in a native host cell under the control of a foreign promoter.

[0057] Although the disclosure describes the use of RRVs comprising a core- or mini-promoter, other "vectors" can includes such core- or mini-promoter constructs to express operably linked genes and sequences. The terms "vector", "vector construct" and "expression vector" mean the vehicle by which a DNA or RNA sequence (*e.g.*, a foreign gene) can be introduced into a host cell, so as to transform the host and promote expression (*e.g.*, transcription and translation) of the introduced sequence. Vectors typically comprise the DNA of a transmissible agent, into which foreign DNA encoding a protein is inserted by restriction enzyme technology. A common type of vector is a "plasmid", which generally is a self-contained molecule of double-stranded DNA that can readily accept additional (foreign) DNA and which can readily introduced into a suitable host cell. A large number of vectors, including plasmid and fungal vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts. However, most vectors have particular size limitations on what can be cloned into the vector (*e.g.*, 12kb for plasmids, 20 kb for lambda bacteriophage, 30-35 kb for cosmids). This is even more restrictive when one considers retroviral vectors. For example, the genome of a typical replication-competent murine retrovirus is about 8.3 kb, whereas that of the alpha retrovirus RSV, which contains a disposable *src* sequences in addition to the normal complement of viral genes, is about 9.3 kb. The maximum size for a replication-competent spleen necrosis virus vector is similar, about 10 kb (Gelinas and Temin 1986) (Retroviruses., Coffin JM, Hughes SH, Varmus HE, editors., Cold Spring Harbor (NY): Cold Spring Harbor Laboratory Press; 1997). Presumably, the size limit on the retroviral genome depends on the size of the folded dimeric RNA. Furthermore, "gutted" or replication defective retroviral vectors can incorporate larger sequence than their replication competent counter parts.

[0058] The disclosure provides retroviral replicating vectors that contain a heterologous polynucleotide encoding, for example, a polypeptide having cytosine deaminase or mutant thereof; a polypeptide having thymidine kinase activity or mutants thereof;

other prodrug activating genes; an microRNA, shRNA or siRNA; a cytokine; an antibody binding domain or combinations thereof that can be delivered to a cell or subject. In addition, to retroviral vectors other viral vector that can be used in the compositions and methods of the disclosure and which can be engineered to contain a core- or mini-prmoter cassette include adenoviral vectors, a measles vectors, a herpes vectors, a retroviral vectors (including a lentiviral vector), a rhabdoviral vectors such as a Vesicular Stomatitis viral vectors, a reovirus vectors, a Seneca Valley Virus vectors, a poxvirus vectors (including animal pox or vaccinia derived vectors), a parvovirus vectors (including an AAV vectors), an alphavirus vectors or other viral vector known to one skilled in the art (see also, *e.g.*, *Concepts in Genetic Medicine*, ed. Boro Dropulic and Barrie Carter, Wiley, 2008, Hoboken, NJ.; *The Development of Human Gene Therapy*, ed. Theodore Friedmann, Cold Springs Harbor Laboratory Press, Cold springs Harbor, New York, 1999; *Gene and Cell Therapy*, ed. Nancy Smyth Templeton, Marcel Dekker Inc., New York, New York, 2000; *Gene Therapy: Therapeutic Mechanism and Strategies*, ed. Nancy Smyth Templetone and Danilo D Lasic, Marcel Dekker, Inc., New York, New York, 2004; *Gene and Cell Therapy: Therapeutic Mechanisms and Strategies*, Third Edition, ed. Nancy Smyth Templeton, CRC Press, 2008); the disclosures of which are incorporated herein by reference).

[0059] As desecribed herein the disclosure provides modified retroviral vectors. The modified retroviral vectors can be derived from members of the retroviridae family. Retroviruses have been classified in various ways, but the nomenclature has been standardized in the last couple of decades (see ICTVdB - The Universal Virus Database, 2012 release, on the World Wide Web (www) at ncbi.nlm.nih.gov/ICTVdb/ICTVdB/ and the text book "Retroviruses" Eds Coffin, Hughs and Varmus, Cold Spring Harbor Press 1997; the disclosures of which are incorporated herein by reference). In one embodiment, the retroviral replicating vector can comprise an Orthoretrovirus or more typically a gamma retrovirus vector.

[0060] In many situations for using a retroviral replicating vector therapeutically, it is advantageous to have high levels of expression of the transgene that is encoded by the retroviral

replicating vector. For example, with a prodrug activating gene such as the cytosine deaminase gene it is advantageous to have higher levels of expression of the CD protein in a cell so that the conversion of the prodrug 5-FC to 5-FU is more efficient. Similarly high levels of expression of siRNA or shRNA lead to more efficient suppression of target gene expression. Also for cytokines or single chain antibodies (scAbs) or binding portion of an antibody it is usually advantageous to express high levels of the cytokine or scAb. In addition, in the case that there are mutations in some copies of the vector that inactivate or impair the activity of the vector or transgene, it is advantageous to have multiple copies of the vector in the target cell as this provides a high probability of efficient expression of the intact transgene. The disclosure provides recombinant replication competent retroviruses capable of infecting a target cell or target cell population multiple times resulting in an average number of copies/diploid genome of 3 or greater. The disclosure also provides methods of testing for this property. Also provided are methods of treating a cell proliferative disorder, using a retroviral replicating vector capable of infecting a target cell or target cell population multiple times resulting in an average number of copies/diploid genome of 5 or greater.

[0061] In one embodiment, the disclosure provides a recombinant retrovirus capable of infecting a non-dividing call, a dividing cell, or a cell having a cell proliferative disorder. The recombinant replication competent retrovirus of the disclosure comprises a polynucleotide sequence encoding a viral GAG, a viral POL, a viral ENV, a therapeutic cassette comprising at least one heterologous polynucleotide preceded by a core- or mini-promoter, encapsulated within a virion.

[0062] The phrase "non-dividing" cell refers to a cell that does not go through mitosis. Non-dividing cells may be blocked at any point in the cell cycle, (*e.g.*, G_0/G_1, $G_{1/S}$, $G_{2/M}$), as long as the cell is not actively dividing. For dividing cells ortho- or gamma-retroviral vectors can be used.

[0063] By "dividing" cell is meant a cell that undergoes active mitosis, or meiosis. Such dividing cells include stem cells, skin

cells (*e.g.*, fibroblasts and keratinocytes), gametes, and other dividing cells known in the art. Of particular interest and encompassed by the term dividing cell are cells having cell proliferative disorders, such as neoplastic cells. The term "cell proliferative disorder" refers to a condition characterized by an abnormal number of cells. The condition can include both hypertrophic (the continual multiplication of cells resulting in an overgrowth of a cell population within a tissue) and hypotrophic (a lack or deficiency of cells within a tissue) cell growth or an excessive influx or migration of cells into an area of a body. The cell populations are not necessarily transformed, tumorigenic or malignant cells, but can include normal cells as well. Cell proliferative disorders include disorders associated with an overgrowth of connective tissues, such as various fibrotic conditions, including scleroderma, arthritis and liver cirrhosis. Cell proliferative disorders include neoplastic disorders such as head and neck carcinomas, squamous cell cancer, malignant melanoma, sinonasal undifferentiated carcinoma (SNUC), brain (including glioblastomas), blood neoplasia, carcinoma's of the regional lymph nodes, lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer lymphoma, oral cancer, pancreatic cancer, leukemia, melanoma, stomach cancer, skin cancer and ovarian cancer (see, *e.g.*, DeVita, Hellman, and Rosenberg's Cancer: Principles and Practice of Oncology 9th edition 2011 Wolters Kluwer/Lippincott Williams & Williams for descriptions of these various neoplasia and their current treatments). The cell proliferative disease also includes rheumatoid arthritis (O'Dell NEJM 350:2591 2004)and other auto-immune disorders (Mackay *et al* NEJM 345:340 2001) that are often characterized by inappropriate proliferation of cells of the immune system.

[0064] As described herein, the vector of the disclosure (*e.g.*, an RRV vector) comprises a core- and/or mini-promoter cassette operably linked to a heterologous nucleic acid sequence. As mentioned above, there may be more than one mini-promoter cassettes in a vector of the disclosure. As used herein, the term "heterologous" nucleic acid sequence or transgene refers to (i) a sequence that does not normally exist in a wild-type retrovirus,

(ii) a sequence that originates from a foreign species, or (iii) if from the same species, it may be substantially modified from its original form. Alternatively, an unchanged nucleic acid sequence that is not normally expressed in a cell is a heterologous nucleic acid sequence.

[0065] Depending upon the intended use of the vector of the disclosure, any number of heterologous polynucleotide or nucleic acid sequences may be inserted into the retroviral vector. Additional polynucleotide sequences encoding any desired polypeptide sequence may also be inserted into the vector of the disclosure. Where *in vivo* delivery of a heterologous nucleic acid sequence is sought both therapeutic and non-therapeutic sequences may be used. For example, the heterologous sequence can encode a therapeutic molecule including an inhibitory nucleic acid molecule (microRNA, shRNA siRNA) or ribozymes directed to a particular gene associated with a cell proliferative disorder or other gene-associated disease or disorder; the heterologous sequence can be a suicide gene (*e.g.*, HSV-tk or PNP or cytosine deaminase; either modified or unmodified), a growth factor or a therapeutic protein (*e.g.*, Factor IX, IL2, GMCSF and the like) and any combination thereof. Other therapeutic proteins or coding sequences applicable to the disclosure are easily identified in the art.

[0066] In one embodiment, the heterologous polynucleotide within the vector comprises a cytosine deaminase that has been optimized for expression in a human cell (see, *e.g.*, SEQ ID NO:3 and 5). In a further embodiment, the cytosine deaminase comprises a sequence that has been human codon optimized and comprises mutations that increase the cytosine deaminase's stability (*e.g.*, reduced degradation or increased thermo-stability) compared to a wild-type cytosine deaminase (see, *e.g.*, SEQ ID NO:3). In yet another embodiment, the heterologous polynucleotide encodes a fusion construct comprising a cytosine deaminase (either human codon optimized or non-optimized, either mutated or non-mutated) operably linked to a polynucleotide encoding a polypeptide having UPRT or OPRT activity. In another embodiment, the heterologous polynucleotide comprises a CD polynucleotide of the disclosure (*e.g.*, SEQ ID NO:3, 5, 11, 13, 15, or 17). In yet another

embodiment, the heterologous polynucleotide is a human codon optimized sequence encoding a polypeptide having thymidine kinase activity (see, *e.g.*, SEQ ID NO:75).

[0067] In another embodiment, a vector of the disclosure (*e.g.*, an RRV) can comprise a heterologous polynucleotide encoding a polypeptide comprising a cytosine deaminase activity and may further comprise a polynucleotide comprising a microRNA or siRNA molecule either as part of the primary transcript from the viral promoter or linked to a promoter, which can be cell-type or tissue specific.

[0068] In another embodiment, the disclosure provides a recombinant retroviral replicating vector that contains a heterologous polynucleotide sequence of the human primary precursor miR-128-2 (SEQ ID NO:32) downstream of the *env* gene. miRNAs that are down-regulated in cancers can be incorporated into the vector for therapeutic gene delivery. For example, let-7, miR-26, miR-124, miR181, MiR181d and miR-137 (Esquela-Kerscher *et al.*, 2008 *Cell Cycle* 7, 759-764; Kumar *et al.*, 2008 *Proc Natl Acad Sci USA* 105, 3903-3908; Kota *et al.*, 2009 *Cell* 137, 1005-1017; Silber *et al.*, 2008 *BMC Medicine* 6:14 1-17).

[0069] The replicating retroviral vectors of the disclosure can be used to treat disease by expressing engineered siRNA, shRNA or miRNA (Dennis, Nature, 418: 122 2002) that switches off or lowers expression of key genes that govern the proliferation or survival of diseased cells including tumor cells. Such targets include genes like Rad 51 a central enzyme in DNA repair, and without which cell growth is drastically restricted. Other targets include many of the signaling pathway molecules that control cell growth (Marquez & McCaffrey Hum Gene Ther. 19:27 2008) or inhibit viral replication (WE Johnson Current Topics in Microbiology and Immunology 371: 123-151, 2013) such as APOBEC3G or tetherin. The siRNA or miRNA may be combined with expression of a cytotoxic gene from the same or different retroviral vector of the disclosure. An example of a suitable cytotoxic gene comprises a cytosine deaminase or modified cytosine deaminase of the disclosure. Examples of siRNA or miRNA that can be expressed from the same vector or a different vector with cytosine deaminase are siRNAs or miRNAs that target

thymidilate synthase, dihydropyrimidine dehydrogenase or other nucleic acid anabolic or synthetic enzymes, that can enhance or complement the action of 5-FU produced locally in a tumor or tissue from 5-FC activation by cytosine deaminase. In such instances, the RRV will comprise a therapeutic cassette having a core- or mini-promoter operably linked to a sequence encoding a polypeptide with CD activity and further includes a polIII promoter cassette operably linked to a sequence the encodes an miRNA.

[0070] In use, the retroviral vector(s) will replicate through the tumor or other target tissue and before growth inhibition occurs the virus first integrates into the host genome and continues to make virus after growth of that cell is inhibited. Methods for selecting functional miRNA or siRNA sequences are known in the art. A retroviral vector of this disclosure can be made using cells from other species for which the corresponding protein is not significantly targeted. Such cells include dog cell lines or chicken cell line. Alternatively the virus is made by transient transfection on human 293 derived cells or other cell line that allows efficient transient transfection. For this use the siRNA or miRNA sequence can simply be inserted at a convenient site on the viral genome. This site includes the region downstream of the envelope and upstream of the 3'LTR of the replicating retrovirus. Alternatively, polIII transcription units can be inserted in the viral genome with the appropriate siRNA or miRNA, typically downstream of the 3' envelope gene. In one embodiment, the transcription direction will be the same as that of the retroviral replicating vector. Several different siRNA or miRNA sequences can be inserted to ensure efficient down regulation of the target gene or down regulation of more than one gene. Suitable sequences and targets can be obtained from commercial and academic sources known to those skilled in the art (*e.g.*, the MIT/ICBP siRNA Database http:(//)web.mit.edu/sirna/; http:(//)katahdin.cshl.org:9331/ RNAi_web/ scripts/main2.pl RNAi resources, including siRNA and shRNA design tools. (Hannon Lab, Cold Spring Harbor Laboratory); http:(//)www.rnaiweb.com/ General resource; http:(//)genomics.jp/ sidirect/; http:(//)[www].rnainterference.org/; http:(//)bioinfo.

wistar.upenn.edu/siRNA /siRNA.htm; http:(//)www(.)ambion.com/ techlib/misc/ siRNA_finder.html (Ambion)).

[0071] The miRNA target can be inserted 3′ to the transgene but before the 3′LTR or upstream of the mini-promoter in the therapeutic cassette but after the 3′ end of the envelope. In general the target would not be inserted into protein coding sequences.

[0072] In yet further embodiments, the heterologous polynucleotide may comprise a cytokine such as an interleukin, interferon gamma or the like. Cytokines that may expressed from a retroviral vector of the disclosure include, but are not limited to, IL-1alpha, IL-1beta, IL-2 (SEQ ID NO:38), IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21, anti-CD40, CD40L, IFN-gamma (SEQ ID NO:36, 37, 38) and TNF-alpha, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), OPG, and neutrokine-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-IBB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153. Angiogenic proteins may be useful in some embodiments, particularly for protein production from cell lines. Such angiogenic factors include, but are not limited to, Glioma Derived Growth Factor (GDGF), Platelet Derived Growth Factor-A (PDGF-A), Platelet Derived Growth Factor-B (PDGF-B), Placental Growth Factor (PIGF), Placental Growth Factor-2 (PIGF-2), Vascular Endothelial Growth Factor (VEGF), Vascular Endothelial Growth Factor-A (VEGF-A), Vascular Endothelial Growth Factor-2 (VEGF-2), Vascular Endothelial Growth Factor B (VEGF-3),

Vascular Endothelial Growth Factor B-1 86 (VEGF-B186), Vascular Endothelial Growth Factor-D (VEGF-D), Vascular Endothelial Growth Factor-D (VEGF-D), and Vascular Endothelial Growth Factor-E (VEGF-E). Fibroblast Growth Factors may be delivered by a vector of the disclosure and include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15. Hematopoietic growth factors may be delivered using vectors of the disclosure, such growth factors include, but are not limited to, granulocyte macrophage colony stimulating factor (GM-CSF) (sargramostim), granulocyte colony stimulating factor (G-CSF) (filgrastim), macrophage colony stimulating factor (M-CSF, CSF-1) erythropoietin (epoetin alfa), stem cell factor (SCF, c-kit ligand, steel factor), megakaryocyte colony stimulating factor, PIXY321 (a GMCSF/IL-3) fusion protein and the like.

[0073] The methods and compositions of the disclosure are useful in combination therapies including therapies with other approved drugs or biologics such as Avastin, Herceptin or various HDAC inhibitors.

[0074] The disclosure provides methods for treating cell proliferative disorders such as cancer and neoplasms comprising administering an RRV vector of the disclosure followed by treatment with a chemotherapeutic agent or anti-cancer agent. In one aspect, the RRV vector is administered to a subject for a period of time prior to administration of the chemotherapeutic or anti-cancer agent that allows the RRV to infect and replicate. The subject is then treated with a chemotherapeutic agent or anti-cancer agent for a period of time and dosage to reduce proliferation or kill the cancer cells. In one aspect, if the treatment with the chemotherapeutic or anti-cancer agent reduces, but does not kill the cancer/tumor (*e.g.*, partial remission or temporary remission), the subject may then be treated with a benign therapeutic agent (*e.g.*, 5-FC) that is converted to a toxic therapeutic agent in cells expression a cytotoxic gene (*e.g.*, cytosine deaminase) from the RRV.

[0075] Using such methods the RRVs of the disclosure are spread during a replication process of the tumor cells, such cells can

then be killed by treatment with an anti-cancer or chemotherapeutic agent and further killing can occur using the RVV treatment process described herein.

[0076] In yet another embodiment of the disclosure, the heterologous gene can comprise a coding sequence for a target antigen (*e.g.*, a cancer antigen). In this embodiment, cells comprising a cell proliferative disorder are infected with an RRV comprising a heterologous polynucleotide encoding the target antigen to provide expression of the target antigen (*e.g.*, overexpression of a cancer antigen). An anticancer agent comprising a targeting cognate moiety that specifically interacts with the target antigen is then administered to the subject. The targeting cognate moiety can be operably linked to a cytotoxic agent or can itself be an anticancer agent. Thus, a cancer cell infected by the RRV comprising the targeting antigen coding sequences increases the expression of target on the cancer cell resulting in increased efficiency/efficacy of cytotoxic targeting.

[0077] Blocking of interactions between cells of the immune system has been shown to have significant immunological effects, either activating or suppressing (Waldmann Annu Rev Med. 57:65 2006; Callahan & Wolchok J Leukoc Biol. 2013 Jul;94(1):41-53. doi: 10.1189/jlb.1212631). Systemic administration of these types of molecules can have undesirable global effects which can at a minimum lead to deleterious side -effects or even death in the case of one CD28 agonist (Suntharalingam *et al.* NEJM 355 1018 2006). Pfizer has been developing one such anti-CTLA-4 blockading antibody (CP-675,206) as an anticancer reagent but has recently stopped development because of significant side effects. Bristol Meyers Squibb has an approved product Yervoy for late stage melanoma which is a CTLA-4 blocking monoclonal antibody, but this is acknowledged to cause significant toxicity. Local delivery of blockading molecules that are released into the local environment, from the tumor after infection with a replication competent vector encoding such molecules that are released into the extracellular space, provides the immune modulation locally and can avoid these serious side effects. The blockading molecules are antibodies, single chain antibodies, soluble versions of the natural ligand or other

peptides that bind such receptors. The blocking targets are various surface molecules that include molecules involved in accessory immune interactions other than CTLA-4, but know to those skilled in the art. Further information on the use of such strategies with RRV with smaller single genes is available in WO2010/036986, WO2010/045002, WO2011/126864 and WO2012/058673 (which are incorporated here by reference) and are similar for the vectors of this disclosure.

[0078] Thus, the disclosure includes various pharmaceutical compositions useful for treating a cell proliferative disorder. The pharmaceutical compositions according to the disclosure are prepared by bringing a retroviral vector containing a heterologous polynucleotide sequence useful in treating or modulating a cell proliferative disorder according to the disclosure into a form suitable for administration to a subject using carriers, excipients and additives or auxiliaries. Further information on the use of such strategies with RRV with smaller single genes is available in WO2010/036986, WO2010/045002, WO2011/126864 and WO2012/058673 and are similar for the vectors of this disclosure.

[0079] For example, and not by way of limitation, a retroviral vector useful in treating a cell proliferative disorder will include an amphotropic ENV protein, GAG, and POL proteins, a promoter sequence in the U3 region retroviral genome, and all cis-acting sequence necessary for replication, packaging and integration of the retroviral genome into the target cell.

[0080] As mentioned above and elsewhere herein, a vector of the disclosure can comprise a core- and/or mini-promoter cassette and can further includes an IRES cassette. An internal ribosome entry sites ("IRES"", Pelletier *et al.*, 1988, Mol. Cell. Biol., 8, 1103-1112; Jang *et al.*, J. Virol., 1988, 62, 2636-2643) refers to a segment of nucleic acid that promotes the entry or retention of a ribosome during translation of a coding sequence usually 3′ to the IRES. In some embodiments the IRES may comprise a splice acceptor/donor site, however, preferred IRESs lack a splice acceptor/donor site. The disclosure contemplates that the therapeutic cassette can comprise a mini-promoter followed further 3′ to the promoter by an IRES.

[0081] Additionally, an RRV of the disclosure comprises a promoter region at the 5' end of the retroviral polynucleotide sequence. The term "promoter region" is used herein in its ordinary sense to refer to a nucleotide region comprising a DNA regulatory sequence, wherein the regulatory sequence is derived from a gene which is capable of binding RNA polymerase and initiating transcription of a downstream (3'-direction) coding sequence. The regulatory sequence may be homologous or heterologous to the desired gene sequence. For example, a wide range of promoters may be utilized, including viral or mammalian promoter as described above. Further information on the use of such strategies with RRV with smaller single genes is available in WO2010/036986, WO2010/045002, WO2011/126864 and WO2012/058673 and are similar for the vectors of this disclosure.

[0082] In one embodiment, the retroviral genome of the disclosure contains mini-promoter comprising a cloning site downstream of the mini-promoter for insertion of a desired/heterologous polynucleotide in operaly frame to effectuate expression of the heterologous polynucleotide. In one embodiment, at least one mini-promoter is located 3' to the *env* gene in the retroviral vector, but 5' to the desired heterologous polynucleotide. Accordingly, a heterologous polynucleotide encoding a desired polypeptide may be operably linked to the mini-promoter.

[0083] In one embodiment, a recombinant retrovirus of the disclosure is genetically modified in such a way that the virus is targeted to a particular cell type (*e.g.*, smooth muscle cells, hepatic cells, renal cells, fibroblasts, keratinocytes, mesenchymal stem cells, bone marrow cells, chondrocyte, epithelial cells, intestinal cells, mammary cells, neoplastic cells, glioma cells, neuronal cells and others known in the art) such that the recombinant genome of the retroviral vector is delivered to a target non-dividing, a target dividing cell, or a target cell having a cell proliferative disorder.

[0084] In a further related embodiment, the targeting of the vector is achieved using a chimeric env protein comprising a retroviral ENV protein operably linked to a targeting polypeptide. The targeting polypeptide can be a cell specific receptor molecule,

a ligand for a cell specific receptor, an antibody or antibody fragment to a cell specific antigenic epitope or any other ligand easily identified in the art which is capable of binding or interacting with a target cell. Examples of targeting polypeptides or molecules include bivalent antibodies using biotin-streptavidin as linkers (Etienne-Julan *et al.*, J. Of General Virol., 73, 3251-3255, 1992; Roux *et al.*, Proc. Natl. Acad. Sci USA 86, 9079-9083, 1989), recombinant virus containing in its envelope a sequence encoding a single-chain antibody variable region against a hapten (Russell *et al.*, Nucleic Acids Research, 21, 1081-1085 (1993)), cloning of peptide hormone ligands into the retrovirus envelope (Kasahara *et al.*, Science, 266, 1373-1376, 1994; Krueger & Albritton, J. Virol., 87:5916-5925, 2013), chimeric EPO/env constructs (Kasahara *et al.*, 1994), single-chain antibody against the low density lipoprotein (LDL) receptor in the ecotropic MLV envelope, resulting in specific infection of HeLa cells expressing LDL receptor (Somia *et al.*, Proc. Natl. Acad. Sci USA, 92, 7570-7574 (1995)), similarly the host range of ALV can be altered by incorporation of an integrin ligand, enabling the virus to now cross species to specifically infect rat glioblastoma cells (Valsesia-Wittmann *et al.*, J. Virol. 68, 4609-4619 (1994)), and Dornberg and co-workers (Chu and Dornburg, J. Virol 69, 2659-2663 (1995); M. Engelstadter *et al.*Gene Therapy 8,1202-1206 (2001)) have reported tissue-specific targeting of spleen necrosis virus (SNV), an avian retrovirus, using envelopes containing single-chain antibodies directed against tumor markers.

[0085] In a further related embodiment, the disclosure provides retroviral vectors that are targeted using regulatory sequences. Cell- or tissue-specific regulatory sequences (*e.g.*, promoters) can be utilized to target expression of gene sequences in specific cell populations. Suitable mammalian and viral promoters for the disclosure are described elsewhere herein. Accordingly, in one embodiment, the disclosure provides a retrovirus having tissue-specific promoter elements at the 5' end of the retroviral genome. Typically, the tissue-specific regulatory elements/sequences are in the U3 region of the LTR of the retroviral genome, including for example cell- or tissue-specific promoters and enhancers to

neoplastic cells (*e.g.*, tumor cell-specific enhancers and promoters), and inducible promoters (*e.g.*, tetracycline).

[0086] Transcription control sequences of the disclosure can also include naturally occurring transcription control sequences naturally associated with a gene encoding a superantigen, a cytokine or a chemokine.

[0087] In addition different viral promoters with varying strengths of activity may be utilized depending on the level of expression desired. In mammalian cells, the CMV immediate early promoter if often used to provide strong transcriptional activation. Modified versions of the CMV promoter that are less potent have also been used when reduced levels of expression of the transgene are desired. When expression of a transgene in hematopoietic cells is desired, retroviral promoters such as the LTRs from MLV or MMTV can be used. Other viral promoters that can be used include SV40, RSV LTR, HIV-1 and HIV-2 LTR, adenovirus promoters such as from the E1A, E2A, or MLP region, AAV ITR, cauliflower mosaic virus, HSV-TK, and avian sarcoma virus.

[0088] Similarly tissue specific or selective promoters may be used to effect transcription in specific tissues or cells so as to reduce potential toxicity or undesirable effects to non-targeted tissues. For example, promoters such as the PSA, probasin, prostatic acid phosphatase or prostate-specific glandular kallikrein (hK2) may be used to target gene expression in the prostate. The Whey accessory protein (WAP) may be used for breast tissue expression (Andres *et al.*, PNAS 84:1299-1303, 1987).

[0089] "Tissue-specific regulatory elements" are regulatory elements (*e.g.*, promoters) that are capable of driving transcription of a gene in one tissue while remaining largely "silent" in other tissue types. It will be understood, however, that tissue-specific promoters may have a detectable amount of "background" or "base" activity in those tissues where they are silent. The degree to which a promoter is selectively activated in a target tissue can be expressed as a selectivity ratio (activity in a target tissue/activity in a control tissue). In this regard, a tissue specific promoter useful in the practice of the disclosure

typically has a selectivity ratio of greater than about 5. Preferably, the selectivity ratio is greater than about 15.

[0090] In certain indications, it may be desirable to activate transcription at specific times after administration of the recombinant retroviral replicating vector of the disclosure (RRV). This may be done with promoters that are hormone or cytokine regulatable. For example in therapeutic applications where the indication is a gonadal tissue where specific steroids are produced or routed to, use of androgen or estrogen regulated promoters may be advantageous. Such promoters that are hormone regulatable include MMTV, MT-1, ecdysone and RuBisco. Other hormone regulated promoters such as those responsive to thyroid, pituitary and adrenal hormones may be used. Further information on the use of controlled or tissue-specific promoter strategies with RRV with smaller single genes is available in WO2010/036986, WO2010/045002, WO2011/126864 and WO2012/058673 and are similar for the vectors of this disclosure.

[0091] In addition, this list of promoters should not be construed to be exhaustive or limiting, those of skill in the art will know of other promoters that may be used in conjunction with the promoters and methods disclosed herein.

[0092] It will be further understood that certain promoters, while not restricted in activity to a single tissue type, may nevertheless show selectivity in that they may be active in one group of tissues, and less active or silent in another group. Such promoters are also termed "tissue specific", and are contemplated for use with the disclosure. For example, promoters that are active in a variety of central nervous system (CNS) neurons may be therapeutically useful in protecting against damage due to stroke, which may affect any of a number of different regions of the brain. Accordingly, the tissue-specific regulatory elements used in the disclosure, have applicability to regulation of the heterologous proteins as well as a applicability as a targeting polynucleotide sequence in the present retroviral vectors.

[0093] The retroviral vectors and methods of the disclosure provide a replication competent retrovirus that does not require helper virus or additional nucleic acid sequence or proteins in

order to propagate and produce virion. For example, the nucleic acid sequences of the retrovirus of the disclosure encode a group specific antigen and reverse transcriptase, (and integrase and protease-enzymes necessary for maturation and reverse transcription), respectively, as discussed above. The viral gag and pol can be derived from a lentivirus, such as HIV or an oncovirus or gammaretrovirus such as MoMLV. In addition, the nucleic acid genome of the retrovirus of the disclosure includes a sequence encoding a viral envelope (ENV) protein. The env gene can be derived from any retroviruses or other virus. The env may be an amphotropic envelope protein which allows transduction of cells of human and other species, or may be an ecotropic envelope protein, which is able to transduce only mouse and rat cells. In one embodiment, the *env* gene is derived from a non-retrovirus (*e.g.*, CMV or VSV). Examples of retroviral-derived env genes include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), gibbon ape leukemia virus (GaLV), human immunodeficiency virus (HIV) and Rous Sarcoma Virus (RSV). Other env genes such as Vesicular stomatitis virus (VSV) (Protein G), cytomegalovirus envelope (CMV), or influenza virus hemagglutinin (HA) can also be used.

[0094] In one embodiment, the retroviral genome is derived from an onco-retrovirus, and more particularly a mammalian onco-retrovirus. In a further embodiment, the retroviral genome is derived from a gamma retrovirus, and more particularly a mammalian gamma retrovirus. By "derived" is meant that the parent polynucleotide sequence is a wild-type oncovirus which has been modified by insertion or removal of naturally occurring sequences (*e.g.*, insertion of mini-promoter, insertion of a heterologous polynucleotide encoding a polypeptide or inhibitory nucleic acid of interest, swapping of a more effective promoter from a different retrovirus or virus in place of the wild-type promoter and the like).

[0095] Unlike recombinant retroviruses produced by standard methods in the art that are defective and require assistance in

order to produce infectious vector particles, the disclosure provides a retrovirus that is replication-competent.

[0096] In yet another embodiment, the disclosure provides plasmids comprising a recombinant retroviral derived construct. The plasmid can be directly introduced into a target cell or a cell culture such as NIH 3T3 or other tissue culture cells. The resulting cells release the retroviral vector into the culture medium.

[0097] In other embodiments, host cells transfected with a retroviral replicating vector of the disclosure are provided. Host cells include eukaryotic cells such as yeast cells, insect cells, or animal cells. Host cells also include prokaryotic cells such as bacterial cells.

[0098] Also provided are engineered host cells that are transduced (transformed or transfected) with a vector provided herein (*e.g.*, a retroviral replicating vector). The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying a coding polynucleotide. Culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, *e.g.*, Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique, 3rd ed. (Wiley-Liss, New York) and stem cells of various kinds (world wide web at stembook.org) and the references cited therein. Such host cells can also be used for delivery of RRV by administering the infected cells to an animal or subject (*e.g.*, a patient).

[0099] Examples of appropriate expression hosts include: bacterial cells, such as *E. coli*, *B. subtilis*, *Streptomyces*, and *Salmonella typhimurium*; fungal cells, such as *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Neurospora crassa*; insect cells such as Drosophila and *Spodoptera frugiperda*; mammalian cells such as CHO, COS, BHK, HEK 293 br Bowes melanoma; or plant cells or explants, *etc.* Typically human cells or cell lines will be used; however, it may be desirable to clone vectors and polynucleotides

of the disclosure into non-human host cells for purposes of sequencing, amplification and cloning.

[00100] The disclosure provides a polynucleotide construct comprising from 5′ to 3′: a promoter or regulatory region useful for initiating transcription; a *psi* packaging signal; a *gag* encoding nucleic acid sequence, a *pol* encoding nucleic acid sequence; an env encoding nucleic acid sequence; a therapeutic cassette comprising (a) a core-promoter and at least one addition promoter, each operably linked to a therapeutic polynucleotide sequence or (b) at least one mini-promoter operably linked to a heterologous polynucleotide encoding a marker, therapeutic or diagnostic polypeptide; and a LTR nucleic acid sequence. As described elsewhere herein the various segment of the polynucleotide construct of the disclosure (*e.g.*, a recombinant replication competent retroviral polynucleotide) are engineered depending in part upon the desired host cell, expression timing or amount, and the heterologous polynucleotide. A replication competent retroviral construct of the disclosure can be divided up into a number of domains that may be individually modified by those of skill in the art.

[00101] For example, the viral promoter can comprise a CMV promoter having a sequence as set forth in SEQ ID NO:19, 20 or 22 from nucleotide 1 to about nucleotide 582 and may include modification to one or more (*e.g.*, 2-5, 5-10, 10-20, 20-30, 30-50, 50-100 or more nucleic acid bases) so long as the modified promoter is capable of directing and initiating transcription. In one embodiment, the promoter or regulatory region comprises a CMV-R-U5 domain polynucleotide. The CMV-R-U5 domain comprises the immediately early promoter from human cytomegalovirus to the MLV R-U5 region. In one embodiment, the CMV-R-U5 domain polynucleotide comprises a sequence as set forth in SEQ ID NO:19, 20 or 22 from about nucleotide 1 to about nucleotide 1202 or sequences that are at least 95% identical to a sequence as set forth in SEQ ID NO:19, 20, or 22 wherein the polynucleotide promotes transcription of a nucleic acid molecule operably linked thereto. The *gag* domain of the polynucleotide may be derived from any number of retroviruses, but will typically be derived from an oncoretrovirus and more

particularly from a mammalian oncoretrovirus. In one embodiment the *gag* domain comprises a sequence from about nucleotide number 1203 to about nucleotide 2819 or a sequence having at least 95%, 98%, 99% or 99.8% (rounded to the nearest 10th) identity thereto. The *pol* domain of the polynucleotide may be derived from any number of retroviruses, but will typically be derived from an oncoretrovirus and more particularly from a mammalian oncoretrovirus. In one embodiment the pol domain comprises a sequence from about nucleotide number 2820 to about nucleotide 6358 or a sequence having at least 95%, 98%, 99% or 99.9% (rounded to the nearest 10th) identity thereto. The *env* domain of the polynucleotide may be derived from any number of retroviruses, but will typically be derived from an oncoretrovirus or gamma-retrovirus and more particularly from a mammalian oncoretrovirus or gamma-retrovirus. In some embodiments the *env* coding domain comprises an amphotropic *env* domain. In one embodiment the *env* domain comprises a sequence from about nucleotide number 6359 to about nucleotide 8323 or a sequence having at least 95%, 98%, 99% or 99.8% (roundest to the nearest 10th) identity thereto. 3' to the env termination codon is a therapeutic cassette comprising at least one core-promoter cassette and/or a mini-promoter cassette and may further include a polIII promoter cassette and/or an IRES cassette, each operably linked to heterologous domain (*e.g.*, a sequence encoding a therapeutic molecule such as a polyeptpdie having cytosine deaminase or thymidine kinase activity). The heterologous domain can comprise a cytosine deaminase or thymidine kinase of the disclosure. In one embodiment, the CD polynucleotide comprises a human codon optimized sequence. In yet another embodiment, the CD polynucleotide encodes a mutant polypeptide having cytosine deaminase, wherein the mutations confer increased thermal stabilization that increase the melting temperature (Tm) by 10^{o}C allowing sustained kinetic activity over a broader temperature range and increased accumulated levels of protein. In another embodiment, the heterologous domain is a human codon optimized sequence comprising SEQ ID NO:75 and encoding a polypeptide having thymidine kinase activity.

[00102] The disclosure also provides a recombinant retroviral vector comprising from 5′ to 3′ a CMV-R-U5, fusion of the immediate early promoter from human cytomegalovirus to the MLV R-U5 region; a PBS, primer binding site for reverse transcriptase; a 5′ splice site; a ψ packaging signal; a gag, ORF for MLV group specific antigen; a pol, ORF for MLV polymerase polyprotein; a 3′ splice site; a 4070A env, ORF for envelope protein of MLV strain 4070A; a therapeutic cassette comprising at least one mini-promoter operably lined to a heterologous polynucleotide encoding a therapeutic molecule (*e.g.*, a modified cytosine deaminase (thermostabilized and codon optimized)); a PPT, polypurine tract; and a U3-R-U5, MLV long terminal repeat.

[00103] In addition, the therapeutic methods (*e.g.*, the gene therapy or gene delivery methods) as described herein can be performed *in vivo* or *ex vivo*. It may be preferable to remove the majority of a tumor prior to gene therapy, for example surgically or by radiation. In some aspects, the retroviral therapy may be preceded or followed by surgery, chemotherapy or radiation therapy. In some embodiments, steroids are co-administered with the vector (before, during or immediately after).

[00104] The following Examples are intended to illustrate, but not to limit the disclosure. While such Examples are typical of those that might be used, other procedures known to those skilled in the art may alternatively be utilized.

EXAMPLES

Example 1: Vector stability of emd.GFP and tk genes

[00105] Early passage of a human glioma cell line U87-MG was cultured in complete culture medium. Naïve cells were seeded at 2e5 cell per well in 6-well plates the day prior to infection. Vector from different plasmids was prepared by transient transfection on 293T cells and the supernatant is collected. Titers are measured as described (WO2010036986, Perez *et al.*, Mol. Ther., 2012) typically around 10^6 TU/ml. pAZ based vectors are similar to pAC3 based vectors, but the starting plasmid has an LTR promoter driving the whole viral RNA transcript rather than the hybrid CMV-LTR promoter (Figure 8. Subsequently the viral particles from both types of plasmid have complete MLV LTRs at both the 5′ and 3′ ends

of the genome. The first cycle of infection is performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells is used for infecting naïve cells. In each infection cycle, infected cells are passaged at d4 post infection into 6-well plates. Viral supernatant from infected cells at d7 post infection is collected for subsequent infection, and cells are harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR are: IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3'(SEQ ID NO:54) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3' (SEQ ID NO:54). The A1 and S1 promoters in the vectors expressing emd (GFP), derived from pAZ.A1.emd and pAZ.S1.emd appear a little more stable than vector derived from pAZ.C1.emd, but experience has shown that vectors stable to passage 6 in this test are useful, appear stable and, when armed with the appropriate gene, are therapeutic in mouse tumor models (CR. Logg *et al.*, Hum Gene Ther 12:921-932, 2001; Logg & Kasahara in *Methods in Molecular Biology, vol. 246: Gene Delivery to Mammalian Cells: Vol. 2: Viral Gene Transfer Techniques pp499-525.* Edited by: W. C. Heiser © Humana Press Inc., Totowa, NJ). For human use, further stability is preferred (out to 8 - 12 passages). The stabilities of the pAZ.S1.sr39tk and pAZ.S1.tko derived vectors had increased stability (and hence utility). The sr39tk gene (M. Black *et al. Cancer Res* 2001;61:3022-3026) is a mutatated functionally optimized version of the Herpes Thymidine Kinase gene and the the tko gene is human codon optimized version of the sr39 gene.

Example 2: Construction and configuration of pAC3 based vectors containing C1 and S1 core promoter driving GFP expression

[00106] The retroviral replicating vectors, pAC3-C1.GFP and pAC3-S1.GFP, were derived from the backbone of pAC3-yCD2. The pAC3 backbone was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of C1.GFP and S1.GFP was isolated by endonuclease digestion of the pAZ-C1.GFP and pAZ.S1.GFP plasmid DNA, respectively, with Mlu I and Not I followed by insertion of the isolated DNA fragment to the corresponding restriction enzyme sites in the pAC3 backbone.

Example 3: Construction and configuration of pAC3 based vectors containing C1, S1 and S2 core promoter driving CD expression

[00107] The retroviral replicating vectors, pAC3-C1.yCD2 and pAC3-S1.yCD2, were derived from the backbone of pAC3-yCD2. The pAC3 backbone was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of C1.yCD2, S1.yCD2 and S2.yCD2 was synthesized with Mlu I and Not I restriction enzyme sites present at each end of the DNA fragment for subsequent cloning to the corresponding sites in the pAC3 backbone.

Example 4: Construction and configuration of pAC3 based vectors containing EMCV IRES and C1 or S1 core promoter driving hGMCSF and mGMCSF expression

[00108] The retroviral replicating vectors, pAC3-hGMCSF and pAC3.S1-hGMCSF, pAC3-mGMCSF and pAC3.S1-mGMCSF (see, *e.g.*, Figure 8), were derived from the backbone of pAC3-yCD2 vector (see, *e.g.*, U.S. Pat. Publ. No. 20110217267A1, incorporated herein by reference). For pAC3-hGMCSF and pAC3-mGMCSF vectors, the pAC3 backbone in the vector was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Psi I and Not I. The cDNA sequence of human and mouse GMCSF gene, respectively, were synthesized with the Psi I and Not I restriction enzyme sites at each end of the DNA fragment and subsequently cloned into the corresponding site in the pAC3 backbone. For pAC3.S1-hGMCSF and pAC3.S1-mGMCSF vectors, the pAC3 backbone in the vector was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of S1-hGMCSF and S1-mGMCSF, respectively, was synthesized with the Mlu I and Not I restriction enzyme sites at each end of the DNA fragment and subsequently cloned into the corresponding site in the pAC3 backbone.

Example 5: Vector stability and transgene expression of pAC3 based vectors containing C1 and S1 core promoter driving GFP expression

[00109] pAC3 based vectors with core promoters driving the expression of emerald GFP (pAC3-C1.emd and pAC3-S1.emd (emd a.k.a. GFP) were constructed as described and compared to pAC3.emd (aka pAC3-GFP, Perez *et al.*, Mol. Ther. 2012), which is the equivalent vector using an internal IRES to drive expression of the emd.GFP gene. Infectious vector was prepared by transient transfection as

before. Early passage of a human glioma cell line U87-MG was cultured in complete culture medium. Naïve cells were seeded at 2e5 cell per well in 6-well plates the day prior infection. The first cycle of infection was performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells was used for infecting naïve cells. In each infection cycle, infected cells were passaged at d4 post infection into 6-well plates. Viral supernatants from infected cells at d7 post infection were collected for subsequent infection, and cells were harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR were: IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3' (SEQ ID NO:54) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3' (SEQ ID NO:55).

[00110] As can be seen in Figure 2A the version of the vector with the C1 core promoter (pAC3-C1.emd) has equivalent stability to the IRES driven emd.GFP expression vector (pAC3-emd), whereas the version with the S1 (SCP1) core promoter (pAC3-S1.yCD2) is even more stable.

[00111] The level of GFP expression in three human glioblastoma cell lines (U87-MG, 1306-MG and T98G) infected with different vectors was examined by measuring the mean fluorescent intensity by flow cytometry using proper gating of GFP positive cells. Naïve cells were seeded at 2e5 cell per well in 6-well plates the day prior infection. Viral infection was performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. At d7 post infection, cells were harvested for flow cytometric analysis to measure the percentage of GFP positive cells and Mean Fluorescence Intensity (MFI). Figure 4A shows the results, demonstrating expression from all these vectors. The IRES dependent expression system showed about 5 fold higher levels of GFP expression in infected cells than the S1 promoter construct for all 3 different glioblastoma cell lines examined here, although absolute levels of expression also varied by a factor of about 5 over the three cell lines.

Example 6: Vector stability of pAC3-based vectors containing C1 and S1 core promoter driving CD expression and comparison to pACE-yCD2

[00112] pAC3 based vectors with core promoters driving the expression of CD (pAC3-C1.CD and pAC3-S1.CD) were constructed as described and corresponding infectious vector preparations were compared to vector from pAC3.yCD2 (O.D. Perez *et al.*, Mol. Ther., 2012). Early passage of a human glioma cell line U87-MG was cultured in complete culture medium. Naïve cells were seeded at 2E5 cell per well in 6-well plates the day prior infection. The first cycle of infection was performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells was used for infecting naïve cells. In each infection cycle, infected cells were passaged at d4 post infection into 6-well plates. Viral supernatant from infected cells at d7 post infection was collected for subsequent infection, and cells were harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR were: IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3' (SEQ ID NO:54) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3' (SEQ ID NO:55). The relative stabilities are shown in Figure 2B and show that the C1.yCD2 vector is less stable than the other two vectors which are roughly equivalent in stability, with the S1.yCD2 vector apparently slightly more stable than the IRES vector (pAC3-yCD2).

Example 7: Transgene expression of pAC3-based vectors containing C1 and S1 core promoter driving CD expression and comparison to pAC3-yCD2, after transfection into 293T cells

[00113] The level of CD expression from the vectors after transfection in 293T cells was detected by immunoblotting using an antibody against CD (Figure 4B). Naïve cells were seeded at 2E6 cell per 10-cm plates the day prior transfection. Transient transfection by calcium phosphate method was performed using plasmid DNA encoding the viral genome of each vector. At 40h post transfection, cells were harvested and lysed to obtain cell lysates. Protein concentration of cell lysates was determined to allow equal protein loading as indicated by GAPDH. Figure 4B shows the results demonstrating expression from all these vectors with the IRES system yielding about 15 fold higher levels of expression

than the S1 promoter construct. Figure 4C shows a Western blot of cell extracts from U87 cells fully transduced with vector derived from pAC3-yCD2 in both pAC3-C1.yCD2 and pAC3-S1.yCD2. While the CD protein band is easily detectable for pAC3-yCD2, there was insufficient CD protein from cells infected with pAC3-C1.yCD2 and pAC3-S1.yCD2 to be detected in this assay.

Example 8: Replication kinetics, vector stability and transgene expression of pAC3 based vectors containing the IRES or S1 core promoter driving human and mouse GM-CSF expression

[00114] The replication kinetics of pAC3-IRES.hGMCSF, pAC3-S1.hGMCSF and pAC3-emd were assessed in U87-MG by qRT-PCR. The replication kinetics of pAC3-IRES.mGMCSF, pAC3-S1.mGMCSF and pAC3-emd were assessed in EMT6 (a mouse breast cancer cell line). Naïve cells were seeded at 1E5 cells (U87-MG) or 5E4 cells (EMT6) in 6-well plate the day prior infection. Viral infection was performed at MOI 0.1 (U87-MG) or MOI 1 (EMT6) according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. Equal number of infected cells were seeded at each passage (every 2 days for U87-MG and 3-4 days for EMT6 cells) during the entire course of infection, and viral supernatant produced from infected cells at various time points is collected and stored in -80°C freezer. Samples of viral supernatant collected were processed to obtain viral RNA (Maxwell 16 LEV simplyRNA Cells Kit, Promega) followed by qRT-PCR. The number of viral RNA copies/ml at each time point is determined from a standard curve included in the qRT-PCR.

[00115] Results of the growth kinetics of the vectors are shown in Figure 5A and B, and demonstrate that the vectors all proliferate in target cells with similar kinetics to the archetypal pAC3-emd vector, in human and mouse cells.

[00116] Early passage of a human glioma cell line U87-MG was cultured in complete culture medium. Naïve cells were seeded at 2e5 cell per well in 6-well plates the day prior infection. A first cycle of infection with infectious viral vector from pAC3-hGMCSF, pAC3-S1.hGMCSF and pAC3-emd was performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells was used for infecting naïve

cells. In each infection cycle, infected cells were passaged at d4 post infection into 6-well plates. Viral supernatant from infected cells at d7 post infection was collected for subsequent infection, and cells were harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR are: IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3' (SEQ ID NO:54) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3' (SEQ ID NO:55). The stability profiles on serial passage are shown in Figure 3 and demonstrate that the vector with the S1 promoter is at least as stable as the IRES-hGMCSF vector, while for the mouse GMCSF the S1 vector is more stable than the IRES version.

[00117] pAC3 based vectors with a core promoter driving the expression of human and mouse GM-CSF (pAC3-S1.hGMCSF and pAC3-S1.mGMCSF) were constructed and compared to pAC3-IRES.hGMCSF and pAC3-IRES.mGMCSF, respectively. Vector preparations were made from the constructs by transient transfection as described. The vector transfected 293T cells were assayed for production of hGMCSF and mGMCSF and Figure 4D and G show that expression of these proteins is observed in transfected cells, and that the transfected cells make about the same levels of human or mouse GMCSF from both the vector using the IRES expression system and the vectors using the S1 core promoter system, respectively. However, Figure 4E and F show that hGMCSF expression driven by the S1 promoter is 3 fold less than the IRES configuration, in fully infected U87 and PC3 cells, respectively. Similarly, Figure 4H shows that in mouse EMT6 cells the S1 promoter is less efficient that the IRES vector in expressing mGMCSF after infection.

Example 9: Poor transgene expression of pAC3 based vectors containing C1 and S1 core promoters driving yCD2 relative to pAC3-yCD2

[00118] The levels of CD expression were detected in 293T cells by immunoblotting using an antibody against CD (Figure 4B). Naïve cells are seeded at 2E6 cell per 10-cm plates the day prior transfection. Transient transfection by calcium phosphate method was performed using plasmid DNA encoding the viral genome of each vector. At 40h post transfection, cells are harvested and lysed to obtain cell lysates. Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH.

Figure 4B shows the results demonstrating expression from all these vectors, with the IRES system yielding about 15 fold higher levels of expression than the S1 promoter construct. In addition, Figure 4C shows expression of CD protein in an immunoblot in fully infected U87-MG cells from cells infected with vector from pAC3-yCD2 (IRES vector) but undetectable expression of yCD2 in both C1. yCD2 and S1.yCD2 vectors.

Example 10: *In vitro* positive selection using pAC3-S1.yCD2 vector in human cells to increase yCD2 expression

[00119] Positive selection of fully infected pAC3.S1.yCD2 vector is performed by concurrently giving N-(phosphonacetyl)-L-aspartate (PALA), an inhibitor of pyrimidine *de novo* synthesis, which leads to pyrimidine depletion-mediated cell death of non-infected cells or cells expression low level of yCD2. With addition of cytosine in culture, it rescues cells expression high level of yCD2 gene via the pyrimidine salvage pathway. The method described below applies to a U87 glioblastoma derived cell line used in the laboratory, but the same procedures can be used with multiple different cell lines derived from different tumor types. In these cases the actual concentrations of reagents and timing of the steps will be determined by the rate of growth of the cells and the initial infection rates of the cell line. Such adjustments can be made as needed by one skilled in the art and will be determined in the course of performing the method. In addition this optimization procedure can be used with any promoter driving a selectable gene in a replicating vector. Also other variations in actual reagent concentrations and timing of selection may be possible.

[00120] The concentration PALA required to kill naïve U87 cells was first determined, U87 cells infected with pAC3-yCD2 vector and for U87 cells with pAC3.S1-yCD2 vector. Cell were seeded at 3E3 cells in 96-well plates the day before. At 24 hour post cell seeding, PALA at 0.00975, 0.039, 0.156, 0.625, 2.5, 10, 40 and 160 uM were added to the culture for 5 consecutive days followed by an MTS assay to determine the cell viability. Figure 6 shows that the IC_{50} of PALA ranges between 8-30 uM. A range of cytosine concentrations (0.2, 1, 5 10 mM) in culture was also determined by

performing the same experiment described above. This shows that the cells can tolerate cytosine in all concentrations tested.

[00121] For positive *in vitro* selection, naïve U87 cells are seeded at 1e5 cells in 6-well plates the day before. The next day, the cells are infected with pAC3-yCD2 vector (positive control) and separately with pAC3.S1-yCD2 vector, respectively, at MOI of 0.1. At 48 hour post infection (~20% infectivity), PALA at 1 uM and cytosine at 10 mM are added to the culture containing naïve U87 cells (negative control), U87 cells infected with pAC3-yCD2 vector (positive control) and U87 cells with pAC3.S1-yCD2 for 5 consecutive days at which time point, the culture supernatant is collected for a new round of infection with naïve U87 cells. The infection cycle in the presence of PALA and cytosine is repeated for 12 rounds with increasing concentration of PALA cycle 1-2: 1 uM; cycle 3-4: 3.3 uM; cycle 5-6: 10 uM, cycle 7-8: 20 uM and cycle 9-12: 30 uM). At the end of the selection, cells are isolated and expanded in the presence of 30 uM PALA and 10 mM cytosine. MTS assay is performed to demonstrate the increase of cell viability as a result of the positive selection. Cells infected with pAC3.S1.yCD2 vector prior to selection are not able to efficiently utilize the salvage pathway due to low CD expression. In contrast, cells infected with pAC3.S1-yCD2 vector post selection show high cell viability that is comparable to cells infected with pAC3-yCD2 vector.

[00122] To confirm that the high cell viability is due to upregulation of CD expression, Western blots are performed to examine CD expression. Cells are harvested and lysed to obtain cell lysates. Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH in the immunoblot. The data show that the CD expression from cell extracts from U87 cells infected with pAC3.S1-yC2 vector is comparable to that of pAC3-yCD2. The genomic DNA is then isolated from U87 cells infected with pAC3.S1-yCD2 vector and amplified the S1-yCD2 region by PCR using the following primer set. IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3' (SEQ ID NO:54) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3'(SEQ ID NO:55). The resulting PCR products are isolated for PCR cloning for sequencing analysis. The

sequencing result show that multiple mutations occur in the S1 core promoter. Subsequently, the S1 promoter with identified mutations is synthesized with Mlu I and Not I site at each end of the DNA fragment for subcloning into pAC3 backbone as described above. The resulting vector with optimized S1 promoter is designated pAC3.mtS1-yCD2.

[00123] Infectious pAC3.mtS1-yCD2 vector is prepared by transient transfection in 293T cells as before. Naïve U87 cells are infected with pAC3.mtS1-yCD2 vector at MOI of 0.1. At day 7 post infection, cells are harvested and lysed to obtain cell lysates. Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH in the immunoblot. The data show that the CD expression of cell extracts from U87 cells infected with pAC3.mtS1-yCD2 vector is comparable to that of pAC3-yCD2 vector driven by the IRES.

[00124] To correlate CD expression with 5-FC sensitivity, U87 cells with no vector, with pAC3-yCD2 vector, and pAC3.mtS1-yCD2 vector, respectively, are seeded at 1e3 cells per well in 96-well plates. They are monitored over an eight day period following treatment with various concentrations of 5-FC, which is first added one day after plating and then replenished with whole medium plus 5-FC every two days. Cell viability is assessed every two days by MTS assay. The data show that IC50 value for U87 cells infected with pAC3.mtS1-yCD2 vector is comparable to those infected with pAC3-yCD2 vector (0.5 ug/mL; Perez *et al.*, 2012). Other promoter configurations can be optimized for gene expression using these techniques.

Example 11: Incorporation of Kozak sequence downstream of the core promoter increases yCD2 gene expression without altering vector stability

[00125] Most eukaryotic mRNAs contain Kozak sequence which facilitates initiation of protein translation. Incorporation of Kozak sequence downstream of the core promoter increases yCD2 expression in both transiently transfected and fully infected cells. The optimized yeast CD gene, yCD2, has 3 in-frame ATG within the first 15 amino acids in the coding region. The spacing in the 5'UTR and the lack of Kozak sequence flanking the initiation codon in yCD2 mRNA was considered suboptimal for efficient protein

translation initiation. Incorporation of Kozak sequence and/or other translational enhancer element may greatly improve the translation initiation and thus protein production of transgenes.

[00126] The pAC3.S1-yCD2 vector contains a core promoter without Kozak sequence. Although the core promoter has demonstrated useful transcription, efficient protein translation is equally important to confer gene expression. This improvement can be combined with others in this specification for improved core promoters or other improved minipromoters.

[00127] The pAC3-kozakS1.yCD2, (AKA pAC3.S1K-yCD2) and pAC3.kozakS2-yCD2 (AKA pAC3.S2K-yCD2) are derived from the backbone of pAC3-yCD2. The pAC3 backbone is isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of kozakS1yCD2 and kozakS2yCd2 are synthesized with Mlu I and Not I restriction enzyme site present at each end of the DNA fragment for subsequent cloning to the corresponding sites in the pAC3 backbone.

[00128] Infectious vectors are prepared by transient transfection in 293T cells as before. Naïve U87 cells are infected with vectors at MOI of 0.1. At day 7 post infection, cells are harvested and lysed to obtain cell lysates. Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH in the immunoblot. Figure 4B shows that the CD expression of cell extracts from 293T transiently transfected with pAC3.S1K-yCD2 vector is approximately 2-5 higher than pAC3.S1-yCD2 vector. Similarly, CD expression of pAC3.S2K-yCD2 is approximately 2-5 higher than pAC3-S2-yCD2 vector in transiently transfected 293T cells. Moreover, the CD expression is comparable between pAC3-S1K-yCD2 and pAC3-S2K-yCD2 in transiently transfected 293T cells. In contrast, Figure 4C shows CD expression is undetectable in maximally infected U87 cells with any one of the four vectors.

[00129] The data show that the CD expression of cell extracts from U87 cells infected with pAC3-kozakS1.yC2 vector is approximately 2-5 higher than pAC3-S1.yCD2 vector.

[00130] To correlate CD expression with 5-FC sensitivity, U87 cells with no vector, with pAC3-yCD2 vector, and pAC3-kozakS1.yCD2 vector, respectively, are seeded at 1E3 cells per well in 96-well

plates. They are monitored over an eight day period following treatment with various concentrations of 5-FC, which is first added one day after plating and then replenished with whole medium plus 5-FC every two days. Cell viability is assessed every two days by MTS assay. The data show that IC_{50} value for U87 cells infected with pAC3-kozakS1.yCD2 vector is approximately 5 fold higher than those infected with pAC3-S1.yCD2 vector, and within 10 fold of the pAC3-yCD2 vector (0.5 ug/mL; Perez *et al.*, 2012).

[00131] For vector stability, naïve U87 cells are seeded at 2E5 cell per well in 6-well plates the day prior infection. The first cycle of infection is performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells is used for infecting naïve cells. In each infection cycle, infected cells were passaged at d4 post infection into 6-well plates. Viral supernatants from infected cells at d7 post infection were collected for subsequent infection, and cells were harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR were: IRES-F: 5′-CTGATCTTACTCTTTGGACCTTG-3′ (SEQ ID NO:54) and IRES-R: 5′-CCCCTTTTTCTGGAGACTAAATAA-3′ (SEQ ID NO:55). The data show that the stability of pAC3.kozakS1-yCD2 vector is comparable to that of pAC3-yCD2 and pAC3.S1-yCD2 vector.

Example 12: Construction and configuration of pAC3 based vectors containing optimized S1 core promoter driving yCD2-UPRT

[00132] The yCD2-UPRT is ~1.2 kb. The mtS1 promoter= optimized S1 promoter (see Example 11). The pAC3-mtS1.yCD2-UPRT vector is derived from the backbone of pAC3-yCD2. The pAC3 backbone is isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of mtS1.yCD2-UPRT is synthesized with Mlu I and Not I restriction enzyme site present at each end of the DNA fragment for subsequent cloning to the corresponding sites in the pAC3 backbone.

Example 13: Vector stability and transgene expression of pAC3 based vectors containing optimized S1 core promoter driving yCD2-UPRT expression

[00133] pAC3 based vectors with optimized core promoters driving the expression of yCD2-UPRT are constructed using similar

techniques as above and compared to pAC3-yCD2-U (aka T50003, Perez *et al.*, Mol.Ther., 2012, WO2010045002), which is the equivalent vector using an internal IRES to drive expression of the yCD2-UPRT fusion gene.

[00134] Infectious pAC3-mtS1.yCD2-UPRT vector is prepared by transient transfection in 293T cells. Naïve U87 cells infected with pAC3kozakS1.yCD2 vector at MOI of 0.1. At day 7 post infection, cells are harvested and lysed to obtain cell lysates. Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH in the immunoblot. The data show that the CD-UPRT expression (~ 44KDa) from cell extracts of U87 cells infected with pAC3-mtS1.yCD2-UPRT vector is comparable to pAC3-yCD2-U and pAC3-yCD2 vectors.

[00135] To correlate CD expression with 5-FC sensitivity, U87 cells with no vector, with pAC3-yCD2, pAC3-yCD2-U, and pAC3-mtS1.yCD2-UPRT vector, respectively, are seeded at 1E3 cells per well in 96-well plates. They are monitored over an eight day period following treatment with various concentrations of 5-FC, which is first added one day after plating and then replenished with whole medium plus 5-FC every two days. Cell viability is assessed every two days by MTS assay. The data show that IC_{50} value for U87 cells infected with pAC3-mtS1.yCD2-UPRT vector is at least equivalent to those infected with pAC3-yCD2 and pAC3-yCD2-U vectors.

[00136] For vector stability, naïve U87 cells are seeded at 2E5 cell per well in 6-well plates the day prior infection. The first cycle of infection is performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells is used for infecting naïve cells. In each infection cycle, infected cells were passaged at d4 post infection into 6-well plates. Viral supernatants from infected cells at d7 post infection were collected for subsequent infection, and cells were harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR were: IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3' (SEQ ID NO:56) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3' (SEQ ID NO:57). The data show that

pAC3-S1.yCD2-UPRT vector has significantly better stability than the IRES driven pAC3-yCD2-U vector.

Example 14: Construction and configuration of pAC3-based vectors containing optimized S1 core promoter driving yCD2 expression and human U6 (Pol III) promoter driving shRNA against TGFb2

[00137] The pAC3-S1.yCD2-polIII promoter-shRNATGFb2 vector is derived from the backbone of pAC3-yCD2. The pAC3 backbone is isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of mtS1.yCD2 and polIII promoter-shRNATGFb2 is synthesized with Mlu I and Not I restriction enzyme site present at each end of the DNA fragment for subsequent cloning to the corresponding sites in the pAC3 backbone.

Example 15: Vector stability and transgene expression of pAC3 based vectors containing optimized S1 core promoter driving yCD2 expression and human pol III promoter promoter driving shRNA against TGFb2

[00138] Infectious pAC3-mtS1.yCD2-polIII promoter-shRNATGFb2 vector is prepared by transient transfection in 293T cells as before. Naïve U87 cells infected with pAC3-kozakS1.yCD2 vector at MOI of 0.1. At day 7 post infection, one portion of cells are harvested and lysed to obtain cell lysates, and another portion of cells are harvested for total RNA extraction. Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH in the immunoblot. The data show that the yCD2 expression from cell extracts of U87 cells infected with pAC3-mtS1.yCD2-polIII promoter-shRNATGFb2 vector is comparable to those from pAC3-yCD2 and pAC3-mtS1.yCD2 vectors.

[00139] To correlate CD expression with 5-FC sensitivity, U87 cells with no vector, with pAC3-yCD2, and pAC3-mtS1.yCD2-polIII promoter-shRNATGFb2 vector, respectively, are seeded at 1E3 cells per well in 96-well plates. They are monitored over an eight day period following treatment with various concentrations of 5-FC, which is first added one day after plating and then replenished with whole medium plus 5-FC every two days. Cell viability is assessed every two days by MTS assay. The data show that IC50 value for U87 cells infected with pAC3-mtS1.yCD2-polIII promoter-shRNATGFb2 vector is comparable to those infected with pAC3-yCD2 or pAC3-mtS1.yCD2 vectors.

[00140] To demonstrate efficient knockdown of TGFb2 in U87 cells infected with pAC3-mtS1.yCD2-polIII promoter-shRNATGFb2 vector, total RNA is extracted from cells harvested at d7 post infection as described above. Gene expression of TGFb2 is measured by qRT-PCR using RNA polIII promoter as an internal control for normalization. The relative expression level of TGFb2 to naïve U87 cells is calculated using $\Delta\Delta C(t)$ method. The data show that at d7 post infection, more than 70% of TGFb2 is downregulated. The infected cells were cultured up to 30 days and observe sustained knockdown of TFGb2.

[00141] For vector stability, naïve U87 cells were seeded at 2E5 cell per well in 6-well plates the day prior infection. The first cycle of infection was performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected cells was used for infecting naïve cells. In each infection cycle, infected cells were passaged at d4 post infection into 6-well plates. Viral supernatants from infected cells at d7 post infection were collected for subsequent infection, and cells were harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR were: IRES-F: 5'-CTGATCTTACTCTTTGGACCTTG-3'(SEQ ID NO:54) and IRES-R: 5'-CCCCTTTTTCTGGAGACTAAATAA-3' (SEQ ID NO:55). The data show that stability of pAC3-mtS1.yCD2-polIII promoter-shRNATGFb2 vector is comparable to pAC3-yCD2 and pAC3-mtS1.yCD2 vectors.

Example 16: Construction and configuration of pAC3-based vectors containing optimized S1 core promoter driving yCD2 expression and optimized S1 core promoter driving tko.

[00142] An optimized thymidine kinase, tko, is used in this example due its high vector stability. The pAC3-mtS1.yCD2-mtS1.tko vector is derived from the backbone of pAC3-yCD2. The pAC3 backbone is isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of mtS1.yCD2-mtS1.tko is synthesized with Mlu I and Not I restriction enzyme site present at each end of the DNA fragment for subsequent cloning to the corresponding sites in the pAC3 backbone.

Example 17: Vector stability and transgene expression of pAC3 based vectors containing an optimized S1 core promoter driving yCD2 expression and an optimized S1 core promoter driving tko.

[00143] Infectious pAC3-mtS1.yCD2-mtS1.tko vector is prepared by transient transfection in 293T cells as before. Naïve U87 cells infected with pAC3-kozakS1.yCD2 vector at MOI of 0.1. At day 7 post infection, cells are harvested and lysed to obtain cell lysates, Protein concentration of cell lysates is determined to allow equal protein loading as indicated by GAPDH in the immunoblot. The data show that the yCD2 and TK expression from cell extracts of U87 cells infected with pAC3-mtS1.yCD2-mtS1.tko vector is comparable to those from pAC3-yCD2 and pAC3-tko vectors mediated by IRES.

[00144] To correlate CD expression with 5-FC sensitivity, U87 cells with no vector, with pAC3-yCD2, and pAC3-mtS1.yCD2-mtS1.tko vector, respectively, are seeded at 1E3 cells per well in 96-well plates. They are monitored over an eight day period following treatment with various concentrations of 5-FC, which is first added one day after plating and then replenished with whole medium plus 5-FC every two days. Cell viability is assessed every two days by MTS assay. The data show that IC_{50} value for U87 cells infected with pAC3-mtS1.yCD2-mtS1.tko vector is comparable to those infected with pAC3-yCD2 vector.

[00145] To correlate tko expression with ganciclovir sensitivity, U87 cells with no vector, with pAC3-tko, and pAC3-mtS1.yCD2-mtS1.tko vector, respectively, are seeded at 1e3 cells per well in 96-well plates. They are monitored over an eight day period following treatment with various concentrations of ganciclovir, which is first added one day after plating and then replenished with whole medium plus ganciclovir every two days. Cell viability is assessed every two days by MTS assay. The data show that IC50 value for U87 cells infected with pAC3-mtS1.yCD2-mtS1.tko vector is comparable to those infected with pAC3-tko vector.

[00146] For vector stability, naïve U87 cells are seeded at 2E5 cell per well in 6-well plates the day prior infection. The first cycle of infection is performed at MOI 0.1 according to calculated titers (TU/mL) in the presence of 4µg/mL polybrene. In subsequent infections, one tenth of the viral supernatant produced by infected

cells is used for infecting naïve cells. In each infection cycle, infected cells are passaged at d4 post infection into 6-well plates. Viral supernatants from infected cells at d7 post infection are collected for subsequent infection, and cells are harvested for genomic extraction for assessment of vector stability by IRES-PCR. The primers used for PCR were: IRES-F: 5′-CTGATCTTACTCTTTGGACCTTG-3′ (SEQ ID NO:54) and IRES-R: 5′-CCCCTTTTTCTGGAGACTAAATAA-3′ (SEQ ID NO:55). The data show that stability of pAC3-mtS1.yCD2-mtS1.tko vector is comparable to pAC3-yCD2 vector and much superior than pAC3-tko vector.

Example 18: Construction, configuration and testing of pAC3 based vectors, pAC3-HOE1.yCD2, pAC3-HOE2.yCD *etc.* containing a hybrid promoter with the human hemoxygenase gene core promoter, selected enhancer segments and a Kozak sequence, driving expression of the yCD2 gene.

[00147] The pAC3 backbone in the vector was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I.

[00148] Six double-stranded synthetic DNA fragments coding for the elements listed in Table 2 and a double-stranded synthetic DNA fragment containing the *Mlu1* recognition site (ACGCGT) were used. Each fragment from Table 2 also has a 5′protrusion of 5-GATC-3 for ligating each other, as did the Mlu1 site. The individual fragments are annealed by heating up to 90°C and slow cooling, phophorylated at the 5′ end by a T4 polynucleotide kinase reaction, then mixed in equimolar amounts along with 1/10 and 1/100 molar kinased Mlu1 sites and ligated. The ligation mixes are digested with Mlu1, the product electrophoresed on a gel and the 40-200 bp portion excised and purified from the gel.

[00149] A sequence corresponding to the human heme oxygenase 1 gene core promoter fused with a Kozak start site and the yCD2 gene is synthesized with a Not1 site on the 3′ end and a Mlu1 site on the 5′ end and digested with both enzymes.

[00150] The synthesized fragment is :

5′-
ACGCGTGGGGCGGGCTGGGCGCGGGCCCCTGCGGGTGTTGCAACGCCCGGCCAGAAAGTGGGCATCA
GCTGTTCCGCCTGGCCCACGTGACCCGCCGAGCATAAATGTGACCGGCCGCGGCTCCGG**C**AGTCAAC
GCCACC*ATGG*TGACCGGCGGCATGGCCTCCAAGTGGGATCAAAAGGGCATGGATATCGCTTACGAGG
AGGCCCTGCTGGGCTACAAGGAGGGCGGCGTGCCTATCGGCGGCTGTCTGATCAACAACAAGGACGG
CAGTGTGCTGGGCAGGGGCCACAACATGAGGTTCCAGAAGGGCTCCGCCACCCTGCACGGCGAGATC
TCCACCCTGGAGAACTGTGGCAGGCTGGAGGGCAAGGTGTACAAGGACACCACCCTGTACACCACCC

TGTCCCCTTGTGACATGTGTACCGGCGCTATCATCATGTACGGCATCCCTAGGTGTGTGATCGGCGA
GAACGTGAACTTCAAGTCCAAGGGCGAGAAGTACCTGCAAACCAGGGGCCACGAGGTGGTGGTTGTT
GACGATGAGAGGTGTAAGAAGCTGATGAAGCAGTTCATCGACGAGAGGCCTCAGGACTGGTTCGAGG
ATATCGGCGAGTGAGCGGCCGC-3' (SEQ ID NO:56);

where the large C is the transcription start site,the first underlined sequence is the Kozak sequence including the ATG start codon (italics) of the yCD2 gene, and the second underlined sequence is the stop codon for yCD2. This fragment is 625 nucleotides, with a 126bp fragment upstream of the transcription start site which is the heme oxygenase promoter. This fragment is ligated to the pAC3Mlu1-Not backbone fragment isolated above, in the presence of excess of the Mlu1 fragments carrying the transcription factor binding site mixtures, and individual clones isolated by bacterial transfections followed by analyses of restriction digest of DNA mini-preps to identify plasmids with the pAC3 backbone the heme oxygenase promoter and CD, and a single copy of the binding site mix, below about 200bp.

[00151] The plasmids that carry the desired sequences are then used to make infectious vector by transient transfection and U87 cells infected and assayed by Western blot for CD protein. Vectors expressing equivalent CD protein to pAC3-yCD2 or above are identified and sequenced to characterize the transcription factor binding site mix. Suitable identified binding site mixes as small as 40 bp are used to make vectors with other genes. Stability of the vectors are tested by serial passage as before.

[00152] Alternatively the ligation mix of transcription factor binding sites, core promoter-CD and pAC3 back bone is used with the PALA selection method in target cells such as U87, to select vectors that express high levels of CD protein.

Example 19: Construction, configuration and testing of pAC3 based vectors, pAC3-cTK.yCD2,. containing a hybrid promoter with the Herpes Virus 1thymidine kinase gene promoter, selected enhancer segments and a Kozak sequence, driving expression of the yCD2 gene.

[00153] The Herpes Thymidine Kinase gene sequence is known to have a cryptic core promoter between the first and third ATG of the normal mRNA coding sequence (Al-shawi *et al.* Mol. Cell. Biol. 11: 4207 1991, Salamon et al Mol. Cell. Biol. 15:5322 1995). This 180bp sequence:

ATGGCTTCGTACCCCTGCCATCAACACGCGTCTGCGTTCGACCAGGCTGCGCGTTCTCGCGGCCATA
GCAACCGACGTACGGCGTTGCGCCCTCGCCGGCAGCAAGAAGCCACGGAAGTCCGCCTGGAGCAGAA
AATGCCCACGCTACTGCGGGTTTATATAGACGGTCCTCACGGGATG (SEQ ID NO:57)

is co-synthesized with both enhancers such as those mixtures isolated in example 18 or in this case with the 72 bp enhancer repeats from SV40 (Gruss et al PNAS 78: 943-9471981, NCBI Reference Sequence: NC_001669.1) a single copy of which is:

5′-
TGGTTGCTGACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCTGGGGACTTT
CCACACC-3′ (SEQ ID NO:58),

upstream of the TK cryptic promoter, and with the yCD2 sequence downstream, starting at the ATG start codon on the 3′ end of the cryptic promoter. The total synthesized sequence has MLu1 and Not1 sites on the 5′ and 3′ ends respectively and is inserted into the pAC3 MLu1-Not 1 backbone fragment isolated as in example 18. The ligation mix is used to transfect bacteria and desired molecular clones isolated and tested for stability and CD expression by Western blot as described in example X. Levels of CD expression are as least as good as for pAC3-yCD2.

Example 20: Construction, configuration and testing of transgene expression of pAC3 based vectors containing SV40 promoter, RSV promoter, a synthetic promoter with selected enhancer segments.

[00154] The pAC3 backbone in the vector was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I sites as described above or by endonuclease digestion of the pAC3-Gluc plasmid DNA with Mlu I and Psi I sites.

[00155] The retroviral replicating vectors, pAC3-SV40-GFP-R, pAC3-SV40-Gluc, pAC3-RSV-Gluc, and pAC3.ES1-Gluc were derived from the backbone of pAC3-yCD2. The pAC3 backbone was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of SV40-GFP-R was synthesized or amplified by polymerase chain reaction (PCR) with Mlu I and Psi I at each end of DNA fragment for subcloning into the pAC3-Gluc backbone to replace the IRES sequence at the corresponding restriction sites.

[00156] In pAC3-SV40-GFP-R construct, the SV40-GFP cassette was placed in a reversed orientation in the 3′UTR to minimize promoter interference in proviral DNA configuration.

[00157] pAC3-SV40-GFP-R viruses are prepared by transient transfection in 293T cells as before. Naïve U87 cells are infected with these vectors at MOI of 0.01. At day 13 post infection, cells are harvested and analyzed by flow cytometry by gating GFP-positive cells and measuring the mean fluorescent intensity of the GFP-positive population. Figure 7 shows that the GFP expression level of pAC3-SV40-GFP-R is higher than pAC3-S1-GFP, but still significantly less than that of pAC3-GFP mediated by IRES.

[00158] pAC3-Gluc, pAC3-SV40-Gluc, pAC3-RSV-Gluc, and pAC3.ES1-Gluc viruses are prepared by transient transfection in 293T cells as before. Naïve U87 cells are infected with these vectors at MOI of 0.01. Supernatant from each cell passage (day 3, day 6 and day 9 post infection) is collected. At each cell passage, same number of cells are seeded and cultured in equal volume of culture medium. A 1:5 serial dilutions of the supernatant of each sample from each time point are made to measure the intensity of luminescence in the presence of the substrate, colenterazine, at a final concentration of 15 uM. The data show that Gluc expression levels mediated by SV40, RSV, and ES1 promoters are 2-3 times less than that mediated by IRES.

Example 21: Construction, configuration and testing of transgene expression of pAC3 based vectors containing RSV promoter, SV40 promoter, S1 core promoter, EC1 synthetic promoter and ES1 synthetic promoter.

[00159] The pAC3 backbone in the vector was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I sites as described above or by endonuclease digestion of the pAC3-Gluc plasmid DNA with Mlu I and Psi I sites.

[00160] The retroviral replicating vectors, pAC3-SV40-Gluc, pAC3-RSV-Gluc, and pAC3.ES1-Gluc were derived from the backbone of pAC3-yCD2. The pAC3 backbone was isolated by endonuclease digestion of the pAC3-yCD2 plasmid DNA with Mlu I and Not I. The DNA sequence of SV40-GFP-R, SV40-Gluc, RSV-Gluc, and ES1-Gluc, respectively, were synthesized or amplified by polymerase chain reaction (PCR) with Mlu I and Psi I at each end of DNA fragment for subcloning into the pAC3-Gluc backbone to replace the IRES sequence at the corresponding restriction sites. In pAC3-SV40-GFP-R construct, the

SV40-GFP cassette was placed in a reversed orientation in the 3'UTR to minimize promoter interference in proviral DNA configuration.

[00161] SV40-Gluc, RSV-Gluc and EC1-Gluc, S1-Gluc and ES1-Gluc cassette with Mlu I and Psi I sites are place in the same orientation as LTR. RVS promoter is 271 nts in length; SV40 promoter is 324 nts in length. Synthetic S1 core promoter is 80 nts in length. EC1, which is a hybrid promoter consists of tandem repeats of CRE (Schlabach *et al.*, 2010 PNAS) and the C1 core promoter (Juven-Gershon *et al.*, 2006 Nature Methods)is 181 nts in length. ES1, which is hybrid of tandem repeats of CRE and S1 core promoter (Juven-Gershon *et al.*, 2006 Nature Methods) is 188 nts in length.

[00162] Gluc expression from pAC3-Gluc, pAC3-RSV-Gluc, pAC3-SV40-Gluc, pAC3-EC1-Gluc, pAC3-S1-Gluc and pAC3-ES1-Gluc were evaluated in transiently transfected 293T or Hela cells. At 48 hours post transfection, the supernatant was collected and Gluc expression level is determined by co-incubation of 1:3 or 1:4 serially diluted supernatant with colenterazine at a final concentration of 15 uM.

[00163] The data is shown in Figure 9. 293T cells, Gluc expression levels mediated by RSV is approximately 3 fold higher than Gluc expression mediated by IRES. Gluc expression level mediated by SV40, EC1 and promoters are comparable to that of IRES. As expected, Gluc expression mediated by S1 core promoter is 3-fold less than that of IRES. For ES1, the promoter activity is about 1/3 less than IRES and EC1, but 2-fold higher than S1 alone.

[00164] In Hela cells, Gluc expression levels mediated by RSV, SV40, and ES1 is approximately 2.5 fold lower than Gluc expression mediated by IRES. The disparity of the RSV results wth those seen in 293T cells (3 fold greater than IRES) is expected as, although the RSV LTR promoter is known to be ubiquitously expressed, unusually, in Hela cells it is specifically suppressd by a 21kD inhibitory protein, not present in most other cell types. The Gluc expression level mediated by the S1 core promoter alone is approximately 10-fold less than that mediated by IRES. However, inclusion of the synthetic enhancer (ES1) increases the promoter

activity by 4-fold. The Gluc expression level mediated by EC1 is slightly higher than that mediated by IRES (Figure 9).

[00165] pAC3-Gluc, pAC3-CMV-Gluc, pAC3-RSV-Gluc, and pAC3-SV40-Gluc viruses are prepared by transient transfection in 293T cells as before. Naïve U87 cells are infected with these vectors at MOI of 0.01. Supernatant from each cell passage (day 3, day 6 and day 9 post infection) is collected. At each cell passage, same number of cells are seeded and cultured in equal volume of culture medium. A 1:3 serial dilutions of the supernatant of each sample from each time point are made to measure the intensity of luminescence in the presence of the substrate, colenterazine, at a final concentration of 15 uM. The data show that Gluc expression levels mediated by RSV, SV40, EC1 and ES1 promoters are comparable to that mediated by IRES.

[00166] A number of embodiments of the disclosure have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the disclosure. Accordingly, other embodiments are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. A recombinant replication competent gammaretrovirus comprising:

a retroviral GAG protein;

a retroviral POL protein;

a retroviral envelope;

a retroviral polynucleotide comprising Long-Terminal Repeat (LTR) sequences at the 3' end of the retroviral polynucleotide sequence, a promoter sequence at the 5' end of the retroviral polynucleotide, said promoter being suitable for expression in a mammalian cell, a *gag* nucleic acid domain, a *pol* nucleic acid domain and an *env* nucleic acid domain;

a therapeutic cassette comprising at least one mini-promoter cassette having a mini-promoter operably linked to a heterologous polynucleotide, wherein the therapeutic cassette is positioned 5' to the 3' LTR and 3' to the *env* nucleic acid domain encoding the retroviral envelope, and wherein when only one mini-promoter cassette is present the heterologous polynucleotide is 1.2kb to 2.0 kb in length; and

cis-acting sequences necessary for reverse transcription, packaging and integration in a target cell.

2. A recombinant replicating retroviral vector comprising:

a retroviral GAG protein;

a retroviral POL protein;

a retroviral envelope;

a retroviral polynucleotide comprising Long-Terminal Repeat (LTR) sequences at the 3' end of the retroviral polynucleotide sequence, a promoter sequence at the 5' end of the retroviral polynucleotide, said promoter being suitable for expression in a mammalian cell, a *gag* nucleic acid domain, a *pol* nucleic acid domain and an *env* nucleic acid domain;

a therapeutic cassette comprising a minipromoter cassette comprising a mini-promoter operably linked to a heterologous polynucleotide, wherein the minipromoter cassette is positioned 5' to the 3' LTR and 3' to the *env* nucleic acid domain

encoding the retroviral envelope, wherein the minipromoter lacks SCP1, Ad or CMV core promoters; and

cis-acting sequences necessary for reverse transcription, packaging and integration in a target cell.

3. The retrovirus of claim 1 or 2, wherein the retroviral polynucleotide sequence is derived from a virus selected from the group consisting of murine leukemia virus (MLV), Moloney murine leukemia virus (MoMLV), Feline leukemia virus (FeLV), Baboon endogenous retrovirus (BEV), porcine endogenous virus (PERV), the cat derived retrovirus RD114, squirrel monkey retrovirus, avian reticuloendotheliosis virus(REV), or Gibbon ape leukemia virus (GALV).

4. The retrovirus of claim 1 or 2, wherein the retroviral envelope is an amphotropic MLV envelope.

5. The retrovirus of claim 1 or 2, wherein the target cell is a cell having a cell proliferative disorder.

6. The retrovirus of claim 1 or 2, wherein the target cell is a neoplastic cell.

7. The retrovirus of claim 5, wherein the cell proliferative disorder is selected from the group consisting of lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer, brain cancer, head and neck cancer, pancreatic cancer, melanoma, stomach cancer and ovarian cancer, lymphoma, leukemia,rheumatoid arthritis or other autoimmune disease.

8. The retrovirus of claim 1 or 2, wherein the promoter sequence is associated with a growth regulatory gene.

9. The retrovirus of claim 1 or 2, wherein the promoter sequence comprises a tissue-specific promoter sequence.

10. The retrovirus of claim 9, wherein the tissue-specific promoter sequence comprises at least one androgen response element (ARE).

11. The retrovirus of claim 9, wherein the tissue-specific promoter sequence comprises at least one glucocorticoid response element

12. The retrovirus of claim 1 or 2, wherein the promoter comprises a CMV-R-U5 domain polynucleotide.

13. The retrovirus of claim 12, wherein the CMV-R-U5 domain comprises the immediately early promoter from human cytomegalovirus linked to an MLV R-U5 region.

14. The retrovirus of claim 1 or 2, wherein the *gag* polynucleotide is derived from a gammaretrovirus.

15. The retrovirus of claim 1 or 2, wherein the *pol* domain of the polynucleotide is derived from a gammaretrovirus.

16. The retrovirus of claim 1 or 2, wherein the mini-promoter is a core promoter.

17. The retrovirus of claim 1, 2 or 16, wherein the mini-promoter is an optimized core promoter.

18. The retrovirus of any of the foregoing claims, wherein the therapeutic cassette comprises (a) at least two mini-promoter cassettes, (b) at least one minipromoter cassette and a polIII promoter cassette or (c) at least one mini-prmoter cassette and an IRES cassette.

19. The retrovirus of claim 1 or 2, wherein the mini-promoter is from about 70-500 bp in length.

20. The retrovirus of claim 1, 2 or 19, wherein the mini promoter comprises a core promoter and further comprises an enhancer element.

21. The retrovirus of claim 1 or 2, wherein the mini-promoter comprises a TATA box, and initiator site, a Motif Ten Element (MTE), a Downstream prmoter element (DPE) and at least one additional element selected from the group consisting of: (a) TFIIB recognition element, upstream (BREu); (b) TFIIB recognition element downstream (BREd); (c) HBV X core promoter elment 1 (XCPE1); (d) HBV X core promoter element 2 (XCPE2); (d) downstream core element site I (CDE SI); (e) downstream core element site II (CDE SII); and (f) downstream core element site III (CDE SIII).

22. The retrovirus of claim 21, wherein the mini-promoter further comprises an enhance element.

23. The retrovirus of claim 1 or 2, wherein the heterologous nucleic acid comprises a polynucleotide having a sequence as set forth in SEQ ID NO:3, 5, 11, 13, 15 or 17.

24. The retrovirus of claim 1 or 2, wherein the heterologous nucleic acid encodes a polypeptide comprising a sequence as set forth in SEQ ID NO:4.

25. The retrovirus of claim 1 or 2, wherein the heterologous nucleic acid is human codon optimized and encodes a polypeptide as set forth in SEQ ID NO:4.

26. The retrovirus of claim 1 or 2, wherein the 3' LTR is derived from a gammaretrovirus.

27. The retrovirus of claim 26, wherein the 3' LTR comprises a U3-R-U5 domain.

28. The retrovirus of claim 1, wherein the heterologous nucleic acid sequence encodes a biological response modifier or an immunopotentiating cytokine.

29. The retrovirus according to claim 28, wherein the immunopotentiating cytokine is selected from the group consisting of interleukins 1 through 15, interferon, tumor necrosis factor (TNF), and granulocyte-macrophage-colony stimulating factor (GM-CSF).

30. The retrovirus according to claim 28, wherein the immunopotentiating cytokine is interferon gamma.

31. The retrovirus according to claim 1 or 2, wherein the heterologous nucleic acid encodes a polypeptide that converts a nontoxic prodrug in to a toxic drug.

32. The retrovirus according to claim 31, wherein the polypeptide that converts a nontoxic prodrug in to a toxic drug is thymidine kinase, purine nucleoside phosphorylase (PNP), or cytosine deaminase.

33. The retrovirus according to claim 1 or 2, wherein the heterologous nucleic acid sequence encodes a receptor domain, an antibody, or antibody fragment.

34. The retrovirus according to claim 1 or 2, wherein the heterologous nucleic acid sequence comprises an inhibitory polynucleotide.

35. The retrovirus according to claim 34, wherein the inhibitory polynucleotide comprises an miRNA, RNAi or siRNA sequence.

36. The retrovirus of claim 35, wherein the therapeutic cassette comprises a mini-promoter operably linked to heterologous nucleic acid and a polIII promoter operably linked to the miRNA, RNAi or siRNA coding domain.

37. A recombinant retroviral polynucleotide genome for producing a retrovirus of claim 1 or 2.

38. A method of delivering a therapeutic molecule to a subject comprising contact the subject with a retrovirus of any of the foregoing claims.

39. A method of treating a cell proliferative disorder comprising contacting the subject with a retrovirus of claim 23 under conditions such that the cytosine deaminase polynucleotide is expressed and contacting the subject with 5-fluorocytosine.

40. The method of claim 39, wherein the cell proliferative disorder is glioblastoma multiforme.

41. The method of claim 39, wherein the cell proliferative disorder is selected from the group consisting of lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer, brain cancer, head and neck cancer, pancreatic cancer, melanoma, stomach cancer and ovarian cancer.

42. A method of treating a cell proliferative disorder in a subject comprising contacting the subject with a retrovirus of claim 1, wherein the heterologous nucleic acid sequence encodes a therapeutic protein that inhibits proliferation of a neoplastic cell.

43. The method of claim 42, wherein the therapeutic protein comprises a polypeptide that converts a non-cytotoxic drug to a cytotoxic drug.

44. The method of claim 43, wherein the polypeptide has cytosine deaminase activity.

45. The method of claim 44, wherein the polypeptide comprises a sequence as set forth in SEQ ID NO:4, 12, 14, 16, or 18.

46. The method of claim 43, wherein the non-cytotoxic drug is 5-fluorocytosine.

47. A method of treating a cell proliferative disorder comprising administering a retrovirus of claim 1 or 2 to a subject having a cell proliferative disorder under conditions such that the retrovirus infects cells with the disorder and contacting the subject with an anti-cancer agent or chemotherapeutic agent.

48. The method of claim 47, wherein the anti-cancer agent is selected from the group consisting of bevacizumab, pegaptanib, ranibizumab, sorafenib, sunitinib, AE-941, VEGF Trap, pazopanib, vandetanib, vatalanib, cediranib, fenretinide, squalamine, INGN-241, oral tetrathiomolybdate, tetrathiomolybdate, Panzem NCD, 2-methoxyestradiol, AEE-788, AG-013958, bevasiranib sodium, AMG-706, axitinib, BIBF-1120, CDP-791, CP-547632, PI-88, SU-14813, SU-6668, XL-647, XL-999, IMC-1121B, ABT-869, BAY-57-9352, BAY-73-4506, BMS-582664, CEP-7055, CHIR-265, CT-322, CX-3542, E-7080, ENMD-1198, OSI-930, PTC-299, Sirna-027, TKI-258, Veglin, XL-184, or ZK-304709.

49. The method of claim 47, wherein the retrovirus is administered from about 10^3 to 10^7 TU/g brain weight.

50. The method of claim 49, wherein the retrovirus is administered from about 10^4 to 10^6 TU/g brain weight.

51. A recombinant retroviral replicating vector (RRV) comprising:

a retroviral GAG protein;

a retroviral POL protein;

a retroviral envelope;

a retroviral polynucleotide comprising Long-Terminal Repeat (LTR) sequences at the 3' end of the retroviral polynucleotide sequence, a promoter sequence at the 5' end of the retroviral polynucleotide, said promoter being suitable for expression in a mammalian cell, a gag nucleic acid domain, a pol nucleic acid domain and an env nucleic acid domain;

a therapeutic cassette comprising a mini-promoter cassette operably linked to a heterologous polynucleotide a miRNA cassette comprising a POLIII PROMOTER promoter linked to a primary precursor miRNA (pri-miRNA)for an miRNA or siRNA sequence;

cis-acting sequences necessary for reverse transcription, packaging and integration in a target cell.

52. The RRV of claim 51, wherein the miRNA is selected from the group consisting of miR-142-3p, miR-181, miR-223, miR 128-1 and miR 128-2.

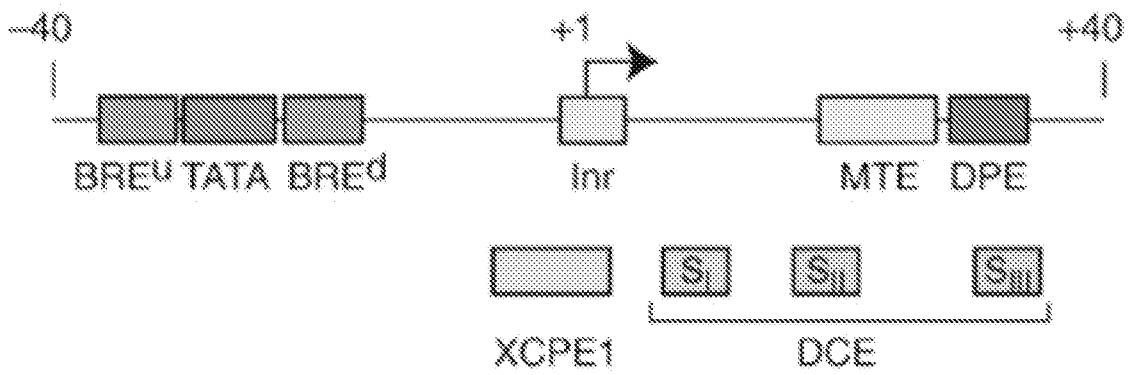

FIGURE 1

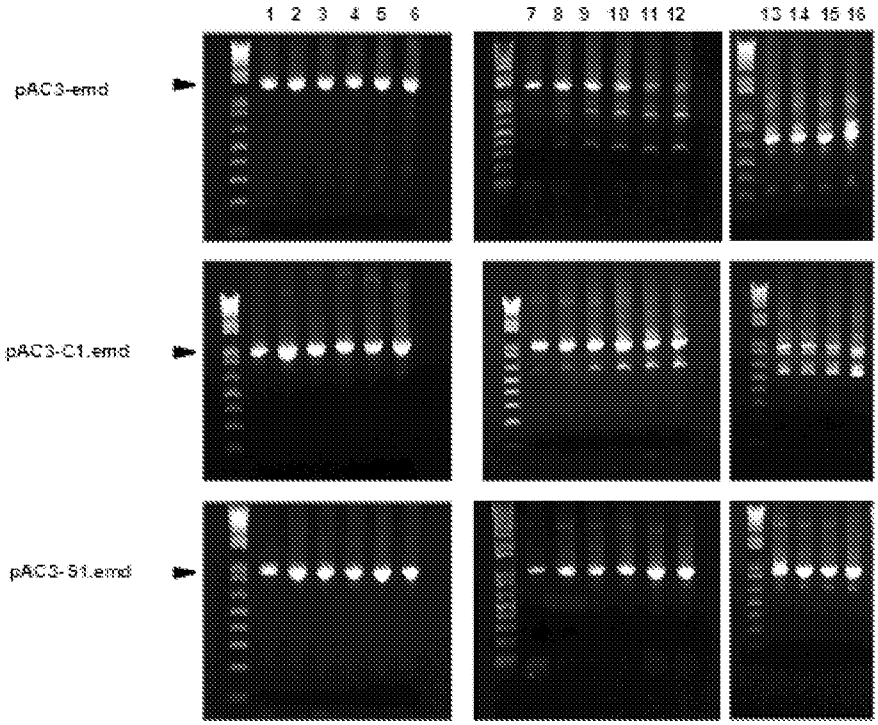

FIGURE 2A

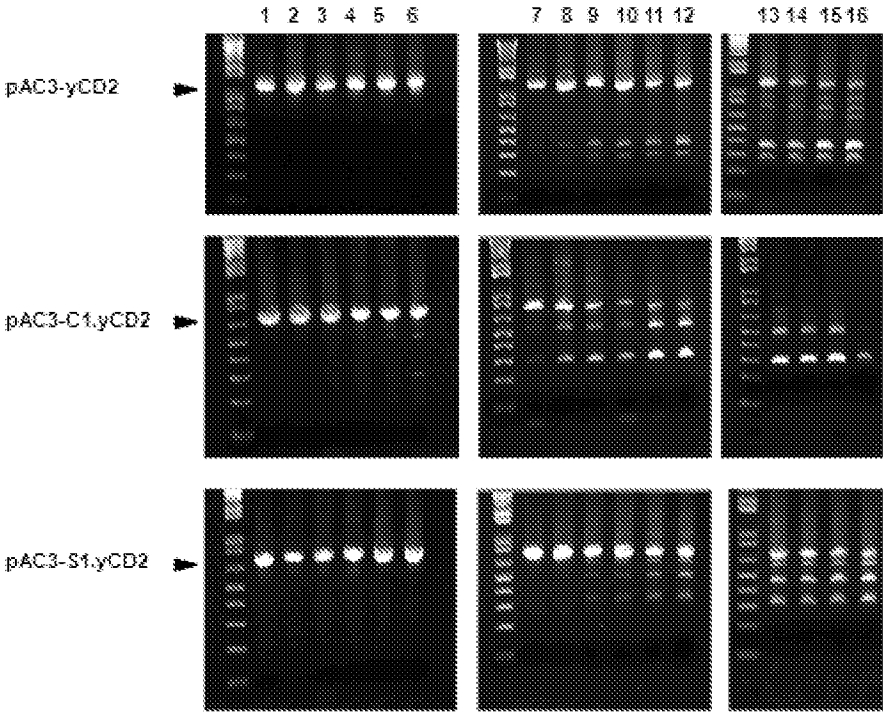
1 2 3 4 5 6
7 8 9 10 11 12
13 14 15 16
pAC3-yCD2
pAC3-C1.yCD2
pAC3-S1.yCD2

FIGURE 2B

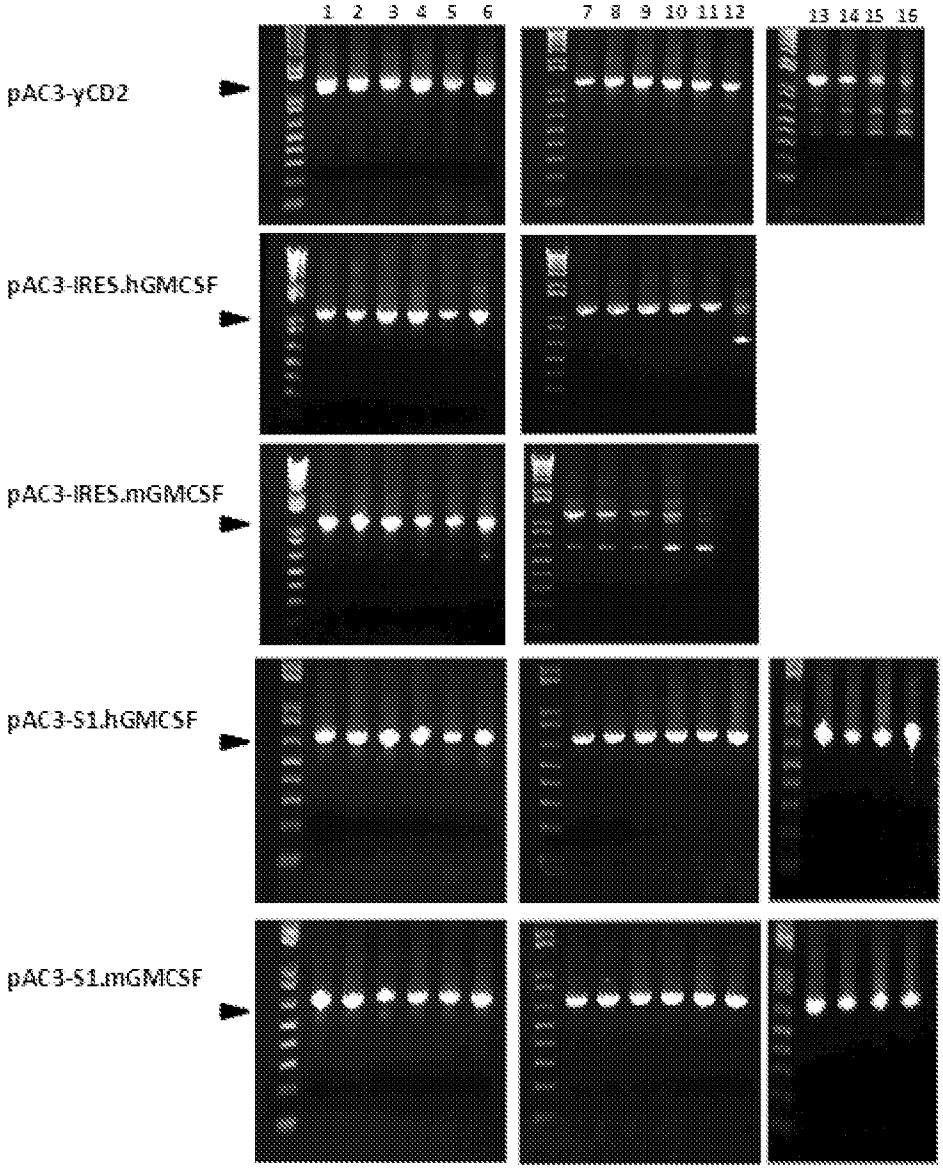
1 2 3 4 5 6
7 8 9 10 11 12
13 14 15 16
pAC3-yCD2
pAC3-IRES.hGMCSF
pAC3-IRES.mGMCSF
pAC3-S1.hGMCSF
pAC3-S1.mGMCSF

FIGURE 3

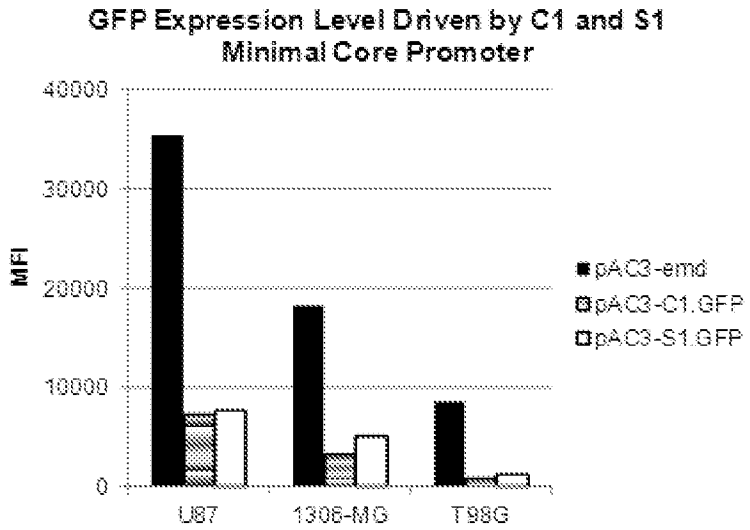

FIGURE 4A

CD Expression Mediated by Core Promoter Derivatives in Transiently Transfected 293T Cells

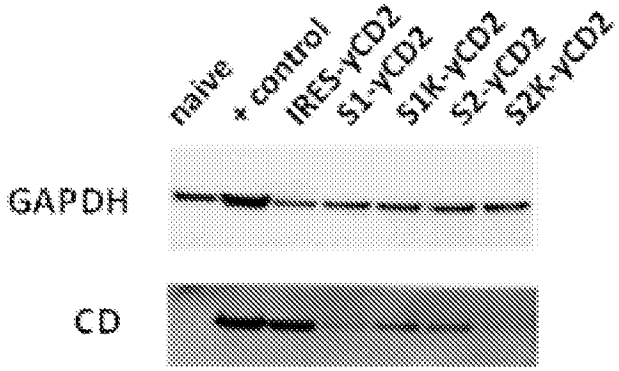

FIGURE 4B

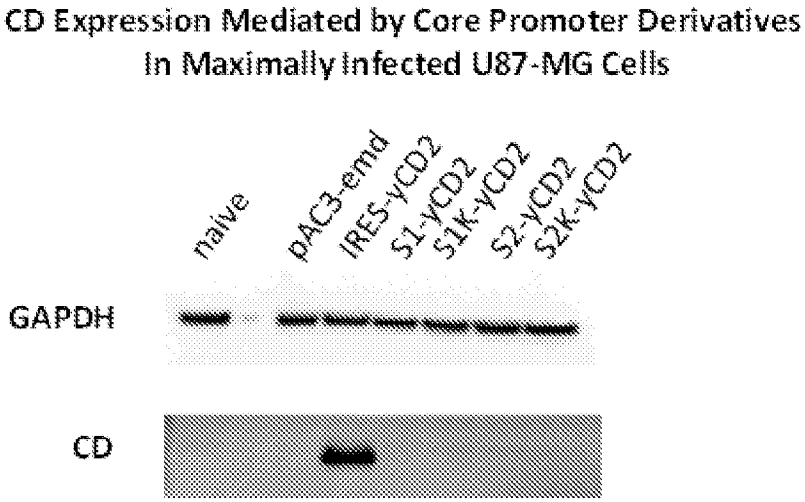

FIGURE 4C

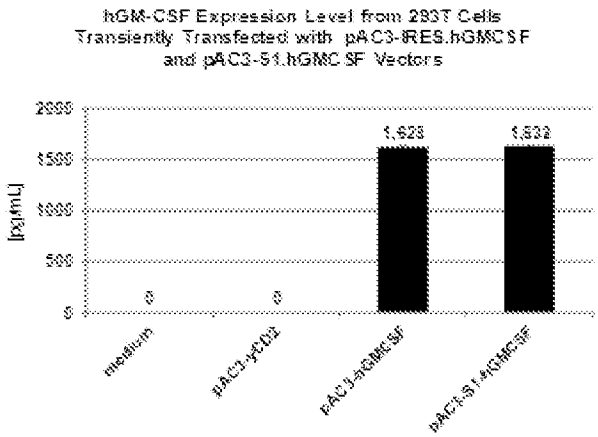

FIGURE 4D

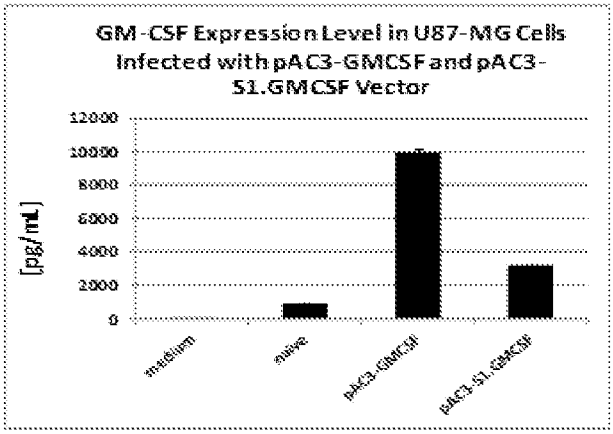

FIGURE 4E

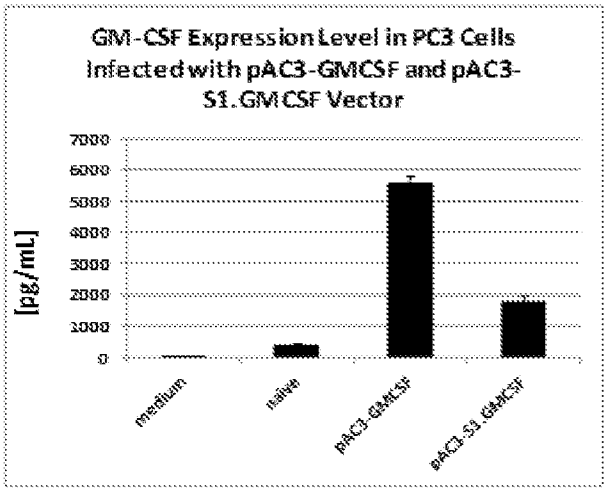

FIGURE 4F

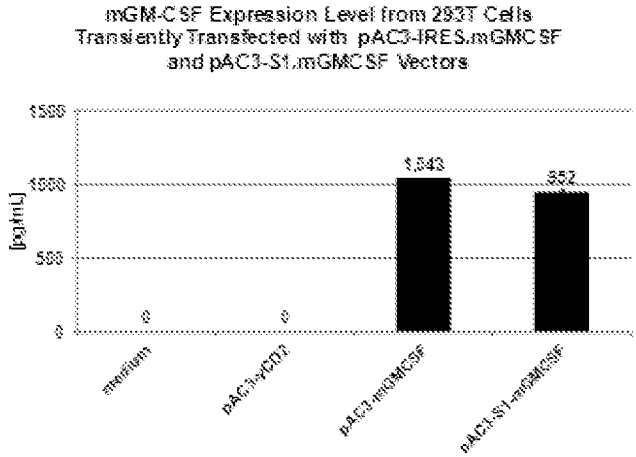

FIGURE 4G

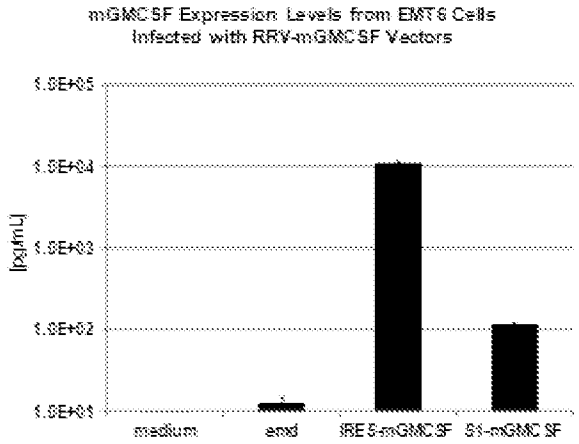

FIGURE 4H

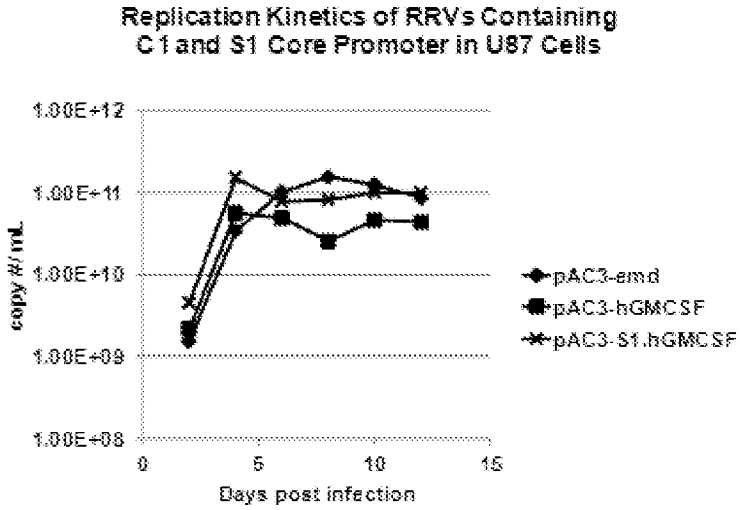

FIGURE 5A

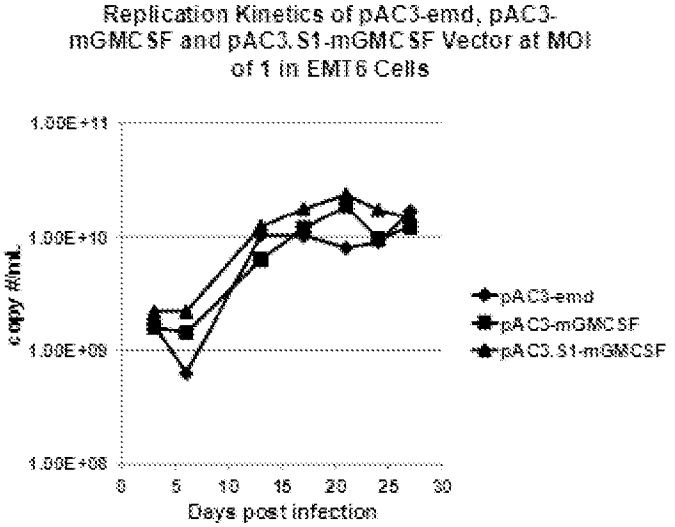

FIGURE 5B

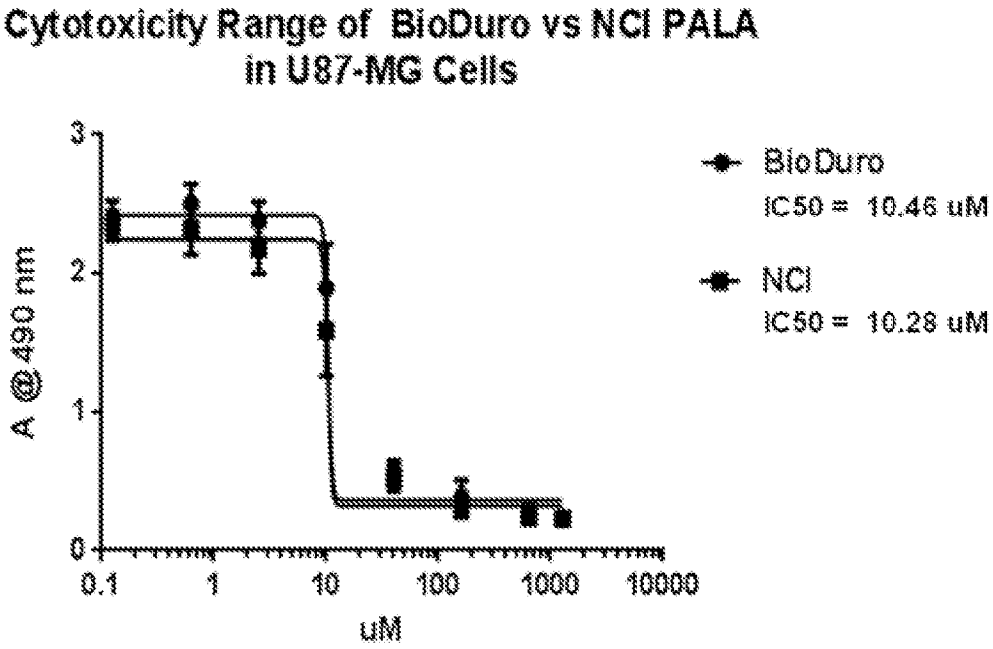

FIGURE 6

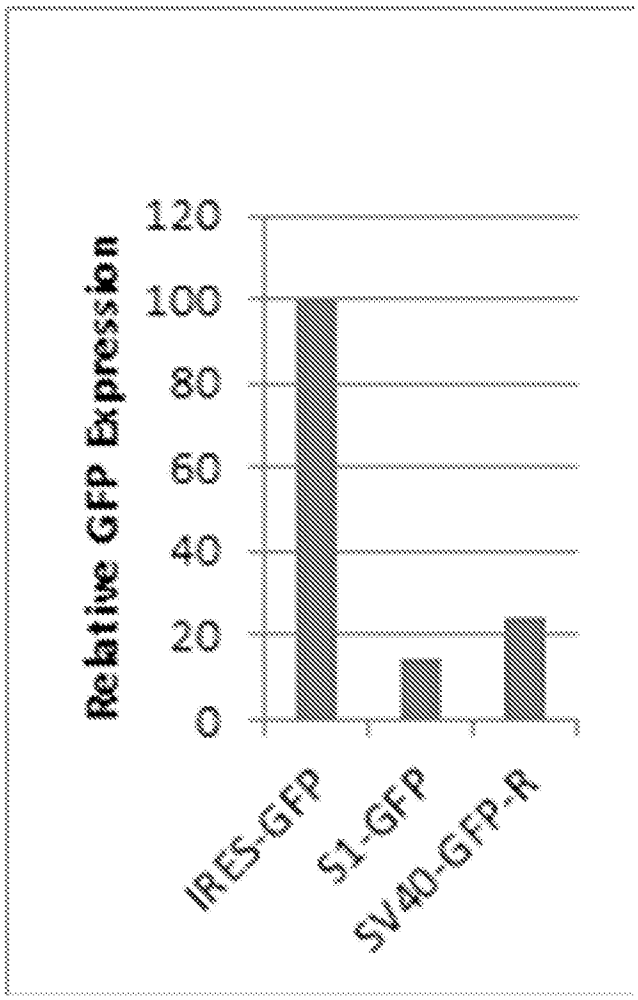
Relative GFP Expression
120
100
80
60
40
20
0
IRES-GFP
S1-GFP
SV40-GFP-R

FIGURE 7

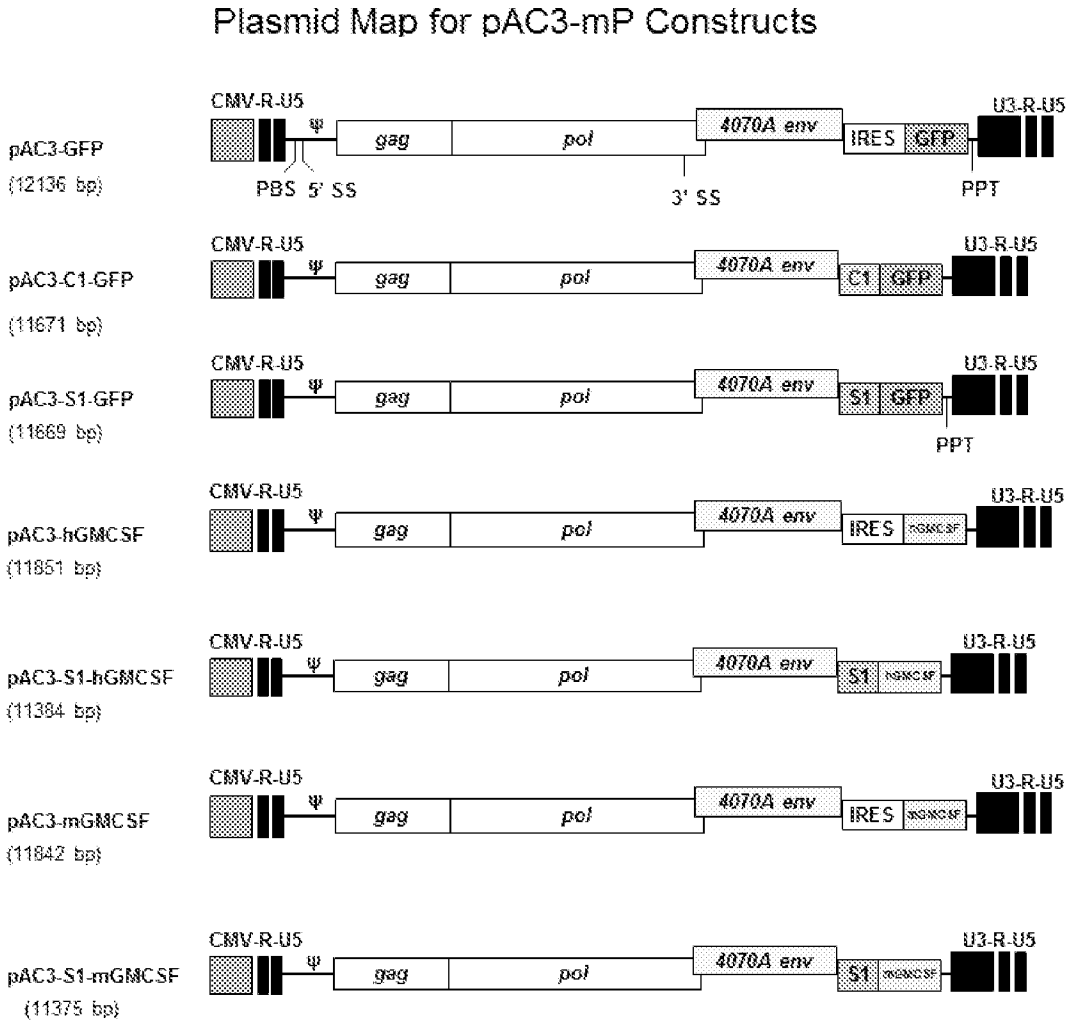
Plasmid Map for pAC3-mP Constructs
pAC3-GFP
(12136 bp)
CMV-R-U5
Ψ
gag
pol
4070A env
IRES
GFP
U3-R-U5
PBS
5' SS
3' SS
PPT
pAC3-C1-GFP
(11671 bp)
C1
pAC3-S1-GFP
(11669 bp)
S1
pAC3-hGMCSF
(11851 bp)
hGMCSF
pAC3-S1-hGMCSF
(11384 bp)
pAC3-mGMCSF
(11842 bp)
mGMCSF
pAC3-S1-mGMCSF
(11375 bp)

FIGURE 8A

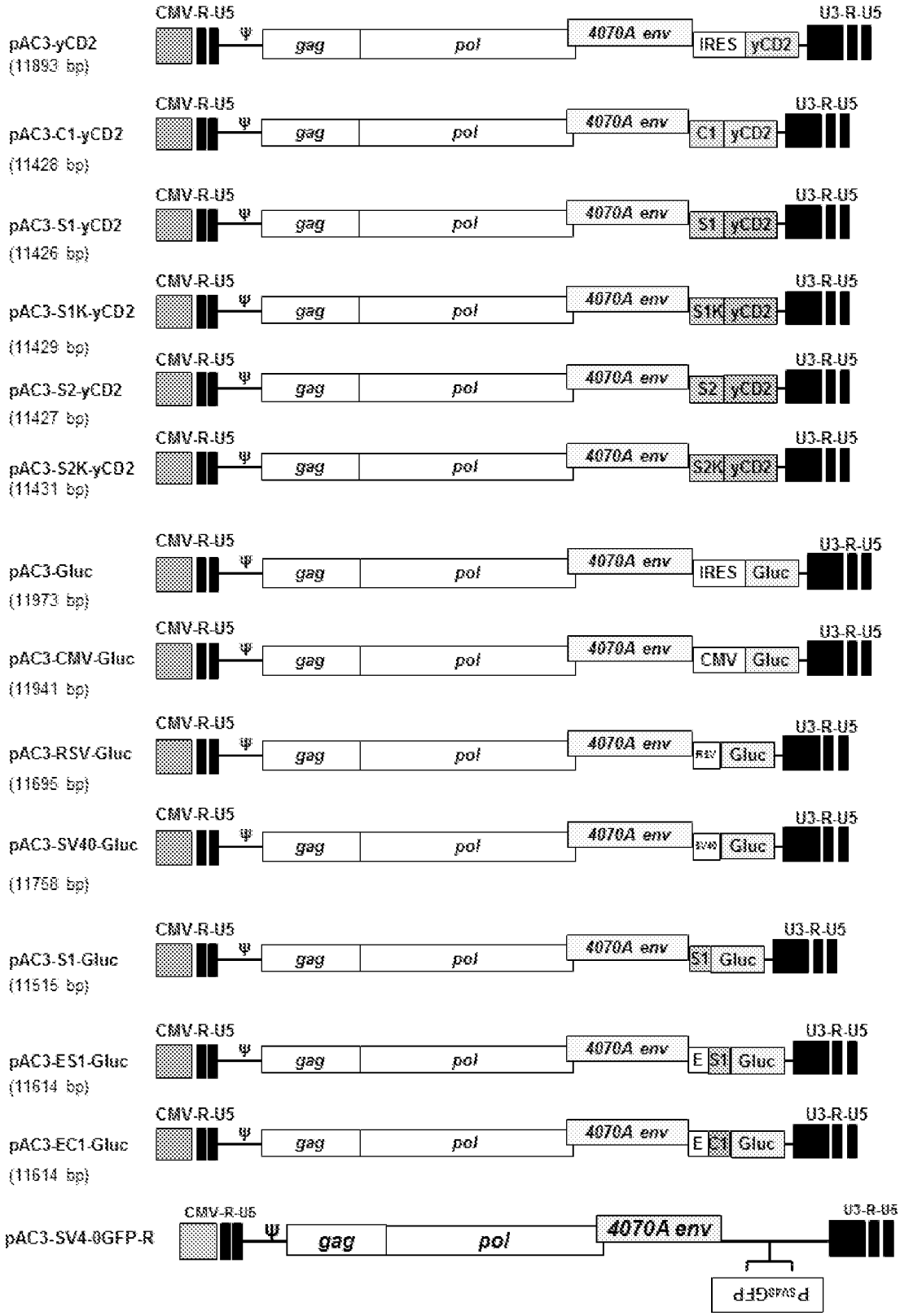
pAC3-yCD2
(11893 bp)
CMV-R-U5
Ψ
gag
pol
4070A env
IRES
yCD2
U3-R-U5
pAC3-C1-yCD2
(11428 bp)
C1
pAC3-S1-yCD2
(11426 bp)
S1
pAC3-S1K-yCD2
(11429 bp)
S1K
pAC3-S2-yCD2
(11427 bp)
S2
pAC3-S2K-yCD2
(11431 bp)
S2K
pAC3-Gluc
(11973 bp)
Gluc
pAC3-CMV-Gluc
(11941 bp)
CMV
pAC3-RSV-Gluc
(11695 bp)
RSV
pAC3-SV40-Gluc
(11758 bp)
SV40
pAC3-S1-Gluc
(11515 bp)
pAC3-ES1-Gluc
(11614 bp)
E
pAC3-EC1-Gluc
(11614 bp)
pAC3-SV4-0GFP-R
PSV40GFP

FIGURE 8B

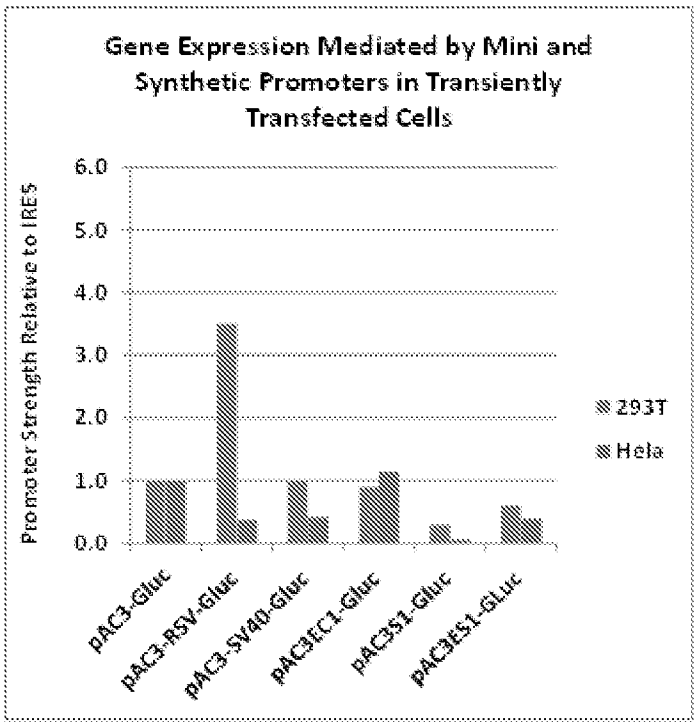
Gene Expression Mediated by Mini and Synthetic Promoters in Transiently Transfected Cells
Promoter Strength Relative to IRES
6.0
5.0
4.0
3.0
2.0
1.0
0.0
293T
Hela
pAC3-Gluc
pAC3-RSV-Gluc
pAC3-SV40-Gluc
pAC3EC1-Gluc
pAC3S1-Gluc
pAC3ES1-GLuc

FIGURE 9

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/066709

A. CLASSIFICATION OF SUBJECT MATTER

C12N 15/867(2006.01)i, C12N 7/01(2006.01)i, A61P 35/00(2006.01)i

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N 15/867; C07H 21/04; C12N 15/82; C12N 9/02; C12N 1/12; C12N 7/01; A61K 38/16; A61K 38/17; C12N 1/20; A61P 35/00

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Korean utility models and applications for utility models
Japanese utility models and applications for utility models

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
eKOMPASS(KIPO internal) & Keywords: retroviral replicating vector, construct, plasmid, gammaretrovirus, mini-promoter, core promoter

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2011-126864 A2 (TOCAGEN INC.) 13 October 2011 See claim 1.	1-16,19,21-37,51,52
A	WO 01-04266 A1 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 18 January 2001 See claim 25.	1-16,19,21-37,51,52
A	US 2012-0052554 A1 (KASAHARA, NORIYUKI et al.) 01 March 2012 See claim 63.	1-16,19,21-37,51,52
A	WO 2012-021794 A1 (PIONEER HI-BRED INTERNATIONAL, INC. et al.) 16 February 2012 See claim 1.	1-16,19,21-37,51,52
A	WO 2006-127980 A2 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 30 November 2006 See claims 1 and 2.	1-16,19,21-37,51,52

☐ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents,such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 January 2014 (27.01.2014)	**28 January 2014 (28.01.2014)**

Name and mailing address of the ISA/KR
Korean Intellectual Property Office
189 Cheongsa-ro, Seo-gu, Daejeon Metropolitan City, 302-701, Republic of Korea
Facsimile No. +82-42-472-7140

Authorized officer
HEO, Joo Hyung
Telephone No. +82-42-481-8150

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/066709

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 39-50
because they relate to subject matter not required to be searched by this Authority, namely:
Claims 39-50 pertain to methods for treatment of the human body by therapy, and thus relate to a subject matter which this International Searching Authority is not required, under Article 17(2)(a)(i) of the PCT and Rule 39.1(iv) of the Regulations under the PCT, to search.

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 17,18,20,38
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required addtional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of any additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/US2013/066709

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2011-126864 A2	13/10/2011	US 2011-0287020 A1	24/11/2011
		WO 2011-126864 A3	19/04/2012
WO 01-04266 A1	18/01/2001	AU 2001-085500 A	30/01/2001
		GB 0203028 D0	27/03/2002
		GB 2368846 A	15/05/2002
		GB 2368846 B	25/08/2004
		WO 01-004266 A9	12/09/2002
US 2012-0052554 A1	01/03/2012	AT 424114 T	15/03/2009
		AU 2000-41900 A	17/04/2000
		CA 2346931 A1	06/04/2000
		CA 2346931 C	29/11/2011
		DE 69940521 D1	16/04/2009
		DK 1115290 T3	22/06/2009
		EP 1115290 A1	18/07/2001
		EP 1115290 A4	04/12/2002
		EP 1115290 B1	04/03/2009
		EP 1932426 A1	18/06/2008
		EP 2386646 A1	16/11/2011
		ES 2323744 T3	23/07/2009
		US 2002-0127697 A1	12/09/2002
		US 6410313 B1	25/06/2002
		WO 00-18240 A1	06/04/2000
WO 2012-021794 A1	16/02/2012	US 2012-0042412 A1	16/02/2012
		US 2012-0042413 A1	16/02/2012
		US 2012-0042414 A1	16/02/2012
		WO 2012-021785 A1	16/02/2012
		WO 2012-021797 A1	16/02/2012
WO 2006-127980 A2	30/11/2006	US 2010-0129863 A1	27/05/2010
		US 7968698 B2	28/06/2011
		WO 2006-127980 A3	30/04/2009