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(54) Title: SYNTHETIC MUSCLE PROMOTERS WITH ACTIVITIES EXCEEDING NATURALLY OCCURRING REGULATORY SEQUENCES IN CARDIAC CELLS

(57) Abstract: Transgenes driven by naturally occurring cardiac promoters have relatively low levels of cardiac transgenic gene expression, and have consequently limited the use of cardiac muscle as a target for plasmid mediated gene supplementation. However, by randomly assembling motifs of E-box, MEF-2, TEF-1 and SRE elements, cardiac-specific synthetic promoter recombinant libraries have been produced. By screening hundreds of resultant clones for transcriptional activity both *in vitro* and *in vivo*, a few cardiac-specific synthetic promoters were discovered comprising a transcriptional potency that greatly exceeds the transcriptional levels obtained from natural myogenic and viral gene promoters. These promoters are used to direct the expression of desirable genes in nucleic acid expression constructs specifically to cardiac cells. Thus, these cardiac specific-synthetic promoters can be utilized for plasmid mediated gene supplementation for serious health conditions, such as ischemic disease, myocardial infarction or heart failure. Thus, one aspect of the current invention is a cardiac specific-synthetic promoter produced by a method that generates a library of randomized synthetic-promoter-recombinant expression constructs. Another aspect of the present invention is directed to a method using the cardiac specific-synthetic expression construct for expression a gene of interest in a cardiac cell.

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SYNTHETIC MUSCLE PROMOTERS WITH ACTIVITIES EXCEEDING NATURALLY OCCURRING REGULATORY SEQUENCES IN CARDIAC CELLS

BACKGROUND

[0001] This application claims priority to U.S. Provisional Patent Application, Serial Number 60/423,536, entitled "Synthetic Muscle Promoters with Activities Exceeding Naturally Occurring Regulatory Sequences in Cardiac Cells," filed on November 4, 2002, the entire content of which is hereby incorporated by reference.

[0002] The ability to program recombinant gene expression in cardiac myocytes *in vitro* and *vivo* holds promise for the treatment of many inherited and acquired cardiovascular diseases (Lin et al., 1990). Cardiac and skeletal muscles are attractive targets for plasmid mediated gene supplementation because of their long life span, and large capacity for protein synthesis and secretion for local or general effects (Draghia-Akli et al., 1999; Vale et al., 1999). Moreover, cardiac and skeletal muscle tissue is highly vascularized and has a high rate of blood flow, thus allowing *de novo* proteins to readily act locally or enter the systemic circulation. Importantly, direct administration of plasmid DNA into heart or muscle leads to expression of recombinant proteins in muscle cells (Mazda, 2002; Prentice et al., 1996). Plasmid DNA can persist in an episomal state directing the expression of recombinant proteins for months to years (Acsadi et al., 1991; Wolff et al., 1992). However, a limiting problem in using plasmid mediated gene supplementation to correct or prevent cardiac disease has been the relatively low levels of expression that have been achieved with muscle specific vectors. Although a low expression level of a recombinant protein is enough to generate an immune response against the expressed protein, therapeutic levels of recombinant proteins have currently not been produced using muscle specific promoters/enhancers (Montgomery et al., 1997). In this report we describe a method for the construction and characterization of synthetic promoters for cardiac and muscle tissue. The transcriptional potency of these synthetic promoters in terminally differentiated muscle greatly exceeds that of the natural myogenic skeletal α -actin gene promoter and viral promoters.

[0003] When delivering therapeutic genes, the use of tissue specific promoters is highly desirable. Numerous strategies have been employed to create or use for therapeutic purposes tissue specific promoters, which support transcription in cardiac and skeletal muscle,

and are essentially silent in other cell types (Keogh et al., 1999; Roell et al., 2002; Rothermel et al., 2001). This approach assures localized transgene activity, without the potential complication of side effects linked to inappropriate expression in non-target tissues or organs. For instance, because of safety issues, components of the beta-adrenergic, Akt or caspase signaling pathway cannot currently be viewed as attractive targets for human gene therapy. Rather, the balance of evidence supports strategies that will target gene products specifically and directly at cardiac regulation, and molecular techniques can be devised to modulate their activity specifically and conditionally (Condorelli et al., 2001; Ding et al., 2002; Webster and Bishopric, 2000). In this report we describe a method for the construction and characterization of synthetic promoters for cardiac and muscle tissue. The transcriptional potency of these synthetic promoters in terminally differentiated muscle greatly exceeds that of the natural myogenic skeletal α -actin gene promoter and viral promoters, and may have important applications in conjunction with therapeutic genes.

[0004] Analysis of the organization of several strong muscle promoters and enhancers, with respect to groupings of cis-acting regulatory elements and their interactions with myogenic regulatory factors led the inventors to formulate a strategy to construct synthetic muscle promoters. Myogenic restricted promoters, such as those of the α -actins, display complex organization. Activation often requires interactions of various myogenic trans-factors with pairs of specific cis-elements. These elements are evolutionarily conserved and primarily responsible for tissue specific expression in adult skeletal muscle, and appeared to be a logical choice for generating synthetic promoters. By randomly assembling these myogenic elements into synthetic promoter ("SP") recombinant libraries, and then by screening hundreds of the resultant clones for transcriptional activity it was possible to create artificial promoters whose transcriptional potency exceeds that of any naturally occurring promoters, as described in United States Patent 6,410,228 ("the '228 Patent"), issued on June 25, 2002 and entitled "Method for the Identification of Synthetic Cell- or Tissue Specific Transcriptional Regulatory Regions" with Schwartz et al., listed as inventors, the entire content of which is hereby incorporated by reference.

[0005] The molecular mechanisms controlling cardiac-specific gene transcription requires the dissection of the cis-elements that govern the complex spatio-temporal expression of these genes. The vertebrate heart is formed during fetal development following a series of complex morphogenetic events that require the functional presence of different proteins,

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tightly regulated by combinatorial interactions of several transcription factors and their cofactors (Nemer and Nemer, 2001; Wang et al., 2001). First, the proximal serum response element (SRE) ('5-CC[A/T]₆GG-3') of the skeletal α -actin promoter was incorporated. Multiple SREs are found in the cardiac, skeletal and smooth muscle α -actin promoters (Chang et al., 2001), and in the promoters of myosin light chain and dystrophin (Bergsma et al., 1986; Carroll et al., 1986). This cis-element is recognized by the trans-acting serum response factor (SRF), and by the competitive inhibitor YY1 (Chow and Schwartz, 1990; Lee et al., 1992; Minty and Kedes, 1986). Serum response factor (SRF) is a key regulator of a number of extracellular signal-regulated genes important for cell growth and differentiation (Zhang et al., 2001). Mutations in the proximal SRE that block SRF binding abolish skeletal α -actin promoter (SK) activity, indicating a fundamental role for this promoter element. Second, MEF-2 sites ('5-[C/T]TAAAAATAAC[C/T]₃-3') that have been found in the promoter/enhancer regions of the myosin light-chain 3 gene were selected. A single MEF-2 site lacks enhancer activity, but has multiple copies that exhibit strong enhancer activity (Gossett et al., 1989). Mutation of the MEF2 site severely reduced promoter activity in embryos, underlining the importance of MEF2 in controlling differentiation in all muscle lineages (Kelly et al., 2002). Third, the MEF-1 sites ('5-CANNTG-3'), or E-boxes that are found in the upstream regulatory region of most, if not all, muscle-specific genes were included (Olson et al., 1991; Weintraub et al., 1990). MEF-1 sites are recognized by the basic helix-loop-helix (bHLH) family of proteins. Multiple MEF-1 sites placed upstream of basal non-muscle promoters are sufficient to direct muscle-specific expression and MyoD-mediated trans-activation in transient assays (Lassar et al., 1991; Weintraub et al., 1990). Finally, the highly conserved muscle-CAT motif, or TEF-1 binding site ('5-CATTCCT-3') was selected. TEF-1 mediates both muscle-specific (SK, cardiac troponin T, cardiac α - and β -myosin heavy chain) and non-muscle specific transcription (simian virus 40 promoter) (Larkin et al., 1996; Stewart et al., 1994).

[0006] In M-CAT dependent promoters, specific sequences immediately flanking the core motif contribute to both the cell specificity and the overall transcriptional strength (O'Connell et al., 2001). While the process of creating synthetic promoters and their muscle specificity have been previously described by us (Li et al., 1999), their cardiac specificity has not been described or demonstrated. For instance, unpublished data from our laboratory proved that the skeletal α -actin 448 (SK448) is expressed exclusively in the skeletal muscle in

transgenic animals, while the longer version of the same promoter, skeletal α -actin 622 (SK622) is expressed both in the skeletal muscle and in the cardiac muscle. Also, data from transgenic animals, an artificial model, cannot be extrapolated to direct transfection or *in vivo* activity after direct injection. For instance, after direct injection or *in vitro* cell transfection, the skeletal α -actin 448 (SK448) is expressed in cardiac cells.

[0007] Transgenes driven by naturally occurring cardiac promoters have relatively low levels of cardiac transgenic gene expression, and have consequently limited the use of cardiac muscle as a target for plasmid mediated gene supplementation. However, by randomly assembling motifs of E-box, MEF-2, TEF-1 and SRE elements, cardiac-specific synthetic promoter recombinant libraries have been produced. By screening hundreds of resultant clones for transcriptional activity both *in vitro* and *in vivo*, a few cardiac-specific synthetic promoters were discovered comprising a transcriptional potency that greatly exceeds the transcriptional levels obtained from natural myogenic and viral gene promoters. These promoters are used to direct the expression of desirable genes in nucleic acid expression constructs specifically to cardiac cells. Thus, these cardiac specific-synthetic promoters are further utilized during plasmid mediated gene supplementation for serious health conditions, such as ischemic disease, myocardial infarction or heart failure. Thus, one aspect of the current invention is a cardiac specific-synthetic promoter produced by a method that generates a library of randomized synthetic-promoter-recombinant expression constructs. A second aspect of the present invention is directed to a method using the cardiac specific-synthetic expression construct for expression a gene of interest in a cardiac cell.

Summary

According to a first embodiment of the invention, there is provided a cardiac-specific synthetic promoter produced by a method comprising:

(a) introducing a library of randomized synthetic promoter-recombinant expression constructs into a first population of cells forming a first test population of cells;

(b) screening the first test population of cells for a first cardiac-specific clone having a first transcriptional activity that is higher than a control transcriptional activity in a comparable population of cells having a control cardiac-specific clone comprising a known promoter operatively linked to the reporter gene forming a control nucleic acid expression construct; and

(c) utilizing the cardiac-specific synthetic promoter from the first cardiac-specific clone as a cardiac-specific synthetic expression construct;

wherein,

each of the randomized synthetic promoter-recombinant expression constructs are operatively linked to a reporter gene to form a nucleic acid expression construct; and

the cardiac-specific synthetic promoter comprises c5-12 (SeqID#5).

According to a second embodiment of the invention, there is provided a method of using a cardiac-specific synthetic expression construct for expressing a gene in a cardiac cell comprising:

delivering into the cardiac cell a cardiac-specific synthetic expression construct;

wherein,

the cardiac-specific synthetic expression construct comprises a cardiac-specific synthetic promoter operatively linked to an expressible gene, and

the cardiac-specific synthetic promoter comprises c5-12 (SeqID#5).

According to a third embodiment of the invention, there is provided a method of synthesizing a cardiac-specific synthetic expression construct comprising:

(a) identifying a cardiac-specific promoter; and

(b) operatively linking the cardiac-specific promoter to an expressible gene to form the cardiac-specific synthetic expression construct;

wherein;

the cardiac-specific synthetic promoter comprises c5-12 (SeqID#5), and a combination of cis-acting regulatory elements; and

the expressible gene comprises a nucleic acid expression construct with or without an operably linked promoter.

According to a fourth embodiment of the invention, there is provided a method of using a cardiac-specific synthetic expression construct for expressing a gene in a cardiac
5 cell comprising:

delivering into the cardiac cell a cardiac-specific synthetic expression construct;

wherein, the cardiac-specific synthetic expression construct comprises a cardiac-specific synthetic promoter comprising c5-12 (SeqID#5), operatively linked to an expressible gene.

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[0009] A second aspect of the current invention is a method for using a cardiac specific-synthetic expression construct for expressing a gene in a cardiac cell. The method comprises delivering into the cardiac cell, a cardiac specific-synthetic expression construct. The cardiac-specific-synthetic expression construct comprises a cardiac-specific-synthetic-promoter operatively-linked to an expressible gene. In a specific embodiment of this invention, the cardiac specific synthetic promoter comprises c5-12 (SeqID#5). Other specific embodiment utilizes other cardiac specific synthetic promoters such as c1-26 (SeqID#16); c2-26 (SeqID#17); c2-27 (SeqID#18); c5-5 (SeqID#19); c6-5 (SeqID#20); c6-16 (SeqID#21); or c6-39 (SeqID#22). The cardiac-specific-synthetic promoters comprise a first-combination of cis-acting regulatory elements, and the first combination of cis-acting regulatory elements were selected from a library of randomized synthetic-promoter-recombinants. The cardiac-specific synthetic promoter drives a transcriptional activity of the expressible gene in a population of cells that is higher than the transcriptional activity of the expressible gene driven by a control-promoter in the same population of cells. The cis-acting regulatory elements utilized for the cardiac-specific synthetic promoter comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4). Certain embodiments describe the expressible-gene comprising a nucleic acid sequence that encodes a growth-hormone-releasing-hormone ("GHRH") or functional biological equivalent thereof. The encoded GHRH is a biologically active polypeptide, and the encoded functional biological equivalent of GHRH is a polypeptide that has been engineered to contain a distinct amino acid sequence while simultaneously having similar or improved biological activity when compared to the GHRH polypeptide. In another specific embodiment, the encoded GHRH or functional biological equivalent thereof is of formula (SEQID#6): The cardiac specific-synthetic expression constructs of this invention also comprises SeqID No: 7, SeqID No: 8, SeqID No: 9, SeqID No: 10, SeqID No: 11, SeqID No: 12, SeqID No: 13, SeqID No: 14, or SeqID No: 15.

BRIEF DESCRIPTION OF FIGURES

[0010] Figure 1 shows the strategy and design of muscle synthetic promoters with the proportion of regulatory elements in different combinations of synthetic promoters, wherein each combination contains at least one of each muscle specific regulatory elements;

[0011] Figure 2 shows the design of muscle synthetic promoters elements in the constructs with the highest *in vitro* reporter gene activity compared with skeletal α -actin 448 promoter ("SK448");

[0012] Figure 3 shows the transcriptional expression of luciferase in fold excess of the SK448 expression, the luciferase reporter gene was driven by the various synthetic promoters and activity was measured at 48 hours post-differentiation;

[0013] Figure 4 shows the transcriptional expression of luciferase in anterior tibialis of adult ICR mice driven by the synthetic promoters SPc1-28, SPc5-12, cytomegalovirus ("CMV"); and SK448, the luciferase activity was measured at 7 days after direct injections in anterior tibialis;

[0014] Figure 5 shows the transcriptional expression of β -galactosidase (" β -gal") in primary chicken muscle culture driven by the synthetic promoters cytomegalovirus ("CMV"), SK448, SPc5-12, and control, the β -gal activity was measured at 24, 48, 72, and 96 hours;

[0015] Figure 6 shows the transcriptional expression of luciferase in primary mouse cardiac culture driven by the synthetic promoters cytomegalovirus ("CMV"), SPc5-12, SK448, SV40, β -gal, and non-transfected cells the luciferase activity was measured at 24, 48, 72, and 96 hours;

[0016] Figure 7 shows a time course table for Beta-galactosidase activity in cardiac myocytes wherein the activity of β -gal was measured at 24, 48, 72, and 96 hours;

[0017] Figure 8 shows the *in vitro* muscle specific expression of β -gal driven by the synthetic promoter SPc5-12, wherein the expression level of β -gal driven by SPc5-12 promoter is comparable with the expression level of β -gal driven by the SK448 promoter in displaying cell type specific expression, and the expression level of β -gal driven by SPc5-12

promoter is at least one order of magnitude less active than the β -gal driven by the CMV promoter in several non-muscle cell lines (CV1, 293, HeLa and 10T1/2);

[0018] Figure 9 shows the expression level of β -gal driven by the synthetic promoter c5-12 is muscle and cardiac specific *in vivo*, a total RNA Northern blot of various tissues (e.g. testis ("T"), brain ("B"), intestine ("I"), lung ("Lg"), stomach ("St"), kidney ("K"), liver ("Lv"), gastrocnemius ("M"), heart ("H"), spleen ("Sp")) from different lines of transgenic mice hybridized with a β -gal cDNA probe and then a mouse 18S probe, was used to show the muscle and cardiac specific expression of a reporter gene driven by SPc5-12;

[0019] Figure 10 shows the *in vivo* expression of a luciferase reporter gene driven by the synthetic promoters cytomegalovirus ("CMV"), SPc5-12, SK448, SV40, and control, wherein the *in vivo* luciferase activity was analyzed at 2 and 4 weeks after direct intra-muscular injection;

[0020] Figure 11 shows the level of mouse growth hormone ("GH") in mice that were injected with a GHRH expression construct driven by the SPc5-12 promoter when compared with control promoters, the GH levels were determined at 7 days post-injection;

[0021] Figure 12 shows the synthetic promoter c1-26 sequence with the regulatory elements marked and with the restriction maps;

[0022] Figure 13 shows the synthetic promoter c2-26 sequence with the regulatory elements marked and with the restriction maps;

[0023] Figure 14 shows the synthetic promoter c2-27 sequence with the regulatory elements marked and with the restriction maps;

[0024] Figure 15 shows the synthetic promoter c5-5 sequence with the regulatory elements marked and with the restriction maps;

[0025] Figure 16 shows the synthetic promoter c5-12 sequence with the regulatory elements marked and with the restriction maps;

[0026] Figure 17 shows the synthetic promoter c6-5 sequence with the regulatory elements marked and with the restriction maps;

[0027] Figure 18 shows the synthetic promoter c6-16 sequence with the regulatory elements marked and with the restriction maps;

[0028] Figure 19 shows the synthetic promoter c6-39 sequence with the regulatory elements marked and with the restriction maps.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

[0029] *Terms:*

[0030] The term "a" or "an" as used herein in the specification may mean one or more. As used herein in the claim(s), and when used in conjunction with the word "comprising", the words "a" or "an" may mean one or more than one. As used herein "another" may mean at least a second or more.

[0031] The term "cis-acting regulatory elements" as used herein refers nucleic acid sequences that comprise transcription factor binding sites. In specific embodiments, the cis-acting regulatory elements comprise the muscle-specific control elements SRE, MEF-1, MEF-2, and TEF-1. It is recognized by one of ordinary skill in the art that other control elements may also be utilized in the present invention.

[0032] The term "operatively linked" as used herein refers to elements or structures in a nucleic acid sequence that are linked by operative ability and not physical location. The elements or structures are capable of, or characterized by accomplishing a desired operation. It is recognized by one of ordinary skill in the art that it is not necessary for elements or structures in a nucleic acid sequence to be in a tandem or adjacent order to be operatively linked.

[0033] The term "plasmid" as used herein refers generally to a construction comprised of extra-chromosomal genetic material, usually of a circular duplex of DNA that can replicate independently of chromosomal DNA. Plasmids, or fragments thereof, may be used as vectors. Plasmids are double-stranded DNA molecule that occur or are derived from bacteria and (rarely) other microorganisms. However, mitochondrial and chloroplast DNA, yeast killer and other cases are commonly excluded.

[0034] The term "plasmid mediated gene supplementation" as used herein refers a method to allow a subject to have prolonged exposure to a therapeutic range of a therapeutic protein by utilizing a nucleic acid expression construct in vivo.

[0035] The term "promoter" as used herein refers to a sequence of DNA that directs the transcription of a gene. A promoter may direct the transcription of a prokaryotic or eukaryotic gene. A promoter may be "inducible", initiating transcription in response to an

inducing agent or, in contrast, a promoter may be “constitutive”, whereby an inducing agent does not regulate the rate of transcription. A promoter may be regulated in a “tissue-specific” or “tissue-preferred” manner, such that it is only active in transcribing the operable linked coding region in a specific tissue type or types. Additionally, promoters may comprise “viral promoters,” “control-promoters,” “naturally-occurring,” or “synthetically” assembled nucleic acid sequences.

[0036] The term “randomized synthetic-promoter-recombinants” as used herein are assembled combinations of randomized cis-acting regulatory elements.

[0037] The term “reporter gene” as used herein are nucleic acid sequences encoding easily assayed proteins. They are used to replace other coding regions whose protein products are difficult to assay. Among the more commonly used reporter genes are those for the following proteins chloramphenicol acetyltransferase (“CAT”), β -galactosidase (“GAL”), β -glucuronidase (“GUS”), luciferase (“LUC”), and green fluorescent protein (“GFP”). It is recognized by one of ordinary skill in the art that other reporter genes are available. It is also recognized by one of ordinary skill in the art that other coding regions (e.g. therapeutic genes) are easily substituted in lieu of the reporter gene.

[0038] The term “transcriptional activity” as used herein refers to the transcription of the information encoded in DNA into a molecule of a RNA, or the translation of the information encoded in the nucleotides of a RNA molecule into a defined sequence of amino acids in a protein.

[0039] The term “vector” as used herein refers to any vehicle that delivers a nucleic acid into a cell or organism. Examples include plasmid vectors, viral vectors, liposomes, or cationic lipids. The term “vector” as used herein more specifically refers to a construction comprised of genetic material designed to direct transformation of a targeted cell by delivering a nucleic acid sequence into that cell. A vector may contain multiple genetic elements positionally and sequentially oriented with other necessary elements such that an included nucleic acid cassette can be transcribed and when necessary translated in the transfected cells. These elements are operatively linked. The term “expression vector” refers to a DNA plasmid that contains all of the information necessary to produce a recombinant protein in a heterologous cell.

[0040] A first aspect of the current invention comprises a cardiac specific-synthetic promoter. This promoter is produced by a method comprising the steps of: introducing a library of randomized synthetic-promoter-recombinant expression constructs into a first-population of cells forming a first-test-population of cells; screening the first-test-population of cells for a first cardiac-specific-clone having a first-transcriptional activity that is higher than a control-transcriptional activity; and utilizing the cardiac specific-synthetic promoter from the first-cardiac-specific clone as the cardiac specific-synthetic promoter for a cardiac-specific-synthetic expression construct. In this way, each of the randomized synthetic-promoter-recombinant expression constructs are operatively linked to a reporter gene to form a nucleic acid expression construct; and the control-cardiac-specific-clone comprises a known-promoter operatively linked to the reporter gene, which forms a control-nucleic acid expression construct having the control-transcriptional activity in the first-population of cells. One specific embodiment of the current invention further comprises a second-screening the first cardiac-specific-clone in a second-test-population of cells before utilizing the cardiac-specific-synthetic promoter as the cardiac-specific-synthetic promoter for the cardiac-specific-synthetic expression construct. When the second-screening is performed, the reporter gene from the first-cardiac-specific-clone has a second-transcriptional activity in the second-population of cells that is higher than a second-control-transcriptional activity of the control-cardiac-specific-clone introduced into the second-population of cells. Additionally, the first-population of cells comprise cells *in vitro*, and the second-population of cells comprise cells *in vivo*. In a specific embodiment of this invention, the cardiac specific synthetic promoter comprises c5-12 (SeqID#5). Other specific embodiment utilizes other cardiac specific synthetic promoters such as c1-26 (SeqID#16); c2-26 (SeqID#17); c2-27 (SeqID#18); c5-5 (SeqID#19); c6-5 (SeqID#20); c6-16 (SeqID#21); or c6-39 (SeqID#22). The cardiac-specific-synthetic promoters comprise a first-combination of cis-acting regulatory elements, and the first combination of cis-acting regulatory elements were selected from a library of randomized synthetic-promoter-recombinants. The cardiac-specific synthetic promoter drives a transcriptional activity of the expressible gene in a population of cells that is higher than the transcriptional activity of the expressible gene driven by a control-promoter in the same population of cells. The cis-acting regulatory elements utilized for the cardiac-specific synthetic promoter comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4).

[0041] A second aspect of the current invention is a method for using a cardiac specific-synthetic expression construct for expressing a gene in a cardiac cell. The method comprises delivering into the cardiac cell, a cardiac specific-synthetic expression construct. The cardiac-specific-synthetic expression construct comprises a cardiac-specific-synthetic-promoter operatively-linked to an expressible gene. In a specific embodiment of this invention, the cardiac specific synthetic promoter comprises c5-12 (SeqID#5). Other specific embodiment utilizes other cardiac specific synthetic promoters such as c1-26 (SeqID#16); c2-26 (SeqID#17); c2-27 (SeqID#18); c5-5 (SeqID#19); c6-5 (SeqID#20); c6-16 (SeqID#21); or c6-39 (SeqID#22). The cardiac-specific-synthetic promoters comprise a first-combination of cis-acting regulatory elements, and the first combination of cis-acting regulatory elements were selected from a library of randomized synthetic-promoter-recombinants. The cardiac-specific synthetic promoter drives a transcriptional activity of the expressible gene in a population of cells that is higher than the transcriptional activity of the expressible gene driven by a control-promoter in the same population of cells. The cis-acting regulatory elements utilized for the cardiac-specific synthetic promoter comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4). Certain embodiments describe the expressible-gene comprising a nucleic acid sequence that encodes a growth-hormone-releasing-hormone ("GHRH") or functional biological equivalent thereof. The encoded GHRH is a biologically active polypeptide, and the encoded functional biological equivalent of GHRH is a polypeptide that has been engineered to contain a distinct amino acid sequence while simultaneously having similar or improved biological activity when compared to the GHRH polypeptide. In another specific embodiment, the encoded GHRH or functional biological equivalent thereof is of formula (SEQID#6): The cardiac specific-synthetic expression constructs of this invention also comprises SeqID No: 7, SeqID No: 8, SeqID No: 9, SeqID No: 10, SeqID No: 11, SeqID No: 12, SeqID No: 13, SeqID No: 14, or SeqID No: 15.

[0042] The randomized synthetic-promoter-recombinants of this invention are prepared by a method comprising: identifying pools of cis-acting regulatory elements; and assembling the cis-acting regulatory elements in a random order to form the library of the synthetic-promoter-recombinants. The cis-acting regulatory elements comprise a double stranded, phosphorylated core motif that is flanked by an adjacent sequence. The assembled cis-acting regulatory elements face a same side of a DNA helix in each recombinant

comprising the synthetic-promoter-recombinant library. The tissue specific synthetic promoter comprises a muscle specificity, wherein the muscle specificity comprises cardiac or skeletal muscle. A specific synthetic promoter of this invention comprises about 5 to about 20 cis-acting regulatory elements, wherein the regulatory elements comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4). One example of a tissue specific synthetic promoter comprise SeqID#5. Additionally, the tissue specific synthetic promoter is utilized for plasmid mediated gene supplementation.

[0043] The regulatory regions of most promoters and enhancers consist of a combination of multiple transcription factor binding sites. Although not wanting to be bound by theory, the composition and arrangement of the binding sites determine the characteristics of regulatory regions. Expression vectors have been frequently modified by combining naturally existing promoters and enhancers (Hartikka et al., 1996; Skarli et al., 1998), and generally these modifications had little or no effect when compared with the transcriptional activity of the native promoters (Franz et al., 1997). In addition, naturally occurring regulatory regions are not always capable of regulating transcription in a desired manner (e.g. enhanced tissue specific regulation). In the invention described herein utilize specific transcription factor binding elements that were incorporated into synthetic promoters. For example, the muscle-specific control elements SRE, MEF-1, MEF-2, TEF-1 were synthesized, randomly assembled, and screened. Fragments containing 5-20 control elements represent synthetic promoter/enhancers were randomly ligated with regulatory sequences that varied in content, location and orientation relative to natural muscle promoters. These fragments were cloned in reporter plasmids in order to identify synthetic promoters with high transcriptional activity both in vitro and in vivo. Over 1000 different clones were evaluated. Since the method to produce and identify synthetic promoters with high transcriptional activity in vitro and in vivo is highly dependent on specific control elements and screening methods, it could not have been predicted by one skilled in the art which elements and control elements were appropriate without laborious and failed experimentations. However, the preferred composition and methods that are outlined for this invention achieve the desired in vitro and in vivo transcriptional activity.

[0044] We observed that multimerized single elements had low activity when compared with the natural skeletal α -actin 448 promoter (SK448), while about 2.5% of the clones derived by combining regulatory elements in the promoter library revealed 2-10 fold

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higher activity. Transfection assays in primary chicken myotubes indicated that one of the specific promoters of this invention (i.e. SPc5-12) had a 6 fold increased activity over a CMV promoter and at least 10 fold greater activity than the control SK448 promoter.

[0045] Transfection assays in primary mouse cardiac cells indicated that SPc5-12 had a 2 fold increased activity over CMV promoter and at least 13 fold greater activity than SK448. Analysis of direct intramuscular injection of DNA plasmids in normal muscle after 2-4 weeks revealed a 3-4 fold increased activity of SPc5-12 over SK448 promoter and a 6-8 fold increase over the CMV promoter. Cardiac and muscle specificity was confirmed with non-muscle cell lines and in transgenic animals.

[0046] Although not wanting to be bound by theory, many transcriptional regulatory regions have been described without the cloning of the corresponding transcription factors. Consequently, these "potential transcription factor regulatory elements" still need to be confirmed as functional for transcription regulation by identification of the corresponding transcription factors. Thus, synthetic promoters of this invention are constructed using combinations of cis-elements whose trans-factors are both known and unknown. Synthetic promoter libraries are also utilized to provide the basis for a desired functional tissue specificity. Because PCR mutagenesis allows the random modification of regulatory regions, this PCR method is utilized to screen even a greater number of regulatory regions by selection assays.

[0047] Although not wanting to be bound by theory, this novel system of designing synthetic promoters/enhancers using individual regulatory elements rather than entire promoters represents a significant improvement over previously generated plasmid DNA expression vectors (Buvoli et al., 2002; Phillips et al., 2002; Xu et al., 2002). For example, organ-specific promoter/enhancer fragments that exhibit persistent and increased expression when compared to naturally occurring sequences were obtained using this novel strategy. Although *in vitro* assays provide a good indication of promoter potency, *in vivo* studies are still required to determine the most appropriate synthetic promoter, as indicated in the specific embodiments of this invention. Although not wanting to be bound by theory, the optimization of plasmid DNA vectors for cardiac and muscle mediated plasmid mediated gene supplementation will increase their utility for delivery of therapeutic proteins including anti-

coagulation factors, superoxide dismutase ("SOD"), hemoxygenase or other therapeutic molecules.

[0048] Construction of synthetic promoter and reporter plasmids. A 144 bp EcoRI/EagI fragment of chicken skeletal α -actin promoter (Chow et al., 1991; Lee et al., 1994) which contains the TATA box at -25bp upstream the cap site, a Sp1 pair in between -35 and -65bp and a TEF-1 site at -65bp, was removed from plasmid p612aACATMLC (Chow and Schwartz, 1990). The fragment was cloned into the EcoRI/EagI sites of pBluescript KS+ to generate pBS-SK144. pBS-SK144 was then cut SacI/HindIII, and the SK144 fragment, now with appropriate cloning sites was moved into the SacI/HindIII sites of pGL-2 basic vector (Promega, Madison, WI, USA) to generate pSK144GL-2. All synthetic fragments had EagI cohesive ends and were cloned into EagI site of pSK144GL-2, to create synthetic promoter constructs driving luciferase. The pSK448GL-2 was utilized as a muscle specific control that contained a 448 bp chicken skeletal α -actin promoter (Draghia-Akli et al., 1997) cloned into the SacI/HindIII sites of the same pGL-2 basic vector. Additional methods for the construction of synthetic promoters and reporter plasmids are described in United States Patent 6,410,228 ("the '228 Patent), issued on June 25, 2002 and entitled "Method for the Identification of Synthetic Cell- or Tissue Specific Transcriptional Regulatory Regions" with Schwartz et al., listed as inventors, the entire content of which is hereby incorporated by reference.

[0049] Two complementary oligonucleotides were synthesized for each individual control element, phosphorylated and annealed to yield short DNA fragments. The oligonucleotide sequences were as follows:

SRE	5' -GACACCCAAATATGGCGACGG-3' (SeqID#1) 3' -CTGTGGGTTTATACCGCTGCC-5'
MEF-1	5' -CCAACACCTGCTGCCTGCC-3' (SeqID#2) 3' -GGTTGTGGACGACGGACGG-5'
MEF-2	5' -CGCTCTAAAAATAACTCCC-3' (SeqID#3) 3' -GCGAGATTTTATTGAGGG-5'
TEF-1	5' -CACCATTCCTCAC-3' (SeqID#4) 3' -GTGTAAGGAGTG-5'

[0050] The phosphorylation/annealing reaction was performed in a total volume of 300 μ l in TEN buffer (10mM Tris-HCl, pH 7.5; 1mM EDTA, 50mM NaCl) using sense and antisens strand oligonucleotides (20 μ M each, equivalent to a total of 600 pmoles), 1mM ATP and 0.5U/ml of T4 polynucleotide kinase by heating to 70⁰C for 15 minutes and cooling down to room temperature over 30 minutes.

[0051] Different combination of SRE, MEF-1, MEF-2 and TEF-1 were then ligated in a total volume of 100 μ l using different molar ratio (Figure 1), maintaining a constant total amount of oligonucleotide of 200 pmoles. The core motif of each regulatory element (underlined) was flanked by adjacent sequence so that the binding sites of the regulatory elements would face the same side of the DNA helix when assembled together. The ligation reaction was completed with T4 ligase in 150 μ l. After ligation, the combination of elements was run on a 6% acrylamide gel. The 75-300-bp region was cut and eluted in 2 volumes of diffusion buffer at 37⁰C overnight. The DNA was extracted using Qiaex II Gel Extraction Kit (Qiagen Inc., Chatsworth, CA, USA) and incubated in 150 μ l with phosphorylated and annealed Sp1 element (2.5 nmoles) and 10U of T4 ligase at 16⁰C overnight. Since each of the Sp1 elements ('5-CCGTCCGCCCTCGG-3') contains EagI half at both ends, an intact EagI restriction site was generated wherever two Sp1 elements were ligated together. The reaction was cleaned up (Qiaquick Nucleotide Removal Kit), digested with EagI and cloned into the EagI site of SK144GL-2 luciferase reporter construct, which resulted in a library of randomized synthetic-promoter-recombinants that were operatively linked to a reporter gene. The clones that gave the best results in the transfection studies were sequenced automatically.

[0052] Amplification and selection of the randomized synthetic-promoter-recombinant clones. The entire library of randomized synthetic-promoter-recombinants was transformed and then amplified in E. coli DH5 α cells, plated on agar growth medium, and individual specific clones screened by transfection into muscle cells. The clones that gave the best results in the transfection studies were then sequenced automatically.

[0053] The nucleic acid sequences reported herein are believed to be correct, however a small percentage of sequence errors may be present. One skilled in the art could readily obtain the correct synthetic regulatory region by identifying the particular elements

and their positions in the region from the sequence provided, and constructing the synthetic regulatory regions from those elements in the same positions and orientations.

[0054] Screening for high transcriptional activity synthetic promoters. Miniprep DNA was used for transfection during the initial screening of synthetic promoters. After plating 4000 cells/well in 96 well dishes, cells were transfected with 15ng plasmid/ well using lipofectamine and collected 72h post-transfection, using the conditions described in the next paragraph.

[0055] Cell culture. Minimal Essential Medium (MEM), heat inactivated horse serum ("HIHS"), gentamycin, Hanks Balanced Salt Solution (HBSS), lipofectamine were obtained from Gibco BRL (Grand Island, NY). Primary chicken myoblast and mouse cardiac cultures were obtained as described (Bergsma et al., 1986). Cells were plated 24h prior to transfection at a density of 1.5 million cells / 100mm plate, in MEM supplemented with 10% HIHS, 5% chicken embryo extract (CEE) and gentamycin. Cells were maintained in a humidified 5% CO₂ 95% air atmosphere at 37°C. Cells were transfected with 4µg of plasmid per 100mm plate, using lipofectamine, according to the manufacturer instructions. After transfection, the medium was changed to MEM which contained 2% HIHS, 2% CEE for at least 24h to allow the cells to differentiate. Media and cells were harvested 24, 48, 72 and 96h post-differentiation. The samples and controls were assayed in quadruplicate in at least two different rounds of transfection. The efficiency of transfection was estimated by β-galactosidase histochemistry of control plates to be 10%. The cells were homogenized in Promega reporter lysis buffer for luciferase, beta-galactosidase and protein assays.

[0056] Northern blot analysis. 10-20µg of total RNA was DNase I treated (Gibco BRL), size separated in 1.5% agarose-formaldehyde gel and transferred to Gene Screen nylon membrane (DuPont Research Products, Boston, MA). The membranes were hybridized with cDNA probes ³²P labeled by random priming (Ready-to-Go DNA labeling kit, Pharmacia Biotech, Piscataway, NJ). Hybridization was carried out at 45°C in a solution which contained 50% formamide, 5xSSPE, 5xDenhardts, 1% SDS, 200µg/ml sheared salmon sperm DNA. Membranes were washed twice for 10 minutes in 2xSSPE/1%SDS at room temperature and twice for 30 minutes in 0.2xSSPE/1%SDS at 68°C. Blots were subsequently exposed to X-ray film (Kodak X-Omat AR; Eastman Kodak, Rochester, NY) at -80°C with intensifying screens.

[0057] **Transgenic animals study.** Transgenic mice carrying E.coli beta-galactosidase ("β-gal") with an NLS under the control of the SPc5-12 promoter were generated by standard oocyte injection. Three different lines of 5 weeks old SPc5-12β-gal mice and control littermates were killed and samples of different organs and skeletal muscles were collected, stored at -80°C. For β-gal histochemistry, tissues were sectioned at 10 μm, fixed and stained.

[0058] **Intramuscular injection of plasmid DNA in adult mice.** Plasmid preparation of SPc5-12 and SK448 were diluted in PBS pH=7.4 to 1mg/ml. ICR male mice (Harlem Laboratories, Houston, TX) were anesthetized with 0.5ml/kg of a combination of ketamine (42.8mg/ml), xylazine (8.2mg/ml) and acepromazine (0.7mg/ml). Fifty micrograms of plasmid in 25μl sterile PBS was injected directly into the anterior tibialis of mice. At 1, 2 and 4 weeks after the injection, the injected muscle was snap frozen in liquid nitrogen. Muscles were homogenized in PBS, pH=7.4 containing 0.2% Triton x-100 and protease inhibitors: leupeptin, 0.7μg/ml, pepstatin 10μg/ml and aprotinin 2μg/ml (Boehringer Mannheim, Indianapolis, IN). Muscle extracts were centrifuged at 10,000xg for 30 minutes at 4°C and the supernatant recovered. Protein assays were performed using Bio-Rad Protein Assay (Bio-Rad Laboratories, Hercules, CA) and luciferase and β-galactosidase activity was measured. At each time point, 6-15 animals were used for each construct. The experiments were repeated twice.

[0059] **Mouse growth hormone RIA.** Mouse GH in plasma was measured with a heterologous rat assay system (Amersham, Arlington Heights, IL). The sensitivity of the assay was 0.16 ng/tube. The intra- and interassay coefficients of variation were 6.5 and 6.8% respectively.

[0060] **Statistics.** Data were analyzed using Microsoft Excel statistics analysis package. Values shown in the figures are the mean ± s.e.m. to exert the desired effect.

[0061] The invention may be better understood with reference to the following examples, which are representative of some of the embodiments of the invention, and are not intended to limit the invention.

EXAMPLE 1.

[0062] Construction of synthetic promoter libraries. Although not wanting to be bound by theory, the endogenous promoter of skeletal α -actin is considered a very strong promoter. For example, when poly-A mRNA is isolated from an adult avian muscle, approximately 9% of the total poly-A mRNA isolated comprises skeletal α -actin mRNA, which is the highest expressed level of any poly-A mRNA species in cardiac or skeletal muscle (Schwartz and Rothblum, 1981). A short core fragment (i.e. SK144) of the chicken skeletal α -actin promoter was used as the minimal sequence to insert synthetic regulatory elements (Lee et al., 1994),(Chow et al., 1991). The core motif of each regulatory element was flanked by adjacent sequences that are conserved in the natural genes to allow the regulatory elements to anneal on the same face of the DNA helix. For example the serum regulatory element ("SRE") sequence corresponds to the proximal SK SRE1, GCTGC motif adjacent to the MEF-1 is conserved in the muscle creatine kinase gene and rat myosin light chain gene. Different combinations of SRE, MEF-1, MEF-2 and TEF-1 oligonucleotide (Figure 1) were annealed and then capped by ligation with Sp1 elements, since Sp1 has been shown to act in synergy with SREs and E-boxes. It has also been shown that Sp1 binding sites are essential for *de novo* methylation protection of CpG islands and non-island DNA regions (Machon et al., 1998). Synthetic promoter libraries were generated from DNA fragments containing about 5-20 regulatory elements and ligated into a minimal actin-reporter plasmid that expresses the luciferase reporter gene.

[0063] Screening synthetic promoters with high transcriptional activity. The *in vitro* luciferase activity was measured in more than 1000 different clones in 96 well dishes containing transiently transfected chicken primary myoblasts to determine the strength of the newly constructed synthetic promoters. A 448bp promoter fragment (-424/+24) ("SK448") of the avian skeletal α -actin gene was used as a specific expression control in cardiac and skeletal muscle (Figure 2). The SK448 promoter control has been shown to be active in differentiated skeletal muscle cells, but not in myoblasts (Bergsma et al., 1986; Chow and Schwartz, 1990; Lee et al., 1994). Cytomegalovirus ("CMV") basic promoter was also used as a ubiquitous promoter control. Newly generated synthetic promoters, CMV promoters, and SK448 promoters were inserted into reporter construct plasmids and transfected into cells then placed into differentiation media for up to 72 hours to initiate withdrawal from the cell cycle

and to induce post-fusion differentiation and muscle-specific promoter activation. At the end of this period the cells were harvested and assayed for the reporter gene activity.

[0064] Promoters consisting of only multimerized single elements such as SREs, E-boxes, MEF-2 or TEF-1 had activities several-fold lower than the skeletal α -actin promoter 448 (data not shown). We observed that some promoters containing a combinatory pool of elements provided a 2 to 10 fold higher luciferase reporter gene activity (Figure 3) when compared to SK448. Clones that displayed transcriptional activity greater than 2 times that of SK448 activity were examined further. Some clones from the first and fifth combinatorial pools, such as c1-28, c5-12, c5-1, c5-5, where SRE, MEF-2, MEF-1, TEF-1 were mixed in the ratio 1:1:1:1 and 1:1:1:4, respectively, had the highest *in vitro* and/or *in vivo* activity (see also Figure 1).

[0065] Cell culture assay systems cannot readily substitute for *in vivo* testing into the skeletal muscle of new plasmid constructs, as it has been shown that some muscle specific regulatory elements with high *in vitro* expression have less activity *in vivo* (Barnhart et al., 1998). Fifty micrograms of the most potent synthetic promoters (SPc1-28 and SPc5-12), SK448 and CMV plasmids were injected into the tibialis anterior muscle of adult ICR mice (n=6 / group). One week later (Figure 4), the activity of CMV and SPc5-12 was similar (16.77 ± 7.43 and $14.59 \pm 9.39 \times 10^6$ RU/ μ g protein, respectively), while SK448 and SPc1-28 were 10 fold less active (1.44 ± 0.76 and $1.58 \pm 0.65 \times 10^6$ RU/ μ g protein, respectively). SPc5-12 was then chosen for further studies.

[0066] SPc5-12 was tested over a 96 hour time-course during primary avian muscle cell myogenesis in culture where replicating myoblasts withdraw from the cell cycle, fuse and form multinucleated terminally differentiated myotubes (Figure 5). CMV promoter was active in both myoblasts and myotubes at similar levels ($1.05 \pm 0.06 \times 10^6$ RU (relative units)/ μ g protein at 24h, $1.22 \pm 0.22 \times 10^6$ RU/ μ g protein at 96h). SK448 expression increased only after 48 hours ($0.17 \pm 0.016 \times 10^6$ RU/ μ g protein at 48h, $0.37 \pm 0.09 \times 10^6$ RU/ μ g protein at 72h, $0.41 \pm 0.06 \times 10^6$ RU/ μ g protein at 96h), which correspond to the pattern of activation of SK promoters, active in myotubes but not in replicating myoblasts (Hayward and Schwartz, 1986). SPc5-12 mimicked the pattern of activation of SK448. However, SPc5-12 was 10 fold more active than SK448 and 2-6 fold higher than CMV promoter at 96h ($2.27 \pm 0.23 \times$

10^6 RU/ μ g protein at 48h, $3.62 \pm 0.91 \times 10^6$ RU/ μ g protein at 72h and $7.25 \pm 0.48 \times 10^6$ RU/ μ g protein at 96h).

[0067] SPc5-12 was tested in primary cardiac myocytes over a 96-hour time course (Figure 6), and compared with the ubiquitous promoters CMV and SV40 and with the muscle specific promoter SK448. As shown, CMV promoter has high initial activity in cardiac cells, which decreases over time. SK448 and SPc5-12 activities increase during the same time period, with long-term activation and higher activity than the baseline. Similarly to the skeletal muscle cells, in cardiac cells at 96 hour post-transfection, the SPc5-12 promoter has 13-fold higher expression than the naturally occurring SK448, and 2-fold higher activity than CMV (Figure 7).

EXAMPLE 4.

[0068] ***In vitro* and *in vivo* specificity of SPc5-12 promoter.** The specificity of SPc5-12 promoter was evaluated by transient transfections in several non-muscle cell lines. In the CV1 line (monkey kidney fibroblasts), HeLa cells (human cervix epitheloid carcinoma), 293 line (human transformed embryonic kidney) and 10T1/2 line (mouse embryonic fibroblasts) specific β -gal activity of SPc5-12 and SK 448 constructs was relatively low compared with the prevalently expressed CMV promoter (Figure 8).

[0069] We then generated lines of transgenic mice carrying *E.coli* β -galactosidase (β -gal) with a nuclear localization signal (nls) under the control of the SPc5-12 promoter to determine its *in vivo* specificity. At the end of 5 weeks, several different SPc5-12 transgenic β -gal mice were killed and samples of different organs (lung, liver, brain, spleen, intestine, stomach, kidney, testis) and heart and skeletal muscles were frozen in liquid nitrogen. β -gal tissue specific expression was evaluated by Northern blot analysis of total RNA (Figure 9) and histochemistry techniques (data not shown). RNA blot analysis revealed β -gal transcripts only in muscle and heart samples in all positive lines of SPc5-12 transgenic mice; no expression was detected in non-myogenic organs. Histologically, β -gal positive nuclei were present in muscle fibers, as with the original SK448 promoter, but not in the control littermates. The pattern of expression was similar in 2 other transgenic lines.

EXAMPLE 3.

[0070] ***In vivo* activity of SPc5-12 promoter.** *In vivo* expression of SPc5-12 promoter was compared to that of the ubiquitous promoters CMV and SV40, and with the muscle specific SK448 promoter, after direct intra-muscular injection in adult immunocompetent mice (Figure 10). At 2 and 4 weeks post-injection, the SPc5-12 driven construct had an activity 3-5 fold higher than that of the SK448 promoter (SPc5-12, 2 weeks: $4.97 \pm 2.07 \times 10^6 \text{RU}/\mu\text{g protein}$, 4 weeks: $3.78 \pm 1.71 \times 10^6 \text{RU}/\mu\text{g protein}$ vs. SK448, 2 weeks: $1.37 \pm 0.43 \times 10^6 \text{RU}/\mu\text{g protein}$, 4 weeks: $1.25 \pm 0.04 \times 10^6 \text{RU}/\mu\text{g protein}$) and 6-8 time greater than that of the CMV promoter (2 weeks: $0.94 \pm 0.4 \times 10^6 \text{RU}/\mu\text{g protein}$, 4 weeks: $0.65 \pm 0.16 \times 10^6 \text{RU}/\mu\text{g protein}$). The SV40 construct was 100 fold less active at each of these time points (2 weeks: $0.05 \pm 0.02 \times 10^6 \text{RU}/\mu\text{g protein}$, 4 weeks: $0.04 \pm 0.008 \times 10^6 \text{RU}/\mu\text{g protein}$). These results show that *in vivo* transfection of the SPc5-12 into skeletal muscle results in significantly higher expression than conventional promoters do.

[0071] The ability of our synthetic promoter to ensure production of therapeutic levels of a secreted protein was determined. Human growth hormone releasing hormone ("hGHRH") cDNA was cloned downstream of the SPc5-12 promoter. The same construct, but with a CMV promoter, was used as a positive control. Biologically active hGHRH secreted by the muscle cells stimulated the secretion of endogenous growth hormone ("mGH") from the anterior pituitary of the injected mice. Seven days after direct intra-muscular injection of 30 micrograms of SPc5-12-GHRH plasmid in adult mice, serum mouse GH ("mGH") was measured using a specific RIA. Serum mGH increased in both SPc5-12-GHRH and CMV-GHRH injected mice compared to control levels ($24.84 \pm 13.15 \text{ng/ml}$ and $21.19 \pm 11.05 \text{ng/ml}$, respectively vs. $1.7 \pm 0.1 \text{ng/ml}$). The values obtained using these synthetic promoters (in a quantity of 30 μg of plasmid) were 1.5 fold higher than that obtained using 100 μg of pSK-GHRH in a previous study in our laboratory (Draghia-Akli et al., 1997), a five fold increase in activation when normalizing for the plasmid quantity.

[0072] The above synthetic promoters can be utilized for organ specific expression of various therapeutic genes in a mammalian host. One skilled in the art recognizes that the promoters described herein can direct the expression of any number of different genes that are useful for plasmid mediated gene supplementation. Methods and compositions for constructing promoters that can be utilized for effective gene transfer of an expression vector

to a host cell in accordance with the present invention to a host cell can be monitored in terms of a therapeutic effect (*e.g.* alleviation of some symptom associated with the particular disease being treated) or, further, by evidence of the transferred gene or high expression of the gene within the host (*e.g.*, using the polymerase chain reaction in conjunction with sequencing, Northern or Southern hybridizations, or transcription assays to detect the nucleic acid in host cells, or using immunoblot analysis, antibody-mediated detection, mRNA or protein half-life studies, or particularized assays to detect protein or polypeptide encoded by the transferred nucleic acid, or impacted in level or function due to such transfer).

[0073] The above tissue specific synthetic promoters can be utilized in diverse vector constructs and administered to a mammalian host for various therapeutic effects. One skilled in the art recognizes that different methods of delivery may be utilized to administer a tissue specific synthetic expression vector into a cell. Examples include: (1) methods utilizing physical means, such as electroporation (electricity), a gene gun (physical force) or applying large volumes of a liquid (pressure); and (2) methods wherein the tissue specific synthetic expression vector is complexed to another entity, such as a liposome or transporter molecule.

[0074] Accordingly, the present invention provides a method of transferring a tissue specific therapeutic gene to a host, which comprises administering the vector of the present invention, preferably as part of a composition, using any of the aforementioned routes of administration or alternative routes known to those skilled in the art and appropriate for a particular application. Effective gene transfer of a tissue specific expression vector to a host cell in accordance with the present invention to a host cell can be monitored in terms of a therapeutic effect (*e.g.* alleviation of some symptom associated with the particular disease being treated) or, further, by evidence of the transferred gene or expression of the gene within the host (*e.g.*, using the polymerase chain reaction in conjunction with sequencing, Northern or Southern hybridizations, or transcription assays to detect the nucleic acid in host cells, or using immunoblot analysis, antibody-mediated detection, mRNA or protein half-life studies, or particularized assays to detect protein or polypeptide encoded by the transferred nucleic acid, or impacted in level or function due to such transfer).

[0075] These compositions and methods described herein are by no means all-inclusive, and further methods to suit the specific application will be apparent to the ordinary

skilled artisan. Moreover, the effective amount of the compositions can be further approximated through analogy to compounds known to exert the desired effect.

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The claims defining the invention are as follows:

1. A cardiac-specific synthetic promoter produced by a method comprising:

(a) introducing a library of randomized synthetic promoter-recombinant expression constructs into a first population of cells forming a first test population of cells;

(b) screening the first test population of cells for a first cardiac-specific clone having a first transcriptional activity that is higher than a control transcriptional activity in a comparable population of cells having a control cardiac-specific clone comprising a known promoter operatively linked to the reporter gene forming a control nucleic acid expression construct; and

(c) utilizing the cardiac-specific synthetic promoter from the first cardiac-specific clone as a cardiac-specific synthetic expression construct;

wherein,

each of the randomized synthetic promoter-recombinant expression constructs are operatively linked to a reporter gene to form a nucleic acid expression construct; and

the cardiac-specific synthetic promoter comprises c5-12 (SeqID#5).

2. The cardiac-specific synthetic promoter of claim 1, wherein the first population of cells comprise cells *in vitro*.

3. The cardiac-specific synthetic promoter of claim 1, further comprising:

second screening the first cardiac-specific clone in a second test population of cells before utilizing the cardiac-specific synthetic promoter as the cardiac-specific synthetic expression construct;

wherein,

the first cardiac-specific clone having a second transcriptional activity in the second population of cells that is higher than a second control transcriptional activity of the control cardiac-specific clone introduced into a comparable population of cells.

4. The cardiac-specific synthetic promoter of claim 3, wherein the first population of cells comprise cells *in vitro*, and the second population of cells comprise cells *in vivo*.

5. The cardiac-specific synthetic promoter of claim 1 further comprising a combination of cis-acting regulatory elements selected from a library of randomized synthetic promoter recombinants.

6. The cardiac-specific synthetic promoter of claim 5, wherein the cis-acting regulatory elements comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4).

7. A method of using a cardiac-specific synthetic expression construct for
5 expressing a gene in a cardiac cell comprising:

delivering into the cardiac cell a cardiac-specific synthetic expression construct;

wherein,

the cardiac-specific synthetic expression construct comprises a cardiac-specific synthetic promoter operatively linked to an expressible gene, and
10

the cardiac-specific synthetic promoter comprises c5-12 (SeqID#5).

8. The method of claim 7, wherein the cardiac-specific synthetic promoter comprises a combination of cis-acting regulatory elements selected from a library of randomized synthetic promoter recombinants; and

15 the cardiac-specific synthetic promoter provides a transcriptional activity of the expressible gene in a population of cells that is higher than the transcriptional activity of the expressible gene driven by a control promoter in a comparable population of cells.

9. The method of claim 8, wherein the cis-acting regulatory elements comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4).

20 10. The method of claim 7, wherein the cardiac-specific synthetic expression construct is delivered into the cardiac cell via electroporation.

11. The method of claim 7, wherein the expressible gene comprises a nucleic acid sequence that encodes a growth-hormone-releasing-hormone ("GHRH") or functional biological equivalent thereof.

25 12. The method of claim 11, wherein the encoded GHRH is a biologically active polypeptide, and the encoded functional biological equivalent of GHRH is a polypeptide that has been engineered to contain a distinct amino acid sequence while simultaneously having similar or improved biological activity when compared to the GHRH polypeptide.

13. The method of claim 11, wherein the encoded GHRH or functional biological
30 equivalent thereof is of the formula (SEQID#6):

$-X_1-X_2-DAIFTNSYRKVL-X_3-QLSARKLLQDI-X_4-X_5-RQQGERNQEQQGA-OH$

wherein the formula has the following characteristics:

X_1 is a D- or L-isomer of the amino acid tyrosine ("Y"), or histidine ("H");

X₂ is a D- or L-isomer of the amino acid alanine ("A"), valine ("V"), or isoleucine ("I");

X₃ is a D- or L-isomer of the amino acid alanine ("A") or glycine ("G");

X₄ is a D- or L-isomer of the amino acid methionine ("M"), or leucine ("L");

X₅ is a D- or L-isomer of the amino acid serine ("S") or asparagine ("N");

or a combination thereof.

14. The method of claim 7, wherein the cardiac-specific synthetic expression construct comprises SeqID No: 7, SeqID No: 8, SeqID No: 9, SeqID No: 10, SeqID No: 11, SeqID No: 12, SeqID No: 13, SeqID No: 14, or SeqID No: 15.

15. A method of synthesizing a cardiac-specific synthetic expression construct comprising:

(a) identifying a cardiac-specific promoter; and

(b) operatively linking the cardiac-specific promoter to an expressible gene to form the cardiac-specific synthetic expression construct;

wherein;

the cardiac-specific synthetic promoter comprises c5-12 (SeqID#5), and a combination of cis-acting regulatory elements; and

the expressible gene comprises a nucleic acid expression construct with or without an operably linked promoter.

16. The method of claim 15, wherein the combination of cis-acting regulatory elements are selected from a library of randomized synthetic promoter recombinants; and

the cardiac-specific synthetic promoter driving a transcriptional activity of the expressible gene in a population of cells that is higher than the transcriptional activity of the expressible gene driven by a control promoter in the population of cells.

17. The method of claim 16, wherein the cis-acting regulatory elements comprise SRE (SeqID#1); MEF-1 (SeqID#2); MEF-2 (SeqID#3); and TEF-1 (SeqID#4).

18. The method of claim 15, wherein the cardiac-specific synthetic expression construct is delivered into the cardiac cell via electroporation.

19. The method of claim 15, wherein the expressible gene comprises a nucleic acid sequence that encodes a growth-hormone-releasing-hormone ("GHRH") or functional biological equivalent thereof.

20. The method of claim 19, wherein the encoded GHRH is a biologically active polypeptide, and the encoded functional biological equivalent of GHRH is a polypeptide

that has been engineered to contain a distinct amino acid sequence while simultaneously having similar or improved biological activity when compared to the GHRH polypeptide.

21. The method of claim 19, wherein the encoded GHRH or functional biological equivalent thereof is of the formula (SEQID#6):

5 -X₁-X₂-DAIFTNSYRKVL-X₃-QLSARKLLQDI-X₄-X₅-RQQGERNQEQGA-OH

wherein the formula has the following characteristics:

X₁ is a D- or L-isomer of the amino acid tyrosine ("Y"), or histidine ("H");

X₂ is a D- or L-isomer of the amino acid alanine ("A"), valine ("V"), or isoleucine ("I");

10 X₃ is a D- or L-isomer of the amino acid alanine ("A") or glycine ("G");

X₄ is a D- or L-isomer of the amino acid methionine ("M"), or leucine ("L");

X₅ is a D- or L-isomer of the amino acid serine ("S") or asparagine ("N");

or a combination thereof.

22. The method of claim 15, wherein the cardiac-specific synthetic expression
15 construct further comprises SeqID No: 7, SeqID No: 8, SeqID No: 9, SeqID No: 10, SeqID No: 11, SeqID No: 12, SeqID No: 13, SeqID No: 14, or SeqID No: 15.

23. A method of using a cardiac-specific synthetic expression construct for expressing a gene in a cardiac cell comprising:

20 delivering into the cardiac cell a cardiac-specific synthetic expression construct;

wherein, the cardiac-specific synthetic expression construct comprises a cardiac-specific synthetic promoter comprising c5-12 (SeqID#5), operatively linked to an expressible gene.

24. The method of claim 23, wherein the expressible gene comprises a nucleic
25 acid sequence that encodes a growth-hormone-releasing-hormone ("GHRH") or functional biological equivalent thereof.

25. The method of claim 24, wherein the encoded GHRH is a biologically active polypeptide, and the encoded functional biological equivalent of GHRH is a polypeptide that has been engineered to contain a distinct amino acid sequence while simultaneously
30 having similar or improved biological activity when compared to the GHRH polypeptide.

26. The method of claim 24, wherein the encoded GHRH or functional biological equivalent thereof is of the formula (SEQID#6):

-X₁-X₂-DAIFTNSYRKVL-X₃-QLSARKLLQDI-X₄-X₅-RQQGERNQEQGA-OH

wherein the formula has the following characteristics:

X₁ is a D- or L-isomer of the amino acid tyrosine ("Y"), or histidine ("H");

X₂ is a D- or L-isomer of the amino acid alanine ("A"), valine ("V"), or
isoleucine ("I");

5 X₃ is a D- or L-isomer of the amino acid alanine ("A") or glycine ("G");

X₄ is a D- or L-isomer of the amino acid methionine ("M"), or leucine ("L");

X₅ is a D- or L-isomer of the amino acid serine ("S") or asparagine ("N");

or a combination thereof.

27. The method of claim 23, wherein the cardiac-specific synthetic expression
10 construct further comprises SeqID No: 7, SeqID No: 8, SeqID No: 9, SeqID No: 10,
SeqID No: 11, SeqID No: 12, SeqID No: 13, SeqID No: 14, or SeqID No: 15.

Dated 30 August, 2011

Inovio Pharmaceuticals, Inc.

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Baylor College of Medicine

Patent Attorneys for the Applicant/Nominated Person

SPRUSON & FERGUSON

Figure 1

Element	Pools of regulatory elements					
	1	2	3	4	5	6
SRE	1	4	1	1	1	4
MEF-2	1	1	4	1	1	1
MEF-1	1	1	1	4	1	4
TEF-1	1	1	1	1	4	1

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Figure 3

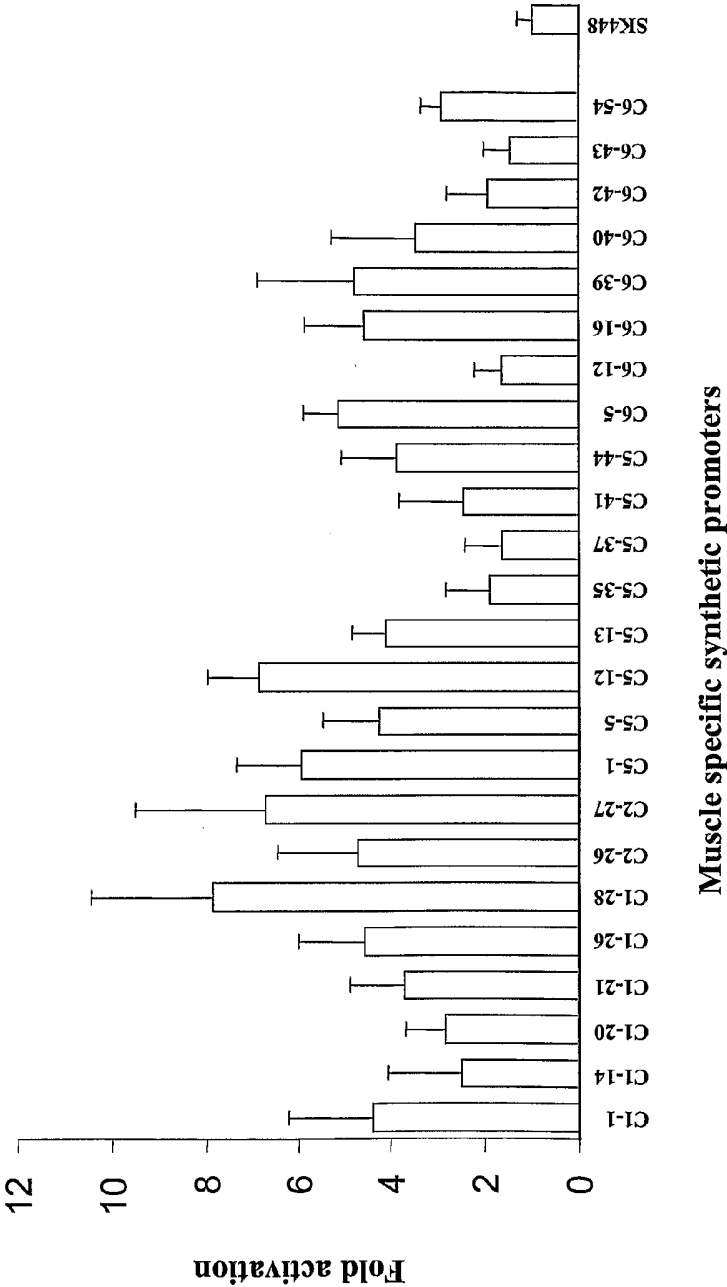
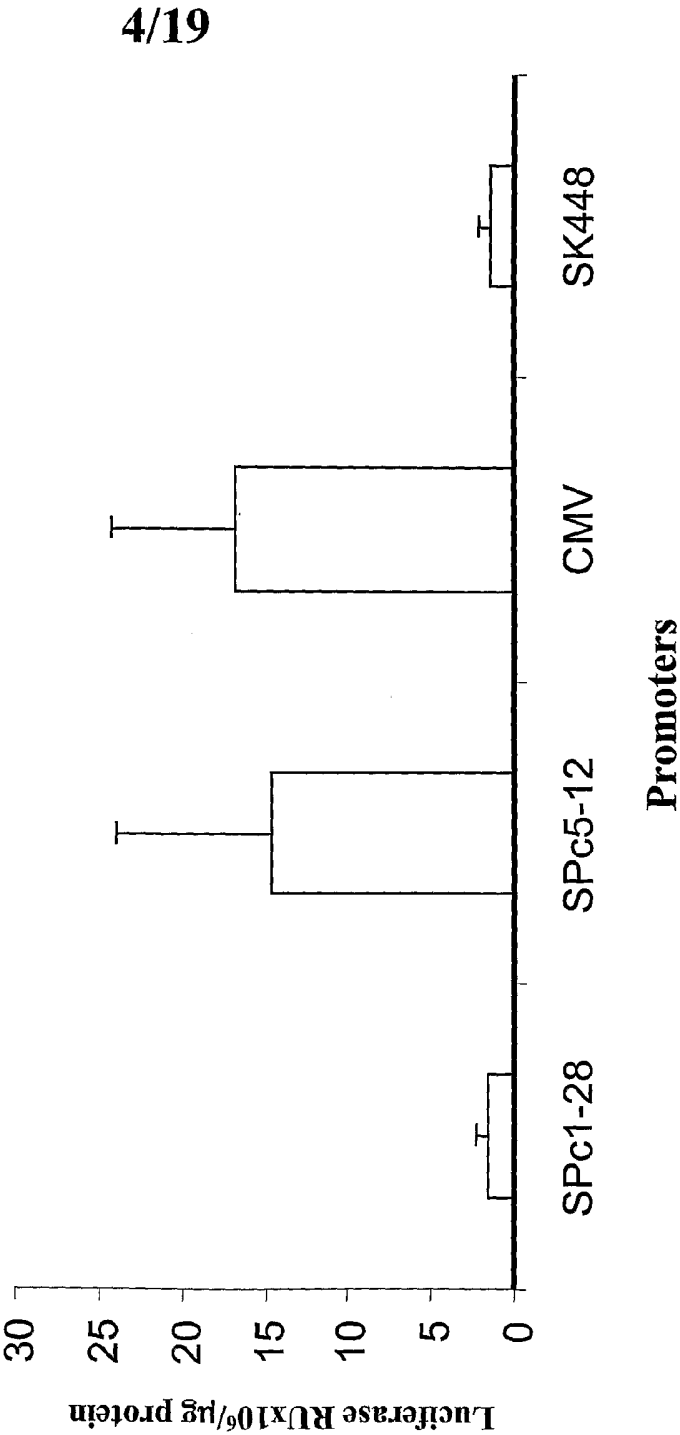
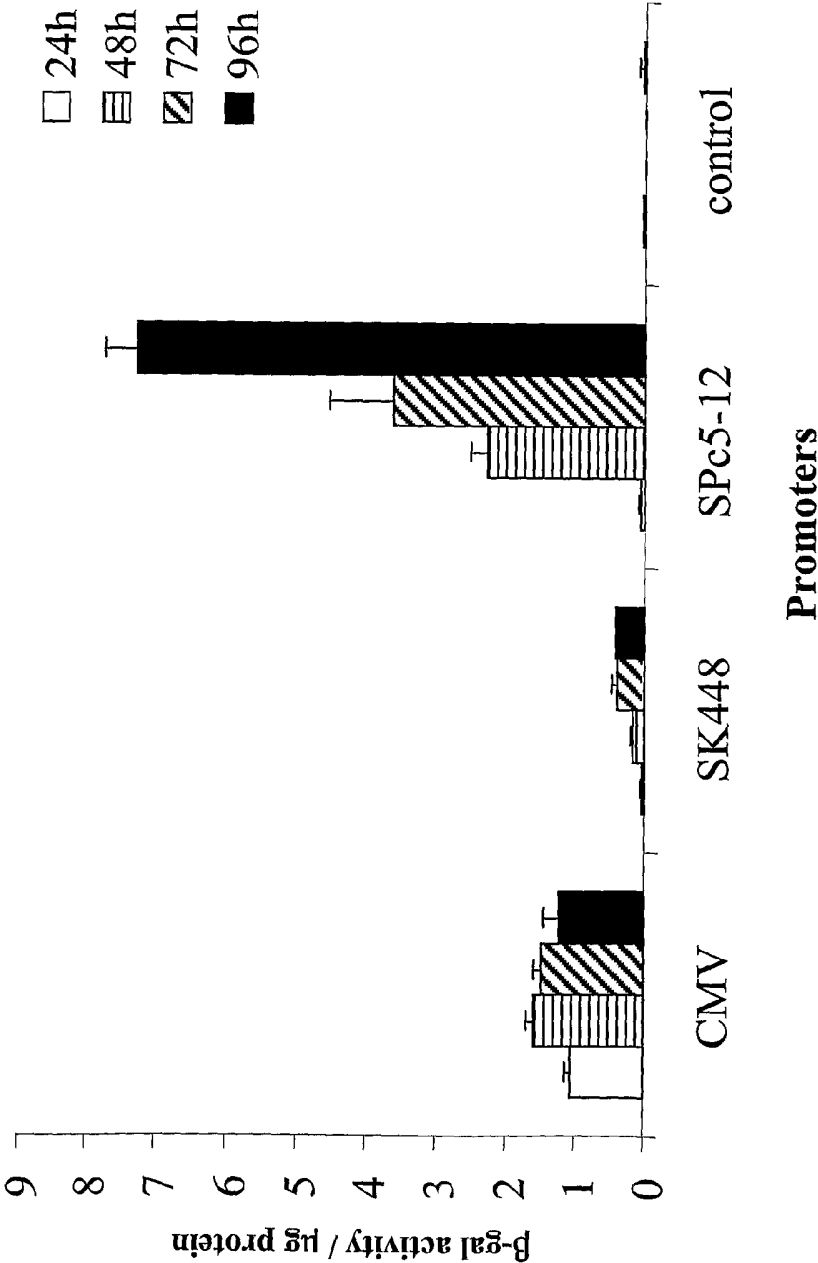


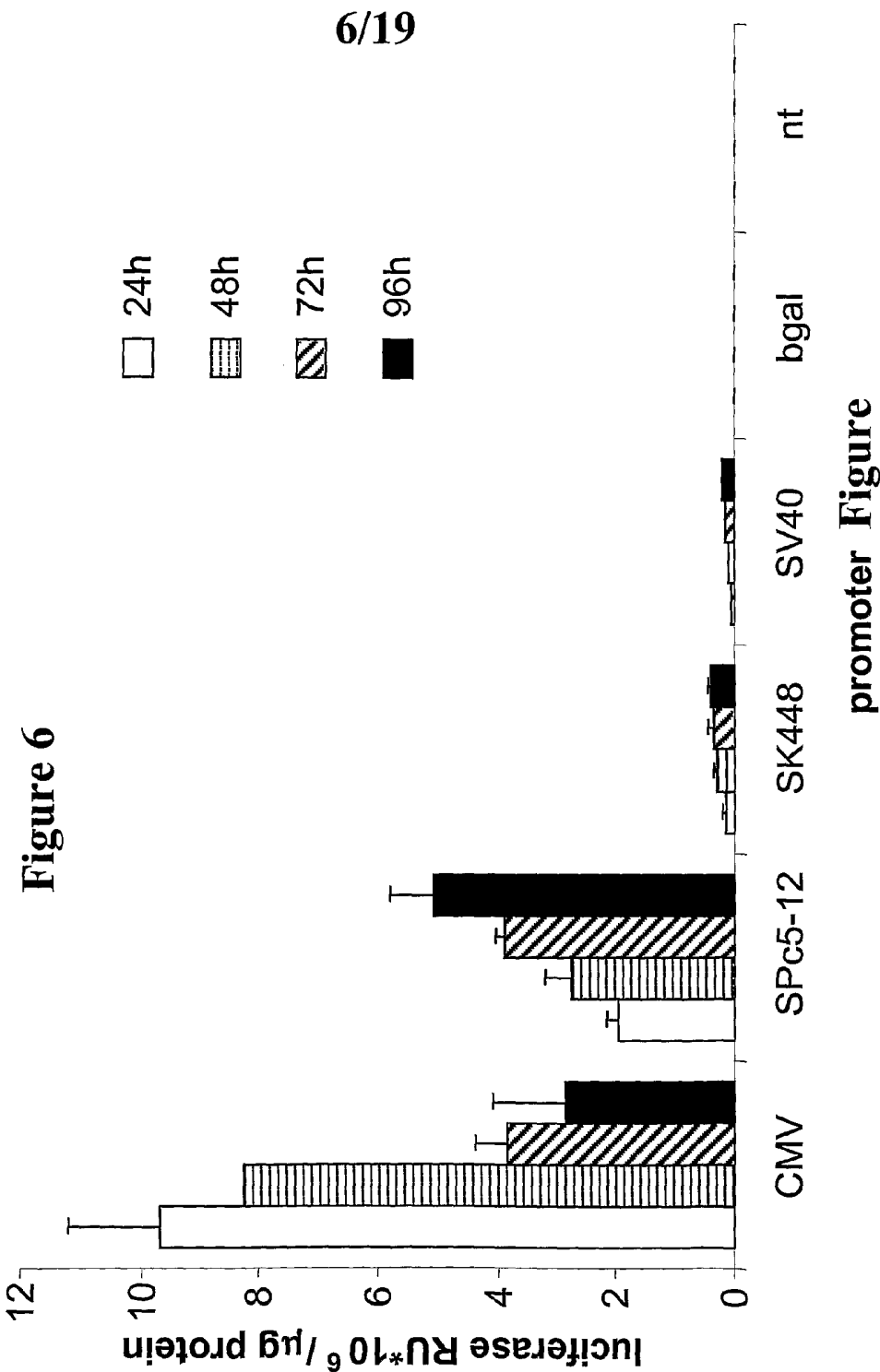
Figure 4



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Figure 5



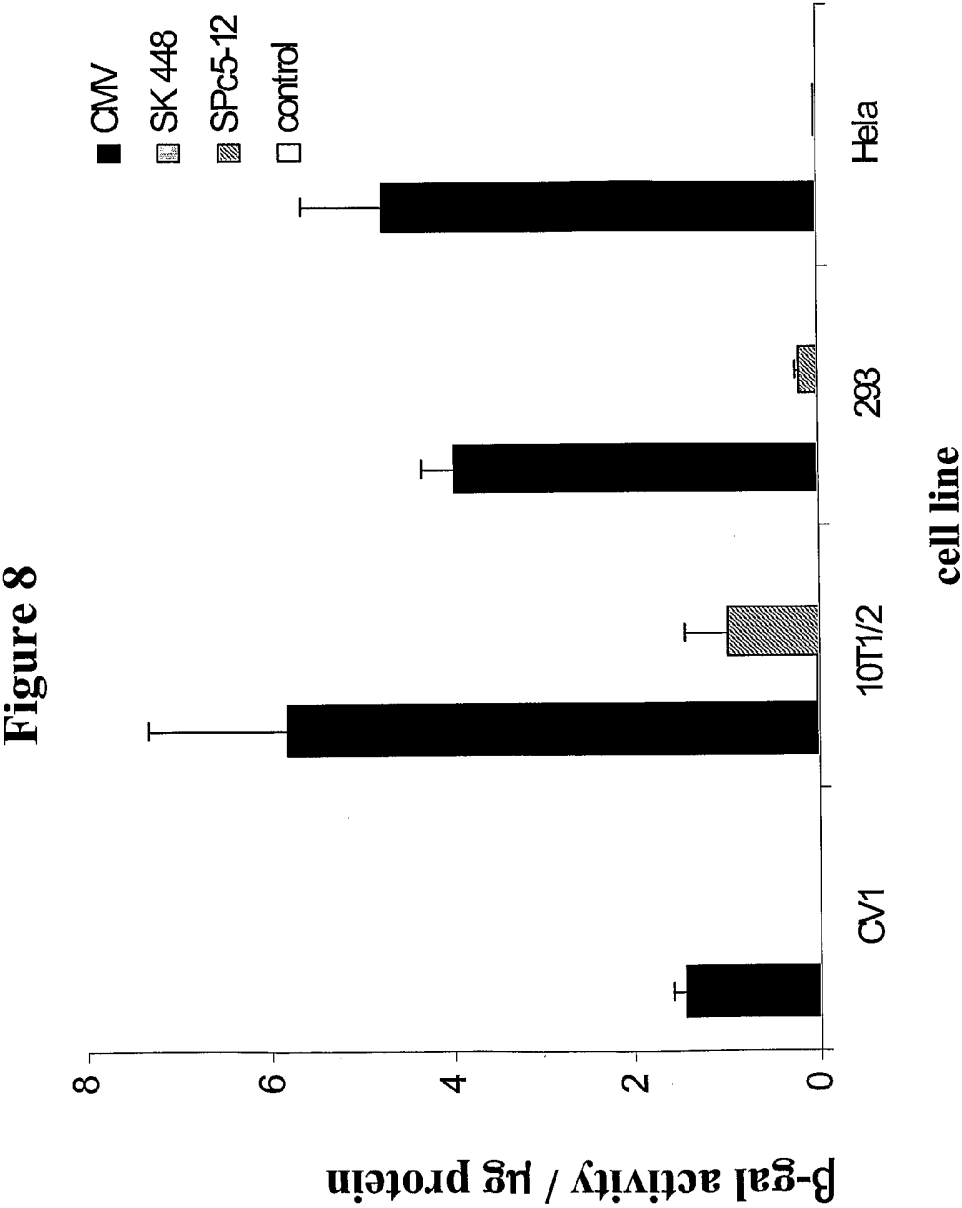


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Figure 7

	24 hours	48 hours	72 hours	96 hours
CMV	9.706	8.240	3.832	2.846
SPc5-12	1.957	2.757	3.893	5.070
SK448	0.167	0.304	0.356	0.383
SV40	0.064	0.112	0.136	0.182
bgal	0.000	0.002	0.003	0.003
nt	0.001	0.002	0.002	0.003

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Figure 9

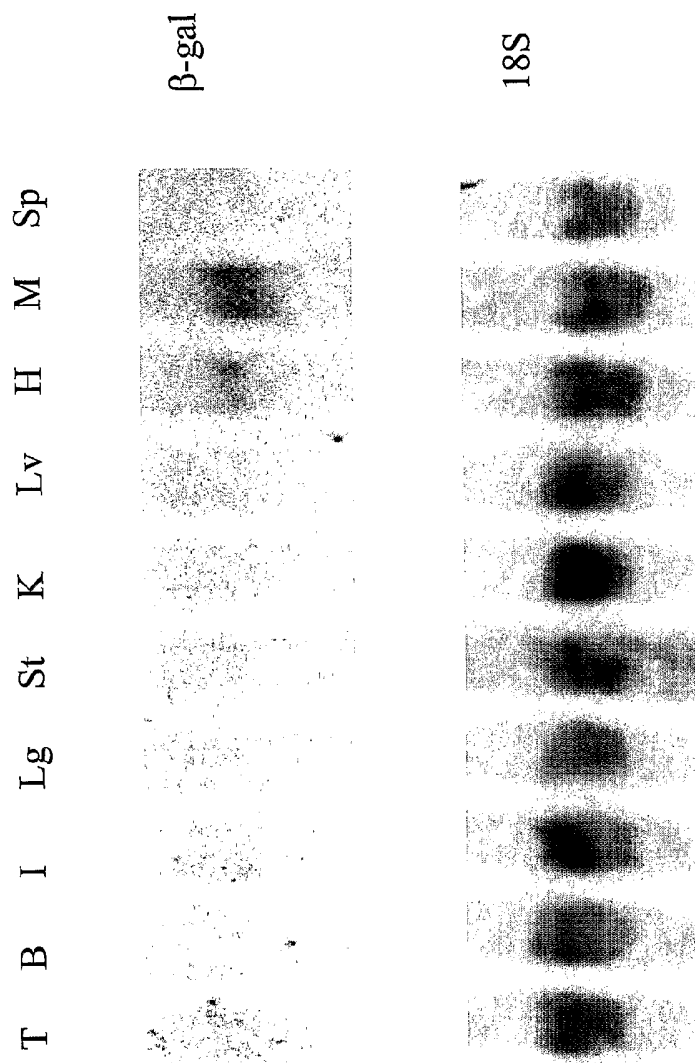
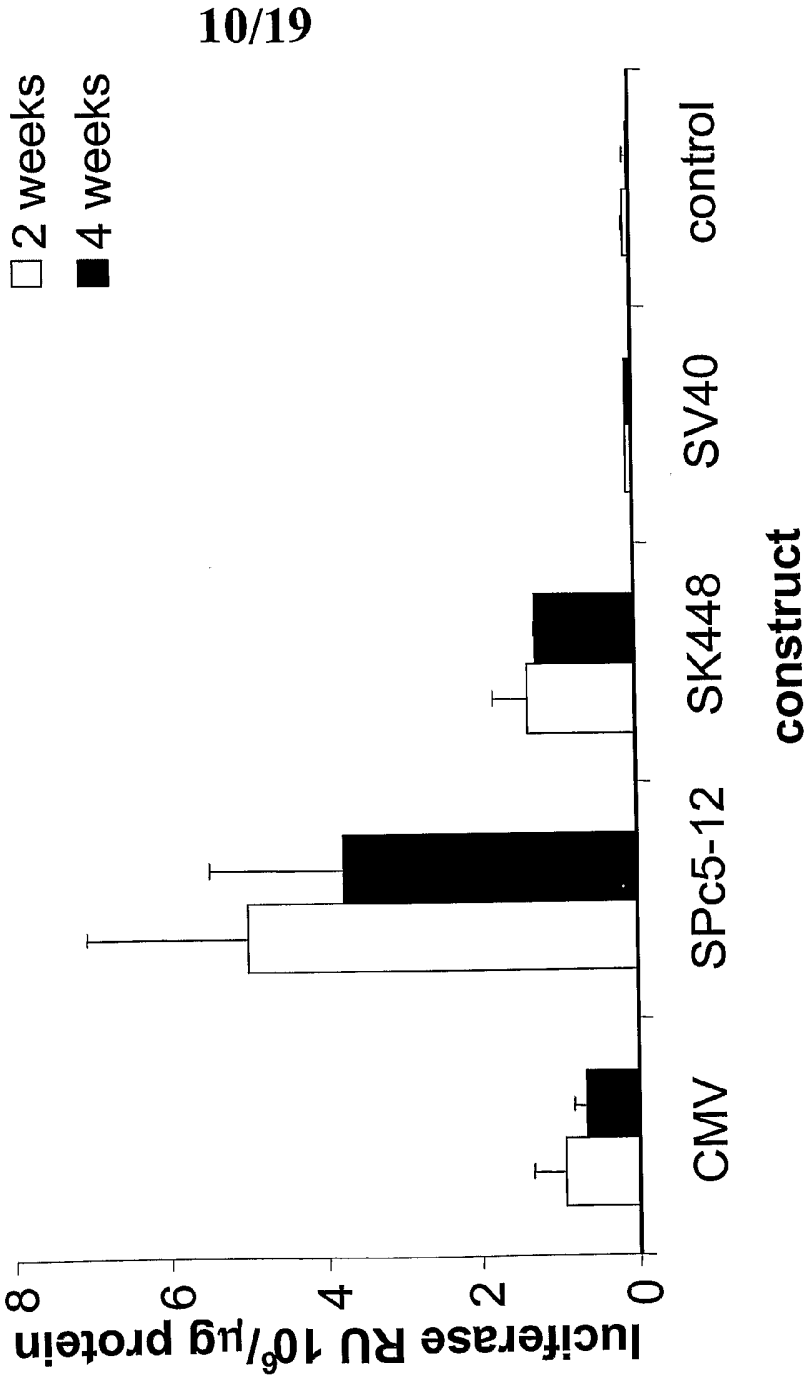
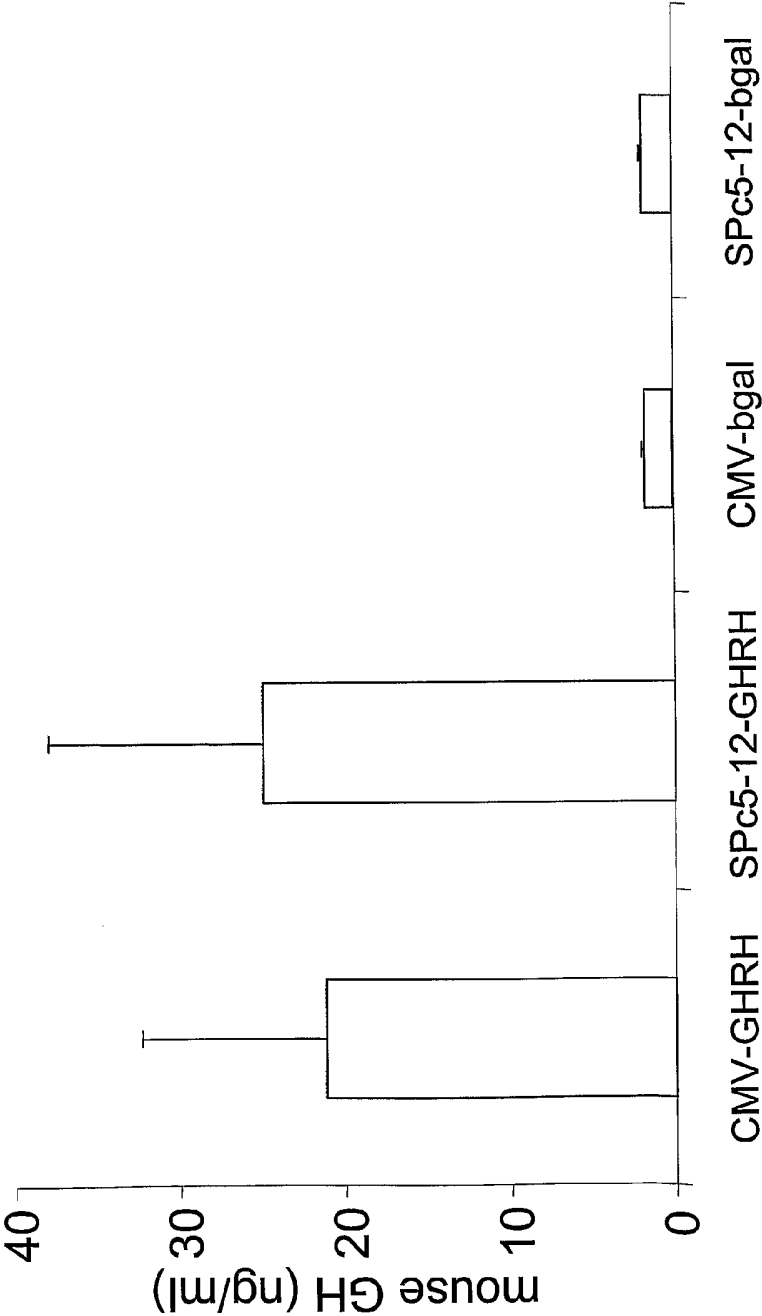


Figure 10



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Figure 11



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c1-26

←MEF-1 TEF-1→ MEF-2
 cggccgaggg cggcggggca ggcagcaggt gttggcacca ttcttcacgg ctctaaaaat 60
 → ←TEF-1 ←SRE SRE→
 aactcccggt aggaatggtg ccgtcgccat atttgggtgt cgacacccaa atatggcgac 120
 ←TEF-1 ←MEF-1 SRE→ MEF-1
 ggggtgaggaa tgggtggcag gcagcaggtg ttgggacacc caaatatggc gacggccaac 180
 MEF-1→ ←MEF-2 ←MEF-2 ←TEF-1
 acctgctgcc tgccgggagt tatttttaga gccgggagtt atttttagag cggtgaggaa 240
 SRE→
 tgggtgacac ccaaatatgg cgacggccgg ggccgcattc ctggggggcgg ggcggtgctc 300
 cggcccgctt cgataaaagg ctccggggcc ggccggcgcc cagcagctac ccggaggagc 360
 gggaggcgcc aagctctaga 380

Figure 12

EagI
 ~~~~~  
 EclXI  
 ~~~~~  
 McrI
 ~~~~~  
 XmaIII  
 ~~~~~  
 BsiEI
 ~~~~~  
 1 GGCGGCCGAG GGCGGCCGGG CAGGCAGCAG GTGTTGGCAC CATTCTCTAC CGCTCTAAAA  
 CCGCCCGCTC CCGCCGCCCC GTCCGTCTGC CACAACCGTG GTAAGGAGTG GCGAGATTTT  
 HincII  
 ~~~~~  
 HindII
 ~~~~~  
 SalI  
 ~~~~~  
 TaqI
 ~~~~~  
 AccI  
 ~~~~~  
 61 ATAACCTCCG TGAGGAATGG TGCCGTCGCC ATATTGTTGGT GTCGACACCC AAATATGGCG
 TATTGAGGGC ACTCCTTACC ACGGCAGCGG TATAAACCCA CAGCTGTGGG TTTATACCGC
 BsmFI
 ~~~~~  
 121 ACGGGTGAGG AATGGTGGGC AGGCAGCAGG TGTGGGGACA CCCAAATATG GCGACGGCCA  
 TGCCCACTCC TTACCACCGG TCCGTCGTCC ACAACCGTGT GGGTTTATAC CGCTGCCGGT  
 181 ACACCTGCTG CCGCCCGGGA GTTATTTTGA GAGCGGGGAG TTATTTTATG AGCGGTGAGG  
 TGTGGACGAC GGACGGCCCT CAATAAAAT CTCGCCCTC AATAAAATC TCGCCACTCC  
 XmaIII BmyI  
 ~~~~~  
 EclXI EcoRII BsiHKAI
 ~~~~~  
 EagI BstNI Bsp1286I  
 ~~~~~  
 McrI MvaI HgiAI
 ~~~~~  
 BsiEI BsmI AspHI  
 ~~~~~  
 241 AATGGTGGAC ACCCAAATAT GGCAGCGGCC GGGGCCGCAT TCCTGGGGGC CGGGCGGTGC
 TTACCACCTG TGGTTTATA CCGCTGCCGG CCCCGGCGTA AGGACCCCGG GCCCGCCAGC
 BmyI
 ~~~  
 BsiHKAI NgoMI  
 ~~~~~  
 Bsp1286I Cfr10I
 ~~~~~  
 HgiAI NaeI

BspMI

BstNI  
~~~  
EcoRII
~~~  
MvaI

EagI

BsmI

Bmy I

BsiHKAI

Ngomi

EcoRII

Bsp1286I

Cfr1.0I

MvaI

Hq:AI

Nae

EstNI

ASDHI

TaqI

BsrFI

121 GGGGGCCGGG CGGTGCTCCC GCCCGCCTCG ATAAAAGGCT CCGGGGCCGG CGGCGGCCCA  
CCCCCGGCCC GCCACGAGGG CGGGCGGAGC TATTTTCCGA GGCCCCGGCC GCCGCCGGGT

BanI

BsaHI

CfoI

HaeII

HhaI

HinP1I

KasI

MaeT

NarI

XbaI

ACYT

BfatT

181 CGAGCTACCC GGAGGAGCGG GAGGCGCCAA GCTCTAGA  
GCTCGATGGG CCTCCTCGCC CTCCGCGGTT CGAGATCT

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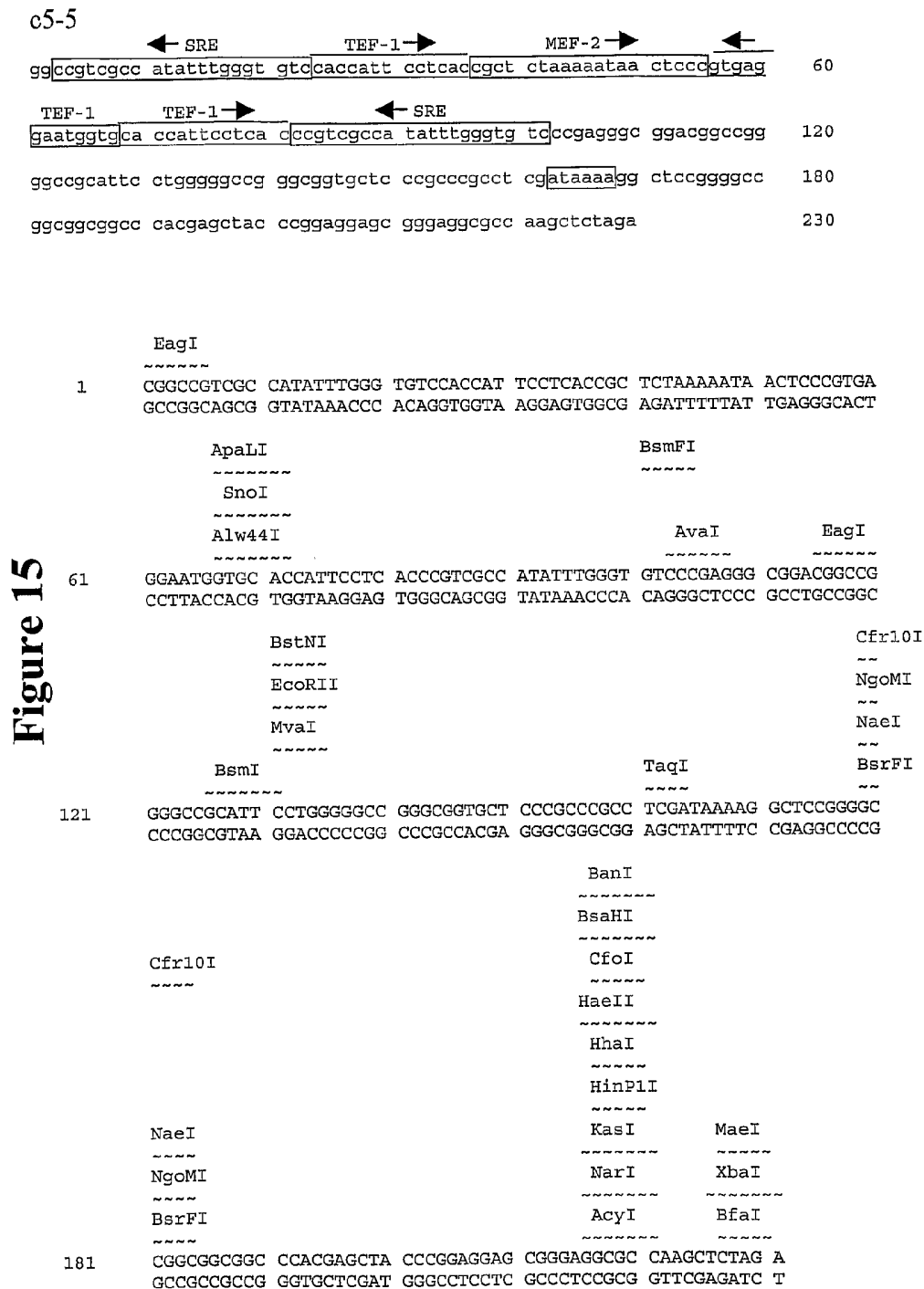
c2-27

← SRE                      MEF-1 →                      SRE →  
 ggccgtcgcc atatttgggt gtc ccaacac tgctgcctgc cgacaccaa atatggcgac 60  
 ← TEF-1                      MEF-1 →                      SRE →  
 gggtgaggaa tgggtgccaac acctgctgcc tgccgacacc caaatatggc gacggccggg 120  
 gccgcattcc tgggggcccgg gcggtgctcc cggccgcttc gataaaaaggc tccggggccg 180  
 gcggcgggccc acgagctacc cggaggagcg ggaggcgcca agctctaga 229

Figure 14

|     |                                                                                                                                        |                   |                                                                                                                                       |
|-----|----------------------------------------------------------------------------------------------------------------------------------------|-------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| 1   | EagI<br>~~~~~                                                                                                                          | BsmFI<br>~~~~~    | CGGCCGTCGC CATATTGGG TGTCCCAACA CTGCTGCCTG CCGACACCCA AATATGGCGA<br>GCCGGCAGCG GTATAAACCC ACAGGGTTGT GACGACGGAC GGCTGTGGGT TTATACCGCT |
| 61  | HphI<br>~~~~~                                                                                                                          | BspMI<br>~~~~~    | EagI<br>~~~~~                                                                                                                         |
|     | CGGGTGAGGA ATGGTGCCAA CACCTGCTGC CTGCCGACAC CCAAATATGG CGACGGCCGG<br>GCCCACTCCT TACCACGGTT GTGGACGACG GACGGCTGTG GGTTTATACC GCTGCCGGCC |                   |                                                                                                                                       |
|     |                                                                                                                                        | BmyI<br>~~~~~     |                                                                                                                                       |
|     | EcoRII<br>~~~~~                                                                                                                        | BsiHKAI<br>~~~~~  | NgoMI<br>~~~                                                                                                                          |
|     | BstNI<br>~~~~~                                                                                                                         | Bsp1286I<br>~~~~~ | Cfr10I<br>~~~                                                                                                                         |
|     | MvaI<br>~~~~~                                                                                                                          | HgiAI<br>~~~~~    | NaeI<br>~~~                                                                                                                           |
|     | BsmI<br>~~~~~                                                                                                                          | AspHI<br>~~~~~    | TaqI<br>~~~~~                                                                                                                         |
| 121 | GGCCGCATTC CTGGGGGCGG GCGGGTGCTC CCGCCCGCCT CGATAAAAGG CTCCGGGGCC<br>CCGGCGTAAG GACCCCCGGC CCGCCACGAG GCGGGCGGA GCTATTTTCC GAGGCCCCGG  |                   |                                                                                                                                       |
|     |                                                                                                                                        | BsaHI<br>~~~~~    |                                                                                                                                       |
|     | Cfr10I<br>~~~                                                                                                                          | CfoI<br>~~~~~     |                                                                                                                                       |
|     |                                                                                                                                        | HaeII<br>~~~~~    |                                                                                                                                       |
|     |                                                                                                                                        | HhaI<br>~~~~~     |                                                                                                                                       |
|     |                                                                                                                                        | HinPII<br>~~~~~   |                                                                                                                                       |
|     | NaeI<br>~~~                                                                                                                            | KasI<br>~~~~~     | MaeI<br>~~~~~                                                                                                                         |
|     | NgoMI<br>~~~                                                                                                                           | NarI<br>~~~~~     | XbaI<br>~~~~~                                                                                                                         |
|     | BsrFI<br>~~~~~                                                                                                                         | BsrBI<br>~~~~~    | AcyI<br>~~~~~                                                                                                                         |
|     |                                                                                                                                        | BfaI<br>~~~~~     |                                                                                                                                       |
| 181 | GGCGGCGGCC CACGAGCTAC CCGGAGGAGC GGGAGGCGCC AAGCTCTAGA<br>CCGCCGCCGG GTGCTCGATG GGCCTCGTCG CCTCCGCGG TTCGAGATCT                        |                   |                                                                                                                                       |

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Figure 16

c5-12

ggcgcgtccgc cttgggcacc atcctcacga caccacaata tggcgacggg tgaggaatgg 60

tggggagtta tttttagagc ggtgaggaag gtgggcaggg agcagggtgt ggcgctctaa 120

aaataactcc cgggagttat ttttagagcg gaggaatggt gacacccaa atatggcgac 180

ggttctctac ccgtcgccat atttgggtgt cgcctcgg cgggggcgc attcctgggg 240

gccggggcgt gctcccgccc gcctcgataa aagggtccgg ggcggcgggc ggcccaacgag 300

ctaccgggag gagcgggagg cgccaagctc taga 334

EagI FokI

1 CGGCCGTCCG CCTTCGGCAC CATCTCAGC ACACCCAAAT ATGGCGACGG GTGAGGAATG

GCCGCGACGC GGAAGCCGTG GTAGGAGTGC TGTGGGTTA TACCGCTGCC CACTCCTTAC

BspMI

BbvI

61 GTGGGGAGTT ATTTTITAGAG CGGTGAGGAA GGTGGGCAGG CAGCAGGTGT TGGCGCTCTA

CACCCCTCAA TAAAAATCTC GCCACTCCTT CCACCCGTCC GTCGTCCACA ACCGCGAGAT

SmaI

XmaI

AvaI

121 AAAATAACTC CCGGGAGTTA TTTTITAGAGC GGAGGAATGG TGGACACCCA AATATGECGA

TTTATTAGAG GGCCCTCAAT AAAAATCTCG CCTCCTTACC ACCTGTGGGT TTATACCGCT

BstNI

EcoRII

MvaI

EagI BsmI

181 CGGTTCTCTA CCGTTCGCCA TATTGGGTG TCCGCCCTCG GCCGGGGCGG CATTCCTGGG

GCCAAGGAGT GGGCAGCGGT ATAAACCCAC AGGCGGGAGC CGGCCCGGC GTAAGGACCC

BmyI

BsiHKAI

Bsp1286I

HgiAI

AspHI

TaqI

NgoMI

Cfr10I

NaeI

BsrFI

241 GGCCGGGCGG TGCTCCCGCC CGCCTCGATA AAAGGCTCCG GGGCCGGCGG CGGCCACGA

CCGCCCCGCC ACGAGGCGCG GCGGAGCTAT TTTCCGAGGC CCCGGCCGCC GCCGGGTGCT

BsaHI

KasI MaeI

NarI XbaI

AcyI BfaI

301 GCTACCCGGA GGAGCGGGAG GCGCCAAGCT CTAGA

CGATGGGCCT CCTCGCCCTC CGCGTTCGA GATCT

17/19

c6-5

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      ← SRE          MEF-2 →          ← MEF-1
ggcgcgtgcc atatttgggt gtcgcgtcta aaaataactc ccggcaggca gcagggtgttg 60

      MEF-1 →          SRE →          ← MEF-1
gccaacacct gctgcctgca gacaccaaat atggcgacgg ggcaggcagc aggtgttgga 120

      SRE →
acacccaaat atggcgacgg ccggggcgcg attcctgggg gcggggcggt gctcccgccc 180

gcctcgataa aaggctccgg ggccggcgcg gggccacgag ctaccgggag gagcggggagg 240

cgccaagctc taga 254

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Figure 17

```

MscI
EagI
1 CGGCCGTCGC CATATTGGG TGTCCGCTCT AAAAATAACT CCCGGCAGGC AGCAGGTGTT
GCCGCGACGC GTATAAACC ACAGGCGAGA TTTTATIGA GGGCCGTCGC TCGTCCACAA

MscI
MluNI
61 GGCCAACACC TGCTGCCTGC CGACACCAAA TATGGCGACG GGCAGGCAG CAGGTGTTGG
CCGTTTGTGG ACGACGGACG GCTGTGTTT ATACCGCTGC CCGTCCGTC GTCCACAACC

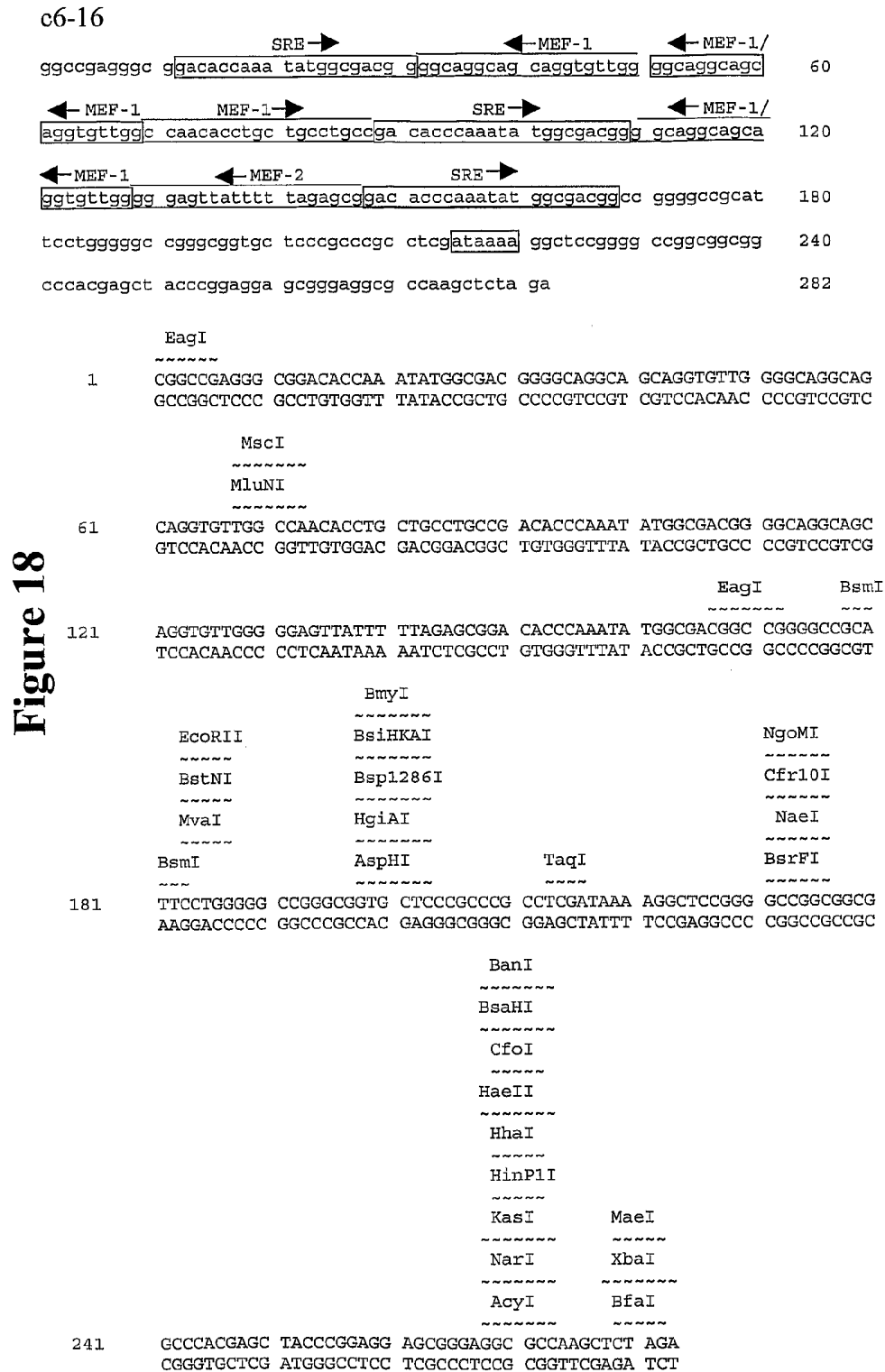
BmyI
EcoRII
BstNI
MvaI
BsmFI
EagI
BsmI
121 GACACCAAAA TATGGCGACG GCCGGGGCGG CATTCCCTGGG GGCCGGGCGG TGCTCCCGCC
CTGTGGGTTT ATACCGCTGC CGGCCCGGC GTAAGGACCC CCGCCCGCC ACGAGGGCGG

BmyI
BsiHKAI
Bsp1286I
HgiAI
AspHI
BanI
BsaHI
HaeII
KasI
NarI
AcyI
181 CGCCTCGATA AAAGGCTCCG GGGCCGGCGG CGGCCACGA GCTACCCGGA GGAGCGGGAG
GCGGAGCTAT TTCCGAGGC CCCGGCCGCC GCCGGGTGCT CGATGGGCTT CCGGCCCTC

BanI
BsaHI
CfoI
HaeII
HhaI
HinPII
KasI
MaeI

```

18/19



19/19

c6-39

SRE → MEF-2 → MEF-1  
 ggccggtccgc cctcgggaca cccaaatatg gcgacggcgc tctaaaaata actccc **ccaa** 60  
 MEF-1 → SRE → ←MEF-1 MEF-2  
**cac**cctgctgc ctgccc **gacac** ccaaatatgg caacggggca ggcagcaggt gtttgg **cgct** 120  
 MEF-2 →  
**cta**aaaaataa ctccc **cccga** gggcggacgg ccggggccgc attcctgggg gccggggcgt 180  
 gctccccccc gctcgg **ataa** aaggctccgg ggcccgccgc ggcccacgag ctaccgggag 240  
 gagcggggagg cgccaagctc taga 264

Figure 19

EagI BsmFI  
 ~~~~~  
 1 CGGCCGTCCG CCTCGGGAC ACCCAAATAT GCGACGGCG CTCTAAAAAT AACTCCCCCA
 GCCGGCAGGC GGGAGCCCTG TGGGTTTATA CCGCTGCCGC GAGATTTTTA TTGAGGGGGT
 61 ACACCTGCTG CCTGCCGACA CCCAAATATG GCAACGGGGC NAGGCAGCAG GTGTTTGGCG
 TGTGGACGAC GGACGGCTGT GGGTTTATAC CGTTGCCCGG NTCCGTCGTC CACAAACCGC
 BstNI
 ~~~~~  
 EcoRII  
 ~~~~~  
 MvaI
 ~~~~~  
 EagI BsmI  
 ~~~~~  
 121 CTCTAAAAAT AACTCCCCCA GAGGGCGGAC GGCCGGGGCC GCATTCTCTGG GGGCCGGGCG
 GAGATTTTTA TTGAGGGGGG CTCCCGCCTG CCGGCCCGCG CGTAAGGACC CCCGGCCCCG
 BmyI
 ~~~~~  
 BsiHKAI  
 ~~~~~  
 Bsp1286I
 ~~~~~  
 HgiAI  
 ~~~~~  
 AspHI TaqI
 ~~~~~  
 181 GTGCTCCCGC CCGCCTCGAT AAAAGGCTCC GGGGCCGGCG GCGGCCACG AGCTACCCGG  
 CACGAGGGCG GCGGAGCTA TTTTCCGAGG CCGCGCCCGC CGCCGGGTGC TCGATGGGCC  
 BanI  
 ~~~~~  
 BsaHI
 ~~~~~  
 KasI MaeI  
 ~~~~~  
 NarI XbaI
 ~~~~~  
 BsrBI AcyI BfaI  
 ~~~~~  
 241 AGGAGCGGGA GCGCCAAGC TCTAGA
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SEQUENCE LISTING

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Baylor College of Medicine

<120> SYNTHETIC MUSCLE PROMOTERS WITH ACTIVITIES EXCEEDING NATURALLY OCCURRING
REGULATORY SEQUENCES IN CARDIAC CELLS

<130> 108328.00161 - AVSI-0027

<150> US 60/423,536
<151> 2002-11-04

<160> 22

<170> PatentIn version 3.1

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<220>
<223> SRE control elements used in the promoters.

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<220>
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<400> 2
ccaacacctg ctgcctgcc 19

<210> 3
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<213> artificial sequence

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13

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<223> Xaa at position 1 may be tyrosine, or histidine

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa at position 2 may be alanine, valine, or isoleucine.

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa at position 15 may be alanine, valine, or isoleucine.

<220>
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<222> (27)..(27)
<223> Xaa at position 27 may be methionine, or leucine.

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa at position 28 may be serine or asparagine.

<400> 6

Xaa Xaa Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Xaa Gln
1 5 10 15

Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Xaa Xaa Arg Gln Gln Gly
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Glu Arg Asn Gln Glu Gln Gly Ala
35 40

<210> 7

<211> 3534

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<220>

<223> Nucleic acid sequence for the HV-GHRH plasmid.

<400> 7

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cattcctggg ggccgggcgg tgctcccgcc cgcctcgata aaaggctccg gggccggcgg      360
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<213> artificial sequence

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<223> Nucleic acid sequence for the TI-GHRH plasmid.

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<210> 10

<211> 3534

<212> DNA

<213> artificial sequence

<220>

<223> Nucleic acid sequence for the 15/27/28 GHRH plasmid.

<400> 10

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<210> 11

<211> 2710

<212> DNA

<213> artificial sequence

<220>

<223> Vector with a mouse codon optimized GHRH analog sequence

<400> 11

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gagttat	240
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agggcgatcg 2710

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<210> 12

<211> 2713

<212> DNA

<213> artificial sequence

<220>

<223> Vector with a rat codon optimized GHRH analog sequence

<400> 12

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agtcaccta gctgccatgg ccctgtgggt gttcttcgtg ctgctgacct tgaccagcgg 480
aagccactgc agcctgcctc ccagccctcc cttcagggtg cgcgggcacg ccgacgccat 540

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cttcaccagc agctacagga ggatcctggg ccagctgtac gctaggaagc tcctgcacga 600
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cagttcatto agagcaccag acaggtcagt tttacaaaac agaactggac gaccctgtgc 2400
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ggaagggcga tcg 2713

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<210> 13
<211> 2704
<212> DNA
<213> artificial sequence

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<220>

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<223> Vector with a bovine codon optimized GHRH analog sequence

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gaaaacagct gcatcagagc aaccaatggg ctgctgtgcc cagtcataac caaacagacg 2460
ttcaaccag gctgccggag aacctgcatg cagaccatcc tgttcaatca tgcgaaacga 2520
tctcatcct gtctcttgat cagatcttga tccctgcgc catcagatcc ttggcgga 2580
gaaagccatc cagtttactt tgcagggtt cccaacctta ccagagggcg cccagctgg 2640
caattccggt tcgcttgctg tccataaaac cgcccagctc agcaactgtt gggaagggcg 2700
atcg 2704

<210> 14
<211> 2704
<212> DNA

<213> artificial sequence

<220>

<223> Vector with a ovine codon optimized GHRH analog sequence

<400> 14

tgtaatacga ctcactatag gggaattgg agctccaccg cgggtggcggc cgtccgccct	60
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ttagagcggg gaggaagggt ggcaggcagc aggtgttggc gctctaaaaa taactcccgg	180
gagttat	240
tcgccatatt tgggtgtccg ccctcggccg gggccgcatt cctggggggc gggcgggtgt	300
cccgcgccgc tcgataaaaag gctccggggc cggcggcggc ccacgagcta cccggaggag	360
cgggaggcgc caagcggatc ccaaggccca actccccgaa ccactcaggg tcctgtggac	420
agctcaccta gctgccatgg tgtgtgggt gttcttcctg gtgaccctga ccctgagcag	480
cggaagccac ggcagcctgc ccagccagcc cctgaggatc cctaggtacg ccgacgccat	540
cttcaccaac agctacagga agatcctggg ccagctgagc gctaggaagc tcctgcagga	600
catcatgaac aggcagcagg gcgagaggaa ccaggagcag ggcgcctgat aagcttatcg	660
gggtggcatc cctgtgacct cccccagtg cctctcctgg ccctggaagt tgccactcca	720
gtgcccacca gccttgcctt aataaaatta agttgcatca ttttgtctga ctaggtgtcc	780
ttctataata ttatgggggtg gaggggggtg gtatggagca aggggcaagt tgggaagaca	840
acctgtaggg ctgcaggggg gggccggtag cagcttttgt tccctttagt gagggttaat	900
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caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcggtt cccctggaa	1200
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tgaagtgggt gcctaactac ggctacacta gaagaacagt atttggtatc tgcgctctgc	1560
tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg	1620

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ctggtagcgg tggttttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc 1680
aagaagatcc tttgatcttt tctacggggc tagcgcttag aagaactcat ccagcagacg 1740
gtagaatgca atacgttgag agtctggagc tgcaatacca tacagaacca ggaaacggtc 1800
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tcctcatcct gtctcttgat cagatcttga tccctgccc catcagatcc ttggcggcaa 2580
gaaagccatc cagtttactt tgcagggtt cccaacctta ccagaggcg cccagctgg 2640
caattccggt tcgcttgctg tccataaaac cgcccagct agcaactgtt gggaaggcg 2700
atcg 2704

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<210> 15

<211> 2713

<212> DNA

<213> artificial sequence

<220>

<223> Vector with a chicken codon optimized GHRH analog sequence

<400> 15

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tgtaatacga ctactatag gggaattgg agtccaccg cggtagggcg cgtccgccct 60
cggcaccatc ctacgacac ccaaatatgg cgacgggtga ggaatgggtg ggagtatttt 120
ttagagcggg gaggaagggt ggcaggcagc aggtgttggc gctctaaaaa taactcccg 180
gagttatttt tagagcggag gaatgggtga caccctaaata tggcgacggg tcctcaccg 240
tcgccatatt tgggtgtccg ccctcggccg gggcgcgatt cctggggggc gggcgggtgt 300
ccgcgccgcc tcgataaaag gctccggggc cggcggcgcc ccacgagcta cccggaggag 360

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aagccactgc	agcctgccac	ccagcccacc	cttcgcgctc	aggcgccacg	ccgacggcat	540
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cctgatggcc	aagcgcgtgg	gcagcggact	gggagacgag	gccgagcccc	tgagctgata	660
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atccggcata	cgagctttca	gacgtgcaaa	cagttcagcc	ggtgccagac	cctgatgttc	2040
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cattgcatca gccatgatag aaactttctc tgccggagcc aggtgagaag acagcaggtc 2220
ctgacccgga acttcaccca gcagcagcca gtcacgacca gcttcagtaa ctacatccag 2280
aactgcagca cacggaacac cagtggttgc cagccaagac agacgagctg cttcatcctg 2340
cagttcatto agagcaccag acaggtcagt tttaacaaac agaactggac gacctgtgc 2400
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tggcggcaag aaagccatcc agtttacttt gcagggcttc ccaaccttac cagagggcgc 2640
cccagctggc aattccggtt cgcttgctgt ccataaaacc gccagctcta gcaactgttg 2700
ggaagggcga tcg 2713

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<210> 16
 <211> 382
 <212> DNA
 <213> artificial sequence

<220>
 <223> This is the synthetic promoter c1-26.

```

<400> 16
ggcggccgag ggcggcgggg caggcagcag gtgttggcac cattcctcac cgctctaaaa 60
ataactccc tgaggaatgg tgccgtcgcc atatttgggt gtcgacaccc aaatatggcg 120
acgggtgagg aatggtgggc aggcagcagg tggtgggaca cccaaatatg gcgacggcca 180
acacctgctg cctgccggga gttattttta gagcggggag ttatttttag agcggtgagg 240
aatggtggac acccaaatat ggcgacggcc ggggcccgc tcttgggggc cgggcggtgc 300
tccgcgccgc ctcgataaaa ggctccgggg ccggcggcgg cccacgagct acccgagga 360
gcgggaggcg ccaagctcta ga 382

```

<210> 17
 <211> 218
 <212> DNA
 <213> artificial sequence

<220>
 <223> This is the synthetic promoter sequence for c2-26.

```

<400> 17
gggccgtcgc catatttggg tgtccgctct aaaaataact cccgacaccc aaatatggcg 60
acggggcagg cagcaggtgt tgggacaccc aaatatggcg acggccgggg ccgcattcct 120
gggggcccgg cggtgctccc gccgcctcg ataaaaggct ccggggccgg cggcggccca 180

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cgagctaccc ggaggagcgg gaggcgcaa gctctaga 218

<210> 18
<211> 230
<212> DNA
<213> artificial sequence

<220>
<223> This is the synthetic sequence for c2-27.

<400> 18
gggccgtcgc catatttggg tgcggcagg cagcaggtgt tggcaccatt cctcaccggt 60
cgccatattt ggggtgtcggc aggcagcagt gttgggacac ccaaatatgg cgacggccgg 120
ggccgcattc ctggggggccg ggcggtgctc ccgcccgcct cgataaaagg ctccggggcc 180
ggcggcgggc cagcagctac ccggaggagc gggaggcgcc aagctctaga 230

<210> 19
<211> 231
<212> DNA
<213> artificial sequence

<220>
<223> This is the synthetic promoter for c5-5.

<400> 19
cggccgtccg ccctcgggac acccaaatat ggcgacgggt gaggaatggt gcaccattcc 60
tcacgggagt tattttttaga gcggtgagga atggtggaca ccaaatatg gcgacggccg 120
gggccgcatt cctggggggcc ggcggtgct cccgcccgc tcgataaaag gctccggggc 180
cgccggcggc ccacgagcta ccggaggag cgggaggcgc caagctctag a 231

<210> 20
<211> 255
<212> DNA
<213> artificial sequence

<220>
<223> This is the synthetic promoter for c6-5.

<400> 20
cggccgtcgc catatttggg tgcaccaaca cctgctgcct gcccgtcgc catatttgggt 60
gtcggcaggc agcagggtgtt ggccaacacc tgctgcctgc cgggagttat ttttagagcg 120
gacacccaaa tatggcgacg gccggggccg cattcctggg ggccgggcgg tgctcccgcc 180
cgccctgata aaaggctccg gggccggcg cggcccacga gctaccggga ggagcgggag 240
gcgccaagct ctaga 255

<210> 21

<211> 283
<212> DNA
<213> artificial sequence

<220>

<223> This is the synthetic promoter for c6-16.

<400> 21
cggccgtcgc catatttggg tgccgctct aaaaataact ccccaacac ctgctgcctg 60
cccgcgcgc atatttgggt gtcggcaggc agcaggtgtt ggccaacacc tgctgcctgc 120
cccaacacct gctgcctgcc ccgtcgccat atttgggtgc cgcctcggc cggggccgca 180
ttcctggggg ccgggcgggt ctccgcccgc cctcgataaa aggctccggg gccggcggcg 240
gccacgagc taccggagg agcgggagg gccagctct aga 283

<210> 22
<211> 263
<212> DNA
<213> artificial sequence

<220>

<223> This is the synthetic promoter for c6-39.

<400> 22
cggccgtccg ccctcggggg agttattttt agagcgccaa cacctgctgc ctgccccgtc 60
gccatatttg ggtgtcggca ggcagcaggc gttgggggag ttatttttag agcgcctgc 120
ccatatttgg gtgtcccag ggcggacggc cggggccgca ttcctggggg ccgggcgggtg 180
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agcgggaggc gccagctct aga 263