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(71) Applicant (for all designated States except US): **THE CHILDREN'S HOSPITAL OF PHILADELPHIA** [US/US]; Research Institute, Abramson Research Center, Suite 140, Office Of Technology Transfer, 3615 Civic Center Boulevard, Philadelphia, PA 19104 (US).

(72) Inventor; and

(75) Inventor/Applicant (for US only): **COUTO, Linda, B.** [US/US]; 258 S. 3rd Street, Unit 6, Philadelphia, PA 19106 (US).

(74) Agents: **RIGAUT, Kathleen, D.** et al.; Dann, Dorfman, Herrell & Skillman, 1601 Market Street, Suite 2400, Philadelphia, PA 19103-2307 (US).

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(54) Title: NUCLEIC ACIDS FOR TARGETING MULTIPLE REGIONS OF THE HCV GENOME

(57) Abstract: Compositions and methods effective for modulating Hepatitis C viral infection are provided. Compositions and methods effective for modulating Hepatitis C viral infection are provided. Specifically, multiple artificial miRNAs targeting different regions of the HCV genome were inserted into a single promoter, polycistronic expression vector. The exogenous anti-HCV miRNAs induced gene silencing. When expressed from an adenovirus associated virus (AAV) delivery system, the vector inhibit the replication of HCV without inducing toxicity.



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NUCLEIC ACIDS FOR TARGETING MULTIPLE REGIONS OF THE HCV GENOME

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Field of the Invention

This invention relates to the field of medicine, molecular biology and treatment of disease. More specifically, the present invention features compositions and methods useful for the treatment of Hepatitis C infection.

10

Background of the Invention

Several publications and patent documents are cited throughout this application in order to more fully describe the state of the art to which this invention pertains. The disclosure of each of these citations is incorporated by reference herein.

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It is estimated that approximately 3% of the world population, or 170 million people, are chronically infected with the hepatitis C virus (HCV); with 3.2 million affected individuals in the United States alone. Most acute HCV infections are asymptomatic, but the infection resolves spontaneously in only about 15-30% of subjects. For the remaining 70-85% of individuals, a chronic infection persists, and decades can elapse before symptoms appear. Chronic HCV infection can lead to serious liver disease, including steatosis, fibrosis, cirrhosis and hepatocellular carcinoma (HCC). Approximately 20% of chronically infected individuals will develop cirrhosis, and 1.2-4% of all those chronically infected will develop HCC.

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The current therapy for HCV infection is a year long treatment with a combination of pegylated interferon- α (INF- α) and ribavirin. This treatment is approximately 80% effective against HCV genotypes 2 and 3, but against the major genotype found in the United States and the world (genotype 1), it is less than 50% effective. In addition, there are numerous serious side effects from these drugs including neutropenia, anemia, nausea, and depression. A number of specific small molecule antiviral therapies are currently under development, and although some have shown good antiviral properties, they are not broadly applicable to all HCV genotypes and drug resistance develops quickly.

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RNA interference (RNAi) based-technology is being developed to treat a wide range of diseases (1), and is a particularly good strategy for treating RNA virus-mediated diseases, such as HIV, HCV, and polio virus infections. RNAi is mediated by a variety of small regulatory RNAs, which differ in their biogenesis (2). Short interfering RNAs (siRNAs) are small double-stranded RNAs of 21-23 nt that are generated in the cytoplasm from longer RNAs (e.g., viral) following enzymatic cleavage by the RNase III enzyme Dicer. In contrast, microRNAs (miRNAs) are derived from long primary RNAs (pri-miRNA) that are transcribed in the nucleus and cleaved by the microprocessor complex, composed of the nuclear enzyme Drosha and its cofactor DGCR8, into ~70 nt precursor stem-loop RNAs (pre-miRNAs). Pre-miRNAs are exported to the cytoplasm by Exportin 5, where they are further processed by Dicer into mature miRNAs. Short hairpin RNAs (shRNAs) (3) are not naturally found in cells, but they are designed to be expressed from plasmids or viral vectors in the nucleus and have a stem-loop structure similar to pre-miRNAs. The shRNAs are also cleaved by Drosha/DGCR8 in the nucleus and are transported to the cytoplasm where they are cleaved into siRNAs by Dicer. The products of these pathways (siRNAs and miRNAs) induce gene silencing after the antisense (AS) or guide strand of the RNA duplex is loaded into the RNA induced silencing complex (RISC), and guides the endonucleolytic cleavage or translational repression of a cognate mRNA. The RNA strand of the siRNA duplex that has the lowest free energy at the 5' end will be loaded into the RISC and will mediate post-transcriptional silencing (4;5) Using this feature, as well as other characteristics that have been identified empirically (6), it is possible to design synthetic siRNAs that are highly effective in silencing cellular and viral genes.

As such, RNAi has become a standard tool to inhibit gene expression, and a variety of nucleic acid species are capable of modifying gene expression. These include antisense RNA, siRNA, shRNA, microRNA (miRNAs). Other approaches to down modulate target gene expression include use of RNA and DNA aptamers. Each of these nucleic acid species have been shown to inhibit target nucleic acid activity, including gene expression, but a need exists to selectively down-regulate the expression of viral genes.

In the case of Hepatitis C virus (HCV), siRNAs targeting the 5' untranslated region (UTR), core, and several non-structural proteins (NS3, NS4B, NS5A, and NS5B) have all been shown to inhibit HCV RNA and protein levels by up to 95%

when tested in cells containing autonomously replicating full genomic or subgenomic HCV replicons (7;8). Likewise, shRNAs targeting the 5'UTR, E2, NS3, and NS5B were also capable of inhibiting virus replication in replicon-containing cells (7;8). However, RNAi-based technologies suffer from the same problems that plague traditional anti-viral drugs; that is, sustained use of single RNAi effectors results in the emergence of RNAi-resistant viral variants, which contain nucleotide substitutions or deletions in the areas targeted by the RNAi effectors. It is now generally agreed that for viruses that are replicated by low fidelity RNA polymerases, such as HCV, antiviral drug therapy involving RNAi should be used in a combined fashion to prevent the emergence of resistant viruses (7;10;11).

Many groups are now developing new approaches to simultaneously deliver multiple RNAi effectors to target HCV and HIV, including the use of pools of siRNAs (12) and the expression of multiple shRNAs (13;14). For example, expression cassettes with four shRNAs have been shown to prevent the emergence of HIV viral escape mutants (14). One important finding from these studies is the importance of avoiding the use of repetitive elements in the expression constructs (e.g., identical promoters) when using lentiviral vectors for delivery, in order to prevent the deletion of one or multiple shRNA cassettes by recombination.

The first group to show that a human microRNA stem-loop RNA precursor (miR-30) could be used as a scaffold to shuttle siRNA sequences also developed design rules for the construction of these so-called artificial miRNAs (15). In addition to a large terminal loop, efficient Drosha processing of a pri-miRNA transcript requires single stranded RNA sequences flanking the 70-80 nt stem-loop structure. Since then many other investigators have utilized artificial miRNAs based on miR-30 and other endogenous miRNAs to express individual RNAi effectors from either Pol II (16-18) or Pol III (19-21) promoters. Artificial miRNA hairpins have also been multimerized in order to express a combination of miRNAs in a single vector (22-27). However, like some of the multiple shRNA constructs, most of these miRNA complexes use repetitive elements, and thus may be genetically unstable in vectors employed for therapeutic use.

Over the past several years, distinct differences have been observed between the use of shRNAs and miRNAs. Recent studies using Pol III-driven shRNAs and miRNAs, that have been carefully designed such that they each generate similar processed siRNAs with the equivalent strand biasing, indicate that shRNAs are more

potent than miRNAs (28). This is likely due to the higher levels of siRNAs that are generated from equivalent amounts of expression plasmids. However, there is also a high level of precursor RNA produced using shRNAs, while there is minimal build-up of pre-miRNAs when using artificial miRNAs (28;29). Furthermore, using a CMV promoter to express miRNAs, no precursors were observed, suggesting that complete processing of Pol II transcripts occurs more efficiently than that of Pol III-expressed miRNAs (17). High levels of precursor RNAs are an indication that the endogenous RNAi machinery is being saturated. Interfering with miRNA biogenesis can have serious consequences since this pathway is involved in critical cellular processes.

There is now general agreement from *in vitro* studies that artificial miRNAs are less likely to lead to this problem, as non-related shRNAs compete with each other and with exogenous and endogenous miRNAs, whereas miRNAs expressed from pol II promoters do not (20;30).

Several *in vivo* studies have highlighted the problems encountered with the use of shRNAs, and have confirmed that interfering with the miRNA pathway leads to toxicity. Expression of several individual shRNAs from an AAV vector caused severe liver damage and fatality at high doses of vector (31). Toxicity was also observed in mouse brain using an AAV vector expressing shRNAs targeting the Huntington or spinocerebellar ataxia type 1 genes (29;32).

It is clear that a need exists for other safe and effective compositions and methods for treatment of HCV and other viral infections, since viruses represent one of the many circumstances where down-regulation of gene target expression is desirable. The present invention satisfies this need and provides related advantages that overcome the deficiencies of the prior art.

Summary of the Invention

In accordance with the present invention, a composition comprising a miRNA expression cassette comprising at least two isolated nucleotide sequences selected from the group consisting of sequences complementary to SEQ ID NOs: 1-5, in a pharmaceutically acceptable carrier is provided. In a preferred embodiment, the cassette comprises at least four isolated sequences. In a particularly preferred embodiment, the cassette comprises all five isolated sequences. In another aspect, the cassette is cloned within a vector. Such vectors include without limitation, AAV vectors, lentiviral vectors, retroviral vectors and AV vectors. Particularly preferred

are AAV vectors, selected from the group consisting of serotypes 1-9. Exemplary cassettes cloned within the AAV vectors contain cluster 1, cluster 2 or cluster 5 respectively.

In yet another embodiment of the invention, a method of reducing HCV viral load in a patient is provided. An exemplary method entails administering to the liver of said patient a therapeutically effective amount of a cluster comprising vector which directs cleavage of target HCV mRNA sequences present in said patient, thereby reducing HCV viral load. In one aspect, the vector may be directly introduced into the liver of said patient. Alternatively, the vector may be introduced via intravenous infusion.

Brief Description of the Figures

Figure 1: Schematic of the miR-17-92 primary RNA and the artificial HCV-mRNA clusters. (A) Structure of endogenous miR-17-92 polycistron. (B) Structure of HCV-miR Cluster 1. (C) Structure of HCV-miR Cluster 1 + Intron. (D) Structure of HCV-miR Cluster 2. Numbers in between pre-miRNAs represent nucleotides. MiRNA stems are not drawn to scale and secondary structures are approximate. ApoE, apolipoprotein E hepatic control region; hAAT, alpha-one antitrypsin promoter; pA, bovine growth hormone polyadenylation signal.

Figure 2: *In vitro* inhibition of luciferase reporters by miRNAs targeting HCV. Huh-7 cells were co-transfected with a RLuc-HCV reporter plasmid (125 ng) and a plasmid expressing one of five anti-HCV miRNAs (125 ng), a plasmid expressing all five anti-HCV miRNAs (125 ng), or pUC19 (125 ng). RLuc reporter plasmids encoded either an individual HCV target (UTR1, UTR2, UTR3, Core, NS5B) or all 5 HCV target sequences (5 Targets). Twenty four hours post-transfection, cell lysates were prepared and dual luciferase (FFLuc and RLuc) assays were performed. Normalized RLuc expression in cells transfected with pUC19 was set as 100% activity or 0% inhibition of the target, and the percent inhibition achieved by each miRNA was compared to the pUC19 control. Mean values of triplicate samples from at least 3 independent experiments (unless stated otherwise) are shown (+/-SD). (A) Inhibitory activity of individually expressed anti-HCV miRNAs (miR-UTR1, miR-UTR2, miR-UTR3, miR-Core, miR-NS5B) against individual reporters or the reporter encoding all 5 targets. (B) Inhibitory activity of anti-HCV miRNAs when

expressed from HCV-miR Cluster 1 or HCV-miR-Cluster 1 + Intron against individual cognate targets or the reporter encoding all 5 targets. (C) Inhibitory activity of anti-HCV miRNAs when expressed from HCV-miR Cluster 2 against individual cognate targets or the reporter encoding all 5 targets (data is from triplicate replicates of 2 independent experiments).

Figure 3: Specificity of miRNAs targeting HCV. Huh-7 cells were co-transfected with a RLuc-HCV reporter plasmid (125 ng) and a plasmid expressing a single anti-HCV miRNA (125ng), HCV-miR Cluster 1 (125 ng), or pUC19 (125ng). Twenty four hours post-transfection, cell lysates were prepared and dual luciferase (FFLuc and RLuc) assays were performed. Normalized RLuc expression the presence of pUC19 was set as 100% activity or 0% inhibition of the target, and the % inhibition achieved by each miRNA was compared to the pUC19 control. Mean values from triplicate replicates of at least 3 independent experiments are shown (+ SD). (A) Inhibitory activity of single anti-HCV miRNAs against WT reporter plasmids (UTR1, UTR2, UTR3, Core, NS5B). (B) Inhibitory activity of HCV-miR Cluster 1 against RLuc-HCV reporters that contained 3 bp mutations in the miRNA target sequences (UTR1-M, UTR2-M, UTR3-M, Core-M, NS5B-M). (C) Inhibitory activity of HCV-miR Cluster 1 against RLuc-HCV reporters that contained the reverse complement of the miRNA target sequences (UTR1-RC, UTR2-RC, UTR3-RC, Core-RC, NS5B-RC).

Figure 4: Cell viability. Huh-7 cells were co-transfected with increasing amounts of the HCV-miR Cluster 1 plasmid (0, 2.5, 10, 50, 125 ng) in the presence or absence of one of the RLuc-HCV reporter plasmids. The total amount of plasmid DNA added to cells was adjusted to 250 ng using pUC19. Twenty four hours post-transfection, 50 μ l of AlamarBlue reagent (Invitrogen Carlsbad, CA) was added directly to the cells and the cells were incubated at 37°C for 4 hours, and fluorescence was measured according to the manufacturer's instructions. Percent survival was calculated relative to cells not transfected with HCV-miR Cluster 1 plasmid DNA. Mean values from triplicate measurements of two independent experiments are shown (+ SD).

Figure 5: *In vivo* inhibition of RLuc reporters by miRNAs targeting HCV. HDTV injections of Balb/c mice were performed using HCV-miR Cluster1 + Intron (12 μ g),

HCV-miR Cluster 2 plasmid (12 μ g), or pUC19 (12 μ g), and one of the RLuc-HCV fusion reporter plasmids (12 μ g) or psiCheck plasmid (12 μ g) in a volume of 2 ml PBS. Two days later, animals were sacrificed, livers harvested, and liver lysates were assayed for both FFLuc and RLuc activity. Normalized RLuc expression in the

5 animals that received the pUC19 negative control plasmid was set as 100% activity or 0% inhibition of the target, and the percent inhibition achieved by each miRNA was compared to the pUC19 control. (A) Inhibitory activity of anti-HCV miRNAs when expressed from HCV-miR Cluster 1 + Intron against individual reporter plasmids, the reporter encoding all 5 HCV targets, or a plasmid encoding no HCV targets

10 (psiCheck). (B) Inhibitory activity of anti-HCV miRNAs when expressed from HCV-miR Cluster 2 against individual reporter plasmids, the reporter encoding all 5 HCV targets, or a plasmid encoding no HCV targets (psiCheck).

Figure 6: Northern blot analyses of miRNA transcripts in murine liver RNA. (A-E)

15 Mice were injected with a plasmid expressing HCV-miRNA Cluster 1 (lane 2), HCV-miRNA Cluster 1 + Intron (lane 3) or pUC19 (lane 4). Synthetic siRNAs were used as probe-specific positive controls: 0.4 fmole (lane 5), 2.0 fmole (lane 6), 10.0 fmole (lane 7), 50.0 fmole (lane 8, D only). A radiolabeled RNA marker was included (lane 1). The miRNA transcripts were detected using radiolabeled oligonucleotide probes

20 specific for the anti-sense strand: (A) miR-UTR1, (B) miR-UTR2, (C) miR-UTR3, (D) miR-Core, (E) miR-NS2B. Blots were stripped and reprobed with a U6 snRNA probe to confirm equal sample loading.

Figure 7: (A-B) Northern blot analyses of miRNA transcripts in murine liver RNA.

25 Mice were injected with a plasmid expressing HCV-miRNA Cluster 1+ Intron (lane 2), HCV-miRNA Cluster 2 (lane 3) or pUC19 (lane 4). Synthetic siRNAs were used as probe-specific positive controls: 0.4 fmole (lane 5), 2.0 fmole (lane 6), 10.0 fmole (lane 7). A radiolabeled RNA marker was included (lane 1). The miRNA transcripts were detected using radiolabeled oligonucleotide probes specific for the anti-sense

30 strand: (A) miR-UTR1, (B) miR-UTR2.

Figures 8A and 8B: Sequence information for Cluster 1. Figure 8B: Sequence information for Cluster 2.

Figure 9: A schematic diagram of the HCV genome. HCV sequence information is available in GenBank.

Figure 10. Construction of HCV-miRNA Cluster 5 encoding five anti-HCV

5 miRNAs. The miRNAs used in Cluster 1 were utilized. The difference is the last miRNA (miR-92) is employed rather than the second miRNA position (miR-18) as a scaffold for miR-UTR-1. Thus this cluster contains miR-UTR2, miR-UTR3, MiR-Core, MiR-NS5B, and miR-UTR1.

10 **Figure 11.** A graph showing in vitro inhibition of RLuc-HCV reporter plasmids by HCV- miRNA-Cluster 5.

Figure 12. AAV vectors expressing HCV-mRNA-Cluster 5 are effective to inhibit HCVcc replication.

15

Figures 13A and 13B. Sequence information for AAV vectors (Fig. 13A) comprising Cluster 5 (Fig. 13. B).

Figure 14. A graph showing that AAV-vectors expressing HCV-miRNA –Cluster 5
20 eliminate HCVcc from infected cells.

Figure 15. A graph showing that scAAV8-HCV-miRNA-Cluster 5 silences all 5 target sequences in vivo.

25 **Figure 16.** A pair of graphs showing that scAAV8-HCV-miRNA-Cluster 5 can be safely delivered to the liver.

Detailed Description of the Invention

30 The present invention provides compositions and methods for reducing the amount of a viral genome in a target cell, where the target cell may be present in vitro or in vivo. The term "reducing the amount of" indicates that the level or quantity of the viral genome in the target cell is reduced by at least about 2-fold, usually by at least about 5-fold, possibly even 10-fold, 15-fold, 20-fold, 50-fold, or 100-fold or

more, as compared to a control (i.e., an untreated target cell). In a preferred embodiment, the viral genome comprises HCV.

As described throughout the application, miRNAs are a class of 15-30 nt non-coding RNAs (ncRNAs) that exist in a variety of organisms, and are conserved throughout evolution. They are processed from hairpin precursors (pre-miRNA) which are derived from primary transcripts (pri-miRNA) through sequential cleavage by RNase III enzymes. Many miRNAs can be encoded in intergenic regions, hosted within introns of pre-mRNAs or within ncRNA genes. MiRNAs also tend to be clustered and transcribed as polycistrons and often have similar spatial temporal expression patterns. They have been found to have roles in a variety of biological processes including developmental timing, differentiation, apoptosis, cell proliferation, organ development, and metabolism by negatively regulating gene expression by base-pairing to a target sequence in an mRNA. In certain embodiments of the instant invention, this negative regulation is exploited for therapeutic advantage.

Previous data indicate that maximal silencing can be achieved with miRNA-based RNAi effectors without the build-up of excessive precursor and non-processed products that may disrupt miRNA biogenesis and function. Since many miRNAs exist naturally in clusters and are transcribed as polycistronic pri-miRNAs in the nucleus by tissue specific pol II promoters, their genomic organization makes them an attractive system for treating "error-prone" RNA viruses. (33). This allows for the simultaneous expression of multiple miRNAs from a single transcription unit and avoids the use of repetitive promoter sequences. This configuration is ideally suited for targeting many different regions of viral genomes and is more likely to yield a potent treatment for viruses such as HCV, HIV, and poliovirus. Recently, two different endogenous miRNA clusters (miR106b-93-25 and miR17-92) have been manipulated to express multiple anti-HIV miRNAs (34;35). Inhibition of HIV target sequences ranged from ~0-80% for different anti-HIV-miRNAs, and silencing activity of individual miRNAs improved when the secondary structure of the endogenous pre-miRNA stems were mimicked, as opposed to having fully-paired stem structures (34).

One feature of the present invention comprises the miR17-92 cluster to allow development of an artificial polycistronic miRNA for treating HCV infection. In certain embodiments, the first five pre-miRNAs of the cluster have been replaced with inhibitory RNAs targeting HCV, and four out of the five miRNAs are active,

inhibiting their cognate sequences by up to 80% *in vitro*. The *in vivo* activity of an artificial polycistronic miRNA cluster was evaluated, and up to 97% inhibition of the HCV targets was observed. The miRNAs are specific for their cognate sequences and fail to inhibit the many non-target sequences tested. In addition, the correct strands of the miRNAs are incorporated into the RISC. In another embodiment, HCV inhibitory RNAs are inserted at miR-17 (UTR-2), miR-19A (UTR-3), miR-20 (Core), miR-19B (NS5B) and miR-92 (UTR-1). In this construct, referred to herein as cluster 5, the miR-18 loop is deleted. However, in an alternative embodiment, this loop may be left intact. In contrast to clusters 1 and 2, all five anti-HCV inhibitory RNAs in cluster 5 were active and inhibited expression of their cognate targets. These findings suggest that the HCV miRNA clusters are active and that off-target effects and toxicity are unlikely using these miRNAs. The findings described herein are exemplified for HCV infection, but can be broadly applied and modified to inhibit other viruses and cellular gene products associated with disease states.

Typically, inhibition of target sequences by RNAi (i.e. miRNAs) requires a high degree of sequence homology between the target sequence and the anti-sense strand of the RNAi molecules. Most important is the seed region 2-8 nt from 5' end. In some embodiments, such homology is higher than 70%, and may be higher than 75%. Preferably, homology is higher than 80%, or 85% or even 90%. More preferably, sequence homology between the target sequence and the sense strand of the RNAi is higher than 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%

Certain embodiments of the invention address a major problem of current anti-viral therapies, which is the emergence of resistant variants, known generally as escape mutants. The high mutation rate of viruses and the use of single drug treatments allow escape mutants to emerge. Thus, one aspect of the present invention neutralizes emergent escape mutants. For example, use of miRNAs targeting multiple regions of the HCV genome can be expressed simultaneously on one polycistronic miRNA construct allowing the targeting of multiple regions within the HCV genome. Thus, expression of multiple miRNA constructs in one transcriptional unit comprises an aspect of the invention. In the HCV context, using the miR-17-92 cluster as a scaffold, multiple constructs can be made based on the hairpin structures. In addition to the miRNA clusters disclosed herein, particular embodiments of the invention feature multiple miRNAs, wherein the pre-miR-18 hairpin is excluded from targeting, and miR-92 is used as a basis for inhibition. See Figure 10. Figure 1A shows the

natural miRNA-17-92 cluster, which can be modified at one or more of the first, third, fourth, fifth, and sixth hairpin structures. In some embodiments of this invention the selection of multiple RNAi sequences (i.e., miRNAs) to treat viral infections can be chosen based on the emergence of escape mutants from treatment of infected cells
5 single sequence of RNAi. Emergent escape mutants are determined by treatment with an expression construct containing a single sequence of RNAi after the cells have been infected with virus. Cells containing resistant viruses that emerge are harvested and the viral genomes sequenced.

10

I. Definitions

The following definitions are provided to facilitate an understanding of the present invention. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the
15 art to which this invention belongs. Generally, conventional methods of molecular biology, microbiology, recombinant DNA techniques, cell biology, and virology within the skill of the art are employed in the present invention. Such techniques are explained fully in the literature, see, e.g., Maniatis, Fritsch & Sambrook, *Molecular Cloning: A Laboratory Manual* (1982); *DNA Cloning: A Practical Approach*,
20 *Volumes I and II* (D. N. Glover, ed. 1985); *Oligonucleotide Synthesis* (M. J. Gait, ed. 1984); *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins, eds. (1984)); *Animal Cell Culture* (R. I. Freshney, ed. 1986); and *RNA Viruses: A Practical Approach*, (Alan, J. Cann, Ed., Oxford University Press, 2000).

For purposes of the invention, "Nucleic acid", "nucleotide sequence" or a
25 "nucleic acid molecule" as used herein refers to any DNA or RNA molecule, either single or double stranded and, if single stranded, the molecule of its complementary sequence in either linear or circular form. In discussing nucleic acid molecules, a sequence or structure of a particular nucleic acid molecule may be described herein according to the normal convention of providing the sequence in the 5' to 3' direction.
30 With reference to nucleic acids of the invention, the term "isolated nucleic acid" is sometimes used. This term, when applied to DNA, refers to a DNA molecule that is separated from sequences with which it is immediately contiguous in the naturally occurring genome of the organism in which it originated. For example, an "isolated nucleic acid" may comprise a DNA molecule inserted into a vector, such as a plasmid

or virus vector, or integrated into the genomic DNA of a prokaryotic or eukaryotic cell or host organism. Alternatively, this term may refer to a DNA that has been sufficiently separated from (e.g., substantially free of) other cellular components with which it would naturally be associated. "Isolated" is not meant to exclude artificial or synthetic mixtures with other compounds or materials, or the presence of impurities that do not interfere with the fundamental activity, and that may be present, for example, due to incomplete purification. When applied to RNA, the term "isolated nucleic acid" refers primarily to an RNA molecule encoded by an isolated DNA molecule as defined above. Alternatively, the term may refer to an RNA molecule that has been sufficiently separated from other nucleic acids with which it would be associated in its natural state (i.e., in cells or tissues). An isolated nucleic acid (either DNA or RNA) may further represent a molecule produced directly by biological or synthetic means and separated from other components present during its production.

According to the present invention, an isolated or biologically pure molecule or cell is a compound that has been removed from its natural milieu. As such, "isolated" and "biologically pure" do not necessarily reflect the extent to which the compound has been purified. An isolated compound of the present invention can be obtained from its natural source, can be produced using laboratory synthetic techniques or can be produced by any such chemical synthetic route.

The term "promoter" or "promoter region" generally refers to the transcriptional regulatory regions of a gene. The "promoter region" may be found at the 5' or 3' side of the coding region, or within the coding region, or within introns. Typically, the "promoter region" is a nucleic acid sequence which is usually found upstream (5') to a coding sequence and which directs transcription of the nucleic acid sequence into mRNA. The "promoter region" typically provides a recognition site for RNA polymerase and the other factors necessary for proper initiation of transcription. Promoters useful in some embodiments of the present invention may be tissue-specific or cell-specific. The term "tissue-specific" as it applies to a promoter refers to a promoter that is capable of directing selective expression of a nucleotide sequence of interest to a specific type of tissue in the relative absence of expression of the same nucleotide sequence of interest in a different type of tissue (e.g., liver). The term "cell-specific" as applied to a promoter refers to a promoter which is capable of directing selective expression of a nucleotide sequence of interest in a specific type of cell in the relative absence of expression of the same nucleotide sequence of interest

in a different type of cell within the same tissue (see, e.g., Higashibata, et al., J. Bone Miner. Res. Jan 19(1):78-88 (2004); Hoggatt, et al., Circ. Res., Dec. 91(12):1151-59 (2002); Sohal, et al., Circ. Res. Jul 89(1):20-25 (2001); and Zhang, et al., Genome Res. Jan 14(1):79-89 (2004)). The term "cell-specific" when applied to a promoter
5 also means a promoter capable of promoting selective expression of a nucleotide sequence of interest in a region within a single tissue. Alternatively, promoters may be constitutive or regulatable. Additionally, promoters may be modified so as to possess different specificities.

The term "vector" relates to a single or double stranded circular nucleic acid
10 molecule that can be infected, transfected or transformed into cells and replicate independently or within the host cell genome. An assortment of vectors, restriction enzymes, and the knowledge of the nucleotide sequences that are targeted by restriction enzymes are readily available to those skilled in the art, and include any replicon, such as a plasmid, cosmid, bacmid, phage or virus, to which another genetic
15 sequence or element (either DNA or RNA) may be attached so as to bring about the replication of the attached sequence or element. An "expression vector" is a specialized vector that contains a gene or nucleic acid sequence with the necessary regulatory regions needed for expression in a host cell. The term "operably linked" means that the regulatory sequences necessary for expression of a coding sequence
20 are placed in the DNA molecule in the appropriate positions relative to the coding sequence so as to effect expression of the coding sequence. This same definition is sometimes applied to the arrangement of coding sequences and transcription control elements (e.g. promoters, enhancers, and termination elements) in an expression vector. This definition is also sometimes applied to the arrangement of nucleic acid
25 sequences of a first and a second nucleic acid molecule wherein a hybrid nucleic acid molecule is generated.

The terms "miRNA" and "microRNA" refer to about 10-35 nt, preferably about 15-30 nt, and more preferably about 19-26 nt, non-coding RNAs derived from endogenous genes encoded in the genomes of plants and animals. They are processed
30 from longer hairpin-like precursors termed pre-miRNAs that are often hundreds of nucleotides in length. MicroRNAs assemble in complexes termed miRNPs and recognize their targets by antisense complementarity. These highly conserved, endogenously expressed RNAs are believed to regulate the expression of genes by binding to the 3'-untranslated regions (3'-UTR) of specific mRNAs. Without being

bound by theory, a possible mechanism of action assumes that if the microRNAs match 100% their target, i.e. the complementarity is complete, the target mRNA is cleaved, and the miRNA acts like a siRNA. However, if the match is incomplete, i.e. the complementarity is partial, then the translation of the target mRNA is blocked.

- 5 The manner by which a miRNA base-pairs with its mRNA target correlates with its function: if the complementarity between a mRNA and its target is extensive, the RNA target is cleaved; if the complementarity is partial, the stability of the target mRNA is not affected but its translation is repressed.

10 The term "RNA interference" or "RNAi" refers generally to a process or system in which a RNA molecule changes the expression of a nucleic acid sequence with which RNA molecule shares substantial or total homology. The term "RNAi agent" refers to an RNA sequence that elicits RNAi.

An "siRNA" refers to a molecule involved in the RNA interference process for a sequence-specific post-transcriptional gene silencing or gene knockdown by providing small interfering RNAs (siRNAs) that have homology with the sequence of the targeted gene. Small interfering RNAs (siRNAs) can be synthesized in vitro or generated by ribonuclease III cleavage from longer dsRNA and are the mediators of sequence-specific mRNA degradation. Preferably, the siRNA of the invention are chemically synthesized using appropriately protected ribonucleoside
15 phosphoramidites and a conventional DNA/RNA synthesizer. The siRNA can be synthesized as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions. Commercial suppliers of synthetic RNA molecules or synthesis reagents include Applied Biosystems (Foster City, CA, USA), Prologo (Hamburg, Germany), Dharmacon Research (Lafayette, Colo., USA), Pierce
20 Chemical (part of Perbio Science, Rockford, Ill., USA), Glen Research (Sterling, Va., USA), ChemGenes (Ashland, Mass., USA) and Cruachem (Glasgow, UK). Specific siRNA constructs for inhibiting HCV may be between 15-35 nucleotides in length.

"Pri-miRNAs" are several hundred to thousands of base pair in size. Pri-miRNA contains at least 1, and up to 6, nucleotide hairpin loop structures when
30 transcribed from polycistronic units. They can be composed of multiple miRNAs, and in a particular arrangement of the invention five miRNAs are processed from one nucleic acid sequence. These sequences can also contain siRNA nucleic acids that repress gene transcription once processed in the RNAi system.

As used herein, "pharmaceutical formulations" include formulations for human and veterinary use which exhibit no significant adverse toxicological effect. The phrase "pharmaceutically acceptable formulation" as used herein refers to a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. The phrase "pharmaceutically acceptable" is used to indicate that the carrier can be administered to the subject without exerting significant adverse toxicological effects. The term "therapeutically effective amount" is the amount present that is delivered to a subject to provide the desired physiological response (e.g., viral load reduction). Methods for preparing pharmaceutical compositions are within the skill in the art, for example as described in Remington's Pharmaceutical Science, 18th ed., Mack Publishing Company, Easton, Pa. (1990), and The Science and Practice of Pharmacy, 2003, Gennaro et al.

A "carrier" refers to, for example, a diluent, adjuvant, preservative (e.g., Thimersol, benzyl alcohol), anti-oxidant (e.g., ascorbic acid, sodium metabisulfite), solubilizer (e.g., Tween 80, Polysorbate 80), emulsifier, buffer (e.g., Tris HCl, acetate, phosphate), bulking substance (e.g., lactose, mannitol), excipient, auxiliary agent or vehicle with which an active agent of the present invention is administered. Pharmaceutically acceptable carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin. Water or aqueous saline solutions and aqueous dextrose and glycerol solutions are preferably employed as carriers, particularly for injectable solutions. Suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin (Mack Publishing Co., Easton, PA); Gennaro, A. R., Remington: The Science and Practice of Pharmacy, 20th Edition, (Lippincott, Williams and Wilkins), 2000; Liberman, et al., Eds., Pharmaceutical Dosage Forms, Marcel Decker, New York, N.Y., 1980; and Kibbe, et al., Eds., Handbook of Pharmaceutical Excipients (3rd Ed.), American Pharmaceutical Association, Washington, 1999.

The term "treating" or "to treat" as used herein means activity resulting in the prevention, reduction, partial or complete alleviation or cure of a disease or disorder. The term "modulate" means altering (i.e., increasing or decreasing) the biological activity of a system. Activity can be modulated by a variety of mechanisms such as modifying expression levels through RNAi.

With respect to single-stranded nucleic acids, particularly oligonucleotides, the term "specifically hybridizing" refers to the association between two single-stranded nucleotide molecules of sufficiently complementary sequence to permit such hybridization under pre-determined conditions generally used in the art (sometimes
5 termed "substantially complementary"). In particular, the term refers to hybridization of an oligonucleotide with a substantially complementary sequence contained within a single-stranded DNA or RNA molecule of the invention, to the substantial exclusion of hybridization of the oligonucleotide with single-stranded nucleic acids of non-complementary sequence. Appropriate conditions enabling specific hybridization of
10 single stranded nucleic acid molecules of varying complementarity are well known in the art.

For instance, one common formula for calculating the stringency conditions required to achieve hybridization between nucleic acid molecules of a specified sequence homology is set forth below (see Sambrook et al. (2001) Molecular Cloning.
15 A Laboratory Manual, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press):

$$T_m = 81.5^{\circ}\text{C} + 16.6\text{Log} [\text{Na}^+] + 0.41(\% \text{ G+C}) - 0.63 (\% \text{ formamide}) - 600/\text{\#bp in duplex}$$

As an illustration of the above formula, using $[\text{Na}^+] = [0.368]$ and 50%
20 formamide, with GC content of 42% and an average probe size of 200 bases, the T_m is 57°C . Depending upon the specific sequence involved, the T_m of a DNA duplex decreases by $0.5 - 1.5^{\circ}\text{C}$ with every 1% decrease in homology. Thus, targets with greater than about 75% sequence identity would be observed using a hybridization temperature of 42°C .

25 The stringency of the hybridization and wash depend primarily on the salt concentration and temperature of the solutions. In general, to maximize the rate of annealing of the probe with its target, the hybridization is usually carried out at salt and temperature conditions that are $20-25^{\circ}\text{C}$ below the calculated T_m of the hybrid. Wash conditions should be as stringent as possible for the degree of identity of the
30 probe for the target. In general, wash conditions are selected to be approximately $12-20^{\circ}\text{C}$ below the T_m of the hybrid. In regards to the nucleic acids of the current invention, a moderate stringency hybridization is defined as hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and $100 \mu\text{g/ml}$ denatured salmon sperm DNA at 42°C , and washed in 2X SSC and 0.5% SDS at 55°C for 15 minutes. A high-

stringency hybridization is defined as hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA at 42°C, and washed in 1X SSC and 0.5% SDS at 65°C for 15 minutes. A very high stringency hybridization is defined as hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA at 42°C, and washed in 0.1X SSC and 0.5% SDS at 65°C for 15 minutes.

"Corresponding" means identical to or complementary to the designated sequence. The sequence may be generated in any manner, including chemical synthesis, DNA replication, reverse transcription or a combination thereof. Being "Complementary" means that a nucleic acid, such as DNA and RNA, encodes the only corresponding base pair that non-covalently connects sequences by two or three hydrogen bonds. There is only one complementary base for any of the bases found in DNA and in RNA, and skilled artisans can reconstruct a complementary strand for any single stranded nucleic acid.

The present invention also includes active portions, fragments, derivatives and functional or non-functional mimetics of the miRNAs of the invention. A "fragment" or "portion" of a sequence means a stretch of residues of at least about five to seven contiguous residues, often at least about seven to nine contiguous residues, typically at least about nine to fifteen contiguous residues and, most preferably, at least about fourteen or more contiguous residues.

For purposes of the present invention, "a" or "an" entity refers to one or more of that entity; for example, "a cDNA" refers to one or more cDNA or at least one cDNA. As such, the terms "a" or "an," "one or more" and "at least one" can be used interchangeably herein. It is also noted that the terms "comprising," "including," and "having" can be used interchangeably. Furthermore, a compound "selected from the group consisting of" refers to one or more of the compounds in the list that follows, including mixtures (i.e. combinations) of two or more of the compounds.

The phrase "consisting essentially of" when referring to a particular nucleotide or amino acid means a sequence having the properties of a given SEQ ID NO. For example, when used in reference to an amino acid sequence, the phrase includes the sequence per se and molecular modifications that would not affect the functional and novel characteristics of the sequence.

A "subject" or "patient" includes, but is not limited to animals, including mammalian species such as murine, porcine, ovine, bovine, canine, feline, equine, human, and other primates.

5 The phrase "viral load" is a measure of the severity of a viral infection, and can be calculated by estimating the amount of virus in an patient. Determination of viral load is part of therapy monitoring during chronic viral infections

A "derivative" of a polypeptide, polynucleotide or fragments thereof means a sequence modified by varying the sequence of the construct, e.g. by manipulation of the nucleic acid encoding the protein or by altering the protein itself. Such derivatives
10 of the natural sequence may involve insertion, addition, deletion or substitution of one or more amino acids, and may or may not alter the essential activity of original the polypeptide. "Derivatives" of a gene or nucleotide sequence refers to any isolated nucleic acid molecule that contains significant sequence similarity to the gene or nucleotide sequence or a part thereof. In addition, "derivatives" include such isolated
15 nucleic acids containing modified nucleotides or mimetics of naturally-occurring nucleotides.

The term "functional" as used herein implies that the nucleic or amino acid sequence is functional for the recited assay or purpose.

"Peptide" and "polypeptide" are used interchangeably herein and refer to a
20 compound made up of a chain of amino acid residues linked by peptide bonds. An "active portion" of a polypeptide means a peptide that is less than the full length polypeptide, but which retains measurable biological activity and retains biological detection.

The term "oligonucleotide" as used herein refers to sequences, primers and
25 probes of the present invention, and is defined as a nucleic acid molecule comprised of two or more ribo- or deoxyribonucleotides, preferably more than three. The exact size of the oligonucleotide can depend on various factors and on the particular application and use of the oligonucleotide.

The term "primer" as used herein refers to an oligonucleotide, either RNA or
30 DNA, either single-stranded or double-stranded, either derived from a biological system, generated by restriction enzyme digestion, or produced synthetically which, when placed in the proper environment, is able to functionally act as an initiator of template-dependent nucleic acid synthesis. When presented with an appropriate nucleic acid template, suitable nucleoside triphosphate precursors of nucleic acids, a

polymerase enzyme, suitable cofactors and conditions such as a suitable temperature and pH, the primer may be extended at its 3' terminus by the addition of nucleotides by the action of a polymerase or similar activity to yield a primer extension product. The primer may vary in length depending on the particular conditions and
5 requirement of the application. For example, in diagnostic applications, the oligonucleotide primer is typically 15-25 or more nucleotides in length. The primer must be of sufficient complementarity to the desired template to prime the synthesis of the desired extension product, that is, to be able anneal with the desired template strand in a manner sufficient to provide the 3' hydroxyl moiety of the primer in
10 appropriate juxtaposition for use in the initiation of synthesis by a polymerase or similar enzyme. It is not required that the primer sequence represent an exact complement of the desired template. For example, a non-complementary nucleotide sequence may be attached to the 5' end of an otherwise complementary primer. Alternatively, non-complementary bases may be interspersed within the
15 oligonucleotide primer sequence, provided that the primer sequence has sufficient complementarity with the sequence of the desired template strand to functionally provide a template-primer complex for the synthesis of the extension product.

Polymerase chain reaction (PCR) has been described in US Patents 4,683,195, 4,800,195, and 4,965,188, the entire disclosures of which are incorporated by
20 reference herein.

The term "gene" refers to a nucleic acid comprising an open reading frame encoding a polypeptide, including both exon and (optionally) intron sequences. The nucleic acid may also optionally include non coding sequences such as promoter or enhancer sequences. The term "intron" refers to a DNA sequence present in a given
25 gene that is not translated into protein and is generally found between exons.

The term "probe" as used herein refers to an oligonucleotide, polynucleotide or nucleic acid, either RNA or DNA, whether occurring naturally as in a purified restriction enzyme digest or produced synthetically, which is capable of annealing with or specifically hybridizing to a nucleic acid with sequences complementary to
30 the probe. A probe may be either single-stranded or double-stranded. The exact length of the probe will depend upon many factors, including temperature, source of probe and method of use. For example, depending on the complexity of the target sequence, the oligonucleotide probe typically contains about 10-50 or more nucleotides, more preferably, about 15-25 nucleotides.

The probes herein are selected to be "substantially" complementary to different strands of a particular target nucleic acid sequence. This means that the probes must be sufficiently complementary so as to be able to "specifically hybridize" or anneal with their respective target strands under a set of pre-determined conditions.

5 Therefore, the probe sequence need not reflect the exact complementary sequence of the target. For example, a non-complementary nucleotide fragment may be attached to the 5' or 3' end of the probe, with the remainder of the probe sequence being complementary to the target strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence
10 has sufficient complementarity with the sequence of the target nucleic acid to anneal therewith specifically.

The terms "percent similarity", "percent identity" and "percent homology" when referring to a particular sequence are used as set forth in the University of Wisconsin GCG software program.

15 The term "delivery" as used herein refers to the introduction of foreign molecule (i.e., protein containing nanoparticle) into cells. The term "administration" as used herein means the introduction of a foreign molecule into a cell. The term is intended to be synonymous with the term "delivery". Administration also refers to screening assays of the invention (e.g., routes of administration such as, without
20 limitation, intravenous, intra-arterial, intramuscular, subcutaneous, intrasynovial, infusion, sublingual, transdermal, oral, or topical).

The term "kit" refers to a combination of reagents and other materials.

II. Therapeutic Uses of miRNAs and polycistronic miRNA constructs

25 The miRNAs and polycistronic miRNA constructs may be used according to this invention, for example, as therapeutic agents that modulate viral infection. The invention also encompasses use of polycistronic miRNAs expressed from transcriptional units inserted into nucleic acid-based vectors. In a preferred embodiment of the present invention, the polycistronic miRNAs may be administered
30 to a patient via infusion in a biologically compatible carrier. The miRNAs may be administered alone or in combination with other agents known to have anti-viral effects. An appropriate composition in which to deliver miRNAs may be determined by a medical practitioner upon consideration of a variety of physiological variables as contemplated hereinbelow. A variety of compositions well suited for different

applications and routes of administration are well known in the art and are described hereinbelow. The preparation containing the polycistronic miRNAs contains a physiologically acceptable matrix and is preferably formulated as a pharmaceutical preparation.

5 Nucleic acid molecules encoding the miRNAs of the invention may be prepared by using recombinant DNA technology methods. The availability of nucleotide sequence information enables preparation of nucleic acid-based molecules of the invention by a variety of means.

 The polycistronic miRNAs may be used for a variety of purposes in
10 accordance with the present invention. In a preferred embodiment of the invention, a nucleic acid delivery vehicle (i.e., an expression vector) for modulating viral infection is provided wherein the expression vector comprises a nucleic acid sequence coding the polycistronic miRNAs, or a functional fragments thereof as described herein. Administration of polycistronic miRNAs or derivatives thereof encoding expression
15 vectors to a patient results in the expression of miRNAs which serve to inhibit viral replication, particularly alleviating HCV infection.

 In a preferred embodiment of the invention, the expression vector comprising nucleic acid sequences encoding polycistronic miRNAs is a viral vector. Viral vectors which may be used in the present invention include, but are not limited to,
20 adenoviral vectors (with or without tissue specific promoters/enhancers), adeno-associated virus (AAV) vectors of multiple serotypes (e.g., AAV-1-9) and recombinant AAV vectors, lentivirus vectors and pseudo-typed lentivirus vectors (e.g., Ebola virus, vesicular stomatitis virus (VSV), and feline immunodeficiency virus (FIV)), herpes simplex virus vectors, vaccinia virus vectors, and retroviral
25 vectors. In preferred embodiments, rAAV-2 will be used in in vitro assays, rAAV-8 will be used in mouse studies and rAAV-6, 8, or 9 will be used as a carrier for in vivo administration of the miRNAs of the invention to primates.

 For some applications, an expression construct may further comprise regulatory elements which serve to drive expression in a particular cell or tissue type.
30 Such regulatory elements are known to those of skill in the art and discussed in depth in Sambrook et al. (1989) and Ausubel et al. (1992). The incorporation of tissue specific regulatory elements in the expression constructs of the present invention provides for at least partial tissue tropism for the expression polycistronic miRNAs. For example, the miRNA constructs can be subcloned into a vector downstream of a

tissue (i.e., liver) specific promoter/enhancer to treat HCV. A preferred embodiment comprises the ApoE, apolipoprotein E, hepatic control region and the hAAT, alpha-one antitrypsin promoter. Additionally, polyadenylation sequences can be inserted downstream of the miRNA cluster in miRNA and polycistronic miRNA clusters.

- 5 Preferably, the bovine growth hormone polyadenylation sequence is used in certain constructs of the invention.

III. Pharmaceutical Compositions

- The expression vectors of the present invention may be incorporated into
10 pharmaceutical compositions that may be delivered to a subject. In a particular embodiment of the present invention, pharmaceutical compositions comprising isolated nucleic acids which enable the recipient to produce therapeutically effective miRNAs that modulate viral infection (i.e., viral load) in the recipient are provided. The compositions may be administered alone or in combination with at least one other
15 agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. In preferred embodiments, the pharmaceutical compositions also contain a pharmaceutically acceptable excipient. Such excipients include any pharmaceutical agent that does not itself induce an immune response
20 harmful to the individual receiving the composition, and which may be administered without undue toxicity. Pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, glycerol, sugars and ethanol.

- Pharmaceutically acceptable salts can also be included therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and
25 the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., 18th Edition,
30 Easton, Pa. (1990).

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of

the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran.

Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. The pharmaceutical compositions of the present invention may be manufactured in any manner known in the art (e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes).

The preparation according to the present invention is especially stable, i.e., it can be allowed to stand in dissolved form for a prolonged time prior to application. The preparation according to the present invention can be made available as a pharmaceutical preparation with the nucleic acid encoding the polycistronic miRNAs in the form of a one-component preparation or in combination with other factors in the form of a multi -component preparation.

Expression vectors comprising polycistronic miRNAs sequences may be administered alone, or in combination with other anti-viral agents. According to the present invention, the expression vectors or combination of therapeutic agents may be administered to the patient alone or in a pharmaceutically acceptable or biologically compatible composition.

After pharmaceutical compositions have been prepared, they may be placed in an appropriate container or kit and labeled for treatment. For administration of polycistronic miRNAs-containing vectors, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the constructs are contained in an effective amount to achieve the intended therapeutic purpose. Determining a therapeutically effective dose is well within the capability of a skilled medical practitioner using the techniques provided hereinbelow. Therapeutic doses will depend on, among other factors, the age and general condition of the subject, the severity of the viral infection, and the strength of the control sequences regulating the expression levels of the polycistronic miRNAs. Thus, a therapeutically effective amount in humans will fall in a relatively broad

range that may be determined by a medical practitioner based on the response of an individual patient to vector-based form of polycistronic miRNAs.

IV. Methods of Treatment and Delivery

5 Nucleic acids encoding the polycistronic miRNAs either in plasmid or viral vector forms alone or in combination with other agents, may be directly infused into a patient in an appropriate biological carrier, preferably by IV administration. One of skill in the art could readily determine specific protocols for using the miRNAs of the present invention for the therapeutic treatment of a particular patient. In this regard,
10 the compositions may be delivered subcutaneously, epidermally, intradermally, intrathecally, intraorbitally, intramucosally, intraperitoneally, intravenously, intraarterially, orally, intrahepatically or intramuscularly. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications.

15 Dosage levels on the order of about 1 µg/kg to 100 mg/kg of body weight per administration are useful in the treatment of a disease or viral infection. In regard to dosage, polycistronic miRNAs can be administered at a unit dose less than about 75 mg per kg of bodyweight, or less than about 70, 60, 50, 40, 30, 20, 10, 5, 2, 1, 0.5, 0.1, 0.05, 0.01, 0.005, 0.001, or 0.0005 mg per kg of bodyweight, and less than 200
20 nmol of polycistronic miRNA per kg of bodyweight, or less than 1500, 750, 300, 150, 75, 15, 7.5, 1.5, 0.75, 0.15, 0.075, 0.015, 0.0075, 0.0015, 0.00075, 0.00015 nmol of polycistronic miRNA per kg of bodyweight. Alternatively AAV doses can be determined using vectors genomes/kg, which in turn can be converted to µg capsid protein/kg. The unit dose, for example, can be administered by injection for example,
25 intravenous, intramuscular, intrathecally, or directly into an organ such as the liver.

Delivery of polycistronic miRNAs directly to an organ can be at a dosage on the order of about 0.00001 mg to about 3 mg per organ, or preferably about 0.0001-0.001 mg per organ, about 0.03-3.0 mg per organ, about 0.1-3.0 mg per organ or about 0.3-3.0 mg per organ. The dosage can be an amount effective modulate viral
30 activity or to treat or prevent a disease or disorder.

One skilled in the art can also readily determine an appropriate dosage regimen for administering the polycistronic miRNAs of the invention to a given subject. For example, the polycistronic miRNAs can be administered to the subject once, e.g., as a single injection or deposition at or near the site of viral replication.

Alternatively, the vectors encoding the polycistronic miRNAs can be administered multiple times to a subject. However, this may require the use of alternative AAV vectors to avoid anti-AAV antibodies that may develop upon initial exposure to the rAAV. It may also be desirable to administer such vectors in conjunction with an immunosuppressive agent in order to suppress this undesired immune response. One skilled in the art will appreciate that the exact individual dosages may be adjusted somewhat depending on a variety of factors, including the specific polycistronic miRNAs being administered, the time of administration, the route of administration, the nature of the formulation, the rate of excretion, the particular infection being treated, the severity of the infection, the pharmacodynamics of the oligonucleotide agent, and the age, sex, weight, and general health of the patient. Wide variations in the necessary dosage level are to be expected in view of the differing efficiencies of the various routes of administration. For instance, oral administration generally would be expected to require higher dosage levels than administration by intravenous or intravitreal injection. Variations in these dosage levels can be adjusted using standard empirical routines of optimization, which are well-known in the art. Optimum dosages may vary depending on the relative potency of individual compounds, and can generally be estimated based on EC₅₀s found to be effective in *in vitro* and *in vivo* animal models.

Changes in dosage may result and become apparent from the results of diagnostic assays. For example, the subject can be monitored after administering polycistronic miRNAs composition. Based on information from the monitoring, an additional amount of the composition can be administered.

V. Kits and Articles of Manufacture

Any of the aforementioned compositions or methods can be incorporated into a kit which may contain at least one miRNA sequence or polycistronic transcript.

If the pharmaceutical composition in liquid form is under risk of being subjected to conditions which will compromise the stability of the polycistronic miRNAs, it may be preferred to produce the finished product containing the polycistronic miRNAs in a solid form, e.g. as a freeze dried material, and store the product in such solid form. The product may then be reconstituted (e.g. dissolved or suspended) in a saline or in a buffered saline ready for use prior to administration.

Hence, the present invention provides a kit comprising (a) a first component

containing miRNAs as defined hereinabove, optionally in solid form, and (b) a second component containing saline or a buffer solution (e.g. buffered saline) adapted for reconstitution (e.g. dissolution or suspension) or delivery of said polycistronic miRNAs.

5 Preferably said saline or buffered saline has a pH in the range of 4.0-8.5, and a molarity of 20-2000 mM. In a preferred embodiment the saline or buffered saline has a pH of 6.0-8.0 and a molarity of 100-500 mM. In a most preferred embodiment the saline or buffered saline has a pH of 7.0-8.0 and a molarity of 120-250 mM. For one embodiment of a kit, the polycistronic miRNAs preferably comprise at least one, or
10 more preferably at least two nucleotides encoded by SEQ ID NO. 1 – SEQ ID NO: 5.

VI. Clinical Applications

As mentioned previously, a preferred embodiment of the invention comprises delivery of at least one miRNA or a polycistronic miRNA transcript to a patient in
15 need thereof. Formulation, dosages and treatment schedules have also been described hereinabove. Phase I clinical trials can be designed to assess the safety, tolerability, pharmacokinetics, and pharmacodynamics of the miRNA constructs of the invention. These trials may be conducted in an inpatient clinic, where the subject suffering from an infection can be observed by full-time medical staff. After the initial safety of the
20 therapy has been performed, Phase II trials can assess clinical efficacy of the therapy; as well as to continue Phase I assessments in a larger group of volunteers and patients. Subsequently, Phase III studies on large patient groups entail definitive assessment of the efficacy of the miRNA constructs for treatment of a viral infection in comparison with current treatments. Finally, Phase IV trials involving the post-launch safety
25 surveillance and ongoing technical support for the polycistronic miRNAs can be completed.

The following examples illustrate certain embodiments of the invention. They are not intended to limit the scope of the invention in any way.

30

Example 1

The following materials and methods are provided to facilitate practice of the invention, and are particularly applicable to the instant example.

DNA constructs

The miR17-92 polycistronic sequence (NCBI GenBank Accession No.: NT_009952.14) was used as a scaffold to construct a gene capable of expressing an artificial pri-miRNA composed of five miRNAs. Secondary structures of the pre-miRNAs as well as the sequence of the mature miRNAs were obtained from the Internet at (mirbase.org). A 783 bp DNA fragment was synthesized (GenScript, Piscataway, NJ) that encoded five anti-HCV miRNA genes embedded in the first five miRNA genes of the endogenous miR17-92 cluster (i.e., miR-17, miR-18, miR-19A, miR-20, miR-19B). The ~11 bp lower stems and loops of each endogenous miRNA was maintained, as well as all the intervening sequences and 91 bp of 5' flanking and 18 bp of 3' flanking DNA sequences. The endogenous sequence was modified slightly by inserting unique restriction sites at the 5' and 3' ends of each miRNA gene to facilitate subcloning. AgeI and BamHI sites flank miR-UTR1, BamHI and ClaI flank miR-UTR2, ClaI and BclI flank miR-UTR3, BclI and EagI flank miR-Core, and EagI and PmeI flank miR-NS5B. The 783 bp fragment contained a SphI site upstream of the first miRNA gene and a PmeI site downstream of the last miRNA gene. In addition, XbaI and BamHI sites were included at the 5' and 3' ends, respectively for bidirectional cloning into pUC57 (GenScript, Piscataway, NJ) to create pUC57-HCV-miR Cluster 1. The plasmid pUC19 was modified to facilitate sub-cloning of the miRNA-containing fragment by inserting a synthetic fragment encoding the restriction sites EcoRI, SphI, PmeI, and HindIII between the EcoRI and HindIII sites of pUC19, creating plasmid pUC19MCSD. The ApoE enhancer and human alpha-one antitrypsin promoter was amplified from plasmid pAAV-hFIX16 by PCR using forward primer 5'-TAGCGAATTCGCTGTTTGTGTGCTGCCTCTGAAG-3' (SEQ ID NO: 11) and reverse primer 5'-TAGCGCATGCACTGTCCCAGGTCAGTGGTGGTGC-3' (SEQ ID NO: 12), and the amplified product was digested with EcoRI and SphI. The polyadenylation (polyA) fragment was generated by PCR amplification of pAAV-hFIX16 using forward primer 5'-TAGCGTTTAAACCTGTGCCTTCTAGT TGCCAGCCAT-3' (SEQ ID NO: 13) and reverse primer 5'-TAGCAA GCTTATAGAGCCCACCGCATCCCCAGCA-3' (SEQ ID NO: 14), and the product was digested with PmeI+HindIII. After enzyme digestion, the ApoE/hAAT promoter fragment, the polyA fragment, and the SphI-PmeI fragment of pUC57-HCV-miR Cluster 1 were cloned into the EcoRI and

HindIII sites of pUC19MCSD, to generate pUC19MCSD-ApoE/hAAT-HCV-miRNA Cluster 1. The human growth hormone intron fragment was generated by PCR amplification of pAAV-LacZ (Stratagene, LaJolla, CA) using forward primer 5'-TAGCGCATGCTTCGAA CAGGTAAGCGCC-3' (SEQ ID NO: 15) and reverse 5'-TAGCGC ATGCAACCTGGGGAGAAACCAG-3' (SEQ ID NO: 16) and was digested with SphI and cloned into the SphI site of pUC19MCSD-ApoE/hAAT-HCV-miRNA cluster 1, generating pUC19MCSD-ApoE/hAAT-HCV-miRNA Cluster 1 + Intron. For construction of HCV-miRNA Cluster 2, a 273 bp DNA fragment was synthesized (GenScript, Piscataway, NJ) that encoded miR-UTR2 and miR-UTR1 embedded in endogenous miR-17 and miR-18 sequences, respectively, and with an AgeI site at the 5' end and a ClaI site at the 3' end. This fragment was initially cloned into pUC57, and then was used to replace the AgeI-ClaI fragment of pUC19MCSD-ApoE/hAAT-HCV-miRNA-Cluster 1, creating pUC19MSCD-ApoE/hAAT-HCV-miRNA Cluster 2. For all single miRNA constructs, the individual miRNA fragments were generated by PCR amplification of pUC19-hAAT/ApoE-HCV-miRNA cluster 1 using different primers. All forward primers had an AgeI site at their 5' ends and the reverse primers had a PmeI site at their 5' ends. The individual miRNA fragments replaced the AgeI-PmeI fragment of pUC19MCSD-ApoE/hAAT-HCV-miRNA Cluster 1, generating pUC19MCSD-ApoE/hAAT-HCV-miR-UTR1, pUC19MCSD-ApoE/hAAT-HCV-miR-UTR2, pUC19MCSD-ApoE/hAAT-HCV-miR-UTR3, pUC19MCSD-ApoE/hAAT-HCV-miR-Core, and pUC19MCSD-ApoE/hAAT-HCV-miR-NS5B.

HCV-miR-Cluster 5 was also generated. This construct encodes five miRNAs by using the last miRNA in the miR17-92 cluster (miR-92), rather than the second miRNA (miR-18), as a scaffold for miR-UTR1. Thus, this cluster contains in order: miR-UTR2, miR-UTR3, miR-Core, miR-NS5B, miR-UTR1 and is shown in Figure 10. For sequence information for AAV vectors comprising Cluster 5, see Figures 13A and 13B.

For construction of pscAAV-HCV-miR Cluster 1, the ApoE HCR/hAAT enhancer/promoter was PCR amplified from pAAV-hFIX16 using forward primer: 5' TAG CGC GAT CGC GCT GTT TGT GTG CTG CCT CTG AAG 3' and reverse primer: 5' TAG CGC ATG CAC TGT CCC AGG TCA GTG GTG GTG C3', to generate a fragment flanked by AsiSI and SphI sites. This fragment was co-ligated with the SphI-PmeI fragment of HCV-miR Cluster 1 (containing the 5 miRNAs) into

the backbone of pscAAV-FIX100 that had first been digested with AsiSI and PmeI. The salient features of the latter fragment are: a wild-type AAV ITR at the 5' end, the bGH pA sequence, a deleted AAV4 ITR at the 3' end, and an ampicillin resistance marker.

5 RLuc-HCV reporter plasmids were generated using the psiCheck-2 plasmid (Promega, Madison, WI). HCV target sequences (wild-type, seed mutation, and reverse complement) were synthesized as duplex primer pairs (40 bp) (IDT, Coralville, IA), and were annealed and ligated between the XhoI and a NotI sites of psiCheck-2, which lie 7-37 nucleotides downstream of the translational stop codon of
10 the RLuc gene. The wild-type reporter primer pairs are as follows: HCV-UTR1 primer pairs: contain HCV1b sequence from 128 to 166 nt, HCV-UTR2 primer pairs: contain HCV1b sequence from 264-304nt, HCV-UTR3 primer pairs: contain HCV1b sequence from 311-349nt, HCV-Core primer pairs: contain HCV1b sequence from 348-387, HCV-NS5B primer pairs contain HCV1b sequence from 7973-8012. The
15 seed mutation reporter plasmids contain a 3 bp substitution at positions 4-6 of the guide strand target region. The reverse complement reporter plasmids contain the anti-sense sequence relative to the wild-type reporters. The 5 Target reporter contains the five wild-type 40 bp target sequences of the miRNAs arranged in tandem.

20 **Transfection and Luciferase Analysis**

The human hepatoma-7 (Huh-7) cell line was maintained in RPMI supplemented with 10% fetal calf serum, 2mM glutamine and 100 U/ml penicillin/streptomycin. Huh-7 cells were seeded in 24-well tissue culture plates at 4×10^4 cells/well two days prior to transfection. The cells were co-transfected in
25 triplicate with a miRNA-expressing plasmid (125ng) or pUC19 (125 ng) and a RLuc-HCV reporter plasmid (125ng). The transfections were performed with Arrest-in (Open Biosystems, Huntsville, AL) according to the manufacturer's instructions. Twenty-four hours after transfection, cells were washed with PBS and lysed using Passive Lysis Buffer (Promega, Madison WI). Firefly and RLuc activities were
30 assessed using the Dual-luciferase assay system (Promega Madison, WI). Luminescence readings were acquired using an automated Veritas luminometer (Turner Biosystems, Sunnyvale CA). Relative light units (RLUs) of RLuc were normalized by dividing by the amount of FFLuc light units. Percent inhibition was calculated by comparing RLUs of the miRNA plasmid-transfected cells to cells

transfected with the pUC19 plasmid. Each condition was tested with n=9 independent transfections, unless otherwise specified, and the results are reported as the mean and SD of these values.

5 Cell viability assay

Cell viability was assessed following transfection of Huh-7 cells with plasmids expressing the miRNAs using the AlamarBlue assay system according to manufacturer's instructions (Invitrogen Carlsbad, CA.) Huh-7 cells were plated in 24 well tissue culture plates at 4×10^4 cells/well in 500 μ l media. Forty eight hours later
10 the cells were transfected using Arrest-In (Open Biosystems, Huntsville, AL) according to the manufacturer's instructions with increasing amounts of the HCV miR Cluster 1 plasmid (0, 2.5, 10, 50 , or 125 ng) and one of the five RLuc reporters (125 ng) or no reporter. The total amount of plasmid DNA added to cells was adjusted to 250 ng using pUC19. Cells were incubated at 37°C for 24 hours and then 50 μ l
15 AlamarBlue reagent was added directly to the cells and they were incubated at 37°C for an additional 4 hours. The oxidized form of this dye is converted to the reduced form by mitochondrial enzyme activity in viable cells, and a shift in fluorescence is measured by excitation at 570nm and emission at 585nm using a Molecular Devices Spectra Max M2 plate reader (Sunnyvale, CA). Percent survival was calculated by
20 comparing the amount of fluorescence emitted from cells transfected with HCV-miR Cluster 1 relative to cells that did not receive this plasmid DNA.

In Vitro HCVcc Inhibition Assays

In Vitro HCVcc Inhibition Assays. HCVcc was produced according to Cai et
25 al.,(2005) J. of Virol. 79:13963-13973 and the physical and infectious titers were determined by quantitative real-time reverse transcription polymerase chain reaction (QRT-PCR) and according to Kato et al., (2006) Nat. Prot. 1: 2334-2339, respectively. For inhibition experiments, Huh-7.5 cells (Apath, Brooklyn, NY) were plated in six-well plates at 2×10^5 cells/well. Twenty-four hours later, cells were
30 infected with either scAAV2-HCV-miR-Cluster 5 or scAAV2-enhanced green fluorescent protein (eGFP), at one of three multiplicities of infection (MOIs; 1×10^4 , 1×10^5 , 1×10^6 vector genomes [vg]/cell), and incubated for 24 hours. At this time, the media was replaced and HCVcc was added (~ 0.2 focus-forming unit [FFU]/cell) for 2 hours. The media was replaced and the cells were incubated for an additional 48

hours. Supernatants were collected from wells for viral RNA isolation and cells were lysed in TRIzol reagent (Invitrogen, Carlsbad, CA) for total cellular RNA purification. Cells from duplicate wells were prepared for western blot analyses.

5 HCV RNA Quantitation.

HCV RNA was quantified by QRT-PCR¹⁹ using in vitro-transcribed JFH-1 (Japanese fulminant hepatitis 1) RNA as a standard

Animal Procedures

10 All animal studies were conducted at the Children's Hospital of Philadelphia with approval from the CHOP Institutional Animal Care and Use Committee. Balb/c mice were purchased from Charles River Labs (Wilmington, MA). HDTV injections of mice (n=4 or 5) were performed as described elsewhere (41) using 12 µg of a miRNA-expressing plasmid or pUC19 DNA, and 12 µg of a RLuc-HCV fusion
15 plasmid in a total volume of 2.0 ml PBS. Two days later, the animals were sacrificed, livers were harvested and stored at -80°C until processing.

Biochemical Analysis

Whole mouse livers were ground using a freezer/mill (Spex CertiPrep,
20 Metuchen, NJ) in liquid nitrogen using three, one minute grinding cycles spaced by three, one minute cooling cycles. Ground livers were stored at -80°C. Lysates of the ground liver were prepared by adding 200µl of 1x Passive Lysis Buffer (Promega, Madison, WI) to ~100 mg liver. The activity of Luc in 10 µl lysate was determined using the Dual Luciferase Assay (Promega, Madison, WI) on a Veritas luminometer
25 (Turner Biosystems, Sunnyvale, CA). Relative light units (RLUs) of RLuc were normalized by dividing by the amount of FFLuc light units. Percent inhibition was calculated by comparing RLUs in the miRNA plasmid-injected mice to animals injected with the pUC19 plasmid. Three independent liver lysates were prepared and analyzed for each liver and the results are reported as the mean and SD of these
30 values.

Northern Blot Analyses.

Ground liver tissue was removed from the -80°C freezer and ~200 mg was added to 2 ml of TRIzol reagent (Invitrogen, Carlsbad, CA), and total RNA was

extracted according to the manufacturer's protocol (yield ~0.9 µg RNA/mg ground liver tissue). Twenty five µg of total RNA was resolved on 15% denaturing polyacrylamide TBE-urea gels (Invitrogen, Carlsbad, CA) . Decade RNA molecular weight markers (Ambion, Austin, TX) were labeled with γ P³²-ATP according to

5 manufacturer's instructions, and were run adjacent to liver RNA samples. RNA was transferred to Bright Star Plus positively charged nylon membranes (Ambion, Austin, TX) at 200 mA for 1 hour and UV-crosslinked using the auto-crosslink function on a Stratlinker 1800 (Stratagene, La Jolla, CA). Blots were prehybridized using UltraHyb-Oligo buffer (Ambion, Austin, TX) for 1 hr at 65°C and subsequently

10 probed with γ -P³²-ATP at room temperature overnight. The blots were washed three times at room temperature and once at 42°C for 30 min with 6X SSC/0.2% SDS, exposed to film, and developed using a Kodak processor. The DNA oligonucleotide sequences used as probes were as follows: miR-UTR1 guide: 5'-CCATAGTGGTCTGCGGAAC-3' (SEQ ID NO: 17), miR-UTR2 guide: 5'-

15 AAAGGCCTTGTGGTACTGCCT-3' (SEQ ID NO: 18), miR-UTR3 guide: 5'-AGGTCTCGTAGACCGTGCA-3' (SEQ ID NO: 19), miR-Core guide: 5'-AACCTCAAAGAAAAACCAAAC-3' (SEQ ID NO: 20), miR-NS5B guide: 5'-GACACTGAGACACCAATTGAC-3' (SEQ ID NO: 21), U6 snRNA: 5'-TATGGAACGCTTCACGAATTTGC-3' (SEQ ID NO: 22). The RNA

20 oligonucleotides used as positive controls were as follows: miR UTR1 (guide strand): 5'-GUUCCGCAGACCACUAUGG-3' (SEQ ID NO: 23), miR UTR2 (guide strand) 5'-AGGCAGUACCACAAGGCCUUU-3' (SEQ ID NO: 24), miR UTR3 (guide strand) 5'-UGCACGGUCUACGAGACCU-3' (SEQ ID NO: 25), miR Core (guide strand) 5'-GUUUGGUUUUUCUUUGAGGUU-3' (SEQ ID NO: 26), miR NS5B

25 (guide strand) 5'-GUCAAUUGGUGUCUCAGUGUC-3' (SEQ ID NO: 27).

Statistical analysis

Two tailed Student's t tests were performed. P values of 0.05 or 0.01 were used to assess statistical significance.

30

RESULTS

Construction of Polycistronic Anti-HCV miRNA vector

To enhance the probability of creating functional miRNAs targeting the HCV genome, the literature was surveyed for siRNAs and shRNAs that had previously been shown to inhibit autonomously replicating full genomic and subgenomic replicons by greater than 80% (7;8). Without being bound by theory, incorporation of these sequences into miRNAs should result in RNAi molecules effective in inhibiting HCV replication. Three of the five siRNAs chosen target the 5'UTR of HCV (UTR1, UTR2, UTR3), and the two others target sequences in one structural (Core) and one non-structural (NS5B) gene. Four of the five targets (UTR1, UTR2, UTR3, and Core) are highly conserved among the six HCV genotypes. The endogenous miR17-92 cluster was utilized to develop a multiplexed platform for inhibiting HCV. This cluster is composed of six genes (36), which are transcribed as a single transcriptional polycistron. The pri-RNA is processed in the nucleus to produce six pre-miRNAs (miR-17, miR-18, miR-19A, miR-20, miR-19B, and miR-92) (Fig. 1), and these are further processed in the cytoplasm to produce seven mature miRNAs. In our first approach, the first five miRNAs of the miR17-92 cluster were replaced with the previously validated anti-HCV siRNAs and shRNAs. siRNA compositions for use in the invention are provided in Tables I and II. The sequences in Table I include several siRNA (i.e., sense sequences for a HCV target region), and Table II provides several sequences of 'anti-sense' strand alone (SEQ ID NOs: 6-10). Those of skill in the art can determine the sequence of an antisense siRNA strand based on the disclosure of the sense strand or target sequence, and will appreciate the difference between "U" and "T" designations in the sequences which correspond to RNA and DNA molecules, respectively. The target sequences, their location in HCV 1b, the names of the miRNAs designed to cleave them, and the miRNAs they replace in the endogenous miR-17-92 cluster are shown Table 1.

TABLE 1

HCV miRNA	HCV Target sequence	Location in HCV 1b	Replaces
miR-UTR1	5'-CCAUAGUGGUCUGCGGAAC-3' (SEQ ID NO: 1)	138-156	miR-17, miR-18 miR-92
miR-UTR2	5'-AAAGGCCUUGUGGUACUGCCU-3'	274-294	miR-17, miR-18,

	(SEQ ID NO: 2)		miR-92
miR-UTR3	5'-AGGUCUCGUAGACCGUGCA-3'	321-339	miR-19A
	(SEQ ID NO: 3)		
miR-Core	5'-AACCUCAAAGAAAAACCAAAC-3'	358-378	miR-20
	(SEQ ID NO: 4)		
miR-NS5B	5'-GACACUGAGACACCAAUUGAC-3'	7983-8003	miR-19B
	(SEQ ID NO: 5)		

Table 1: Names and target sequences for the five anti-HCV miRNAs and their location within the HCV 1b genome. Also shown are the endogenous miRNAs within the miR-17-92 cluster that the anti-HCV miRNAs replace.

5

Table 2 provides the miRNA sequences (i.e, miRNA) that are incorporated into the pri-miRNAs to inhibit HCV.

TABLE 2

HCV miRNA	miRNA antisense sequence
miR-UTR1	5'-GUUCCGCAGACCACUAUGG-3' (SEQ ID NO: 6)
miR-UTR2	5'-AGGCAGUACCACAAGGCCUUU-3' (SEQ ID NO: 7)
miR-UTR3	5'-UGCACGGUCUACGAGACCU-3' (SEQ ID NO: 8)
miR-Core	5'-GUUUGGUUUUUCUUUGAGGUU-3' (SEQ ID NO: 9)
miR-NS5B	5'-GUCAAUUGGUGUCUCAGUGUC-3' (SEQ ID NO: 10)

10 **Table 2:** Sequences useful for targeting regions of the HCV genome which can be incorporated into a polycistronic transcript for therapeutic benefit.

A 783 bp DNA fragment was synthesized that encoded the five HCV miRNAs embedded in endogenous miR17-19B genomic DNA (Fig. 1; Fig. 8A). The ~11 bp
 15 lower stems and loops of each endogenous miRNA was maintained, as well as all the intervening sequences and 91 bp of 5' flanking and 18 bp of 3' flanking DNA sequences. Unique restriction sites were engineered around each of the five miRNAs to facilitate assembly of different miRNA clusters and to create plasmids expressing individual miRNAs. Since the HCV miRNAs are 2-4 nt shorter than the endogenous
 20 miRNAs they replaced, it was possible to insert them at the 5' or 3' end of the original miRNA sequence. They were inserted at the 5' end because it has been demonstrated

that this orientation results in the generation of more efficient miRNAs (35), and because it is important that the miRNA seed region (2-8 nt from the 5' end) contains HCV antisense sequences rather than endogenous miRNA sequences. The Sfold algorithm (37) was then used to create miRNAs with low internal stability at the 5' ends of the intended mature miRNA (i.e., guide stand). This feature promotes efficient entry of the antisense or guide strand of the mature miRNAs into RISC (4;5). In some cases this involved creating wobble or mismatches by changing the sequence of the sense or passenger strand in the miRNA hairpin structures to manipulate the internal stability of the hairpin. The secondary structure of the endogenous miRNAs were also mimicked by introducing mismatches and bulges into the stem of the HCV miRNAs, as this has been shown to increase the probability that the guide strand will be incorporated into the RISC (34). Unlike the endogenous miRNAs, the anti-HCV miRNAs were designed to be entirely complementary to their targets, and thus are predicted to mediate site-specific cleavage of their cognate targets.

In order to minimize any potential off-target effects by ectopic expression of miRNAs, the synthesized DNA fragment was subcloned into a vector downstream of a liver-specific enhancer/promoter, the ApoE hepatic control region and the alpha-one antitrypsin promoter. This regulatory element has been previously used to drive high level liver-specific expression of coagulation factor IX in rodents, dogs, non-human primates, and humans (38). The bovine growth hormone polyadenylation sequence was inserted downstream of the miRNA cluster, and some constructs contained an intron, which was cloned just upstream of the miRNA sequences.

Four HCV miRNA clusters were constructed. Cluster 1 contains in order: miR-UTR1, miR-UTR2, miR-UTR3, miR-Core, and miR-NS5B (with or without an intron), and Cluster 2 contains in order: miR-UTR2, miR-UTR1, miR-UTR3, miR-Core, and miR-NS5B (Fig. 1; Figs. 8A and 8B). Cluster 5 contains in order, miR-UTR-2, miR-UTR-3, miR-Core, miR-NS5B and miR-UTR-1. In cluster 5, miR-18 is deleted. In addition, plasmids expressing the individual miRNAs were constructed by removing four out of five miRNAs from Cluster 1. It should be noted that other miRNA sequences targeting different sequences within the HCV genome can be used in accordance with the teachings herein. See Figure 9: The full length sequence of HCV is known as are the sequences encoding each of the structural and functional proteins of the virus. Accordingly, other regions of the genome may be targeted and clusters designed to incorporate this sequence information. Varying the regions

targeted by the cluster is particularly desirable in certain situations, particularly to treat escape mutants that may emerge following administration of the constructs described herein.

5 *In Vitro Activity of Anti-HCV miRNAs*

A series of renilla luciferase (RLuc)-HCV reporter plasmids were constructed by fusing HCV target sequences downstream of the RLuc gene in plasmid psiCHECK. These were used to evaluate the ability of the miRNAs to cleave their target sequences. In addition, a reporter plasmid that contained all five HCV target sequences was constructed. Each plasmid also contained a firefly luciferase (FFLuc) gene to normalize for transfection efficiency. To evaluate the individually expressed miRNAs, Huh-7 cells were co-transfected with an RLuc-HCV reporter plasmid and a miRNA-expressing plasmid, and were compared to cells that were co-transfected with the same reporter plasmid and pUC19. Twenty four hours later, dual luciferase assays were performed on cell lysates. Normalized RLuc expression (RLuc/FFLuc) in the presence of pUC19 was set as 100% activity or 0% inhibition of the reporter plasmid. The normalized RLuc activity in cells transfected with the miRNA-expressing plasmid was then divided by the activity measured in the cells transfected with pUC19 to obtain the % inhibition of the target. Figure 2A demonstrates that four out of five of the miRNAs were able to inhibit their cognate HCV sequence when they were expressed individually. Expression of miR-UTR1 inhibited its target by 63 +/- 6%, miR-UTR3 by 34 +/- 4.7%, miR-core by 84 +/- 3.1%, and miR-NS5B by 47 +/- 14% ($P < 0.01$ for these four miRNAs). However, expression of miR-UTR2 resulted in no silencing of its cognate target. Similar results were observed when a reporter encoding all five targets was used. Specifically, miR-UTR1, miR-UTR3, miR-Core, and miR-NS5B silenced this reporter by 71 +/- 2%, 49.8 +/- 7.4%, 77.6 +/- 0.7%, and 57 +/- 2% ($P < 0.01$ for these four miRNAs), respectively, while miR-UTR2 had low level activity (27 +/- 5.6%; $P < 0.01$), indicating the potential for non-specific activity by the miRNA that showed no activity against its cognate target (Fig 2A).

A plasmid expressing the HCV miR Cluster 1, which encodes in order, miR UTR-1, miR-UTR2, miR UTR-3, miR-Core, and miR-NS5B was simultaneously evaluated. When this Cluster was evaluated for silencing of the individual RLuc reporters, a 61 +/- 5%, 1 +/- 9%, 64 +/- 13%, 68 +/- 7%, and 68 +/- 9 % inhibition of the corresponding targets was observed, respectively (Fig. 2B). Four of five of these

values were statistically significant relative to their controls ($P < 0.01$). In addition, 79 $\pm 5\%$ ($P < 0.01$) inhibition of the reporter containing all five targets was observed.

These results demonstrate that expression of miRNAs as part of a polycistronic mRNA does not negatively affect their activity, and in some cases improves their efficacy. For example, expression of miR-UTR3 and miR-NS5B from Cluster 1 resulted in statistically more inhibition of their cognate targets compared to expression of these miRNAs alone. This observation is significant because others have shown that competition exists between shRNAs when they are simultaneously expressed from a single vector (30). This competition is not observed using the constructs described herein.

In order to determine whether incorporation of an intron in the primary miRNA transcript would improve the efficacy of the miRNA cluster, a 278 bp intron was inserted downstream of the promoter and upstream of the miRNA cluster. As shown in Fig 2B, similar levels of inhibition were observed using this construct, including the lack of activity by miR-UTR2.

In HCV miR Cluster 1, miR-UTR2 was inserted into endogenous miR-18. Interestingly, the incorporation of a miRNA targeting the polymerase region of HIV was also inactive when it replaced endogenous miR-18 (35). It was suggested that because the hairpin structure of the endogenous miRNA is relatively unstable, misfolding of the hairpin RNA may result, negatively impacting its function. Since the predicted mature miR-UTR2 should have the same sequence as a siRNA that has previously been demonstrated to inhibit an HCV replicon, one explanation was that the mature miRNA was not properly processed from the pri-miRNA or pre-miRNA. By moving it to another position in the miRNA cluster, it may be possible to rescue its activity. Therefore, a second cluster (HCV Cluster 2) was constructed which contained the same five miRNAs but in a different order: miR-UTR2, miR-UTR1, miR-UTR3, miR-Core, and miR-NS5B. Thus, in this cluster miR-UTR2 replaces endogenous miR-17, and miR-UTR1 replaces endogenous miR-18. In this orientation, miR-UTR2 was active and was able to inhibit its target by 72 $\pm 0.5\%$ (Fig 2C). In contrast, this change resulted in a loss of activity for miR-UTR1. The other three miRNAs maintained their activity with miR-UTR3 demonstrating 44.5 $\pm 9\%$ inhibition, miR-Core demonstrating 62 $\pm 2\%$ silencing, and NS5B showing 56 $\pm 11\%$ inhibition. There was no significant difference between expression of miR-UTR3, miR-Core, and miR-NS5B when expressed from Cluster 1 or Cluster 2. These

results indicate that mature miRNAs are not processed correctly from the miR-18 scaffold. When they are inserted into another endogenous miRNA, they can be processed to their mature forms and their activity can be restored. The new cluster, Cluster 2, was also able to silence a reporter that contains all five miRNA targets by
5 ~80 +/-2% (P<0.01).

Safety Evaluation of Anti-HCV miRNAs

Off-targeting, or the inappropriate cleavage of unintentional targets, represents a potentially serious risk for RNAi-based agents. It is triggered by downregulation of
10 targets when pairing between the seed region (positions ~2-8 nt from the 5' end of the miRNA) of the miRNA guide strand and complementary sequences in the 3'UTR of off-targeted transcripts occurs (39).

The relative sequence specificity of the individually expressed miRNAs for their targets was evaluated by determining their ability to inhibit non-cognate reporter plasmids. As shown in Figure 3A, miR-UTR1 inhibited its cognate target, but did not
15 inhibit the RLuc-UTR2 or RLuc-UTR3 reporters, and only low levels of inhibition ($\leq 10\%$) were observed against the RLuc-Core and RLuc-NS5B reporters. As shown above, miR-UTR2 was unable to inhibit its cognate reporter and the data in Figure 3A indicate that it was also ineffective against non-target reporters, with the exception of
20 the NS5B reporter where 14 +/-7.6% inhibition was observed. Again, this indicates that this miRNA may induce low levels of non-specific silencing. The miR-UTR3, miR-Core, and NS5B miRNAs were only able to inhibit their cognate reporters, and no inhibition of non-specific reporters was detected. Thus, the four active miRNAs show good specificity in inhibiting the target sequences that they were designed to
25 silence.

Additional evaluation of the sequence specificity of miRNAs was assessed using RLuc-HCV reporter plasmids that contained three bp mutations in the area corresponding to the seed region of the miRNA. In these experiments, the HCV-miRNA Cluster 1 plasmid was used. As shown in Figure 3B, co-transfection of this
30 plasmid with the RLuc-UTR1 mutant reporter resulted in 7 +/-6% inhibition. When it was co-transfected with the UTR2, UTR3, Core, and NS5B mutant RLuc reporters, 1 +/-2%, 13 +/-9%, 12 +/-5%, and 7 +/-5% inhibition of the target was observed. This is in contrast to the 60-80% inhibition of wild-type reporters observed in Figure 2B ,

demonstrating that the HCV miRNAs have good specificity for the wild-type HCV genome, minimizing the potential for off-target effects.

Another potential concern with the generation of artificial miRNAs is that the wrong strand of the miRNA duplex will be incorporated into the RISC, resulting in passenger strand-mediated off-target effects. Strand selection by the RISC is governed by strand asymmetry (4;5) with the 5' end of the guide strand having lower base-pairing stability than the passenger strand. This results in preferential assembly of the guide strand into the RISC, which is accompanied by destruction of the passenger strand. It has been shown that in order to obtain good discrimination between strands in the RISC incorporation, it is important to mimic the secondary structure of the endogenous miRNA closely (34). Close attention was paid to this in the design of the pre-miRNAs by introducing mutations in the passenger strand to create bulges, while retaining the guide strand sequence. To evaluate how successful the design of the HCV miRNAs was in ensuring guide strand assembly into the RISC, five RLuc-HCV reporter plasmids that contained the reverse complement HCV target sequences were generated. Inhibition of RLuc activity would represent incorporation of the passenger strand into the RISC and would be a concern for passenger strand-mediated off-target effects and low potency of miRNAs. As evidenced by Figure 3C, very low levels of inhibition of the reverse complement targets was observed (ranging from 0-7%). These data, coupled with the data from Figure 2B using the wild type RLuc reporters, demonstrate that the proper strand (i.e. guide) of the miRNAs was loaded into the RISC.

Further evaluation of off-targeting was evaluated by determining proliferation of Huh-7 cells after transfection of miRNA expressing plasmids. Fedorov et al. (40) demonstrated that off-target effects induced by siRNAs can be manifested as strong quantifiable phenotypes, such as an inhibition of cell growth. To evaluate the potential toxic effect of the HCV miRNAs, Huh-7 cells were transfected with increasing amounts of HCV miR Cluster 1 and one of the five RLuc reporters or no reporter. Twenty-four hours later, cell proliferation was analyzed. Figure 4 demonstrates that in the presence of a reporter plasmid, expression of miRNAs from HCV miRNA Cluster 1 does not affect cell proliferation. In addition, in the absence of a reporter plasmid, a situation which might enhance off-target effects, no effect on cell viability was seen. The combined data demonstrate that the HCV miRNAs are specific for their targets, incorporate the proper strand into the RISC, and do not affect

cell viability. Thus, expression of these miRNAs from a polycistronic transcript appears to be safe *in vitro* and the likelihood of off-target effects is minimal.

In Vivo Activity of Anti-HCV miRNAs

5 The efficacy of an artificial polycistronic miRNA has not been previously evaluated *in vivo*. The efficacy of the five HCV miRNAs was evaluated in mouse liver by co-injecting the HCV miRNA plasmids (Cluster 1, Cluster 1 + Intron, and Cluster 2) with the RLuc-HCV reporter plasmids via hydrodynamic tail vein injection (41). Two days following the injection, mice were sacrificed, livers were harvested,
10 and dual luciferase assays were performed on liver lysates. The efficacy of miR-UTR1 to target its reporter when expressed from miR Cluster 1 with and without an intron was compared, and similar levels of inhibition (~90%), with no statistical difference, were observed. Subsequently, miR Cluster 1 + Intron was chosen for all analyses. As shown in Figure 5A, four of the five miRNAs expressed from HCV
15 Cluster 1 + Intron were highly active in inhibiting their cognate reporters. For example, miR-UTR1 inhibited its reporter by 89 +/-1.4 %, and miR-UTR3, miR-Core, and miR-NS5b silenced their cognate RLuc reporters by 65.5 +/-10.5%, 95%+/3.5%, and 93+/-1.7%, respectively ($P<0.01$ for these four miRNAs). Similar to what was found in Huh-7 cells, miR-UTR2 was completely inactive. HCV-miR Cluster 1 +
20 Intron was also evaluated against the RLuc reporter containing all five HCV targets and saw 94 +/- 2 % ($P<0.01$) inhibition of this target. In all cases, higher silencing activity by the four active miRNAs was observed *in vivo* as compared to that seen *in vitro*. The higher activity was not due to non-specific silencing as demonstrated by the failure of HCV-miR Cluster 1 + Intron to inhibit a reporter lacking HCV
25 sequences (psiCHECK) (Figure 5A). In addition, the lack of inhibition of the RLuc-HCV UTR1 reporter by HCV-miR-Core alone also demonstrated that the higher levels of inhibition observed *in vivo* are not due to non-specific targeting.

 As mentioned above, a second miRNA cluster (HCV-miR Cluster 2) was constructed to evaluate the activity of miR-UTR2 when inserted into endogenous
30 miR-17, rather than miR-18. This change in position resulted in a highly active miR-UTR2, capable of inhibiting its target by 97+/-0.5 % ($P<0.01$) (Figure 5B). As was the case *in vitro*, the reciprocal placement of miR-UTR1 into endogenous miR-18 from miR-17, completely abolished its activity, again suggesting that mature miRNAs are not processed correctly from a pre-miR-18 scaffold. The three other miRNAs (UTR3,

Core, NS5B) were able to inhibit their targets by 79 +/- 4.3%, 97 +/- 0.9%, and 92 +/- 1.4% ($P < 0.01$ for these three miRNAs), respectively. Similar to Cluster 1, Cluster 2 was also able to silence the HCV reporter containing all five targets by 92 +/- 2.7 % ($P < 0.01$) (Figure 5B). Thus, two separate HCV-miR Clusters are able to express four
5 potent miRNAs that target HCV sequences.

Active miRNAs are Properly Processed from pri-RNAs

The data hereinabove indicate that four out of five miRNAs expressed from HCV miR Cluster 1 and 2 are properly processed from the pri-miRNA and that their
10 guide strands are selectively incorporated into the RISC, where they mediate inhibition of their cognate HCV targets. To confirm this, Northern blot analyses of total RNA from the livers of mice that had been injected with HCV-miR Cluster 1 and HCV-miR Cluster 1 + Intron was performed. Using sense strand RNA probes to detect the guide strand, mature forms of the four active miRNAs were observed
15 (Figure 6A, 6C-6E). Very little pre-miRNA, which is expected to range from 70-87 nucleotides, was observed, indicating that efficient processing of miR-UTR1, miR-UTR3, miR-Core and miR-NS5B from the pre-miRNA was achieved. Synthetic siRNA standards were included on the blots to estimate the amount of each miRNA that was produced. Approximately equal amounts (~1 fmole) of the four active
20 miRNAs are present in 25 μ g of liver RNA. This indicates that these four miRNAs are processed from the pri-miRNA with similar efficiencies. In contrast, no mature miR-UTR2 was observed following transfection of mouse liver with HCV-miR Cluster 1 or HCV-miR Cluster 1 + Intron (Figure 6B), consistent with the lack of inhibition of the RLuc-HCV UTR2 reporter plasmid, that was observed in the dual
25 luciferase assays. Overexposure of this blot failed to detect the miR-UTR2 transcript.

When the orientation of miR-UTR1 and miR-UTR2 were reversed in HCV-miR Cluster 2, a highly active miR-UTR2 was produced, while miR-UTR1 was inactive, as measured by RLuc activity. This correlated with the production of mature miRNAs as Northern blot analyses demonstrated that RNA isolated from mice
30 injected with HCV-miR Cluster 2 contained mature miR-UTR2 and very little pre-miRNA (Figure 7B). As was predicted by the silencing data, no mature miR-UTR1 was produced from HCV miRNA Cluster 2 (Figure 7A). These data indicate that miRNAs are not efficiently processed from the miR-18 scaffold and that the use of this scaffold for the generation of artificial miRNAs requires further optimization.

However, the other four miRNA scaffolds can be used successfully to produce highly active miRNAs.

A Northern blot was also probed with the miR-UTR3 anti-sense strand probe to assess the amount of passenger strand present in the liver. Consistent with what was found using the reverse complement RLuc HCV reporter, no evidence of the passenger strand was detected, supporting the idea that the guide strand of the mature miR-UTR3 is stable and active, while passenger strand is degraded.

Given the problems with expressing an HCV inhibitory RNA from the miR-18 loop, we generated another HCV-miRNA cluster (HCV-miR-Cluster 5) that encodes five miRNAs by using the last miRNA in the miR17-92 cluster (miR-92), rather than the second miRNA (miR-18), as a scaffold for miR-UTR1. Thus, this cluster contains in order: miR-UTR2, miR-UTR3, miR-Core, miR-NS5B, miR-UTR1 (Figure 10).

The plasmid encoding HCV-miRNA-Cluster 5 was evaluated for the ability to silence six different RLuc-HCV reporter plasmids in Huh-7 cells. Huh-7 cells were co-transfected with 125 µg of an RLuc-HCV reporter plasmid (UTR1, UTR2, UTR3, Core, NS5B, or 5 Targets) and 125 µg of a plasmid expressing HCV-miR-Cluster 5, or pUC19. Twenty four hours post-transfection, cell lysates were prepared and dual luciferase (Firefly Luc and Renilla Luc) assays were performed. Normalized RLuc expression in cells co-transfected with pUC19 was set as 100% activity or 0% inhibition of the target, and the percent inhibition achieved by each miRNA was compared to the pUC19 control. In contrast to the previous clusters, all five anti-HCV miRNAs were active and inhibited their cognate targets by up to 73% and inhibited expression from the 5 Target reporter by 87% (Figure 11).

To evaluate the inhibitory potential of scAAV2-HCV-miRNA-Cluster 5 on HCVcc replication, Huh7-5 cells were plated at 2×10^5 cells per well in a 6 well plate. Twenty-four hours later, cells were infected with HCVcc and either scAAV2-HCV-miRNA-Cluster 5 or the control vector, scAAV2-eGFP, at one of four MOIs (1×10^3 , 1×10^4 , 1×10^5 , 1×10^6 vg/cell). Media was changed after 2 hrs and the cells were incubated for 72 hrs, at which time cell supernatants and cell lysates were harvested. Viral RNA and total cellular RNA was purified from supernatants and cell lysates, respectively. Two independent experiments were performed, and average % inhibition is shown. A negative control included wells of Huh 7.5 cells that were not transduced by AAV vectors, but were treated with HCVcc. As shown in Figure 12A, the amount of HCV sequences observed in the total cellular RNA, as determined by

quantitative real-time RT-PCR (QRT-PCR), decreased in a dose-dependent manner. Using 10^3 , 10^4 , 10^5 , and 10^6 vg/cell of scAAV2-HCV-miR-Cluster 5, 25, 45, 91, and 93 % inhibition of HCVcc was achieved, respectively. The decrease in cellular HCV RNA levels correlated with a decrease in the levels of HCV RNA observed in the supernatants (Figure 12B). These data demonstrate that that scAAV2-HCV-miR-Cluster 5 has the ability to inhibit *bona fide* HCV replication by up to 96%.

AAV vectors expressing HCV-miRNA-Cluster 5 eliminate HCVcc from infected cells

Previously, we demonstrated that scAAV2-HCV-miRNA-Cluster 5 was able to inhibit HCVcc replication by up to 96% when added to Huh7.5 cells at the time of HCVcc infection. We now show that the Cluster 5 vector can completely eliminate an HCVcc infection. In order to model how the AAV-Cluster 5 vector would perform in an *in vivo* setting, where hepatocytes do not divide and the vector is stably maintained, Huh7.5 cells were first infected with both HCVcc and scAAV2-HCV-miRNA-Cluster 5. Forty eight hours later, a portion of the supernatant was transferred to Huh7.5 cells that had previously been transduced with scAAV2-HCV-miRNA-Cluster 5. Another portion of the supernatant, as well as the cells, was analyzed for HCVcc copies by quantitative RT-PCR. This process was repeated for a total of six rounds. Another set of cells was first infected with HCVcc and an AAV vector that expresses just a single miRNA (i.e., miR-Core). Controls in this experiment included cells that were infected with HCVcc and transduced with AAV-GFP, cells that were infected with HCVcc and treated with IFN- α , HCVcc only-infected cells, and cells that were not treated with either HCVcc or AAV. The data in Figure 14 demonstrate that by the fourth round of HCVcc propagation in AAV-Cluster 5-transduced cells, HCVcc was eliminated from the culture (blue bars). This represents at least a 5 log decrease in HCVcc levels (assay limit of quantitation (LOQ)=100 copies). In contrast, HCVcc was not eliminated from un-treated cells (red bars) or cells transduced with AAV-GFP (green bars). Although a 96% decrease in HCVcc levels were observed in cells repeatedly transduced with AAV-miR-Core, HCVcc was not eliminated from the culture (purple bars). IFN- α was also able to clear the HCV infection over time (orange bars). These data suggest that in an infected liver, the stable expression of miRNAs from scAAV2-HCV-miRNA-Cluster 5 will result in the elimination of HCV from transduced hepatocytes.

scAAV8-HCV-miRNA-Cluster 5 silences all 5 target sequences in vivo

We have previously shown that plasmid DNA encoding HCV-miRNA-Cluster 5 was capable of silencing the five cognate miRNA target sequences. We have now cloned this expression cassette into an AAV vector backbone and packaged it into scAAV8 vector particles for efficient gene transfer to the liver. The scAAV8-HCV-miRNA-Cluster 5 vector was evaluated for its ability to express the five anti-HCV miRNAs and to silence their cognate HCV target sequences in vivo. Mice were injected with one of three doses of the vector (2.5×10^9 , 2.5×10^{10} , and 2.5×10^{11} vector genomes/mouse; n=5). In addition, a cohort of animals was injected with 2.5×10^{11} vector genomes of the control vector, scAAV8-GFP. Two weeks later, one of five Renilla luciferase /HCV reporter plasmids was injected. Animals were sacrificed two days later and liver lysates were analyzed for dual luciferase activity. The percent inhibition of the targets was determined relative to the scAAV8-GFP-treated control animals. The data in Figure 15 demonstrates that at the low vector dose, gene silencing of the UTR1 and UTR2 target sequences was observed, but no silencing of the other three targets was seen. However, at the middle dose, all five HCV target sequences were inhibited by 54-93 %, and at the high vector dose, silencing of up to 98% was observed. Northern blot data (not shown) confirmed a dose response in the expression of the miRNAs, with no or low expression of the miRNAs seen at the low dose, and clearly detectable miRNAs observed at the two higher doses.

scAAV8-HCV-miRNA-Cluster 5 can be safely delivered to the liver

A study was performed to evaluate potential hepatotoxicity following scAAV8-HCV-miRNA-Cluster 5 administration to mouse liver. It has been reported that the administration of AAV-vectors expressing short hairpin RNAs results in toxicity and lethality at high doses, whereas delivery of miRNA mimics has been reported to be safe. Thus, to evaluate this novel AAV vector, mice were injected with three different doses of scAAV8-HCV-miRNA-Cluster 5 (2.5×10^9 , 2.5×10^{10} , and 2.5×10^{11} vector genomes/mouse; n=5), and serum was collected at 4-5 different time points for liver enzyme analyses. As shown in Figure 16, no differences in the levels of the two major indicators of hepatotoxicity, alanine amino transferase (ALT) and alkaline phosphatase (AP), were observed between the negative control cohort (scAAV8-GFP) and the three scAAV8-HCV-miRNA-Cluster 5 -treated animal

cohorts, indicating that the miRNA-expressing vector can be safely delivered to mouse liver.

In conclusion, the combined data demonstrate that the scAAV8-HCV-miRNA-Cluster 5 vector is effective at inhibiting HCV replication and completely eliminating it from cell culture systems. In addition, it expresses five biologically active anti-HCV miRNAs in mouse liver without inducing hepatotoxicity. This AAV vector is a viable clinical candidate for use in the treatment of chronic HCV infection.

DISCUSSION

In this example, four miRNA clusters were generated to express five miRNAs targeting different regions of the HCV genome. Three of the miRNAs target the 5'UTR of HCV, one is specific to the Core region, and one targets the NS5B transcript. The pre-miRNAs were constructed by incorporating validated siRNA and shRNA sequences into the endogenous miR-17-92 cluster. The mature miRNAs were designed to mimic the secondary structure of their endogenous counterparts and to have low internal stability at their 5' ends. These characteristics have been associated with preferential incorporation of the guide strand into the RISC (4;5). The miRNAs are expressed from a liver specific promoter so they can ultimately be evaluated for inhibition of HCV replication in hepatocytes. Using RLuc reporter plasmids, the data indicates that four of the five miRNAs inhibit their cognate sequence by approximately 35-80% *in vitro*, when expressed individually. Co-expression of the miRNAs from a polycistronic pri-miRNA led to ~60-70% knockdown of cognate targets *in vitro*, demonstrating that simultaneous expression of the miRNAs does not sacrifice their activity, and in some cases enhances it. The miRNAs that were active *in vitro* (i.e., miR-UTR1, miR-UTR3, miR-Core, miR-NS5B) showed even higher levels of inhibition *in vivo*, achieving 65-95% silencing from HCV-miR Cluster 1 + Intron and 79-97% inhibition from HCV-miR Cluster 2. In both *in vitro* and *in vivo* settings, one of the miRNAs in HCV-miR Cluster 1 (miR-UTR2) was completely inactive. This miRNA was incorporated into the endogenous miR-18 scaffold. When it was instead incorporated into the endogenous miR-17 scaffold (HCV-miR Cluster 2), it became highly active, inhibiting its cognate target by 72% and 97% *in vitro* and *in vivo*, respectively. Interestingly, the reciprocal change, that is, moving miR-UTR1 from the miR-17 scaffold to the miR-18 scaffold, resulted in the loss of activity of this miRNA. These data indicate that mature miRNAs are not processed from the miR-18

scaffold. This was confirmed by Northern blot analyses which demonstrated that miR-UTR2 was not produced from HCV-miR Cluster 1, but was expressed at high levels from HCV-miR cluster 2. Conversely, miR-UTR1 was expressed from HCV-miR Cluster 1, but was not produced from HCV-miR Cluster 2. Although the endogenous miR18 is not expressed at lower levels than the other miRNAs in this cluster in all tissues, it appears to be expressed at lower levels in the liver (43). Thus, it might not be possible to manipulate this miRNA scaffold to achieve high level expression of mature miRNAs in the liver, and the use of the last miRNA in the cluster (i.e., miR-92) as an artificial miRNA scaffold may be a better choice. In view of these data, Cluster 5 was constructed wherein the use of the miR-18 loop was avoided and instead miR-92 was employed to expression an HCV inhibitory RNA targeting UTR-1. This construct, when expressed from an AAV2 vector, scAAV2-HCV-miR-Cluster 5, has the ability to inhibit *bona fide* HCV replication by up to 96% as it demonstrates effective inhibition of all 5 HCV targeted sequences.

The Northern blots demonstrate that slightly more of the miRNAs are expressed from HCV-miR Cluster 1 + Intron as compared to HCV-miR Cluster 1. This is consistent with data suggesting that it is important to include introns in gene therapy vectors so transcripts can be efficiently assembled into spliceosome complexes and be protected from degradation in the nucleus (44). However, at least for miR-UTR1, which was the only miRNA analyzed from both of these two clusters, no difference in silencing activity was observed between the two plasmids. Using the synthetic siRNA controls to estimate the levels of the miRNAs in liver tissue, the amount of the four active miRNAs expressed from HCV-miR Cluster 1+ Intron is ~1.0 fmole (or 6×10^8 miRNAs) in 25 μ g total liver RNA (or ~28 mg tissue, based on yields). This is in the same range as Real-Time PCR measurements for several artificial miRNAs that were expressed from the EF1 α promoter and delivered to cells by lentiviral vectors (27). Equivalent levels of miRNAs from a cluster are not necessarily expected for miRNAs expressed from a polycistronic transcript, but the data indicate that the four active miRNAs are present in roughly equal amounts. Using the hepatocellularity number that has been reported for mice of 1.38×10^8 cells/g liver tissue (45), 155 miRNAs were calculated to be expressed per cell. Since only ~20-40% of the hepatocytes can be expected to be transfected using the HDTV procedure (41), the transduced hepatocytes can be estimated to express ~400-800

miRNAs/cell. It has been reported that the copy number of HCV in hepatocytes is less than 10 copies/cell (46), and thus expression of miRNAs from HCV-miR Cluster 1 + Intron would be expected to be sufficient for inhibiting HCV replication.

There have been a number of reports indicating that siRNAs can result in alterations in mRNA expression (47) and in toxicity *in vitro* (40). In addition, serious toxicity and fatalities have been observed following sustained expression of shRNAs in mouse liver (31) and brain (29;32). However, the use of artificial miRNAs, as opposed to shRNAs, prevented competition between exogenous and endogenous shRNA and miRNAs (30), and eliminated the CNS toxicity seen in mouse brains (29;32). For these reasons the miRNA platform was utilized to design a therapeutic strategy for HCV. The anti-HCV-miRNAs used in the present example resulted in no toxicity in Huh-7 cells, as measured by cell viability, supporting the notion that the miRNAs do not induce off-target effects (40). In addition, the anti-HCV miRNAs are specific for their targets and the guide strands of the miRNA hairpin structures are preferentially loaded into the RISC. A correlation has been found between toxicity and the presence of a four bp motif (UGGC) in the siRNA strand entering the RISC (40), and other motifs, such as GUCCUCAA and UGUGU have been implicated in the induction of an immune response. None of these sequences are present in the anti-HCV miRNAs. Thus, the combined data strongly indicate that the anti-HCV miRNAs are safe.

For therapeutic purposes, it will be necessary to incorporate this cluster into a clinically relevant delivery system that allows for efficient delivery to the liver. Viral vectors are being developed for delivery of many RNAi-mediated therapies. Although individual miRNAs have been evaluated previously *in vivo* (17;18;29;32), artificial polycistronic pri-miRNAs have been evaluated in *in vitro* studies only (34;35). Four of the anti-HCV miRNAs expressed from the clusters described hereinabove target conserved regions in all six HCV genotypes and the combination of all five miRNAs has the potential to prevent the emergence of escape mutants (10). The use of a liver-specific promoter ensures expression in hepatocytes, the site of HCV replication, while minimizing off-target effects in non-target tissues. Thus, the ability to express multiple RNAi effectors simultaneously from a single tissue-specific promoter has the potential to provide both enhanced efficacy and safety. Recombinant adeno-associated viral vectors (rAAV) of serotype 8 are particularly effective in transducing mouse liver (50) and this serotype may prevent some of the

immune complications associated with the use of rAAV2 vectors (51). Recombinant AAV vectors encoding HCV-miR Cluster 1 or 2 can be used to test the efficacy of the individual miRNAs against a bonafide HCV infection. Other AAV vectors suitable for delivering exogenous nucleic acids to cells are described in US Patents 7,351,813 (wherein the miRNA cassette described herein can be substituted for the FIX encoding nucleic acid); 7,282,199; 7,261,544; 7,259,151; 7,241,447; 6,936,243 and 6,156,303. In addition to HCV, the miRNA clusters could be generated to inhibit other viruses and cellular gene products associated with disease and will also be useful for basic research applications.

10

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While certain of the preferred embodiments of the present invention have been described and specifically exemplified above, it is not intended that the invention be limited to such embodiments. Various modifications may be made thereto without departing from the scope of the present invention, as set forth in the following claims.

What is claimed is:

1. A composition comprising a miRNA expression cassette comprising at least two isolated nucleotide sequences selected from the group consisting of sequences complementary to SEQ ID NOs: 1-5, , in a pharmaceutically acceptable carrier.
5
2. The composition of claim 1, comprising at least four isolated sequences.
3. The composition of claim 1, comprising all five isolated sequences.
- 10 4. The composition of claim 1, wherein said construct is contained in a vector.
5. The composition of claim 4, wherein said vector is selected from the group consisting of AAV vectors, lentiviral vectors, retroviral vectors and AV vectors.
- 15 6. The composition of claim 5, wherein said vector is a recombinant AAV vector having a serotype selected from the group consisting of AAV-2, AAV-6 and AAV-8 comprising a sequence selected from the group consisting of the sequence of cluster 1, cluster 2 or cluster 5.
- 20 7. The composition of claim 6, wherein said vector is AAV-6 or AAV-8, comprising a sequence selected from the group consisting of the sequence of cluster 1 or cluster 2.
8. The composition of claim 4, wherein the expression of nucleotides is under the control of a single promoter.
- 25 9. The composition of claim 8, wherein said promoter is a tissue-specific promoter.
10. The composition of claim 9, wherein said promoter is a liver-specific alpha-one antitrypsin promoter, said composition additionally comprising a liver-specific
30 enhancer and a polyadenylation signal.
11. The composition of claim 10, wherein said enhancer is the apolipoprotein E hepatic control region.

12. The composition of claim 10, wherein said polyadenylation signal is the bovine growth hormone polyadenylation signal.
13. The composition of claim 4, wherein said composition comprises an intron.
14. The composition of claim 13, wherein said intron is downstream of said promoter and upstream of said at least two nucleotide sequences .
15. The composition of claim 14, wherein said intron is derived from human growth hormone.
16. A method of reducing HCV viral load in a patient comprising administering to the liver of said patient a therapeutically effective amount of the composition of claim 4 which directs cleavage of target HCV mRNA sequences present in said patient, thereby reducing HCV viral load.
17. The method of claim 16, wherein said composition is introduced directly into said patient.
18. The method of claim 17, wherein said introduction is via intravenous infusion.
19. The method of claim 16, wherein said method results in inhibition of HCV replication in said patient.
20. The method of claim 14, wherein introducing the vector to a cell, tissue, or organ of interest comprises: ligating the miRNA cassette into a viral delivery vector to form a viral miRNA expression construct; packaging the viral miRNA expression construct into viral particles; and delivering the viral particles to the cell, tissue, or organ of interest.
21. The method of claim 20, wherein the miRNA cassette comprising nucleic acids which target multiple regions of a HCV genome.

22. The method of claim 21, wherein said vector is an AAV vector and the miRNA cassette is cluster 5.

Figure 1

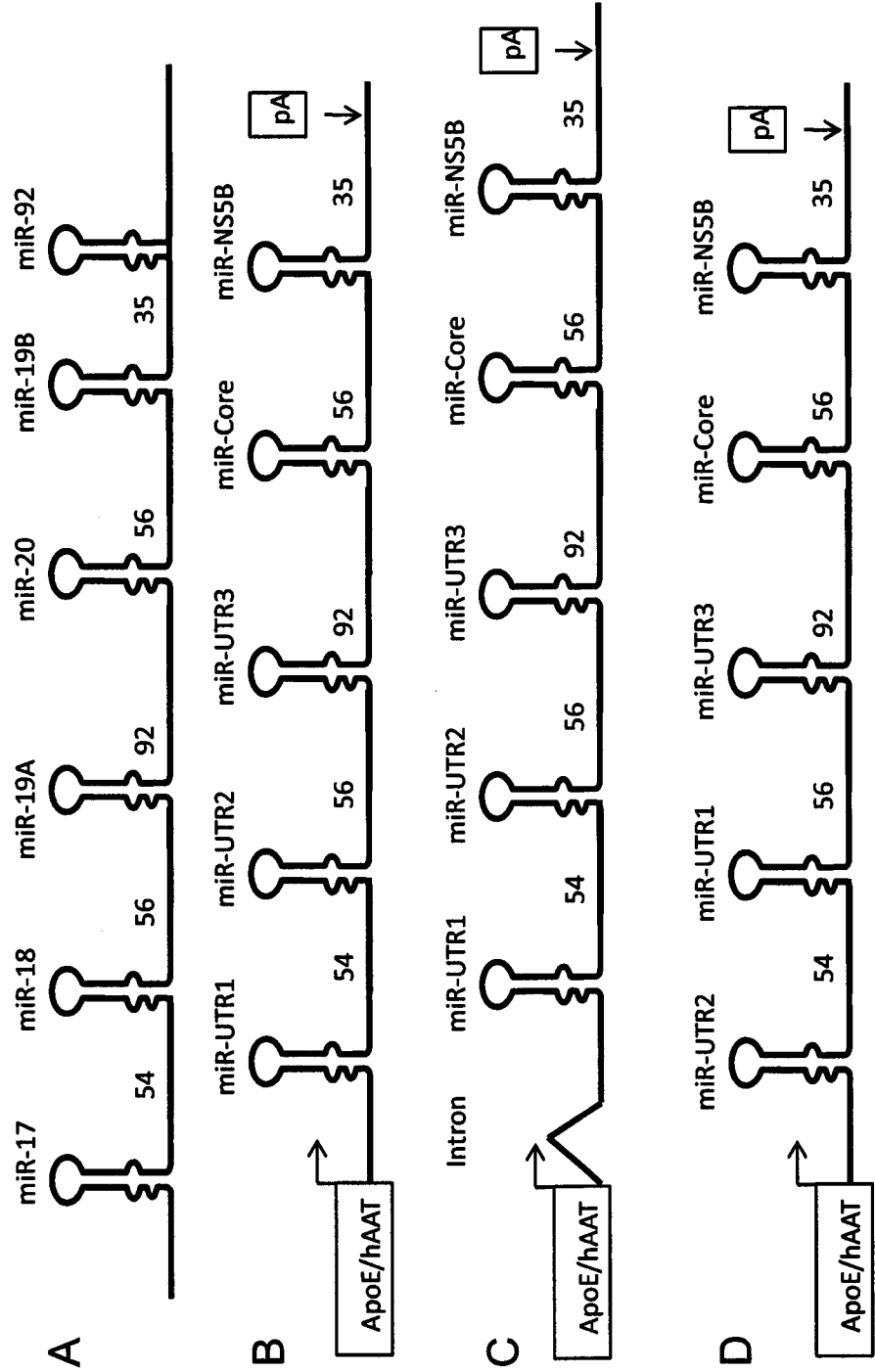
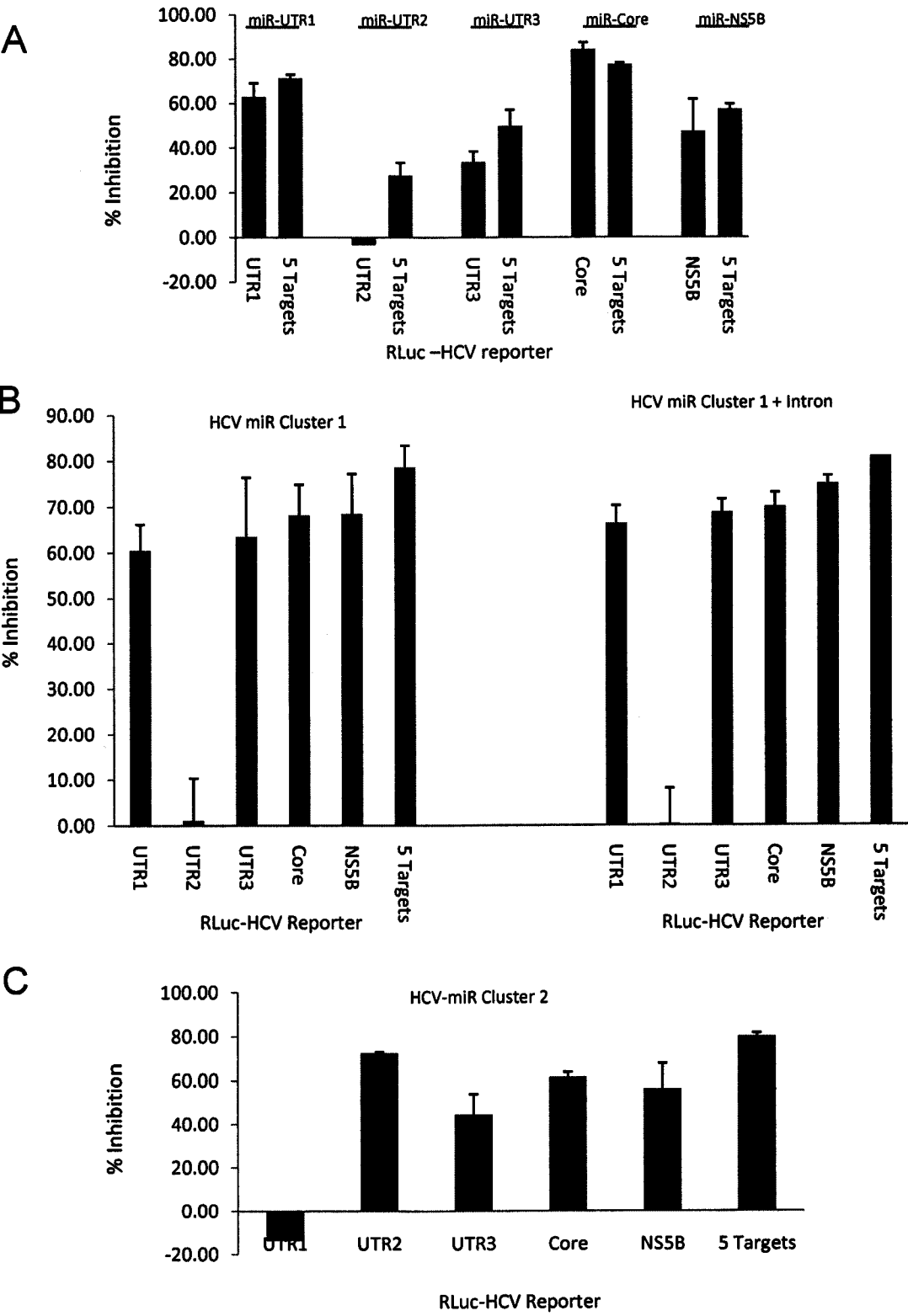
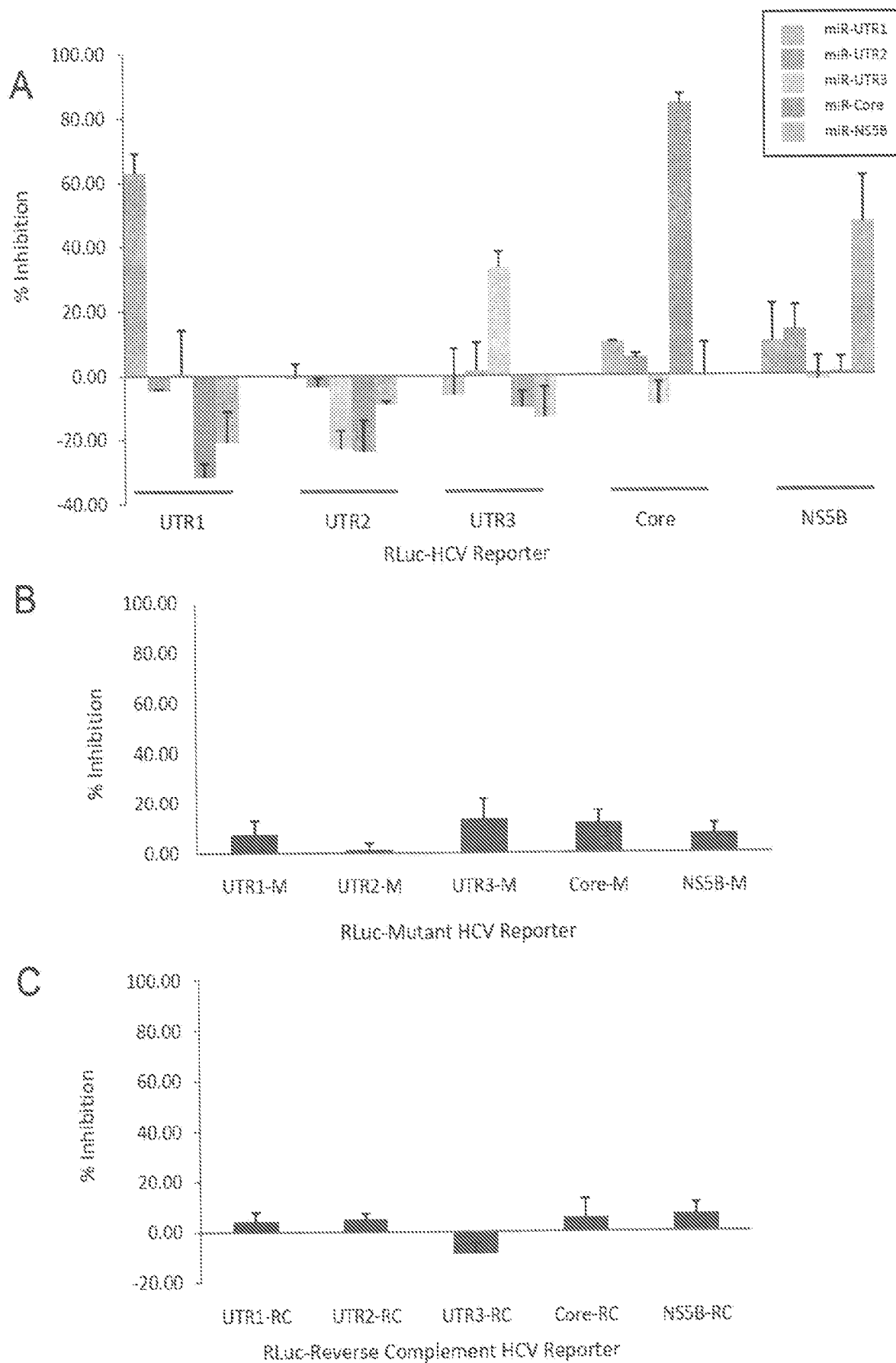
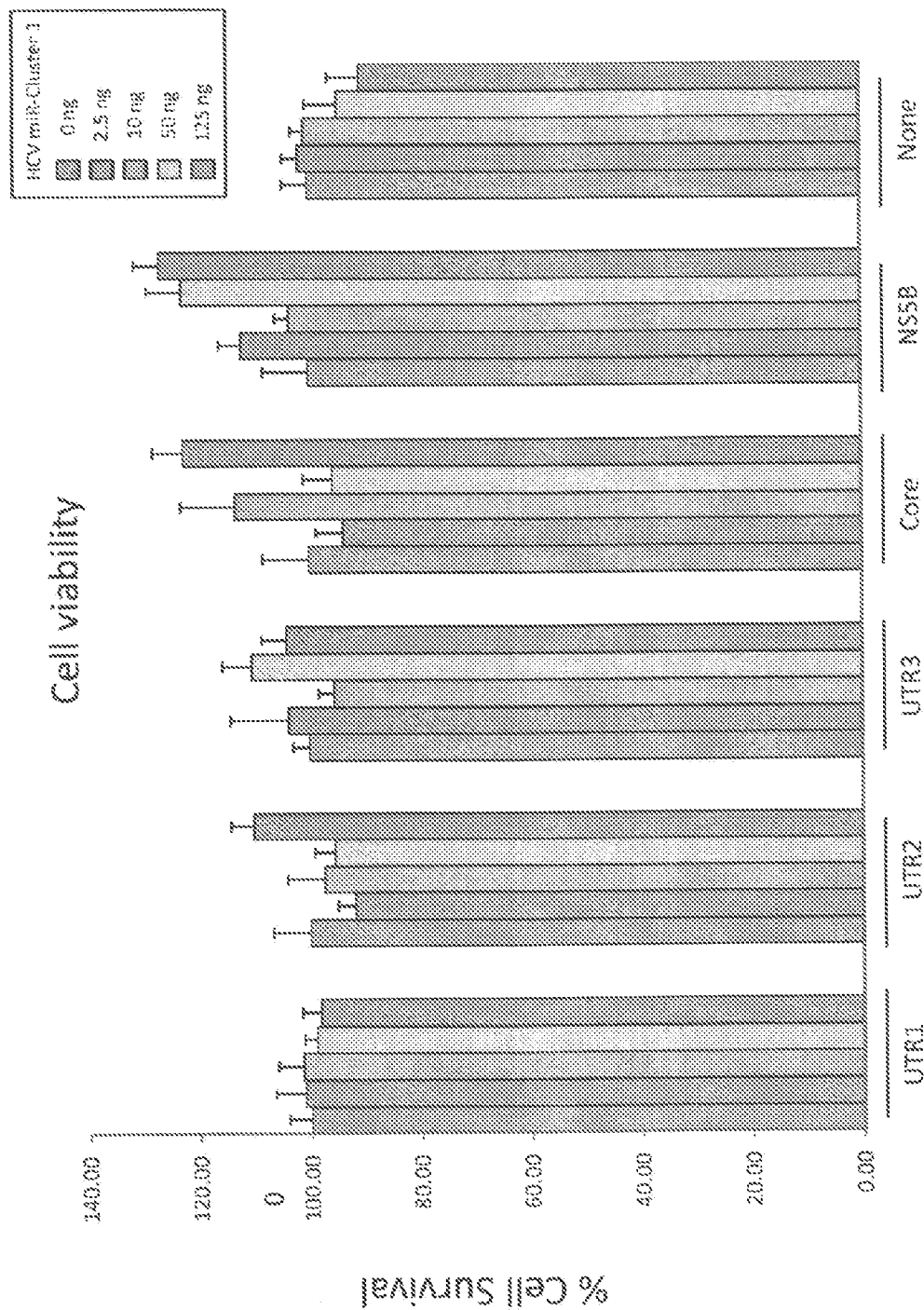


Figure 2



**Figure 3**

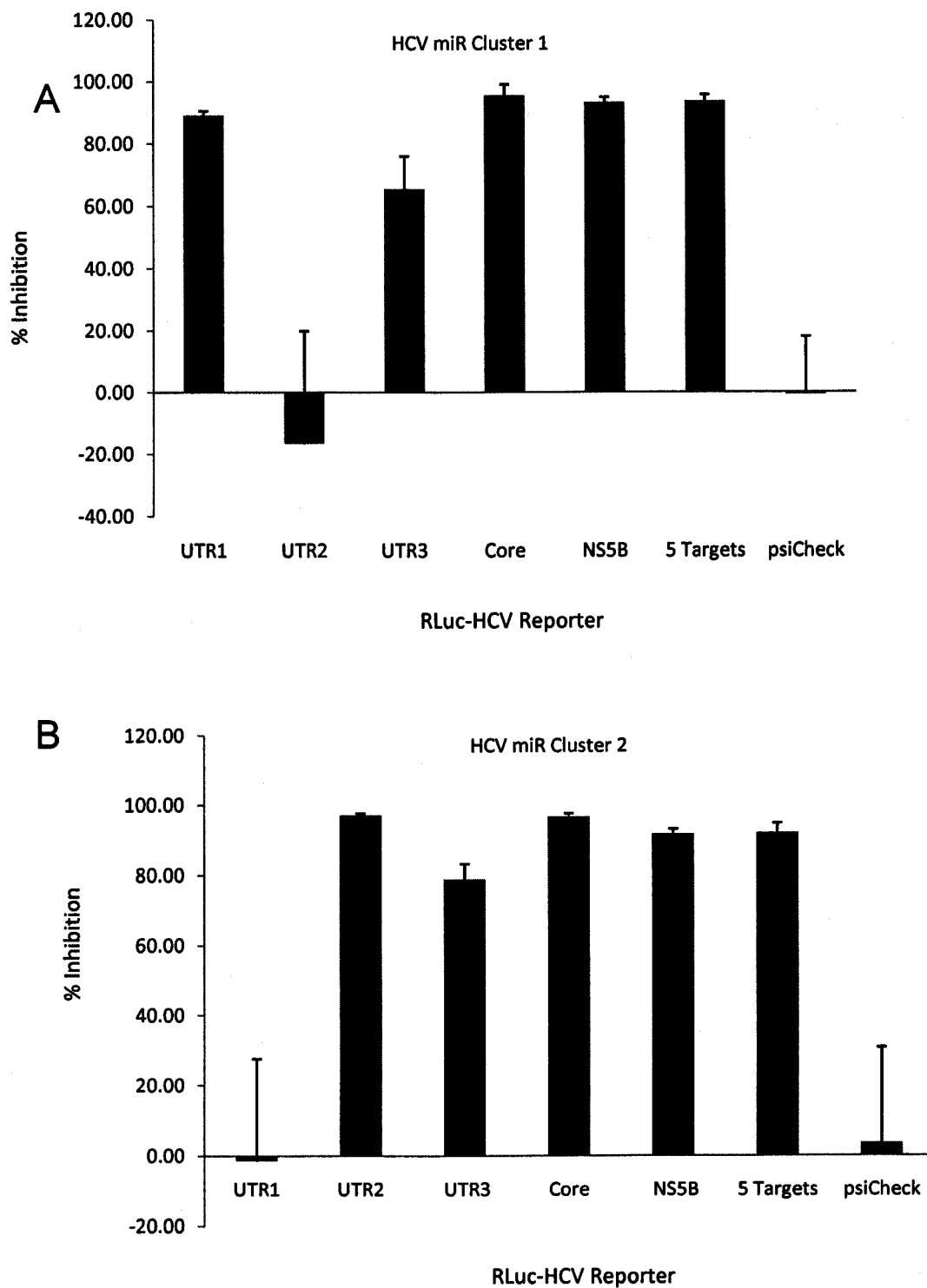
4/21

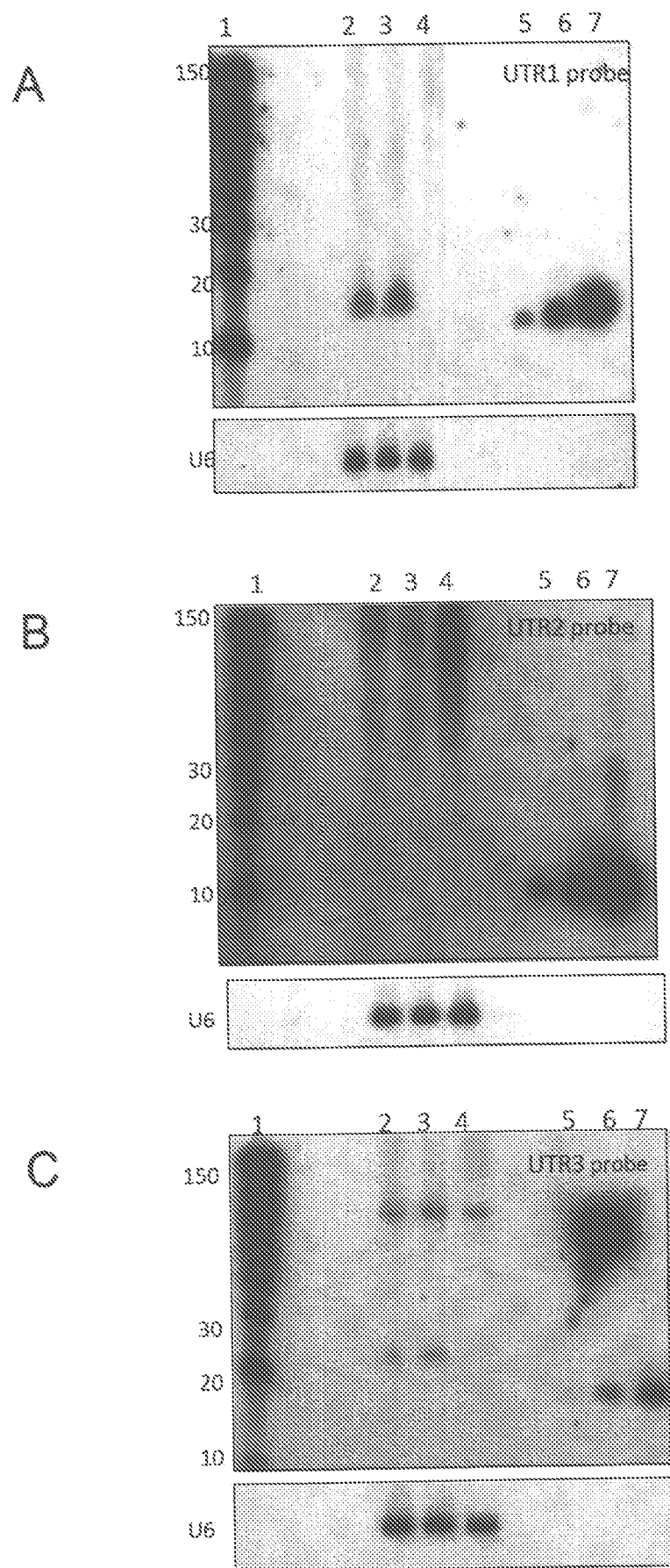


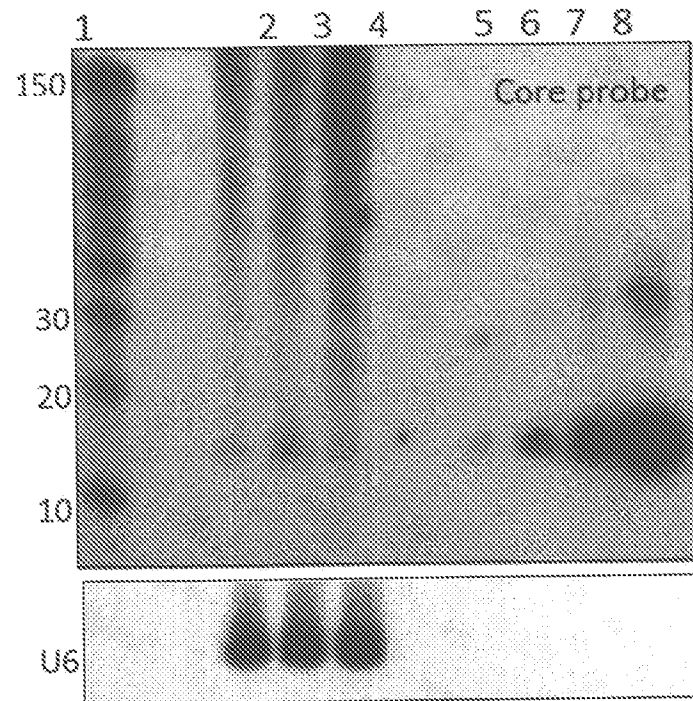
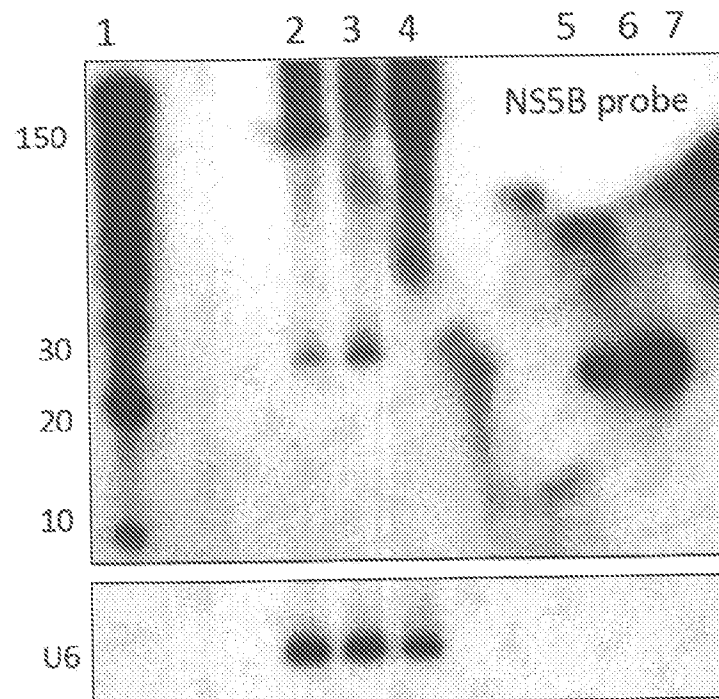
Luc-HCV Reporter

Figure 4

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Figure 5



D**E****Figure 6**

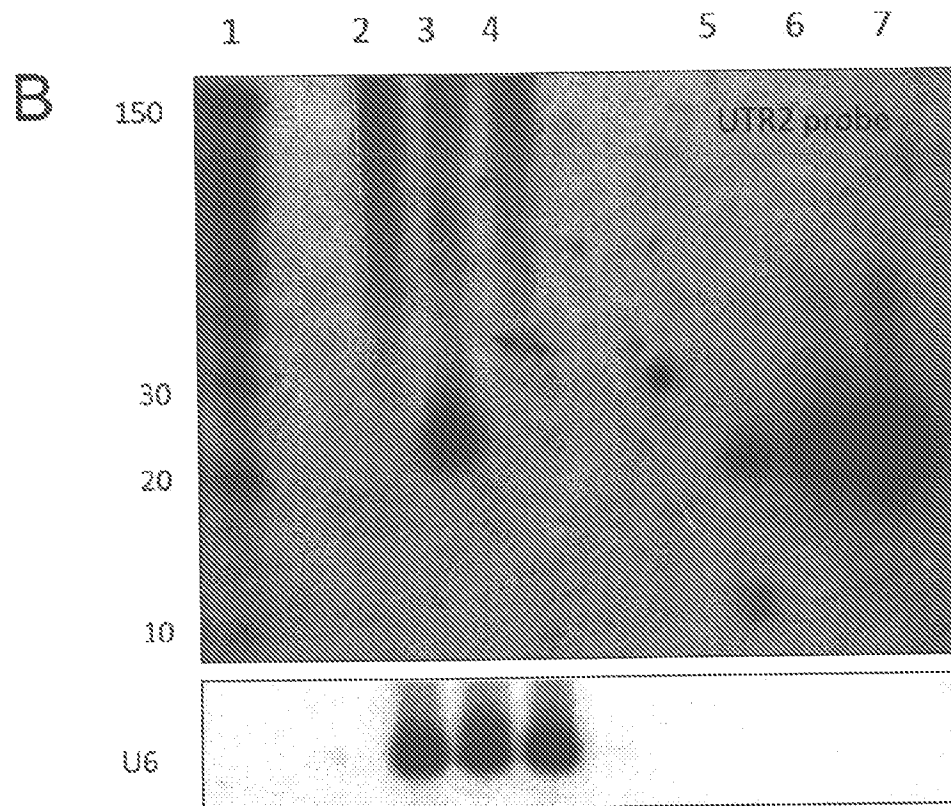
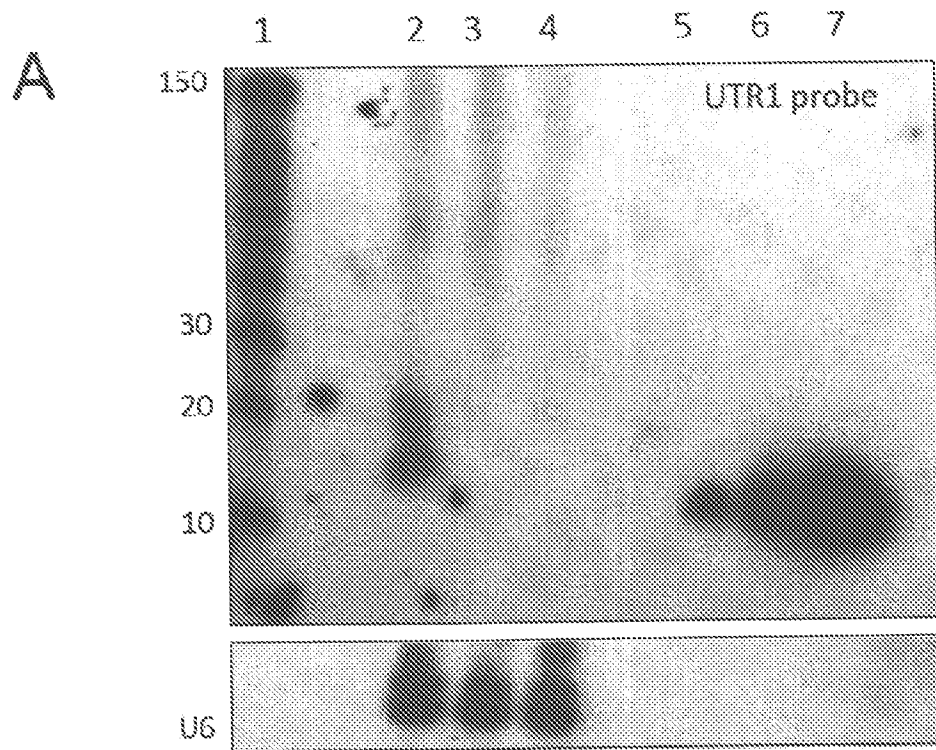


Figure 7

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ApoE/hAAT-HCV miRNA Cluster 1

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T

FIGURE 8A

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ApoE/hAAT-HCV miRNA Cluster 2

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FIGURE 8B

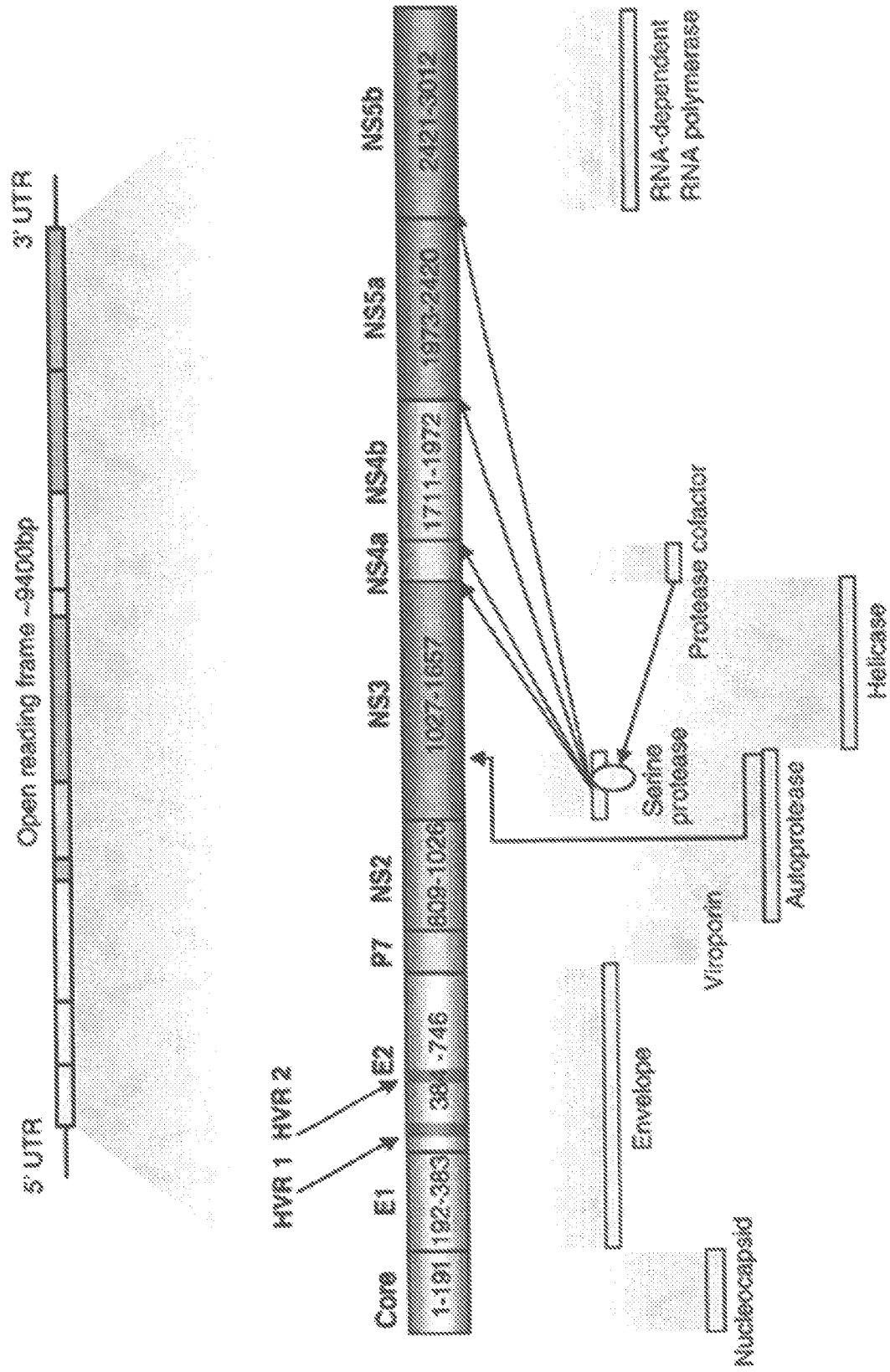
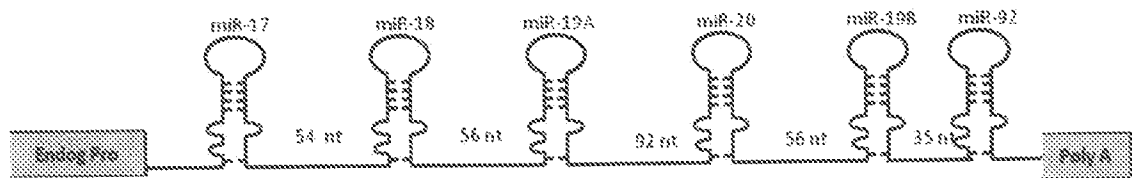


Figure 9

Endogenous miR17-92 cluster



Replace mature miR-17, miR-19A, miR20, miR-19B, and miR-92 sequences of miR 17-92 with sequences targeting HCV

Endogenous HCV-miR Cluster 5

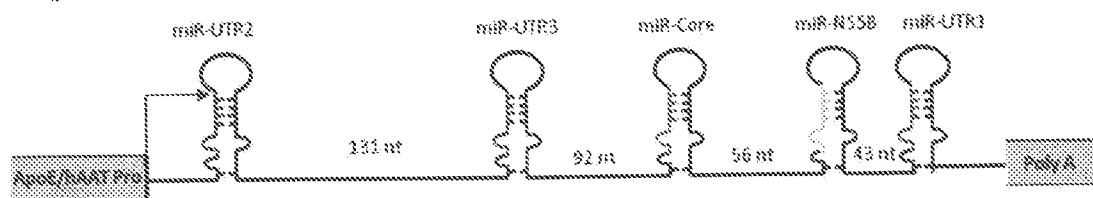


Figure 10

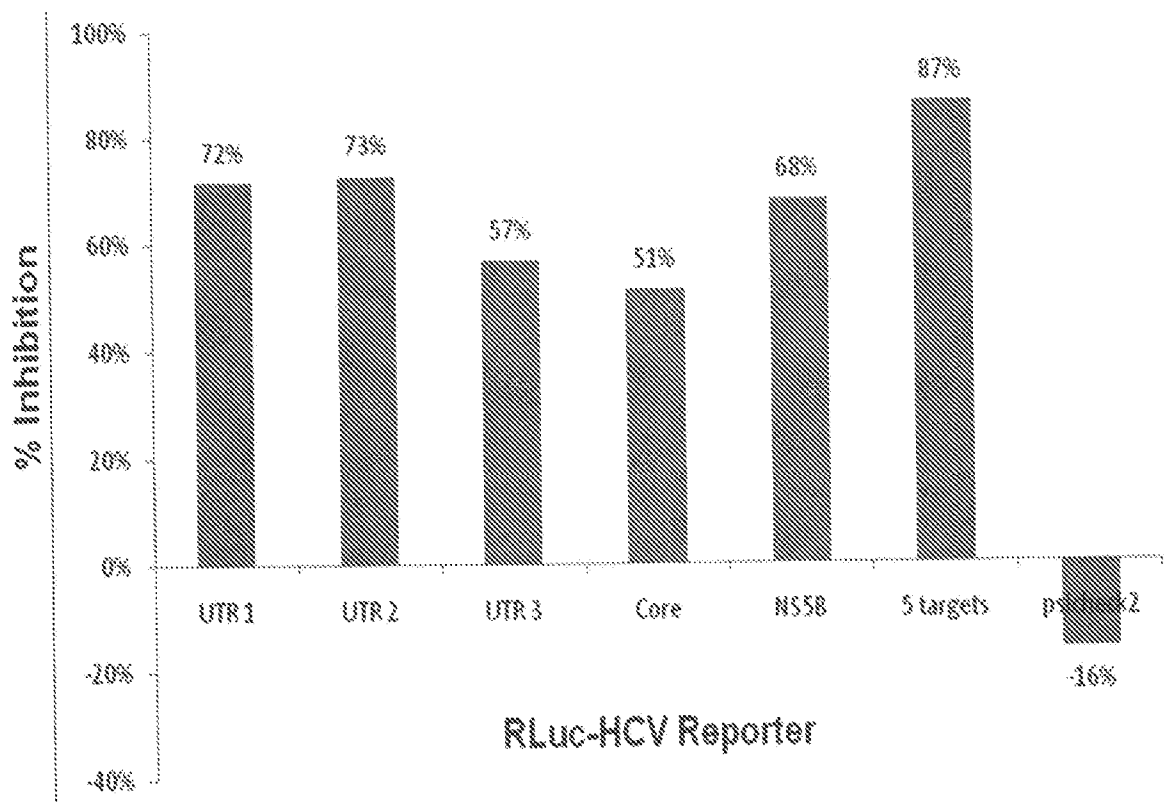


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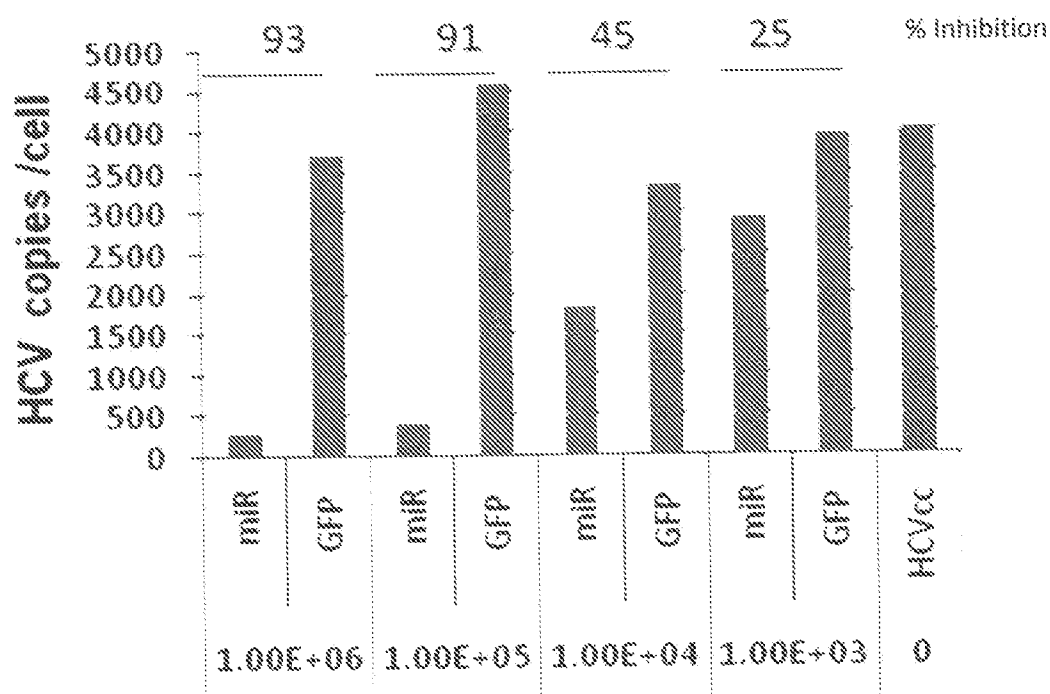
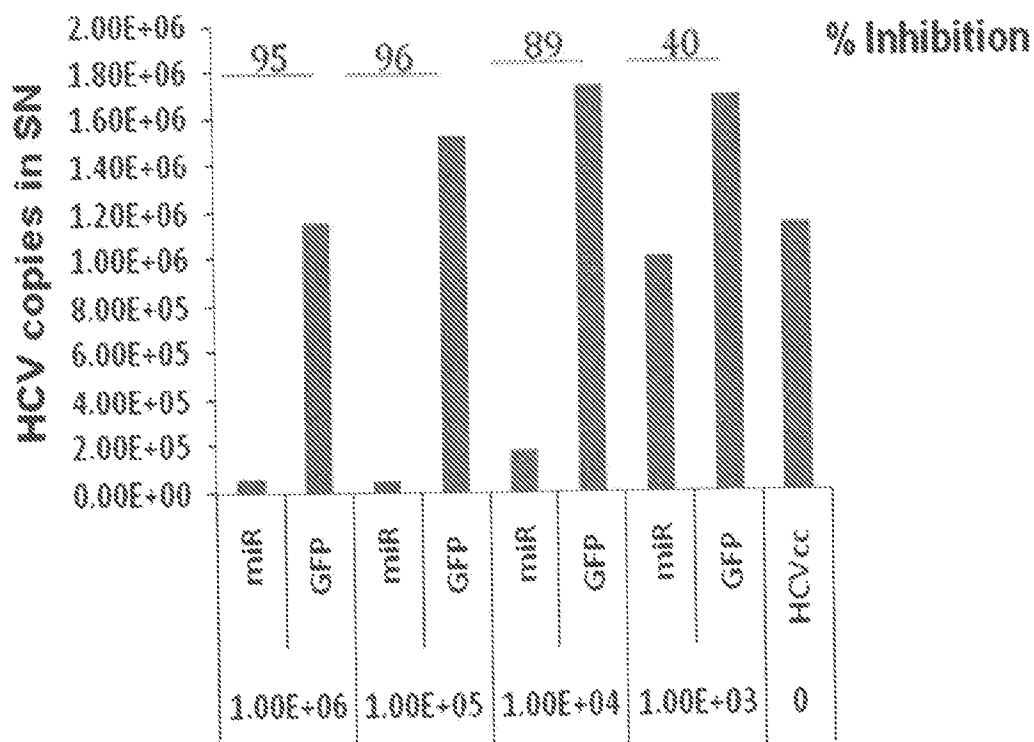
A**B**

Figure 12

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Figure 13A

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//

Figure 13B

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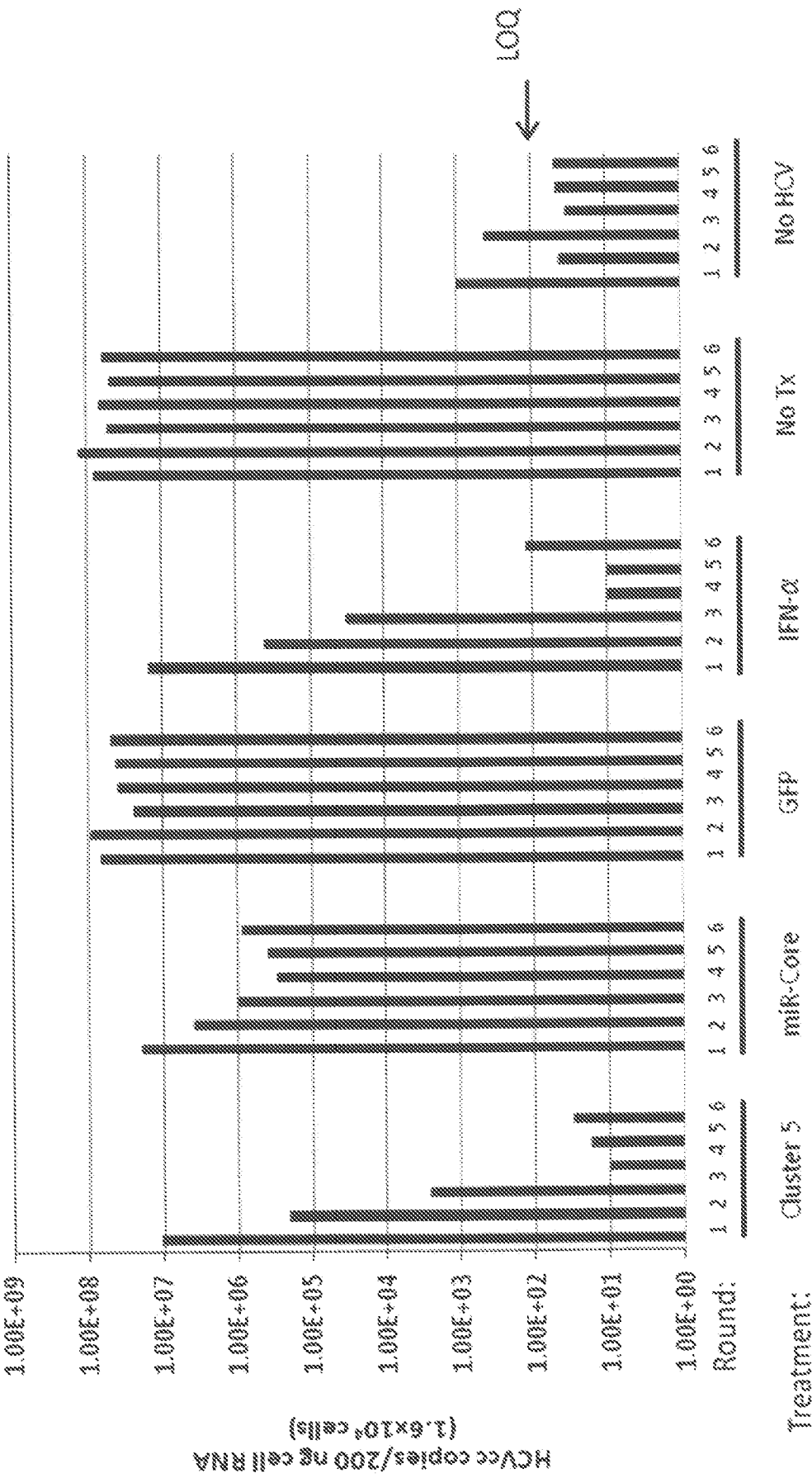


Figure 14

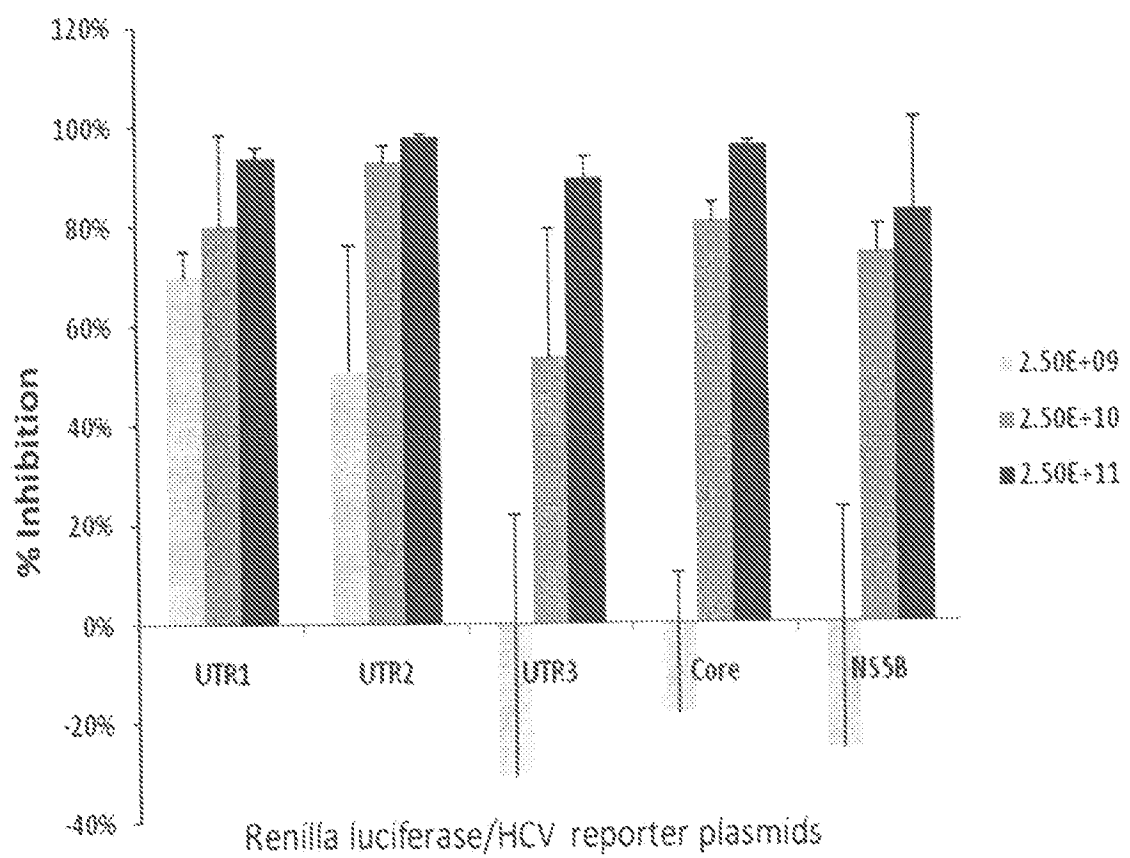


Figure 15

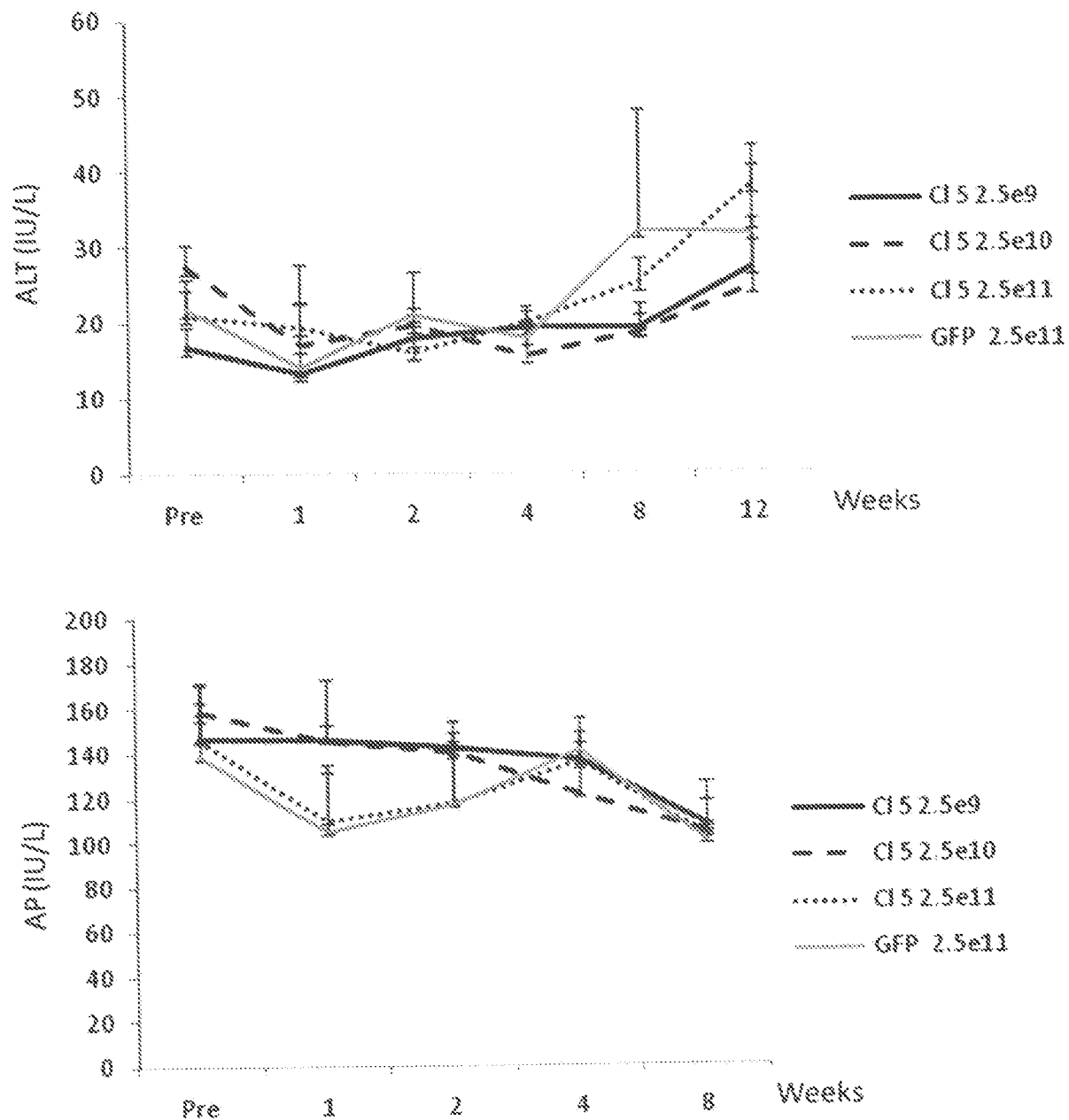


Figure 16

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 11/26666

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - A61K 31/7088; C12N 15/113 (2011.01)
USPC - 514/44A

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)
USPC: 514/44A

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
USPC: 514/44A (text search)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Electronic data bases: PubWEST (PGPB, EPAB, USPT, JPAB); Google Scholar; GenCore sequence search (NT)
Search terms: Hepatitis C Virus (HCV); microRNA polycistron, miRNA expression cassette, artificial miRNA, multiple miRNA, RNAi, vector, AAV vector, lentiviral vector, miR-UTR1, miR-UTR2, miR-UTR3, miR-Core, miR-NS5B, liver-specific promoter

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 20070025969 A1 (ROELVINK et al.) 1 February 2007 (01.02.2007). Especially SEQ ID NO: 8, para [0006], [0023], [0033], [0036], [0056], [0077], [0081], [0099], pg. 10 table 1, sheet 1 fig 1, sheet 2 fig 2B, sheet 9 fig 7B.	1-22
Y	HU et al. Construction of an artificial MicroRNA expression vector for simultaneous inhibition of multiple genes in mammalian cells. Int J Mol Sci; 14 May 2009; Vol. 10, No. 5; Pages 2158-2168. Especially abstract.	1-22
Y	US 2009/0306184 A1 (McSWIGGEN et al.) 10 December 2009 (10.12.2009). Especially SEQ ID NOs: 82, 1626, 51, para [0014], [0736-0740]	1-22
Y	US 2008/0070854 A1 (PACHUK et al.) 20 March 2008 (20.03.2008); Especially SEQ ID NO: 45, para [0010].	2, 3, 6, 7, 22
Y	US 2009/0099124 A1 (JAYASENA et al.) 16 April 2009 (16.04.2009); Especially SEQ ID NO: 9, para [0023]	3, 6, 7, 22
Y	US 2005/0276787 A1 (COUTO et al.) 15 December 2005 (15.12.2005). Especially para [0158], [0016]	10-15, 20-22
X,P	YANG et al. Inhibition of hepatitis C virus replication using adeno-associated virus vector delivery of an exogenous anti-hepatitis C virus microRNA cluster. Hepatology; ePub 7 October 2010; Vol. 52, No. 6; Pages 1877-1887. Especially abstract, entire article.	1-22

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

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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"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

2 June 2011 (02.06.2011)

Date of mailing of the international search report

05 JUL 2011

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P.O. Box 1450, Alexandria, Virginia 22313-1450

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Authorized officer:

Lee W. Young

PCT Helpdesk: 571-272-4300
PCT OSP: 571-272-7774