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(54) Title: PROMOTION OF CARDIOMYOCYTE PROLIFERATION AND REGENERATIVE TREATMENT OF THE HEART BY INHIBITION OF MICRORNA-128

(57) Abstract: Inhibitors of miRNA-128 capable of promoting cardiomyocyte mitotic cell proliferation and methods effective for regeneration of heart tissue.



**PROMOTION OF CARDIOMYOCYTE PROLIFERATION AND
REGENERATIVE TREATMENT OF THE HEART BY INHIBITION OF
MICRORNA-128**

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GOVERNMENT RIGHTS

This invention was made with government support under Contract Nos.
10 HL130042-01A1, HL107957, and HL110740, awarded by the National Institute of
Health (NIH National Heart, Blood and Lung Institute). The government has certain
rights in the invention.

TECHNICAL FIELD

15 The present disclosure relates to therapeutic regenerative medicine; namely
inhibitors of miRNA-128 and methods for promoting proliferation of mitotic
cardiomyocytes and regeneration of heart tissue for the treatment of cardiac disorders
and diseases.

20 **BACKGROUND**

The adult human heart fails to replenish the massive loss of cardiomyocytes
(CMs) caused by ischemia, which is the leading cause of death worldwide. Intensive
25 research has recently focused on the development of regenerative therapies for
ischemic heart disease. Current regenerative approaches are designed to repopulate lost
CMs through transplantation of exogenous stem cells from various sources with
committed cardiogenic potential. Unfortunately, the inability to differentiate

efficiently, poor cell survival, immaturity of differentiated CM, and arrhythmia, have all hampered the application of stem cell-based therapy in clinical settings.

Alternatively, cell-free approaches (such as stimulation of endogenous CM proliferation) have emerged as an attractive option for implementing myocardial

5 regeneration.

There has been a longstanding dogma that adult mammalian CMs are incapable of cell division. Recent studies, however, have shown that the 1-day-old neonatal mouse can regenerate its heart through dedifferentiation and proliferation of pre-existing CMs (see, e.g. Porrello, E.R., *et al. Proc Nat'l Acad of Sci US* 110, 187-192 (2013), and Porrello, E.R., *et al. Science* 331, (2011) 1078-1080, the entire disclosures of which are incorporated herein), a phenomenon that is observed in lower vertebrates such as adult zebrafish and amphibians. Unlike the adult zebrafish, the capacity of the neonatal mouse heart to regenerate is diminished as early as 1 week after birth and remains limited throughout adulthood. Various hypotheses have been proposed to explain the different capacities of different species to undergo cardiac regeneration. Recent compelling evidence showing that CMs have the potential to divide implies there is a latent regenerative potential when endogenous CMs are triggered to proliferate. Most exciting is the recent finding of limited self-renewal of human adult CMs using measurements of carbon-14 (^{14}C) content by accelerator mass spectrometry (see, e.g. Bergmann, O., *et al. Cell* 161, 1566-1575 (2015), Bergmann, O., *et al. Circ Res* 110, e17-18, and Bergmann, O., *et al. Science* 324, 98-102 (2009)). Reactivation of CM proliferation, therefore, becomes even more appealing for the

potential of heart regeneration. Whether, how and to what extent the endogenous proliferative ability of CM is sufficient to restore adult heart function, however, remains largely unknown.

5 MicroRNAs (miRNAs) constitute a class of small noncoding RNAs that bind to 3' untranslated region (3'UTR) of target mRNAs, resulting in the reduction of protein expression predominantly by destabilizing the target mRNAs and/or by inhibiting translation (Eulalio, A., *et al. Nature* (2012), Liu, N. & Olson, E.N. *Dev Cell* 18, 510-525 of CMs during MI (Qian, L., *et al. The Journal of experimental medicine* 208, 10 549-560 (2011), the entire disclosure of which is incorporated herein).

 However, the miRNAs that regulate CM proliferation during homeostasis and injury are not fully understood. Dissecting the mechanisms by which adult CMs exit the cell cycle arrest is fundamental for therapeutic manipulation capable of stimulating 15 endogenous CMs to proliferate in the adult myocardium. Although several CM cell cycle mediators have been identified, manipulation of the genes encoding these mediators has been insufficient for full recovery of heart function in response to injury.

 Clearly, identification of target miRNA implicated in CM proliferation and 20 provision of regenerative therapies based on modulating the target miRNA remain a compelling need in the art.

SUMMARY

Accordingly, the present invention provides embodiments directed miRNA-128 inhibitors capable of promoting CM mitotic cell proliferation and methods effective for regeneration of heart tissue.

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The cardinal miRNA implicated in governing heart growth during homeostasis and following injury was identified by the inventors as miRNA-128. Using small RNA sequencing, miRNA-128 expression was shown to be upregulated during the postnatal switch to terminal differentiation, at a time when most cardiomyocytes exit the cell cycle. It was further found that cardiac-specific overexpression of miRNA-128 in a transgenic mouse model impairs CM proliferation and cardiac function in the neonate. Cardiac-specific deletion of miRNA-128, in contrast, extends the proliferation window of postnatal CMs, with no deleterious effects on cardiac function. Moreover, miRNA-128 deletion modulates the expression of cell cycle-related genes, in part through targeting the chromatin modifier *Suz12*. Deletion of miRNA-128 leads to enhanced enrichment of SUZ12 on the cyclin-dependent kinase inhibitor (CDKI) *p27* promoter, with consequent repression of *p27* expression and activation of *Cyclin E* and *CDK2* of downstream positive cell cycle regulators that promote proliferation. Furthermore, deletion of miRNA-128 promotes re-entry of adult CMs into the cell cycle, thereby reducing the level of fibrosis, and attenuating cardiac dysfunction in response to MI. In aggregate, these results demonstrate that miRNA-128 is a critical regulator of endogenous CM proliferation, and provides a novel therapeutic target for heart repair.

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Accordingly, one embodiment provides methods for treating a subject suffering from a cardiac disorder. The methods comprise the step of delivering a therapeutically effective amount of a miRNA-128 inhibitor to a myocardial region of the subject. The
5 inhibitor can be delivered via transfection by a plasmid or vector comprising a genetic construct of the miRNA-128 inhibitor to the subject, or it may be delivered by enhanced transmission.

Another embodiment provides a miRNA-128 inhibitor selected from an antisense
10 nucleic acid against miRNA-128. In some embodiments the anti-miRNA oligonucleotide comprises between 4 and 21 nucleotides. According to other embodiments the miRNA-128 inhibitor is a small molecule inhibitor. In still other embodiments regenerative mitotic CMs in which proliferative capacity has been restored by inhibition of miRNA-128 are administered to a myocardial region of the heart. The
15 mitotic CMs may derive from the subject.

Embodiments directed to pharmaceutical compositions comprising at least one miRNA-128 inhibitor or at least one plasmid or vector engineered to transfect a cardiomyocyte with at least one miRNA-128 inhibitor, and a pharmaceutically
20 acceptable vehicle aspect are also provided.

Yet another embodiment is directed to methods for promoting proliferation of cardiomyocyte cells. The methods comprise adding an effective amount of a miRNA-

128 inhibitor to a culture medium comprising the cardiomyocyte cells, and observing proliferating regenerative cardiomyocyte cells. Compositions of regenerative cardiomyocyte cells may be directly administered to a myocardial region of a subject that would benefit from regenerative therapy.

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In some embodiments, pharmaceutical compositions of the invention may be administered directly to the myocardial region in a subject in need of regenerative therapy, for example by catheter-based injection. Direct injection may be guided by imaging technology, for example angiographic computed tomography image or real time magnetic resonance.

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These and other embodiments and aspects of the invention will be more fully explained and clarified by reference to the Figures and detailed description, below.

15 BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1A) The level of miRNA-128 increases as the heart progresses from neonatal to adult, sets forth custom qPCR array of miRNA expression in wild type (WT) mouse hearts at postnatal day 1 (P1) and P7; **Fig. 1B)** stereomicroscopic morphology of wild type mouse (WT) hearts at P1, P7, and P28; **Fig. 1C and Fig. 1D)** evaluation of cardiomyocyte (CM) cell-cycle activity using Ki67 (cell cycling marker) immunostaining; **Fig. 1E)** qPCR data of miRNA-128 expression of P1, P7 and P28 heart; **Fig. 1F)** Representative image of adult mouse (P28) ventricular cross-sections analyzed by in situ hybridization using digoxigenin-labeled miRNA-128 probe; **Fig.**

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1G) qPCR data of miRNA-128 expression in neonatal and adult CM. Statistical significance was calculated using ANOVA in D-E and Student's t-test in G. Data are means $\pm$ SEM (n=5). *P <0.05.

5 **Fig. 2A)** Overexpression of miRNA-128 impairs cardiac homeostasis, generation of CM-specific miRNA-128 overexpression mice; **Fig. 2B)** experimental design for CM-specific overexpression of miRNA-128 at P1(left), qPCR analysis of miRNA-128 expression in control miRNA-128^{TetRE} mice (Ctrl) and miRNA-128 overexpression ice (miR-128^{OE}); **Fig. 2C)** gross morphology of P1 hearts (upper),
 10 representative image of Masson Trichrome staining on hearts at P1(bottom); **Fig. 2D)** heart weight (HB) to body weight (BW) ratio in P1 mice (n=8); **Fig. 2E)** wheat germ agglutinin (WGA) staining of hearts (n=8); **Fig. 2F)** quantification of CM size as shown in WGA staining; **Fig. 2G)** heart function analyzed by echocardiography in P1 mice, as measured by left ventricular ejection fraction (EF%) (n=6); **Fig. 2I)**
 15 evaluation of CM cell-cycle activity by Ki67 immunostaining; **Fig. 2J)** quantification data of Ki67⁺CM number in P1 heart (n=6). Statistical significance was calculated using Student's t-test. Data are means $\pm$ SEM. *P<0.05.

Fig. 3A) overexpression of miRNA-128 induce dilated cardiomyopathy, gross
 20 morphology of adult (4 months old) hearts (left), Heart weight (HB) to body weight (BW) ratio (right), (n=5); **Fig. 3B)** gross morphology of lung (left), quantification data of lung weight (n=5); **Fig. 3C)** wheat germ agglutinin (WGA) staining of hearts (left), quantification of CM size as measured by WGA staining (right) (n=6); **Fig. 3D)**

heart function analyzed by echocardiography in adult mice, as measured by left ventricular diastolic diameter (LVDd), systolic diameter (LVDs), ejection fraction (EF%), and fraction shortening (FS%) (n=6). Statistical significance was calculated using Student's t-test. Data are means $\pm$ SEM. *P < 0.05.

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Fig. 4A) Cardiac miRNA-128 deletion promoted postnatal CM proliferation without cardiac dysfunction, a schematic diagram depicting the generation of cardiac-restricted miRNA-128 knockout (miRNA-128^{-/-}) mice; **Fig. 4B)** qPCR analysis of miRNA-128 expression in Ctrl (miRNA-128^{fl/fl}) and miRNA-128^{-/-} hearts (n=6); **Fig. 4C)** Masson Trichrome staining of mouse hearts at P7; **Fig. 4D)** heart weight (HW) to body weight (BS) ratio in Ctrl and miRNA-128^{-/-} mice (n=6); **Fig. 4E)** cardiac function analyzed by left ventricular ejection fraction (EF%) and fraction shortening (FS%) (n=6); **Fig. 4F)** cell size determined by wheat germ agglutinin (WGA) staining (n=6); **Fig. 4G)** Evaluation of CM cell-cycle activity and sarcomere structure in P7 hearts by immunofluorescence analysis of cTnT and Ki67; **Fig. 4H, Fig. 4I, and Fig. 4J)** quantification of Ki67+ CM, sarcomere disassembled CM and Ki67⁺ disassembled CM (n=6); **Fig. 4K)** a schematic diagram depicting EdU intraperitoneal (i.p) injection to label the proliferating CM; **Fig. 4L)** representative image of EdU+ CM in Ctrl hearts and MiRNA-128^{-/-} hearts at P14; **Fig. 4M)** schematic diagram depicting EdU i.p injection to label the proliferating CM; **Fig. 4N)** quantification of EdU+ CM on P21 hearts; **Fig. 4O and Fig. 4P)** cardiac miRNA-128 deletion promoted postnatal CM proliferation without cardiac dysfunction, heart function analyzed by echocardiography in adult mice, as measured by left ventricular diastolic diameter

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(LVDd), systolic diameter (LVDs), ejection fraction (EF%), and fraction shortening (FS%) (n=6). Statistical significance was calculated using Student's t-test. Data are means $\pm$ SEM. *P<0.05.

5 **Fig. 5A)** miRNA-128 deletion coordinates activation of cell cycle-related genes, shows the predictive conserved target site of miRNA-128 in 3'UTR of SUZ12 within different species; **Fig. 5B)** western blotting analysis of SUZ12 expression in mouse hearts at P1, P7, and P28; **Fig. 5C)** Quantification of SUZ12 expression in P1, P7, and P28 hearts (n=5); **Fig. 5D** and **Fig. 5E)** western blotting analysis of SUZ12
 10 expression in neonatal CMs treated with either vehicle (Ctrl), miRNA-128 mimic (miRNA-128) or miRNA-128 inhibitor (Anti-128) (n=3); **Fig. 5F)** Luciferase reporter assay for wild type and mutant Suz12 3' UTR in cells treated with either vehicle (Ctrl) or miRNA-128 inhibitor (Anti-128) (n=3); **Fig. 5G – Fig. 5H)** western blot assay for cell cycle-related protein expression in Ctrl and miRNA-128^{-/-} hearts at P7 (n=5); **Fig.**
 15 **5I)** ChIP-qPCR assay for SUZ12, EZH2, and H3K27me3 enrichment on the p27 promoter (n=5); **Fig. 5J)** evaluation of cell proliferation by immunofluorescence staining of Ki67 in miRNA-128^{-/-} neonatal CM transfected with either control siRNA (si-Ctrl) or SUZ12 siRNA (si-Suz12); **Fig. 5K)** Quantification of CM proliferation by Ki67 immunostaining (n=5); **Fig. 5L)** Proposed model of miRNA-128 deletion
 20 promoting CM proliferation through coordinating the expression cell cycle-related genes. Statistical significance was calculated using ANOVA in C, E, and K and Student's t-test in F, H, and I. Data are means $\pm$ SEM. *P<0.05.

Fig. 6A) miRNA-128 overexpression inhibits neonatal cardiac regeneration after injury; sets forth a schematic diagram depicting the generation of apex resection (AR) model in miRNA-128 overexpressing mice (miRNA-128^{OE}); **Fig. 6B)** Masson trichrome staining for Ctrl (miRNA-128^{TetRE}) and miR128^{OE} hearts at day 21 after AR; **Fig. 6C)** evaluation CM proliferation by EdU incorporation assay; **Fig. 6D)** Quantification of EDU+ CM in Pa hearts at day 21 post AR (n=6); **Fig. 6E)** wheat germ agglutinin (WGA) staining in mouse hearts at day 21 after AR; **Fig. 6F – Fig. 6G)** heart function analyzed by echocardiography and quantification by left ventricular diastolic diameter (LVDd), systolic diameter (LVDs), ejection fraction (EF%), and fraction shortening (FS%) (n=6). Statistical significance was calculated using Student's t-test in D, F, and G. Data are means $\pm$ SEM. *P<0.05.

Fig. 7A) miRNA-128 deletion promoted adult CM dedifferentiation and proliferation, sets forth a schematic diagram depicting TAM-inducible miRNA-128 deletion (iKO) in adult hearts (P56); **Fig. 7B)** evaluation of CM proliferation by EdU incorporation assay (n=6); **Fig. 7C)** wheat germ agglutinin (WGA) staining in Ctrl and iKO hearts (n=6); **Fig. 7D)** quantification data of heart weight to body weight ratio (HW/BW) (n=6); **Fig. 7E)** quantification data of cell size determined by WGA staining (n=6); **Fig. 7F)** representative images of isolated adult CMs in Ctrl and iKO hearts; **Fig. 7G)** quantification of CM number in Ctrl and iKO mouse (n=6); **Fig. 7H)** schematic of TAM-inducible dual-lineage tracing transgenic mouse model (α -MHC^{MerCreMer}:MiRNA-128^{fl/fl}:Rosa-tdTomato, designated as iKO-tdTomato); **Fig. 7I)** qPCR data of miRNA-128 expression in hearts (n=5); **Fig. 7J)** in vivo sarcomere

structure analysis by CtnT immunofluorescence staining (n=6); **Fig. 7K**) qPCR analysis of gene expression in adult hearts, including sarcomere gene, fetal gene, and cell proliferation associated gene (n=6). Statistical significance was calculated using Student's t-test in B, D, E, G, I, and K. Data area means $\pm$ SEM. *P<0.05. NS = not significant.

Fig. 8A) miRNA-128 deletion promoted adult cardiac regeneration after MI, the experimental design for adult cardiac regeneration analysis following MI in TAM-inducible miRNA-128 knockout (iKO) mice; **Fig. 8B)** Masson's Trichrome-stained hearts at 28 days after MI, serial sections were cut at 500 μ m intervals; **Fig. 8C)** quantification of the fibrotic areas in heart section (n=8); **Fig. 8D** and **Fig. 8E)** heart function analyzed by echocardiography and quantified by left ventricular diastolic diameter (LVDd), LV systolic diameter (LVDs), ejection fraction (EF%), and fraction shortening (FS%). Statistical significance was calculating using Student's t-test in C and E. Data area means $\pm$ SEM. *P<0.05. NS = not significant.

Fig. 9) sets forth a schematic diagram showing that miRNA-128 inhibition activates endogenous cardiac regeneration by promoting cardiomyocyte proliferation in an infarcted heart.

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DETAILED DESCRIPTION

Embodiments of the invention provide a novel therapeutic target for treatments

that activate endogenous cardiac proliferation and cardiac function recovery after heart damage.

The presently disclosed subject matter may be embodied in many different
5 forms and should not be construed as limited to the embodiments set forth herein;
rather, these embodiments are provided so that this disclosure will satisfy applicable
legal requirements. Indeed, many modifications and other embodiments of the
presently disclosed subject matter set forth herein will come to mind to one skilled in
the art to which the presently disclosed subject matter pertains having the benefit of
10 the teachings presented in the foregoing descriptions and the associated Figures.
Therefore, it is to be understood that the presently disclosed subject matter is not to be
limited to the specific embodiments disclosed and that modifications and other
embodiments are intended to be included within the scope of the appended claims.

15 Involvement of microRNAs (miRNA or miR) has been invoked as one
mechanism underlying regulation of cell proliferation. miRNAs are an abundant class
of small (approximately 22 nucleotides) endogenous non-coding RNAs that direct
post-transcriptional regulation of gene expression. Metazoan miRNAs regulate a wide
range of biological processes, including developmental timing, apoptosis,
20 differentiation, cell proliferation and metabolism. Evidence is accumulating that
dysregulation of individual or entire families of miRNA is associated with the
pathogenesis of human diseases, such as cancer, CNS disorders, viral infections,
cardiovascular and metabolic diseases. Identification and experimental validation of

miRNA targets is a key prerequisite for uncovering the widespread biological roles of miRNAs and miRNA-mediated gene regulatory networks.

The present investigators surprisingly discovered that inhibition of miRNA-128 in vivo promotes cardiac regeneration by activating CM proliferation, and, as illustrated by the Examples set forth below, have empirically demonstrated: 1) miRNA-128 expression is upregulated after birth and this upregulation is associated with the cell cycle exit of CMs during postnatal development; 2) overexpression of miRNA-128 expression leads to premature cell cycle arrest and cardiac hypertrophy; 3) miRNA-128 regulates some cell cycle genes in vivo, including p27; 4) overexpression of miRNA-128 inhibits CM proliferation and neonatal heart regeneration; and 5) inhibition of miRNA-128 prolongs the postnatal CM proliferation window and activates endogenous cardiac regeneration capacity in adult heart.

It was previously known that as a neuronal-enriched miRNA, miRNA-128 is associated with central nervous system development and is downregulated in gliomas. Downregulation of miRNA-128 accelerates glioma-initiating neural stem cell proliferation and contributes to the development of gliomas. According to the present investigations, miRNA-128 is revealed as a negative regulator of the CM cell cycle, in which deletion of miRNA-128 prolongs the postnatal CM proliferation window, as evidenced by pronounced sarcomere disassembly and expression of markers of cycling cells such as pH3, Ki67, and EdU incorporation. Normal growth in the developing heart requires a proper balance between cycling cells and cells that exit the cycle.

Disturbance in this balance can be associated with hypertrophy. Consistently, the transgenic mice with miRNA-128 overexpression displayed cardiac hypertrophy and cardiac dysfunction due to the premature cell cycle exit. Thus, activation miRNA-128 may participate in pathogenesis of congenital heart disease involving abnormalities of myocardial growth.

Cell cycle exit in CMs is accompanied by downregulation of positive cell cycle regulators and upregulation of CDKIs. Among the target genes regulated by miRNA-128, is Suz12, whose expression was significantly lower in adult hearts. This finding suggests that Suz12 plays a primary role in cardiomyocyte cell cycle regulation in the later stages of heart development and in neonatal cell cycle withdrawal. Results of the present studies demonstrate that knockdown of SUZ12 resulted in a reduction of CM proliferation, which is consistent with its reported function of catalyzing the trimethylation of H3K27 to mediate gene silencing and playing a fundamental role in mouse development. Accompanied with the upregulation of SUZ12, downregulation of negative cell cycle regulators (such as p27) and upregulation of downstream positive cell cycle regulators such as Cyclin E and CDK2 was observed in the miRNA-128 deficient heart.

P27, as a major member of CIP/KIP CDKI family, has been implicated in CM cell cycle arrest, and deletion of P27 promotes CM entry into S-phase. P27 can also negatively modulate the activity of Cyclin E dependent kinase, a requirement for entry of cells into S phase. In keeping with these observations, the present investigations

suggest that elimination of miRNA-128 activates cell cycle-related genes, in part through SUZ12-regulated histone modification, thereby promoting CM proliferation.

Since SUZ12 is chromatin associated protein that is broadly distributed, it is likely that it regulates other genes involved in CM proliferation. Thus, it would be informative to perform ChIP-Seq and RNA-Seq to systemically identify SUZ12 target genes to better understand how SUZ12 modulates the activity of EZH2, the enrichment of H3K27me3 and transcriptional output.

Using a gain-of-function genetic approach in neonatal cardiac injury model, the investigators found that miRNA-128 overexpression inhibited CM proliferation and neonatal heart regeneration. These findings highlight the involvement of miRNA-128 in the molecular pathway that arrests CM proliferation and cardiac regeneration after birth.

15

To assess the potential therapeutic benefit of miRNA-128 inhibition in the heart after cardiac damage, a cardiac-specific, tamoxifen-inducible miRNA-128 knockout mouse model was developed. The effect of miRNA-128 deletion on the cell cycle was evident in adult stages, when adult CMs become profoundly differentiated and quiescent and their ability to divide is quite limited. Using genetic lineage tracing, the results provide proof that preexisting CMs rather than progenitor cells are, in fact, the target cells that respond to miRNA-128 deletion during regeneration after cardiac damage. These adult CMs lacking miRNA-128 can be 'rejuvenated' to an immature

stage that allows them to dedifferentiate and enter a proliferative state, an endogenous program for natural heart regeneration occurred in the zebrafish and neonatal mice in response to injury.

5 Of particular note, the changes in cellular capabilities induced by loss of miRNA-128 results in increased cellular plasticity that allows significant anatomical and functional capacity upon injury, but does not impair heart function under normal conditions.

10 Embodiments of the invention provide methods for activating endogenous cardiomyocyte proliferation by targeting miRNA-128, and treatment methods of inducing myocardial regeneration. Other embodiments are directed to therapeutic agents and compositions effective for inducing CM proliferation and heart tissue regeneration.

15 One embodiment is directed to methods for treating a subject suffering from a cardiac disorder. Contemplated cardiac disorders include any disease or condition of the heart benefited by proliferation of cardiomyocytes and regeneration of heart tissue. Non-limiting examples include ischemic cardiomyopathy, including but not limited to
20 myocardial infarction; non-ischemic cardiomyopathy, including but not limited to hypertrophic cardiomyopathy, dilated cardiomyopathy and diabetic cardiomyopathy; valvular heart disease; heart failure; myocardial stunning, intermittent claudication; tachycardia; stroke; hypotension; embolism; thromboembolism (blood clot); sickle cell

disease; and combinations thereof. The methods comprise delivering a therapeutically effective amount of a miRNA-128 inhibitor to a myocardial region of the subject.

5

Embodiments of the invention provide inhibitors of human miRNA-128 (miRNA-128 Homo sapiens UCACAGUGAACCGGUCUCUUU (SEQ ID NO: 1)) and the identical murine miRNA-128 (Mus musculus UCACAGUGAACCGGUCUCUUU). The present oligonucleotide inhibitor sequesters and/or binds to the miRNA-128 sequence and blocks its activity. In specific embodiments the anti-miRNA oligonucleotide comprises at least 4, at least 5, at least 6, at least 7 or at least 8 nucleotides of the sequence AGUGUCACUUGGCCAGAGAAA (SEQ ID NO: 2).

Additional miRNA-128 inhibitor embodiments include, but are not limited to:

15 **1).** miRNA sponges. DNA vectors that express “microRNA sponges” that are competitive inhibitors of miRNAs have been disclosed. Adenovirus-associated vectors (AAV)-based constructs are currently being used in several clinical trials for gene therapy, and the safety profiles are encouraging (see, e.g. Aalbers et al. “Advancements in adeno-associated viral gene therapy approaches: exploring a new horizon” (2011) F1000 Med Rep 3: 17, and Ebert, M. S. et al. (2007) Nat Methods, 4, 721-726, the entire disclosures of which are incorporated herein by this reference). AAV as gene therapy

20 vector can infect both dividing and quiescent cells with persistent expression. An additional attractive feature of AAV is not integrating into the genome of the host cell. Therefore, transcripts expressed from plasmids possessing multiple tandem binding sites

for targeted miRNA-128 can be constructed into AAV;

2). Chemically modified miRNA-targeting antisense oligonucleotides. A nucleic acid sequence complementary to miRNA-128 can be conjugated to fatty acids, lipids, 5 saccharides, peptides, proteins, locked nucleotide analogues (LNAs), morpholino oligomers or other bioactive molecules to enhance the bio-stability. Chemically modified single-stranded oligonucleotides such as 2'-O-methyl (2'-OMe) RNA (Hutvagner, G et al. (2004) PLoS Biol, 2, E98; Meister, G et al. (2004) Rna, 10, 544-550, incorporated herein by reference), locked nucleic acid (LNA), and "antagomirs" (Orom, 10 U. A. et al. (2006) Gene, 372, 137-141; Knutzfeldt, J. et al. (2005) Nature, 438, 685-689, incorporated herein by reference) are known. These reagents are chemically synthesized to have complementarity towards mature miRNAs and are designed to be introduced into cells by transfection. They are resistant to cellular nucleases, and may function as substrates not cleaved by RISC.

15

3). Small-molecule inhibitors. Small molecule inhibitors have been designed to target at least the three steps of the miRNA transcription, assembly, and function. Additionally, these miRNA-128 inhibitors can be encapsulated into a lipid-based formulation or nanoparticles that enhance tissue-specific delivery.

20

Recent interest in the therapeutic potential for various microRNA species has spurred substantial development in the synthesis/discovery of expression modulators, including inhibitors. Although generation of antimiRNAs for specific miRNA inhibition

is routine, optimization of the oligonucleotides for increased binding affinity, improved nuclease resistance and *in vivo* delivery is required. According to specific embodiments, the miRNA-128 inhibitor comprises an oligonucleotide comprising an antisense nucleic acid against miRNA-128, wherein the oligonucleotide may be chemically modified or
5 unmodified. Anti-miRNA oligonucleotides (AMOs) appear to work primarily through a steric blocking mechanism of action. According to very specific embodiments the inhibitor compound is a synthetic reverse complement that tightly binds and inactivates miRNA-128. A variety of chemical modifications can be used to improve the performance and potency of AMOs. In general, modifications that confer nuclease
10 stability and increase binding affinity improve AMO performance. Chemical modifications and/or certain structural features of the AMO may also facilitate invasion into the miRNA-induced silencing complex. In particular, it is essential that the AMO binds with high affinity to the miRNA 'seed region', which spans bases 2-8 from the 5'-end of the miRNA.

15

One embodiment provides an isolated nucleic acid molecule comprising (a) a nucleotide sequence as shown in SEQ ID NO: 1, or a precursor of SEQ ID NO: 1 and/or (b) a nucleotide sequence which is the complement of (a), and/or (c) a nucleotide sequence which has an identity of at least 80% to a sequence of (a) or (b), and/or (d) a
20 nucleotide sequence which hybridizes under stringent conditions to a sequence of (a), (b) and/or (c) wherein said isolated nucleic acid molecule comprises at least one modified building block, wherein the modified building block is selected from the group consisting of nucleobase-modified building blocks, sugar-modified building blocks,

backbone-modified building blocks and combinations thereof. Such methods are set forth in detail in Stenvang et al. "Inhibition of microRNA function by anti-miR oligonucleotides" *Silence* 2012; 3: 1, the entire disclosure of which is incorporated herein in its entirety by this reference.

5

Modified nucleotide building blocks may be selected from nucleobase-, sugar- and backbone-modified building blocks and combinations thereof, i.e. building blocks having several modifications, e.g. a sugar and a backbone modification. Nucleobase-modified building blocks comprise a non-standard nucleobase instead of a standard nucleobase (e.g. adenine, guanine, cytosine, thymine or uracil) such as a uracil or cytosines modified at the 5-position, e.g. 5-methylcytosine, 5-(2-amino)propyluracil, 5-bromouracil, adenines or guanines modified at the 8-position, e.g. 8-bromoguanine, deazapurine nucleobases, e.g. 7-deaza-adenine and O— or N-alkylated nucleobases, e.g. N6 alkyl-adenine.

15

In some embodiments, the modified nucleotide building blocks encompass sugar-modified building blocks, particularly sugar-modified ribonucleotide building blocks, wherein the 2'OH group is replaced by a group selected from H, OR, R, halo, SH, SR, NH, NHR, NR₂ or CN, wherein R is C₁-C₆ alkyl, C₂-C₆ alkenyl or C₂-C₆ alkynyl and halo is F, Cl, Br or I. Further preferred sugar-modified nucleotides are selected from LNA or morpholino nucleotides. In certain aspects of the backbone-modified building blocks, the phosphoester group connecting to adjacent building blocks is replaced by a modified group, e.g. by replacing one or more O atoms of the phosphoester group by S, Se, NR or

20

CR₂, wherein R is as defined above. It should be noted that the above modifications may be combined.

The nucleic acid molecule may be conjugated to heterologous molecules, e.g.
5 non-nucleic acid molecules such as fatty acids, lipids, saccharides, peptides, proteins, antibodies, nanoparticles, peptide nucleic acids (PNAs), locked nucleotide analogues (LNAs).

In very specific embodiments, sequence (c) has a sufficient sequence
10 complementarity to miRNA-128 and/or a precursor thereof in order to mediate target-specific inhibition, e.g. by forming a double-stranded hybrid with the target. Preferably, the sequence has a complementarity of at least 50%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95% or up to 100% in the portion which corresponds to the target.

15

The isolated nucleic acid molecule may be single-stranded or double-stranded. In very specific embodiments, the isolated nucleic acid molecule is a miRNA molecule or an analog thereof having a length of from 18-25 nucleotides, or a miRNA precursor molecule having a length of 50-120 nucleotides or a DNA molecule coding
20 therefor. Even more specifically, the isolated nucleic acid molecule is an RNA molecule.

According to some embodiments, the isolated nucleic acid molecule is suitable

for the diagnosis, treatment or prevention of a disorder involving cardiomyocyte death, including but not limited to ischemic cardiomyopathy (including but not limited to myocardial infarction), non-ischemic cardiomyopathy (including but not limited to hypertrophic cardiomyopathy), dilated cardiomyopathy, diabetic cardiomyopathy, 5 valvular heart disease, heart failure, myocardial stunning, stroke, hypotension, embolism, thromboembolism (blood clot), and combinations thereof.

Embodiments directed to pharmaceutical compositions comprising an inhibitor of miRNA-128 are also contemplated. In specific embodiments the inhibitor is an isolated 10 nucleic acid molecule comprising at least one modified building block and has sufficient complementarity to miRNA-128 to form a hybrid under physiological conditions. The inhibitor may be a single-stranded or double-stranded nucleic acid molecule. In very specific embodiments the inhibitor is an RNA molecule comprising at least one modified building block selected from the group consisting of nucleobase-modified building 15 blocks, sugar-modified building blocks, backbone-modified building blocks and combinations thereof.

In one embodiment, the inhibitor may be an siRNA, that is, a double-stranded RNA molecule capable of RNA interference which is directed against a transcript 20 comprising miRNA-128 or precursors thereof. In specific embodiments the siRNA molecule is a double-stranded RNA molecule, wherein each strand has a length of 15-30, preferably 19-25 nucleotides, which optionally has at least one 3'-overhang having a length of 1-5 or 1-3 nucleotides. Typical siRNA molecules are for example described in

WO 02/044321, the content of which is incorporated herein by reference.

In another embodiment, the nucleic acid inhibitor is an antagomir, which is a single-stranded RNA molecule having a length of from 10 to 30 nucleotides, preferably
5 from 12 to 25 nucleotides and even more preferably from 15 to 22 nucleotides. The antagomir may be perfectly complementary to its specific miRNA target with mispairing at the cleavage side of Ago2 and/or the presence of at least one modified building block to inhibit Ago2 cleavage. Antagomirs are for example disclosed in Krützfeldt et al., 2005, Czech, 2006 or Fiedler et al., 2011, the contents of which are incorporated herein
10 by reference. Preferred antagomirs are cholesterol-conjugated, LNA-conjugated or FMOE-conjugated. In a very specific embodiment the antagomirs are directed against miRNA-128.

The nucleic acid inhibitors of the invention may be prepared by conventional
15 methods, e.g. by chemical synthesis methods usually involving solid-phase synthesis according to standard protocols. The inhibitors can also be prepared by enzymatic transcription from synthetic DNA templates or from DNA plasmids, e.g. isolated from recombinant bacteria. Typically, phage RNA polymerases are used, such as T7, T3 or SP6 RNA polymerase. Several commercial sources exist for specific miRNA inhibitors.
20 Although human data is scarce, several companies have developed, for example, anti-miRNA-122-based therapeutics for the treatment of HCV infections (See, e.g. Hildebrandt-Eriksen et al. "A unique therapy for HCV inhibits microRNA-122 in humans and results in HCV RNA suppression in chronically infected chimpanzees

results from primate and first-in-human studies” *Hepatology*. 2009; 50:LB19, and Landford RE et al. “Therapeutic silencing of microRNA-122 in primates with chronic hepatitis C virus infection” *Science* 2010; 327:198–201, and Janssen et al. “Treatment of HCV infection by targeting microRNA” *N Engl J Med*. 2013; 368:1685–1694, the entire
5 disclosures of which are incorporated herein by this reference.). Data from the reported trials has shown that short-term use of inhibitor of miRNA-122 in patients with chronic HCV genotype 1 infection is safe and well tolerated and provides long-lasting antiviral activity without evidence of viral resistance. The results of these studies demonstrate that pharmacological modulation of miRNA activity is a feasible therapeutic strategy in
10 human patients.

Thus, dozens of miRNA species inhibitors have recently been developed and optimized and any particularly desired inhibitor species are readily synthesized as either vector-based expression clones or as synthetic oligonucleotides. Vector-based
15 expression clones are typically available in lentiviral and non-viral vectors. MiRNA inhibitor clones bind specifically to their target miRNA’s allowing transient as well as stable suppression of the target gene. Selection of promoter allows constitutive expression of inhibitors in all types of mammalian cells. MiRNA-128 inhibitors are commercially available; for example, from Genecopoeia
20 (<http://www.genecopoeia.com/product/mirna-inhibitor>) and Sigma Aldrich (see <http://www.sigmaaldrich.com/life-science/functional-genomics-and-rnai/mirna/mirna-inhibitors-introduction.html>).

According to some embodiments, miRNA-128 inhibitor may be administered as a pharmaceutical composition comprising a pharmacologically acceptable carrier and diluent. Delivery of anti-miRNA-128 oligonucleotide is via transfection or assisted uptake. In some embodiments the oligonucleotide is unconjugated or 3'-cholesterol modified. Administration methods potentially include injection, including intravenous and intraperitoneal injection, viral transfer, application of liposomes, and systemic/oral intake. The following references provide guidance on effective delivery/administration of anti-miRNA oligonucleotides and the disclosures of all are incorporated herein by reference, Broderick JA et al. "MicroRNA therapeutics" *Gene Ther.* 2011;18:1104–1110; Rooij E., et al. "The art of microRNA research" *Circ Res.* 2011;108:219–234; and Stenvang J. et al. "MicroRNAs as targets for antisense-based therapeutics" *Expert Opin Biol Ther.* 2008;8:59–81.

In one aspect, the step of delivering comprises administering a plasmid/vector comprising a genetic construct of the miRNA-128 inhibitor to the subject. According to other aspects, the step of delivering comprises systemic administration of a vehicle comprising the inhibitor, said vehicle designed for targeted delivery to a myocardial region of the subject. Targeted delivery, for example, may be achieved by designing a liposome or micro/nanoparticle to specifically target heart tissue and release contents comprising miRNA inhibitor into a myocardial region of the subject.

20

Validation of myocardial viability and wall-motion assessment by noninvasive tests (e.g NOGA mapping system, single photon emission computed tomography (SPECT), PET, echocardiography, MRI and cardiac nuclear medicine imaging) may be

necessary to assist target delivery of miRNA-128 inhibiting gene constructs or drugs in the myocardium. With delineation of the myocardial viability by noninvasive methods (e.g NOGA mapping system) catheter-based direct intramyocardial injection of cells or gene constructs reduces the likelihood of systemic toxicity of the injected substance,
5 resulting in minimal washout, limited exposure of nontarget organs, and precise localization to ischemic and peri-ischemic myocardial regions in patients with chronic myocardial ischemia.

Systemic administration includes intravenous or oral. Delivery may also be
10 intraperitoneal, such as directly into a myocardial region of the subject. According to specific embodiments, the step of delivering comprises directly administering a plasmid or viral vector engineered to transfect cardiomyocyte cells located in the myocardial region of the subject with the inhibitor. In more specific embodiments, directly administering comprises injecting or pressure injecting a composition comprising
15 microRNA inhibitor directly into a myocardial region of a subject. In very specific embodiments directly injecting is via catheter-based direct intramyocardial injection to an ischemic or peri-ischemic myocardial region of the subject.

In some embodiments, validation of myocardial viability and wall-motion
20 assessment by noninvasive tests (e.g NOGA mapping system, single photon emission computed tomography (SPECT), PET, echocardiography, MRI and cardiac nuclear medicine imaging) is employed to assist targeted delivery of gene constructs or drugs in the myocardium. With delineation of the myocardial viability by noninvasive methods

(NOGA mapping system; see, e.g. Gyöngyösi M. et al. "Diagnostic and prognostic value of 3D NOGA mapping in ischemic heart disease" *Nat Rev Cardiol.* 2011; 17; 8(7):393-404 and Kastrup J. et al. "Direct intramyocardial plasmid vascular endothelial growth factor-A165 gene therapy in patients with stable severe angina pectoris: A randomized double-blind placebo-controlled study: the Euroinject One trial" *J Am Coll Cardiol.* 2005 5; 45(7):982-8, the entire disclosures of which are incorporated herein by this reference), catheter-based direct intramyocardial injection of cells or gene constructs reduces the likelihood of systemic toxicity of the injected substance, resulting in minimal washout, limited exposure of nontarget organs, and precise localization to ischemic and peri-
10 ischemic myocardial regions in patients with chronic myocardial ischemia.

It is widely reported that decreasing expression of miRNA-128 may be associated with increasing susceptibility to certain cancers, to proliferation of tumor cells in extant tumors, and to decreased responsiveness to cancer therapeutics. In particular, inhibition
15 of miRNA-128 is associated with certain proliferative disorders of the brain. Therefore it is desirable that the therapeutic effects of treatment with miRNA inhibitor be localized and transient. In very specific embodiments the desired therapeutic inhibition of microRNA expression in cardiomyocytes lasts for a duration sufficient to regenerate cardiac tissue to normal functioning and to avoid deleterious effects.

20

The following Examples are provided to evidence, illustrate and clarify certain embodiments and aspects of the invention and should not be construed as limiting the scope of the invention as defined by the appended claims.

EXAMPLES

The following examples collectively demonstrate that the level of cardiac
5 miRNA-128 is lower in neonates than in adults, and is further reduced during neonatal
heart regeneration. Furthermore, cardiac-specific overexpression of miRNA-128 in
early postnatal mice suppressed CM proliferation and caused impaired cardiac
function. Conversely, knockout of miRNA-128 reactivated CM proliferation and
cardiac regeneration in adult mouse, in part through modulation of cell cycle genes by
10 targeting *Suz12* in the heart.

Example 1.

15 **This example demonstrates that the level of miRNA-128 increases as the
heart progresses from neonate to adult.**

Small RNA sequencing in mouse cardiac ventricles was performed on postnatal
days 1, 7, and 28 (P1, P7, and P28) to identify potential miRNAs involved in the
20 regulation of postnatal heart. One of the most robustly upregulated miRNAs during
this period was miRNA-128 (**Fig. 1A**). As previously reported, miRNA-128 is
predominantly expressed in brain tissue; but is also expressed in the heart (**Fig. 1B**).
Its expression in adult myocardium was further confirmed by *in situ* hybridization
(ISH) (**Fig. 1C**). To investigate the role of miRNA-128 in cell cycle withdrawal
25 during heart development, mouse hearts were harvested and sectioned at P1, P7, and
P28 as shown in **Fig. 1A**. As neonates progress to adulthood (from P1 to P28), CMs

underwent a maturation process characterized by suppression of cell proliferation as evidenced by decreased numbers of Ki67⁺ CMs (**Fig. 1C** and **D**). To adapt to the increase in size of an organism, cardiac mass increases (**Fig. 1B**) primarily by an increase in CM size rather than in number (**Fig. 1E** and **Fig. 1F**). The level of

5 miRNA-128 was found to be significantly elevated in P7 and P28 hearts compared with P1 hearts (**Fig. 1G**). In order to examine whether the postnatal upregulation of *miRNA-128* occurs specifically in the CMs, CMs in neonatal (P1) and adult (P28) hearts were isolated and significantly higher levels of miRNA-128 were found in P28 CMs when compared to P1 CMs (**Fig. 1H**). Moreover, miRNA-128 in CMs was

10 significantly higher than that of non-CMs (i.e. cardiac fibroblasts, CF) (**Fig. 1I**). These data indicate a potential critical role played by miRNA-128 in regulating CM proliferation.

Example 2

15

This example demonstrates that overexpression of miRNA-128 impairs cardiac homeostasis.

To elucidate the specific function of miRNA-128 in the heart, a mouse model

20 was developed in which miRNA-128 expression is under control of α -myosin heavy chain (α -MHC) promoter that is under temporal regulation by doxycycline (Dox). This “Tet-off” transgenic mouse (α -MHC-tTA; miRNA-128^{TetRE}) was produced by crossing α -MHC-tTA mice with miRNA-128^{TetRE} mice (**Fig. 2A**). In α -MHC-tTA; miRNA-128^{TetRE} mice, the TetRE portion of tTA binds to the TetO sequences after

Dox withdrawal, and subsequently induces the CM-specific overexpression of *miRNA-128* (designated as *miRNA-128^{OE}* mice) in defined temporal windows (**Fig. 2A and Fig. 2B**). In general, induced transgene expression begins during the second week of Dox withdrawal due to the slow clearance of Dox from tissues. Withdrawal of Dox from *miRNA-128^{OE}* fetuses starting at embryonic day 6 (E6) resulted in significant induction of *miRNA-128* in *miRNA-128^{OE}* hearts at the P1 neonatal stage as determined by qPCR (**Fig. 2B**). At P1, the explanted hearts from *miRNA-128^{OE}* mice were markedly enlarged (**Fig. 2C**) compared with hearts from *miRNA-128^{TetRE}* mice (Control mice, designated as Ctrl). The higher heart-to-body weight ratios (HW/BW) of *miRNA-128^{OE}* mice relative to Ctrl showed a progressive increase of heart mass (**Fig. 2D**). Morphologically, CM size was measured by staining with Wheat Germ Agglutinin (WGA) and showed that *miRNA-128^{OE}* CMs were significantly larger than Ctrl CMs (**Fig. 2E-F**), implying the development of cardiac hypertrophy. Then, cardiac functions in Ctrl and *miRNA-128^{OE}* mice were evaluated at P1 by echocardiography (**Fig. 2G**). Left ventricular (LV) ejection fraction (EF) and fraction shortening (FS), the parameters of cardiac contractile function, were reduced in *miRNA-128^{OE}* hearts (**Fig. 2H**). In contrast, Dox treatment did not induce cardiac dysfunction in Ctrl mice (data now shown).

To explore the cellular mechanisms underlying the observed hypertrophy, heart sections were immunostained to assess proliferation and apoptosis. The *miRNA-128^{OE}* hearts displayed diminished proliferation of CMs based on the reduced number of

Ki67⁺ CMs compared with Ctrl (**Fig. 2I** and **Fig. 2J**). However, there was no significant increase in apoptotic CMs in miRNA-128^{OE} hearts when assessed by TUNEL staining (**Fig. 2C**). Interestingly, miRNA-128^{OE} mice displayed pathologically dilated cardiomyopathy that was consistent with focal replacement fibrosis, CM hypertrophy, and severe heart failure compared with Ctrl mice at the same adult stage (data not published). Taken together, these data indicate that CM-specific overexpression of miRNA-128 induces early CM cell cycle exit and compensatory pathological growth of CM (hypertrophy), and impaired cardiac homeostasis.

Example3.

This example illustrates that deletion of miRNA-128 stimulates postnatal CM proliferation.

Having established a correlation between miRNA-128 overexpression and inhibition of CM proliferation, the question of whether loss of miRNA-128 is causal for CM proliferation arises. When miRNA-128 was knocked down in cultured neonatal rat CMs *in vitro* using specific miRNA-128 inhibitor (designated as Anti-miRNA-128) (**Fig. 3A**), the CMs became dedifferentiated, based on sarcomere disassembly assessed by immunostaining for Cardiac troponin T (cTnT), the sarcomere structure marker (**Fig. 3B-Fig. 3D**). Consistent with sarcomere disassembly, qPCR showed that expression of sarcomere genes (*Myh6* and *cTnT*) was reduced (data not shown). In addition to inducing dedifferentiation, silencing of *miRNA-128* increased the number of mitotic CMs as determined by immunostaining for

phosphorylated histone3 (pH3⁺) as compared with control CMs (Ctrl) (**Fig. 3E and Fig. 3G**). Silencing of miRNA-128, however, did not induce apoptosis in these cells (**Fig. 3F and Fig. 3G**).

5 Given the evidence that silencing of miRNA-128 induces CM proliferation *in vitro*, the next step is to determine what effects the deletion of miRNA-128 would have on CM proliferation *in vivo*. Cardiac-specific conditional miRNA-128 knockout mouse were generated by crossing miRNA-128^{flox/flox} (miRNA-128^{fl/fl}) mice (**Fig. 4A**) with *Nkx2.5*^{Cre} mice, resulting in deletion of miRNA-128 during cardiogenesis

10 (*Nkx2.5*^{Cre}; miRNA-128^{fl/fl} mice, designated as miRNA-128^{-/-}) (**Fig. 4B**). Hearts from miRNA-128^{fl/fl} (Control mice, Ctrl) and miRNA-128^{-/-} mice were harvested and analyzed at P7, at the time when most CMs have exited the cell cycle and become post mitotic. Downregulation of miRNA-128 in hearts from miRNA-128^{-/-} mice was confirmed by qPCR (**Fig. 3A-Fig. 3B**). Phenotypic characterization of *miRNA-128*^{-/-}

15 mice at P7 demonstrated that heart size (**Fig. 3C**) and heart function by echocardiography (**Fig. 3E**) were unaffected by miRNA-128 deletion. Although the heart weight-to-body weight ratio (HB/WB) of miRNA-128^{-/-} and Ctrl mice at P7 was similar (**Fig. 3D**), CMs in miRNA-128^{-/-} hearts were smaller (**Fig. 3F**). This could indicate an increased number of CMs in these hearts due to persistent

20 proliferation resulting from miRNA-128 deletion. To test this proposition, CMs were stained with Ki67 to assess the number of cycling cells. The results show that loss of miRNA-128 results in a striking increase in CM proliferation (**Fig. 3G-Fig. 3H**).

Sarcomere disassembly, a characteristic of CM dedifferentiation and proliferation, was also prominent in miRNA-128^{-/-} hearts compared with Ctrl group (**Fig. 3G** and **Fig. 3I**). In addition to the CMs with disassembled sarcomeres, a significantly higher number of Ki67-positive cells were identified in miRNA-128^{-/-} hearts (**Fig. 3J**). No obvious CM apoptosis was observed in miRNA-128^{-/-} hearts (data not shown). By 5-ethynyl-2'-deoxyuridine (EdU) incorporation assay (**Fig. 3K-Fig. 3N**), we also found a significant increase in the number of EdU⁺ CMs in miRNA-128^{-/-} hearts at P14 (**Fig. 3K-Fig. 3L**) as well as P21 (**Fig. 3M-Fig. 3N**) when compared with Ctrl. These mice developed normally to adulthood without compromised cardiac dysfunctions (**Fig. 5 A-B**). These data suggested that miRNA-128 deletion is sufficient to extend the postnatal CM proliferation window.

Example 4.

This example demonstrates that cardiac miRNA-128 deletion reconfigures cell cycle-related gene expression in the postnatal heart.

To identify miRNA-128 target genes that may be responsible for CM proliferation, online databases TargetScan and miRanda and others were mined with selective focus on genes that were downregulated in adult hearts relative to neonatal hearts. The data predicted that *Suz12*, the core component of polycomb repressive complex 2 (PRC2), is a putative miRNA-128 target (**Fig. 4A**). When assayed by Western blotting, the levels of SUZ12 were lower in the adult heart than in the neonatal heart (**Fig. 4B-C**), consistent with this prediction. To investigate whether

miRNA-128 regulates *Suz12* expression, mouse neonatal CM were transfected with a negative control (Ctrl), a mimic of miRNA-128 (*miRNA-128*), or an inhibitor of miRNA-128 (Anti- miRNA-128) and assessed for the level of SUZ12 by Western blotting. Overexpression of miRNA-128 significantly reduced the protein level of SUZ12, whereas inhibition of miRNA-128 led to its increased expression (**Fig. 4D-E**). To further test whether miRNA-128 regulates *Suz12* expression, a vector containing a luciferase reporter vector with a DNA sequence encoding the complete 3' untranslated region (3'UTR) from mouse *Suz12* (designated as WT), and a mutated vector (designated as Mut) containing mismatches in the predicted miRNA-128 binding site in the 3'UTR (**Fig. 4F**) were constructed. Co-transfection of HEK293T cells with the *Suz12* 3'UTR plasmid (WT) and *miRNA-128* mimic resulted in a significant decrease in luciferase activity compared with cells co-transfected with negative control or the mutated 3'UTR target sequence (Mut), indicating that *Suz12* is a direct target of miRNA-128.

To better delineate how the miRNA-128 -*Suz12* interaction might mediate cell proliferation *in vivo*, the expression of cell-cycle related genes in miRNA-128^{-/-} hearts at P7 was analyzed. As predicted, the level of SUZ12 was elevated in miRNA-128^{-/-} P7 hearts compared with control mice (Ctrl) while CDKi p27 target was downregulated (**Fig. 4G-H**). SUZ12 can catalyze the trimethylation of histone H3K27 to H3K27me3, a transcriptional repressive mark. Since SUZ12 appears to be regulated by miRNA-128, it was hypothesized that in miRNA-128 - deficient hearts SUZ12 should be associated with H3K27me3 and directly repress the transcription of genes encoding cell cycle inhibitors. When assayed by chromatin immunoprecipitation

(ChIP)-qPCR, SUZ12 and H3K27me3 were significantly enriched on the *p27* promoter in miRNA-128^{-/-} hearts compared with hearts from Ctrl mice (**Fig. 4I**).

Since miRNA-128 seems to exerts its inhibitory effects by recruiting SUZ12 to the promoters of the gene encoding cell cycle effectors and repressing their expression, the question of whether targeting of *Suz12* by *miRNA-128* is sufficient to account for the enhanced proliferation observed in miRNA-128^{-/-} CMs was examined. Direct inhibition of *Suz12* by siRNA (si-*Suz12*) in *miRNA-128*^{-/-} neonatal mouse hearts reversed the pro-proliferative effect imparted by miRNA-128 deletion (miRNA-128^{-/-}), as evidenced by a significant decrease in the number of Ki67⁺ CMs in si-*Suz12* group in contrast to control group (si-Ctrl) (**Fig. 4J-K**). Collectively, these data indicated that miRNA-128 deletion stimulates proliferation of CMs, in part through epigenetic modulation of cell-cycle related genes via targeting of *Suz12* (**Fig. 4L**).

Example 5.

This example illustrates that overexpression of *miRNA-128* inhibits neonatal cardiac regeneration after injury.

To enable assessment of temporal gene expression during cardiac regeneration an apex resection (AR) model in neonatal mice at P1 was developed (**Fig. 6A**). Histological analysis verified that by day 7 post-AR, the initial large blood clot in the apex had been replaced by newly formed CMs and limited fibrotic tissue (**Fig. 6B**). Also at day 7 post-AR, genes associated with cell proliferation were significantly activated, whereas miRNA-128 expression was significantly diminished (**Fig. 6C-D**). These data imply that downregulation of miRNA-128 was associated with neonatal

heart regeneration.

To test whether miRNA-128 regulates cardiac regenerative capacity in neonatal mice, the miRNA-128^{OE} mouse model in which miRNA-128 is overexpressed in a CM specific and temporally controlled (by Dox withdrawal) manner was utilized (**Fig. 5A**). The miRNA-128^{OE} mice and control miRNA-128^{TetRE} mice (Ctrl) were subjected to AR at P1, and hearts from both groups were examined histologically. At 21 days post-AR, the miRNA-128^{OE} hearts showed left ventricle dilation and defective regeneration compared with Ctrl groups (**Fig. 5B**). The miRNA-128^{OE} hearts showed fewer proliferating CMs, as quantified by the decreased number of EdU⁺ CM nuclei in the injured apex and border area (**Fig. 5C** and **Fig. 5D**), and a greater extent of CM hypertrophy (**Fig. 5E**). In addition, systolic function was significantly impaired in the miRNA-128^{OE} group relative to Ctrl group (**Fig. 5F** and **Fig. 5G**). These findings suggest that inhibition of CM proliferation by miRNA-128 overexpression is sufficient to impair cardiac regeneration in a neonatal mouse model.

15

Example 6.

This example demonstrates that deletion of miRNA-128 increases CM proliferation and promotes adult cardiac regeneration

20

To investigate whether loss of miRNA-128 in the adult is capable of promoting CM proliferation, a cardiac specific, tamoxifen (TAM) inducible miRNA-128 knockout mice was then generated by crossing α -MHC^{MerCreMer} mice with *miRNA-128*^{fl/fl} mice (**Fig. 6A**). TAM was administered at P21 to induce *miRNA-128* knockout at adult stage. The adult *miRNA-128*-deleted mice were designated iKO, and the

knockout was validated by qPCR. Phenotypic characterization showed that neither heart size nor function was affected in the iKO mice by *miRNA-128* deletion (data not shown). The heart weight-to-body ratio (HB/WB) was unchanged in iKO mice.

Staining with WAG, however, showed that the size of the iKO CMs was smaller than

5 the control CMs (**Fig. 6C-E**), suggesting that loss of *miRNA-128* in the adult heart increase the number of CMs. This increase in CM number following *miRNA-128* deletion was further confirmed by analysis of EdU incorporation into CMs (**Fig. 6B**). Furthermore, the total number of adult CMs and percentage of mono-nucleated CMs was significantly increased in iKO hearts 2 weeks after TAM induced *miRNA-128* deletion (**Fig. 6F-G**).

To determine whether cells in the myocardial lineage dedifferentiate following deletion of *miRNA-128*, a TAM inducible dual-lineage tracing system was generated by crossing α -MHC^{MerCreMer} mice with *miRNA-128*^{fl/fl} mice followed by crossing with Rosa26-tdTomato reporter mice to produce α -MHC^{MerCreMer}; *miRNA-128*^{fl/+}; R26R-tdTomato mice (designated as iKO-tdTomato) (**Fig. 6H**). In these transgenic mice, *miRNA-128*-deficient CMs were labeled red (tdTomato, red fluorescence) following TAM administration. After TAM- induced *miRNA-128* deletion (**Fig. 6J**), the α -MHC myocardial lineage positive CMs in iKO- tdTomato mouse displayed a disorganized sarcomere structure and reduced sarcomere- related gene expression compared with control mice (α -MHC^{MerCreMer}; R26R-tdTomato, designated as Ctrl-tdTomato) (**Fig. 6J** and **Fig. 6K**). No apoptosis was observed in hearts from iKO-tdTomato mice (**Fig. 7A-B**). There was, however, increased expression of genes associated with cell proliferation (*Nuspa1*, *RacGap1* and *Myh10*) and fetal genes

associated with negative regulation of CM differentiation (*Nppa* and *Nppb*) in iKO-tdTomato hearts detected by qPCR (**Fig. 6K**). However, in iKO mice, cardiac morphology remained unchanged and heart functions were normal (**Fig. 7C-D**). These results indicate that deletion of miRNA-128 in the adult heart results in dedifferentiation of CMs and reentry of CMs into the cell cycle.

To determine whether induction of cardiac proliferation following miRNA-128 deletion in adult mice is sufficient to allow adult heart repair following MI, we subjected adult iKO mice to permanent ligation of the left anterior descending coronary artery (LAD). One day after MI, TAM was administered to delete miRNA-128 in CMs (**Fig. 7A**). Seven days after the MI, a decrease in CM death (**Fig. 8B**) and increased proliferation in iKO hearts was detected (**Fig. 8C-D**). In the iKO hearts, analysis of sarcomere structures revealed robust dedifferentiated cardiac muscle in border areas and remote areas, and analysis of EdU incorporation was indicative of increased DNA synthesis (**Fig. 8C**). In addition to dedifferentiation and enhanced proliferation (**Fig. 8D**) iKO hearts showed significantly less fibrosis than Ctrl groups 4 weeks after MI (**Fig. 7B-C**). Similarly, diminished cardiac function was significantly reversed in iKO mice, as evidenced by increased ejection fraction (EF) and fractional shortening (FS) after MI when compared with the Ctrl animals (**Fig. 7D-E**). Cardiac remodeling was also significantly reversed in iKO mice with reduced LVDd and LVDs (**Fig. 7D**). Collectively, these data indicate that inhibition of miRNA-128 promotes CM proliferation and improved endogenous cardiac regeneration after MI (**Fig. 7F**).

5 The following protocols apply to one or more of the examples disclosed herein.

Laboratory animals

All research protocols conformed to the Guidelines for the Care and Use of
10 Laboratory Animals published by the National Institutes of Health (National Academies
Press, eighth edition, 2011). All animal use protocols and methods of euthanasia
(pentobarbital overdose followed by thoracotomy) used in this study were preapproved
by the University of Cincinnati Animal Care and Use Committee. An independent
review and approval of cell and chemical drug used in this study was conducted by the
15 Institutional Biosafety Committee (IBC).

Generation of mice with conditional overexpression of miRNA-128

A construct was engineered for knock-in of the miRNA-128 (miRNA-128-3p)
gene into Rosa26 locus. A ~1.1 kb and a ~4.3 kb Rosa26 genomic DNA fragments
20 (served as 5' and 3' homology arms, respectively) were amplified from C57BL/6 BAC
DNA and cloned into the pBasicLNeoL vector sequentially by in-fusion cloning and
confirmed by sequencing. The miRNA-128 gene, under the control of tetO-minimum
promoter, was also cloned into the vector in between the two homology arms. In
addition, the targeting construct also contains a loxP sites flanked Neomycin cassette
25 for positive selection and a DTA cassette for negative selection. The construct was
linearized with ClaI and electroporated into C57BL/6N ES cells. After G418 selection,
7 positive clones were identified from 121 G418 resistant clones by PCR screening. Six
positive clones were expanded and further analyzed by Southern blot analysis, among

which four clones were confirmed with correct targeting with single copy integration. Correctly targeted ES cell clones were injected into blastocysts, and the blastocysts were implanted into pseudopregnant mice to generate chimeras by Cyagen Biosciences Inc. Chimeric males were bred with Cre delete mice from Jackson Laboratories to
5 generate Neomycin-free knockin mice. The correct insertion of miRNA-128 cassette and the successful removal of Neomycin cassette were confirmed by the PCR assay with the following primers: 5'-TGAGCCAGACCTCCATCGC-3' and 5'-
AGCTCGGTACCATTAATCG-3' for the 559 bp fragment from targeted allele. A PCR with the following primers 5'- ACTCCAAGGCCACTTATCACC-3' and 5'-
10 ATTGTTACCAACTGGGACGACA-3' was used as an internal control, which amplifies a 413 bp fragment from wt allele.

Doxycycline-inducible cardiomyocyte-specific overexpression of miRNA-128 (miRNA-128-3p) mice were generated by crossing α -MHC-tTA (The Jackson
15 Laboratory) mice with miRNA-128^{TetRE} mice, in which tetracycline-responsive transcriptional activator (tTA) expression is under the control of α -MHC promoter. Doxycycline (Dox, Harland Laboratories) containing diet was administered to repress transgene expression.

Generation of mice with a conditional deletion of miRNA-128

20 A construct was engineered for conditional disruption of the miRNA-128 (miRNA-128-3p) gene in which a 1.7 kb fragment spanning the miRNA-128 gene was flanked by two loxP sites. The 1.7 kb fragment, the 5.4 kb left homology arm and the 2.9 kb right homologous arm were amplified from C57BL/6 BAC DNA and cloned

into the pBasicLFNeoFL vector sequentially by in-fusion cloning and confirmed by sequencing. In addition to conditional knockout (cKO) region and homology arms, the targeting construct also contains Frt sites flanked Neomycin cassette for positive selection and a DTA cassette for negative selection. The construct was linearized with

5 NotI and electroporated into C57BL/6N ES cells. After G418 selection, 3 positive clones were identified from 280 G418 resistance clones by PCR screening. The positive clones were expanded and further analyzed by Southern blot. The random integration of extra copies of targeting construct was excluded by hybridization with a neomycin probe. To generate chimeras, ES cell clones were microinjected into

10 blastocysts, and the blastocysts were implanted into pseudo-pregnant foster mice by Cyagen Biosciences Inc. Chimeric males were bred with Flp delete mice from Jackson Laboratories to generate Neomycin-free floxed mice. The correct integration of loxP sites and the successful removal of Neomycin cassette were confirmed by the following PCR

15 assays: 1). Primers 5'-TCATAGCTGTACTTACTGGATG-3' and 5' - CACTTGGGCTTGGAAGATAG-3' for the 234 bp fragment from wt allele and the 289 bp fragment from targeted allele. 2). Primers 5' - GCCCTAATTTGATCATCAGAACC-3' and 5' - CATTGTTGTAGCCACACCCC-

20 3' for the 483 bp from wt allele and the 605 bp fragment from targeted allele.

Cardiac specific miRNA-128 knockout mice (miRNA-128^{-/-}) were generated by crossing

25 Nkx2.5^{Cre} (The Jackson Laboratory) mice with miRNA-128^{floxP/floxP} mice (miRNA-128^{fl/fl}).

Tamoxifen (TAM) inducible cardiomyocyte-specific miRNA-128 knockout mice (iKO) were generated by crossing α -MHC^{MerCreMer} mice (Tg(α -MHC-cre/Esr*)1Jmk/J, The Jackson Laboratory) with miRNA-128^{fl/fl} mice. Induction of Cre recombinase activity was achieved using a two dose of tamoxifen (Sigma, 0.25mg/g body weight) dissolved in corn oil (Sigma) administrated intraperitoneally (IP). A dual-lineage tracing system was established to investigate the origin of regenerated cardiomyocytes. α -MHC^{MerCreMer} mice were crossed with Rosa26-tdTomato (R26R-mTmG, The Jackson Laboratory) reporter mice and miRNA-128^{fl/fl} mice to generate iKO-mTmG mice (α -MHC^{MerCreMer} ;miRNA-128^{fl/+};R26R-mTmG) to label miRNA-128 deleting CM with red color following tamoxifen administration. All mice were maintained on a C57BL/6 background.

Neonatal cardiomyocyte isolation and culture

Neonatal rat cardiomyocytes were isolated from ventricles of 1-day-old neonatal Sprague–Dawley rats (Harland) using a neonatal cardiomyocyte isolation kit (Worthington Biochemical) according to the manufacturer's instructions. Neonatal mouse cardiomyocytes were isolated from 1-day-old (P1) C57BL/6 mice with a modified protocol as previously described. The mouse neonatal cardiomyocytes were cultured in 0.1% gelatin plus with 10 μ g/ml fibronectin (Sigma-Aldrich) coated slides with 68% DMEM high glucose medium supplemented with 17% M-199, 4% horse serum (Gibco), 10% FBS, and 1% penicillin/streptomycin (hereafter referred to as 'complete-medium') at 37⁰C and 5% CO₂.

Adult cardiomyocyte isolation and culture

Adult mouse cardiomyocytes were isolated from adult C57BL/6 mice with modified protocol as previously described. The adult mouse CMs were cultured in laminin (10µg/ml, Life technologies) coated slides with AW medium (Cellutron life technologies) with 10% FBS. After the cells were allowed to adhere for 48 hours in
5 complete-medium, miRNA mimic miRNA inhibitor, siRNA transfection were performed according to the manufacturer's instructions. After 72 hours, cells were harvested for analysis.

Luciferase reporter assay

10 The DNA fragment containing 3'-untranslated regions (3'UTR) was amplified by PCR and cloned into luciferase reporter vector-psiCheck2 (Promega). The reporter vector containing mutant 3'UTR was generated by Site-Directed Mutagenesis Kit (New England Biolabs). HEK-293 cells were transfected using DharmaFECT Duo reagent (Dharmacon) according to the manufacturer's instructions with luciferase
15 reporter vector and miRNA-128 mimic (Dharmacon). Cells were harvested and assayed for luciferase activity using Dual-GloTM kit (Promega) 48 hours after transfection as previously described.

Quantitative real-time PCR (qPCR)

20 Total RNA was isolated using Trizol reagent (Invitrogen), followed by DNase treatment and purification using RNeasy mini column kit (Qiagen). cDNA was synthesized using miScript PCR Starter Kit (Qiagen) in a 20-µl reaction mixture. qPCR was performed on the CFX96 Real Time PCR system (Bio-Rad) using the protocol of miScript PCR Starter Kit (Qiagen). The fold changes of each target mRNA expression
25 relative to GAPDH under experimental and control conditions were calculated based on

the threshold cycle (CT) as $r = 2^{-\Delta(\Delta CT)}$, where $\Delta CT = CT(\text{target}) - CT(\text{GAPDH})$ and

$\Delta(\Delta CT) = \Delta CT(\text{experimental}) - \Delta CT(\text{control})$. The primers for qPCR include:

H3K27me3-p27-F: GAGATCCTACGGTGGGAAGCG;

H3K27me3-p27-R: CTTAGCTGGGGTGCGGAATC;

5 miRNA-128: CGTCACAGTGAACCGGTCTCT;

U6-F: CTCGCTTCGGCAGCACA;

U6-R: AACGCTTCACGAATTTGCGT;

Racgap1-F: CAGATCCAGTGACAATGTTCCA;

Racgap1-R: TCCACCATCATGAACTGATTCC;

10 Nusap1-F: GAGGAGGAAGAAGCACAAGAC;

Nusap1-R: CTACTATCAGTTCCTTTTCATCTCCAA;

Myh10-F: GAATTCGAGAGGCAGAACAA;

Myh10-R: AAGGCTCGCTTGGATTTCTC;

Nppa- F: CTGAGGTGCCTCCCTGGAC;

15 Nppa-R: ACTCTGGGCTCCAATCCTGTC;

Nppb-F: AAGGACCAAGGCCTCACAAA;

Nppb-R: GCCAGGAGGTCTTCCTACAAC;

Myh6- F: GGACGCCCAGATGGCTGACT;

Myh6-R: CCTTGTCATCAGGCACGAAGCAC;

20 Myh7-F: GTTTGTCAAGGCCAAGATCGTGT;

Myh7-R: AGCATGGCCATGTCCTCGAT.

Chromatin Immunoprecipitation-qPCR (ChIP-qPCR) assay

ChIP assay was performed as we described previously to evaluate the enrichment

of SUZ12, EZH2, and H3K27me3 on the p27 promoter. SUZ12 (Active Motif), EZH2 (Abcam) and H3K27me3 antibody (Millipore) and normal mouse IgG (Millipore) were used.

Western blots

5 Cells were lysed with ice-cold cell lysis buffer plus protease inhibitor (Sigma-Aldrich). Protein samples (40 µg) were mixed and resolved in 4×SDS/PAGE sample buffer and boiled for 15 mins before loading onto 10% polyacrylamide gels (Bio-Rad). The electrophoresed proteins were transferred from the gel to nitrocellulose
10 membranes (Bio- Rad). Equal loading and transfer of proteins was confirmed by quantitative Ponceau red staining. Membranes were incubated for 60 mins with 5% dry milk and Tris-buffered saline to block nonspecific binding sites. Membranes were immunoblotted overnight at 4°C with antibodies against Cyclin E (Santa Cruz), SUZ12, CDK2, p27 (Cell Signaling Technology) and GAPDH (Sigma-Aldrich) on a
15 rocking platform. After three 5-mins washings with Tris-buffered saline, the membranes were incubated for 60 mins with HRP-conjugated secondary antibody, washed three times with Tris-buffered saline, and finally developed with the ECL plus kit (Thermo Scientific).

Neonatal Mouse Apex resection

20 Apex resection (AR) was performed on neonatal mice on postnatal day 1 (P1) as previously described. The hearts were harvested at 6 hours, 24 hours, 3 days, 7 days, 14 days, and 21 days post AR. Sham-operated mouse groups (control) underwent chest opening without apex resection.

Myocardial infarction (MI) model

An MI model was developed in female mice, as previously described. Briefly, mice (8- 10 weeks old) were anesthetized by spontaneous inhalation and maintained under general anesthesia with 1–2% isoflurane. Animals were mechanically ventilated using a rodent ventilator (Harvard Apparatus) connected to an endotracheal tube. The heart was exposed by a left side limited thoracotomy and the LAD was ligated with a 6-0 polyester suture 1 mm from the apex of the normally positioned left auricle.

Echocardiography

Transthoracic echocardiography (Visual Sonics Vevo 2100) was performed with a 40-MHz probe. Hearts were imaged in 2D long-axis view at the level of the greatest left ventricular (LV) diameter in animals under light general anesthesia. This view was used to position the M-mode cursor perpendicular to the LV anterior and posterior walls. LV end-diastolic (LVDd) and end-systolic diameters (LVDs) were measured from M-mode recordings. LV ejection fraction (EF) was calculated as:

$$EF\% = [(LVDd)^3 - (LVDs)^3] / (LVDd)^3 \times 100$$

LV fractional shortening (FS) was determined as: $FS\% = (LVDd - LVDs) / LVDd \times 100$. All measurements were performed according to the American Society for Echocardiography leading-edge technique standards, and were averaged over three consecutive cardiac cycles.

EdU pulse-chase

For EdU (5-ethynyl-2'-deoxyuridine, Life technology) labeling experiments *in vivo*, animals were injected intraperitoneally (IP) at 200ug/g body weight. EdU staining was performed with Click-iT EdU Imaging kit (Thermo Fisher Scientific) according to the manufacturer's instructions.

Analysis of left ventricular (LV) fibrotic area

Masson's trichrome staining was performed to quantify fibrosis area in the left ventricle post injury. An Olympus BX41 microscope equipped with CCD (Magna-Fire TM) camera captured LV area images on each slide. LV fibrosis area and total LV area of each image were measured using the Image J and fibrosis area was reported as a percentage of the total LV area.

Immunohistochemistry assay

After deparaffinization and microwaving antigen retrieval in citric acid buffer, heart sections were incubated for 1 h at 37⁰C or overnight at 4⁰C with the following antibodies: Anti-cTnT antibody (Thermo Fisher Scientific) was used to identify CM. Anti-Ki67 (Abcam), anti-EdU (Life technology), anti-phosphorylated-histone 3 (pH3, Millipore) antibodies were used to analyze cell-cycle activity, DNA synthesis, karyokinesis, and cytokinesis respectively. After triple washing in PBS, slides were incubated for 45 mins at 37⁰C with fluorescence conjugated second antibodies (Jackson Immuno Research). For wheat germ agglutinin (WGA) staining, slides were incubated for 30 mins at 37⁰C with primary antibody against conjugated to Alexa Fluor 488 (Thermo Fisher Scientific) in PBS. To quantify apoptotic CMs, additional mouse hearts were stained with TUNEL (Promega) and cTnT (Thermo Fisher Scientific) according to the manufacturer's instructions. To quantify CM proliferation, cells were stained with Ki67, pH3. DAPI was used for nuclear counterstaining. Four fields of each section were examined for quantification. Fluorescent imaging was performed with an Olympus BX41 microscope equipped with an epifluorescence attachment.

25 Statistical analysis

Results were statistically analyzed with the use of the StatView 5.0 software package (Abacus Concepts Inc., Berkeley, CA). All values are expressed as mean $\pm$ S.E.M. Student's *t*-test was applied appropriately for comparison between two
5 treatment groups. One-way ANOVA (using the post-hoc Bonferroni/Dunn test) was performed for comparisons of multiple groups in each of the specific experimental designs presented in the figures.

The many features and advantages of the invention are apparent from the
10 detailed specification, and thus, it is intended by the appended claims to cover all such features and advantages of the invention which fall within the true spirit and scope of the invention. Further, since numerous modifications and variations will readily occur to those skilled in the art, it is not desired to limit the invention to the exact construction and operation illustrated and described, and accordingly, all suitable
15 modifications and equivalents may be resorted to, falling within the scope of the invention.

What is Claimed:

1. A method for treating a subject suffering from a cardiac disorder, the method comprising the step of delivering a therapeutically effective amount of an
5 miRNA-128 inhibitor to a myocardial region of the subject.
2. The method according to claim 1, wherein the delivery method comprises administering one of the following: a plasmid/vector comprising a genetic construct of the miRNA-128 inhibitor, one or more chemically synthesized
10 antisense oligonucleotides targeting miRNA-128, one or more small molecular inhibitors targeting miRNA-128, and combinations thereof.
3. The method according to claim 1, wherein delivering comprises systemic administration of a carrier comprising the inhibitor, said carrier designed for
15 targeted delivery to a myocardial region of the subject.
4. The method according to claim 1, wherein the cardiac disorder comprises any disease or condition benefited by proliferation of cardiomyocytes and/or regeneration of heart tissue.
20
5. The method of claim 4, wherein the cardiac disorder is selected from ischemic cardiomyopathy (including but not limited to myocardial infarction), non-ischemic cardiomyopathy (including but not limited to hypertrophic cardiomyopathy), dilated cardiomyopathy, diabetic cardiomyopathy, valvular
25 heart disease, heart failure, myocardial stunning, stroke, hypotension, embolism, thromboembolism (blood clot), and combinations thereof.
6. The method according to claim 2, wherein the plasmid or vector comprises a DNA vector adapted to express an miRNA-128 sponge.
30

7. The method according to claim 2, wherein the plasmid or vector is engineered to transfect the cardiomyocytes with at least one antisense oligonucleotide against miRNA-128.
- 5 8. The method according to claim 2, wherein the plasmid or vector is engineered to transfect the cardiomyocytes to block transcription or biogenesis of miRNA-128
9. The method according to claim 8, wherein the plasmid or vector is engineered to transfect the cardiomyocytes with an siRNA, an shRNA targeting miRNA-128,
10 or an shRNA targeting a precursor sequence of miRNA-128.
10. The method according to claim 2, wherein the miRNA-128 inhibitor comprises chemically synthesized antisense oligonucleotides targeting miR-128.
- 15 11. The method according to claim 10, wherein the oligonucleotide is modified by conjugation to one or more of a fatty acid, lipid, saccharide, peptide, protein, locked nucleotide analogue (LNA), and morpholino oligomer.
12. The method according to claim 2, wherein the miRNA-128 inhibitor comprises a
20 small molecule inhibitor and the vehicle comprises a liposome designed for targeted delivery to cardiomyocytes.
13. The method according to any of the preceding claims, wherein the inhibition is transient.
- 25 14. The method according to claim 2, wherein the step of delivering comprises administering a plasmid or viral vector engineered to transfect cardiomyocytes located in the myocardial region with the inhibitor.
- 30 15. The method according to claims 1 or 2, wherein the step of delivering comprises injecting the miRNA-128 inhibitor directly to a myocardial region of the subject.

16. The method according to claim 15, wherein direct injection is via catheter-based direct intramyocardial injection to a damaged myocardial region of the subject.
- 5 17. A pharmaceutical composition comprising at least one miRNA-128 inhibitor and a pharmaceutically acceptable vehicle.
18. The pharmaceutical composition according to claim 18, further comprising a pharmaceutical carrier selected from liposomes, microparticles and nanoparticles
10 and being formulated for targeted delivery to myocardium.
19. A method for promoting proliferation of cardiomyocytes, the method comprising adding an effective amount of an miRNA-128 inhibitor to a culture medium comprising cardiomyocytes *in vitro*, and observing proliferating regenerative
15 cardiomyocytes.
20. The method according to claim 19, wherein the regenerative cardiomyocytes are comprised of mitotic cells.
- 20 21. A pharmaceutical composition comprising regenerative cardiomyocytes according to claim 19, and a pharmaceutically acceptable vehicle.
22. A method of treating a subject suffering from a cardiac disorder, the method comprising administration of a therapeutically effective amount of the
25 pharmaceutical composition according to claim 21.
23. The method of treating according to claim 22, wherein administering comprises direct injection of the pharmaceutical composition via catheter-based direct intramyocardial injection to a damaged myocardial region of the subject.
30
24. An isolated nucleic acid molecule comprising (a) a nucleotide sequence as set

forth in SEQ ID NO: 1, or a precursor of SEQ ID NO: 1 and/or (b) a nucleotide sequence which is the complement of (a), and/or (c) a nucleotide sequence which has an identity of at least 80% to a sequence of (a) or (b), and/or (d) a nucleotide sequence which hybridizes under stringent conditions to a sequence of (a), (b) and/or (c) wherein said isolated nucleic acid molecule comprises at least one modified building block selected from the group consisting of nucleobase-modified building blocks, sugar-modified building blocks, backbone-modified building blocks and combinations thereof.

25. The isolated nucleic acid molecule according to claim 24, wherein the identity of sequence (c) is at least 90%.

26. The isolated nucleic acid molecule according to claim 24 comprising a single-stranded or double-stranded nucleic acid molecule.

27. The isolated nucleic acid molecule according to claim 24, wherein said isolated nucleic acid molecule is a miRNA molecule or an analog thereof having a length of from 18-25 nucleotides, or a miRNA precursor molecule having a length of 50-120 nucleotides, or a DNA molecule coding therefor.

28. The length of the miRNA molecule or analog according to claim 27 consisting of 21 or 22 nucleotides.

29. The isolated nucleic acid molecule according to claim 24 comprising an RNA molecule.

30. The isolated nucleic acid molecule according to claim 24, wherein said isolated nucleic acid molecule is suitable for the diagnosis, treatment or prevention of a disorder involving cardiomyocyte death.

31. The isolated nucleic acid molecule according to claim 30, wherein the disorder

- involving cardiomyocyte death is selected from the group consisting of ischemic cardiomyopathy (including but not limited to myocardial infarction), non-ischemic cardiomyopathy (including but not limited to hypertrophic cardiomyopathy), dilated cardiomyopathy, diabetic cardiomyopathy, valvular heart disease, heart failure, myocardial stunning, stroke, hypotension, embolism, thromboembolism (blood clot), and combinations thereof.
- 5
32. The isolated nucleic acid molecule according to claim 25, wherein the identity of sequence (c) is at least 95%.
- 10
33. A pharmaceutical composition comprising an inhibitor of miRNA-128, wherein the inhibitor is an isolated nucleic acid molecule comprising at least one modified building block.
- 15
34. The composition according to claim 33, wherein the inhibitor has sufficient complementarity to miRNA-128 to form a hybrid under physiological conditions.
- 20
35. The composition according to claim 33, wherein the inhibitor is a single-stranded or double-stranded nucleic acid molecule.
36. The composition according to claim 33, wherein the inhibitor is an RNA molecule comprising at least one modified building block.
- 25
37. The composition according to claim 36, wherein the modified building block is selected from the group consisting of nucleobase-modified building blocks, sugar-modified building blocks, backbone-modified building blocks and combinations thereof.
- 30
38. The composition according to claim 33, wherein the inhibitor is a siRNA molecule or an antagomir.

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Fig. 1A

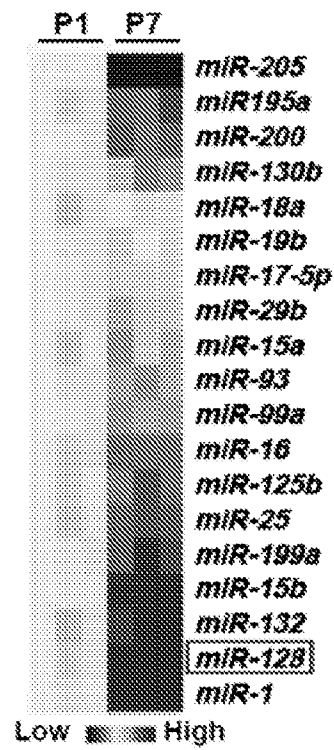
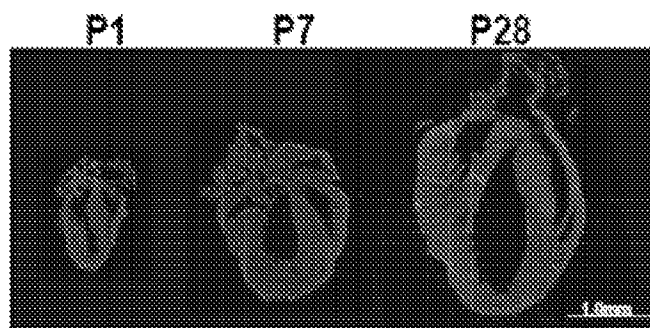
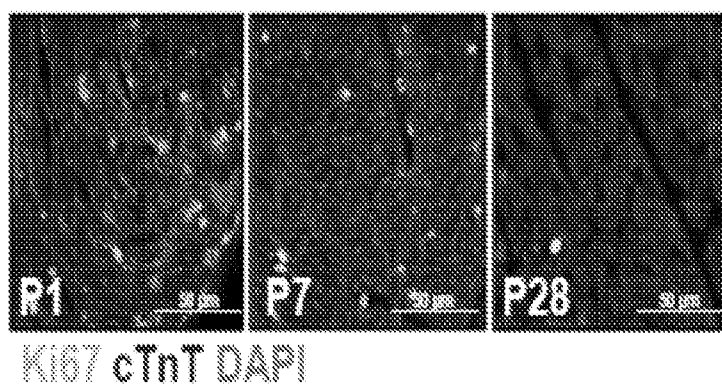


Fig. 1B



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Fig. 1C



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Fig. 1D

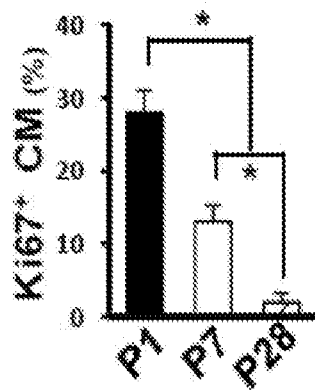


Fig. 1E

(expression miR-128)

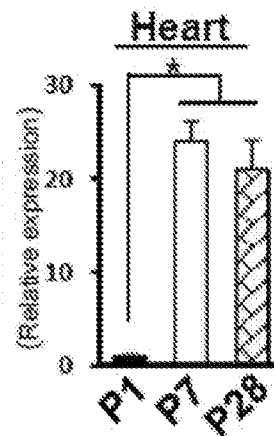


Fig. 1F

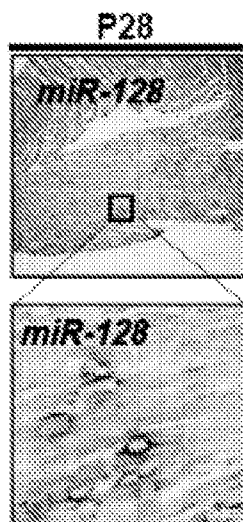
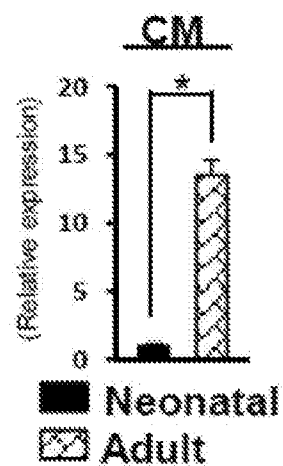


Fig. 1G

(expression miR-128)



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Fig. 2A

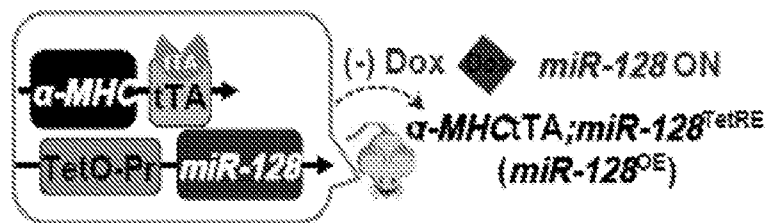


Fig. 2B

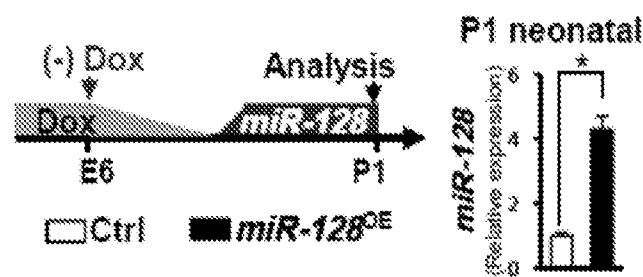


Fig. 2C

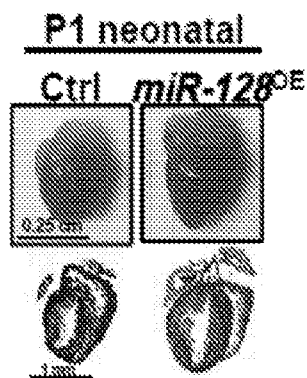


Fig. 2E

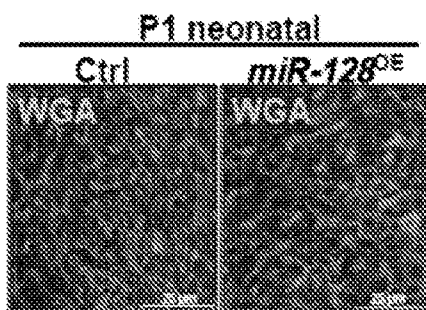


Fig. 2D

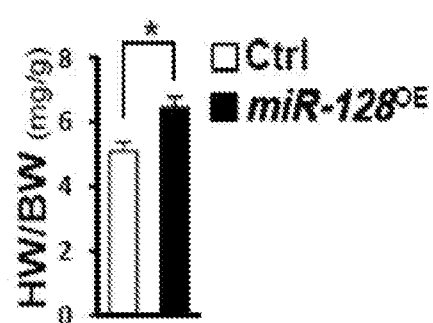
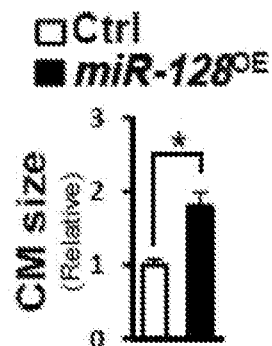


Fig. 2F



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Fig. 2G

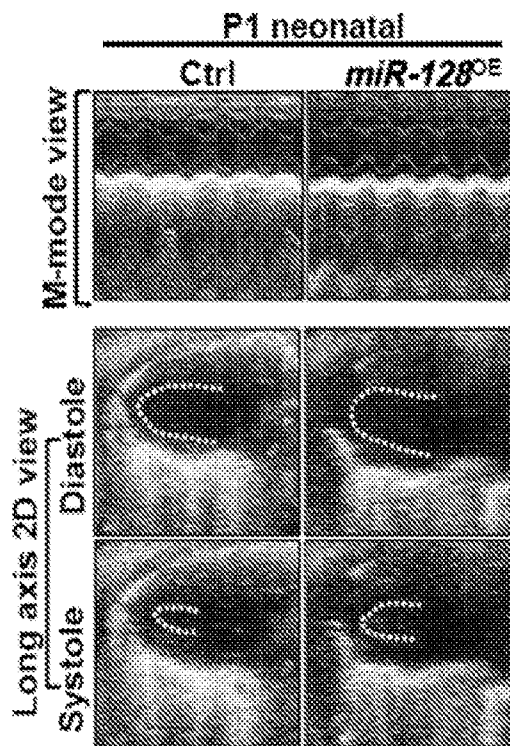


Fig. 2H

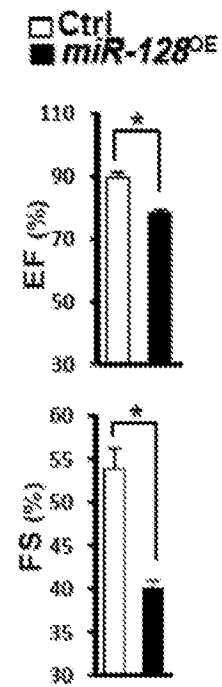


Fig. 2I

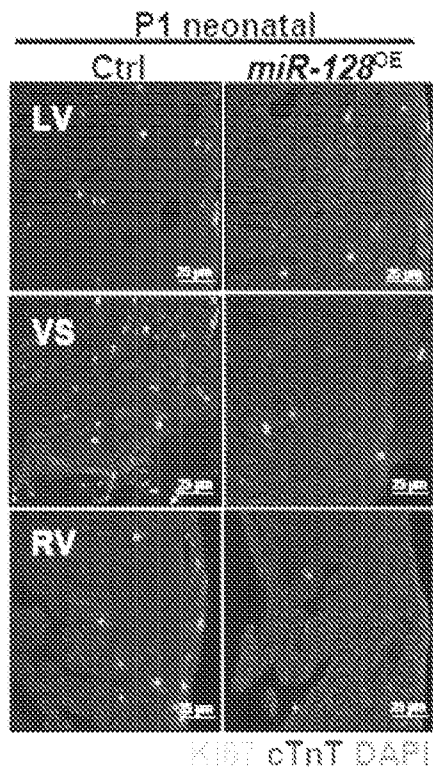


Fig. 2J

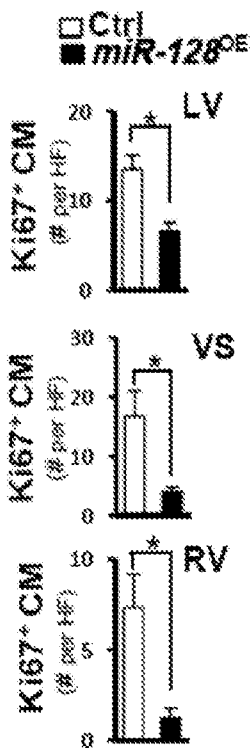


Fig. 3A

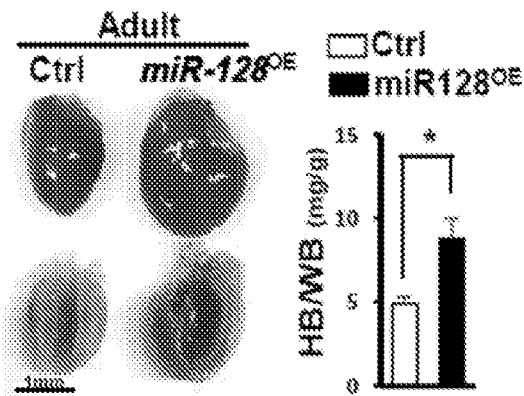
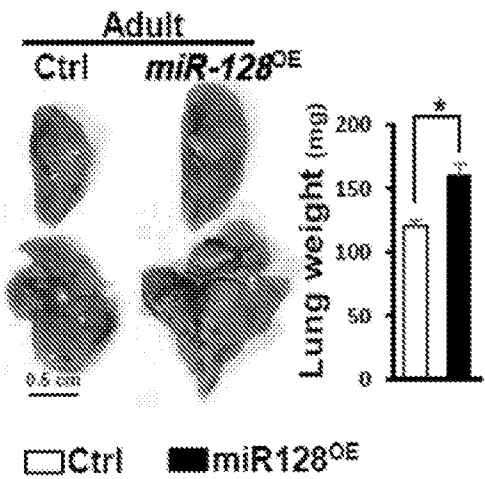


Fig. 3B



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Fig. 3C

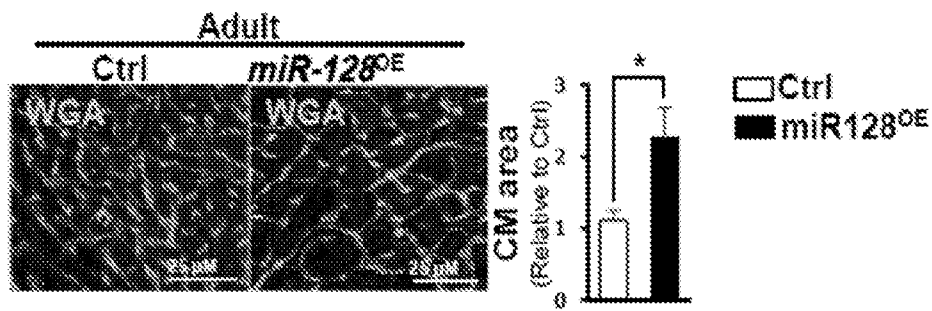
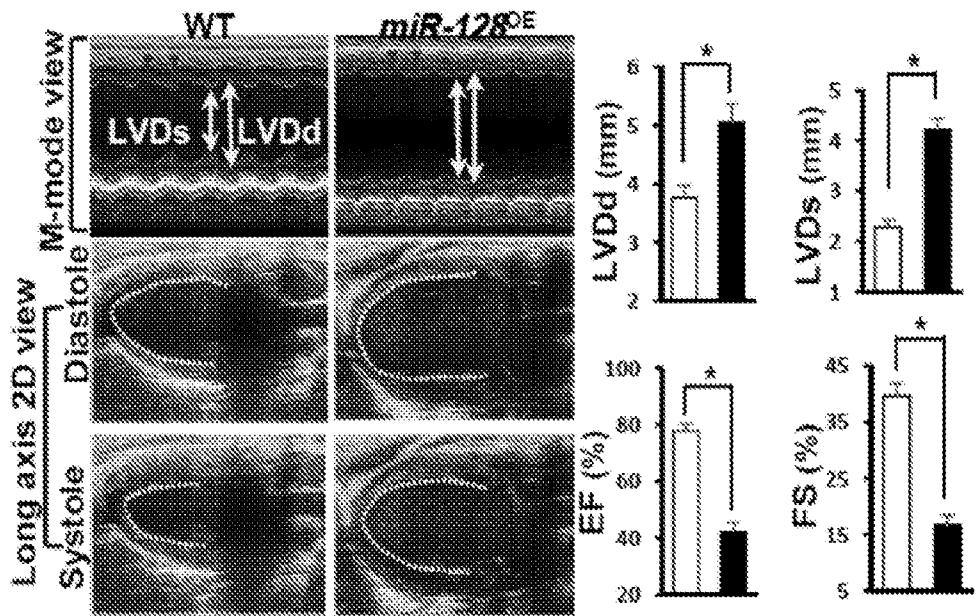


Fig. 3D



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Fig. 4A

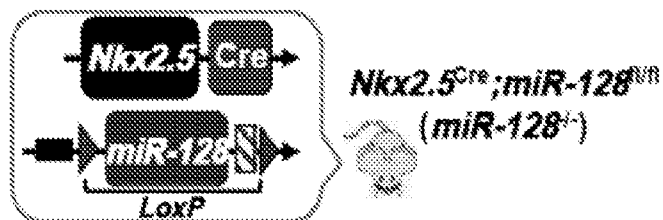


Fig. 4B

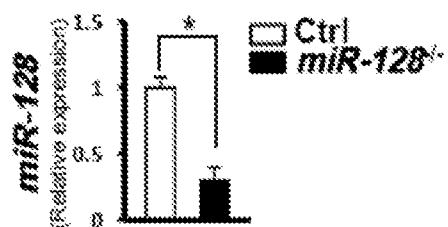


Fig. 4C

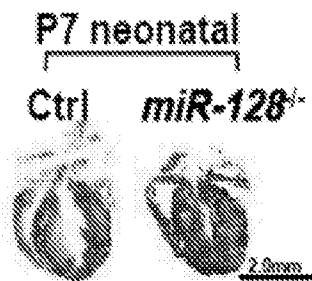


Fig. 4D

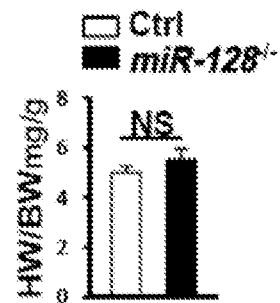


Fig. 4E

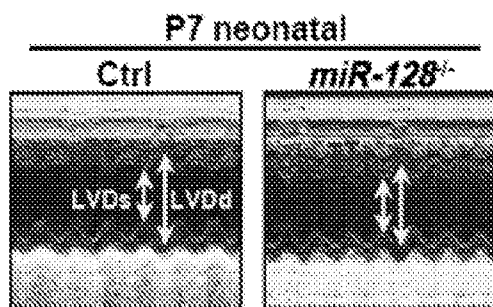
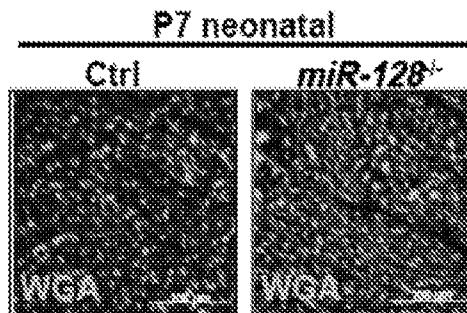


Fig. 4F



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Fig. 4G

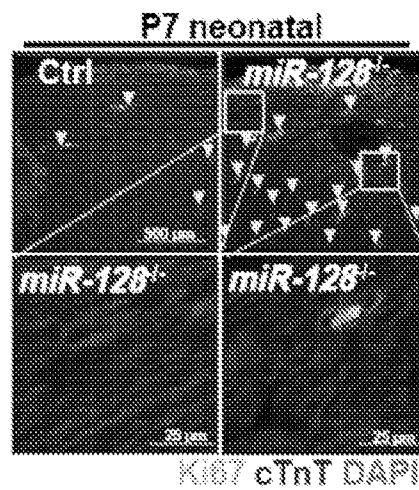


Fig. 4H

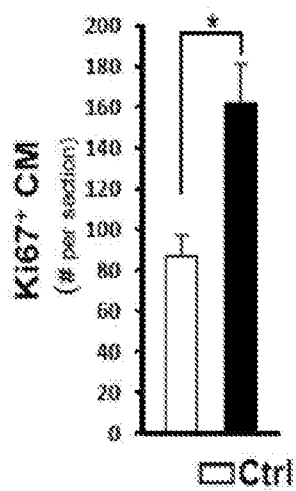


Fig. 4I

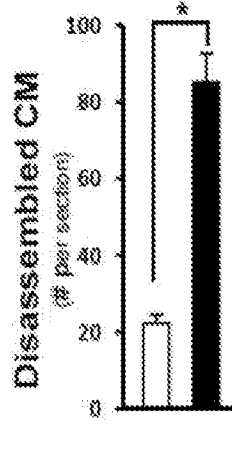
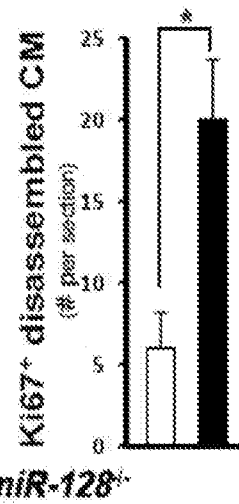


Fig. 4J



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Fig. 4K

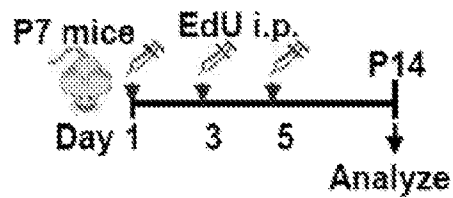


Fig. 4L

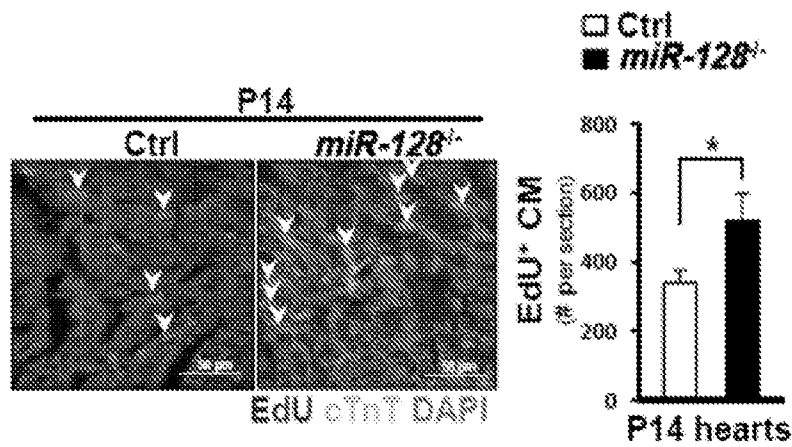


Fig. 4M

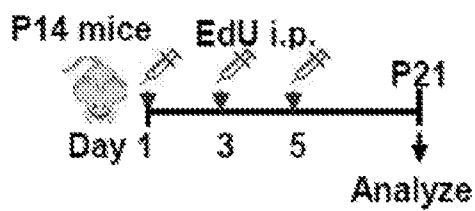
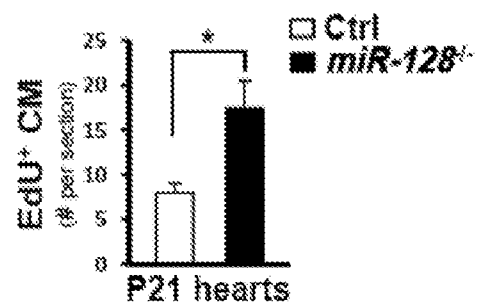


Fig. 4N



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Fig. 4O

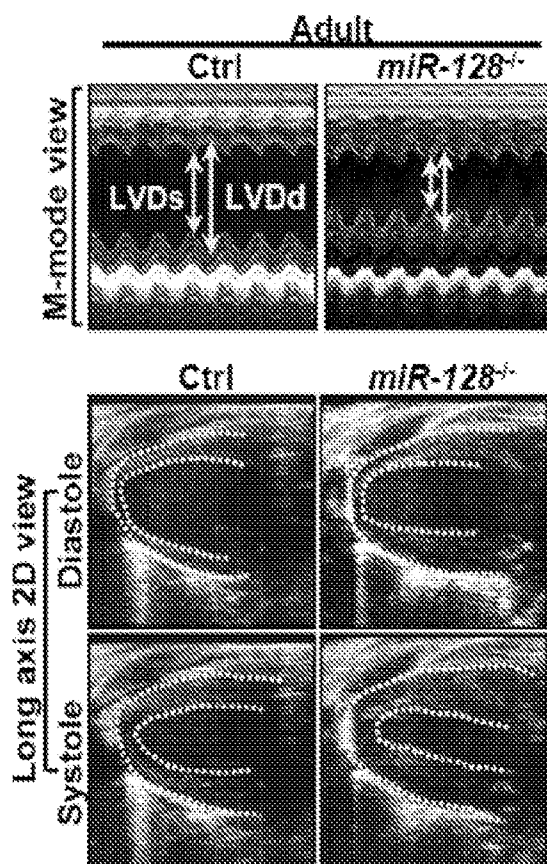
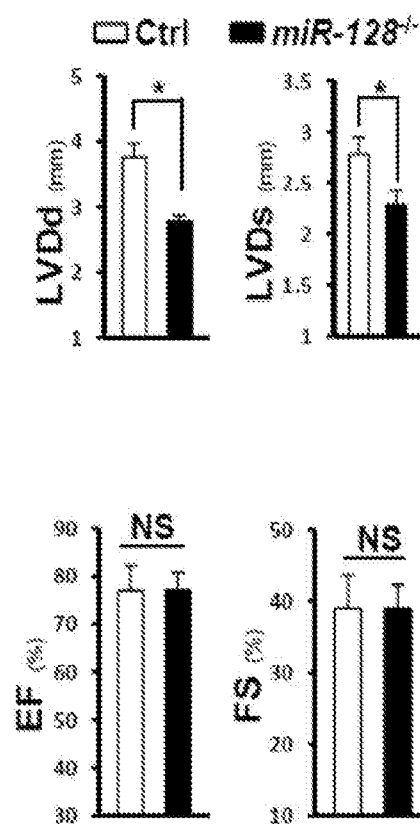


Fig. 4P



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Fig. 5A

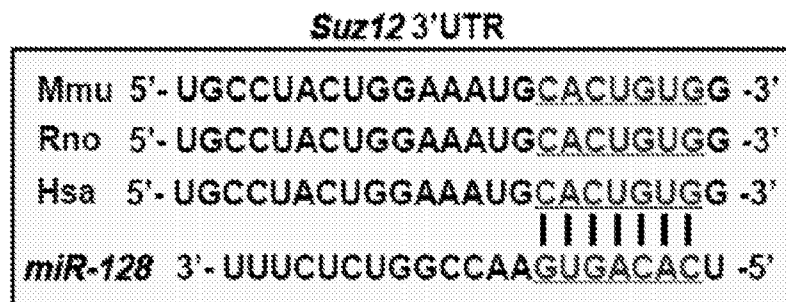


Fig. 5B

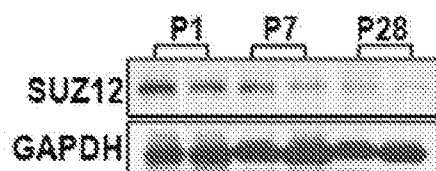


Fig. 5C



Fig. 5D

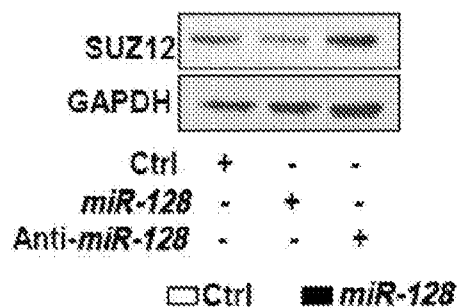


Fig. 5E

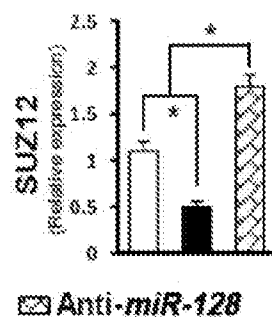
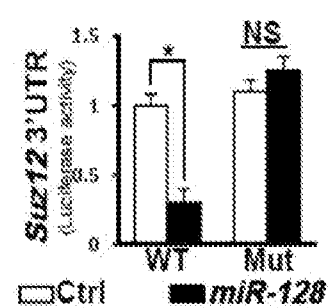


Fig. 5F



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Fig. 5G

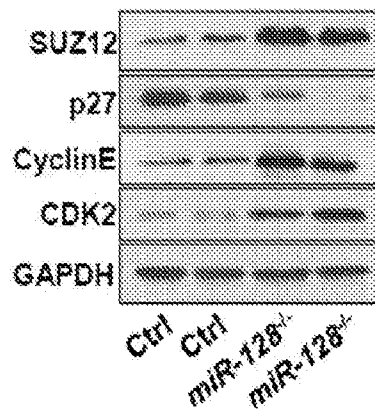


Fig. 5H

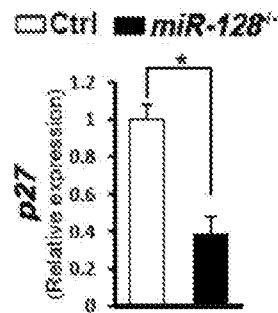


Fig. 5I

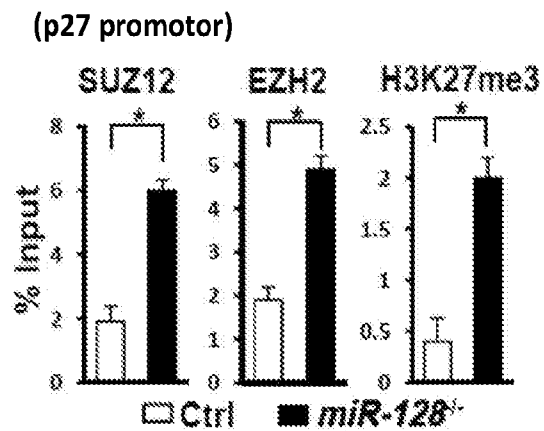


Fig. 5J

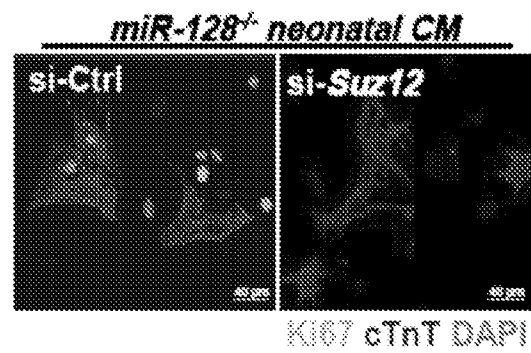


Fig. 5K

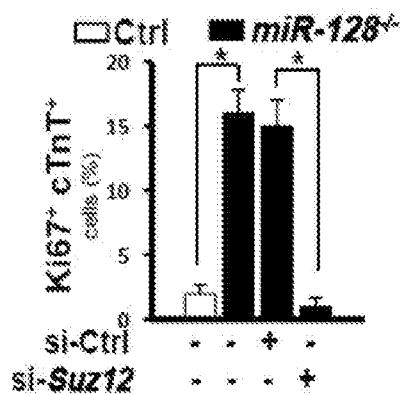
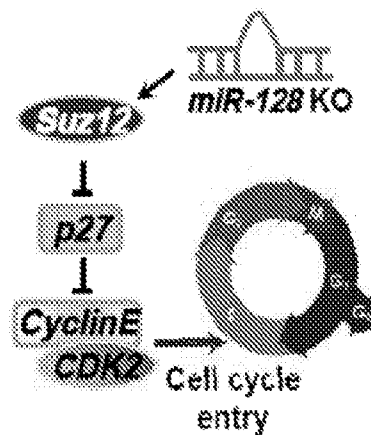


Fig. 5L



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Fig. 6A

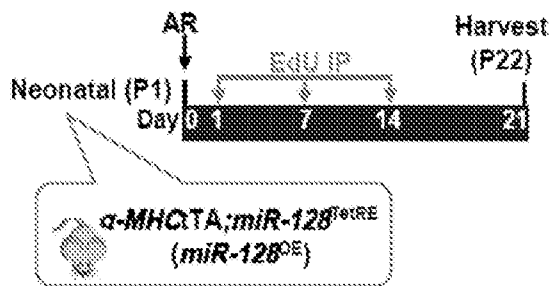


Fig. 6B

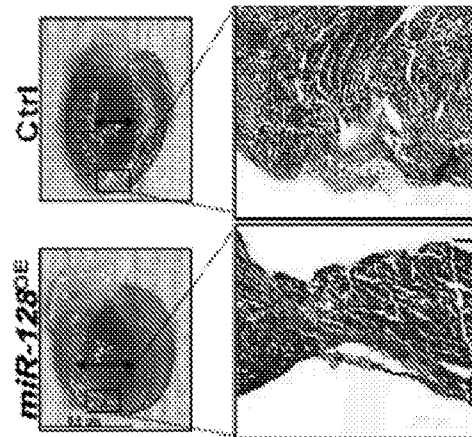


Fig. 6C

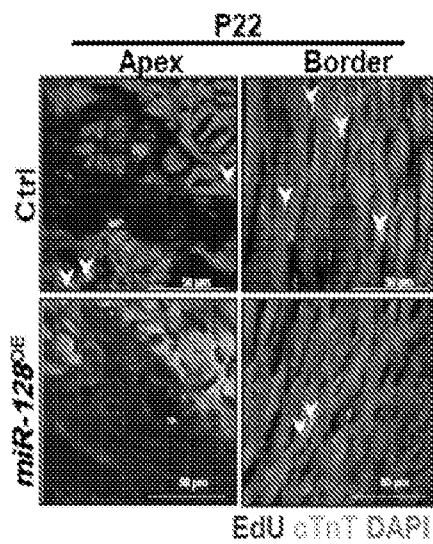


Fig. 6D

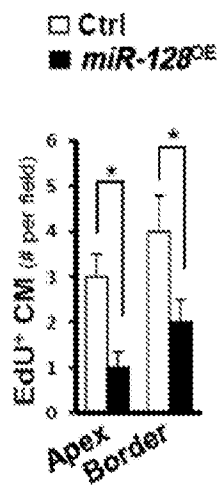
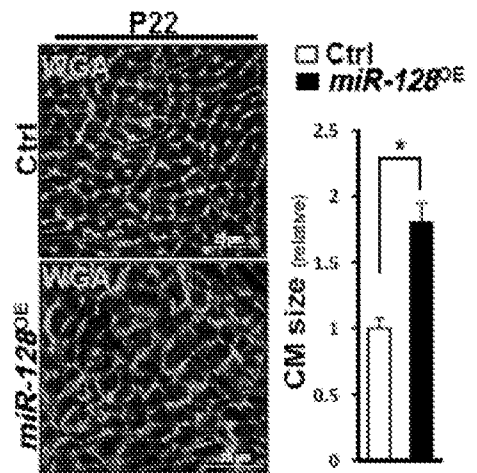


Fig. 6E



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Fig. 6F

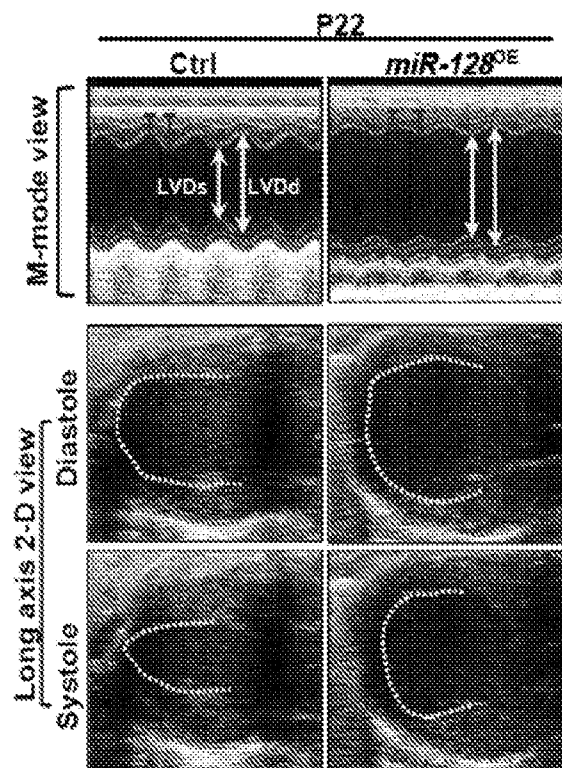
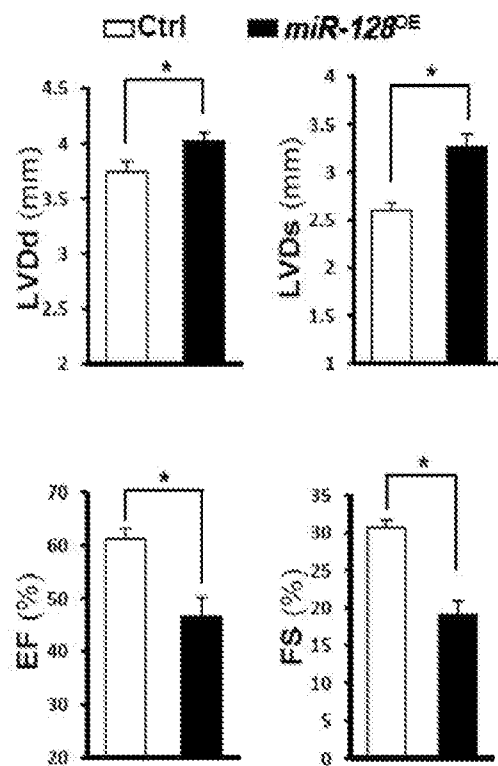


Fig. 6G



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Fig. 7A

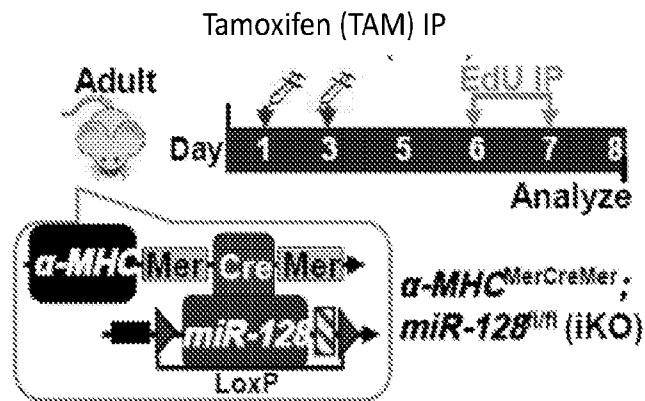


Fig. 7B

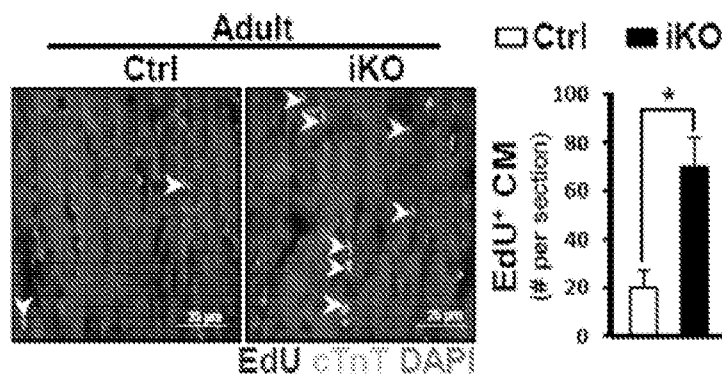


Fig. 7C

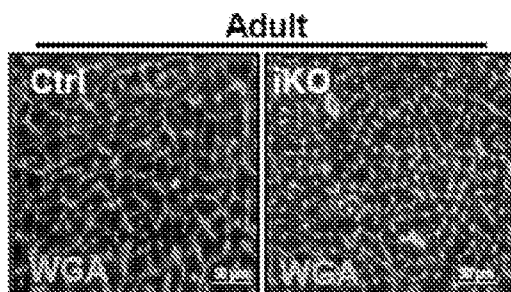


Fig. 7D

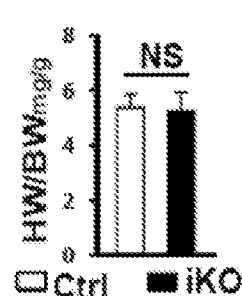
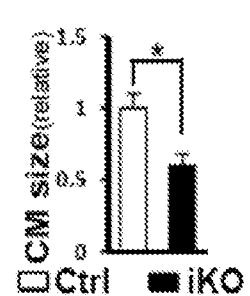


Fig. 7E



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Fig. 7F

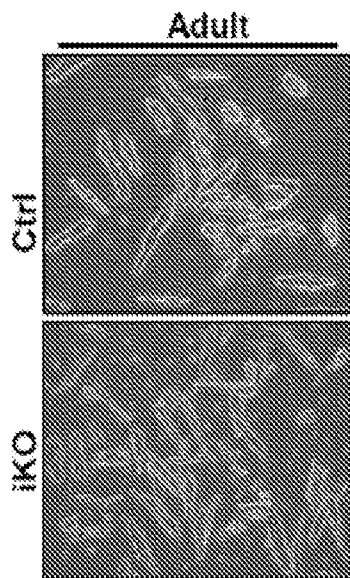


Fig. 7G

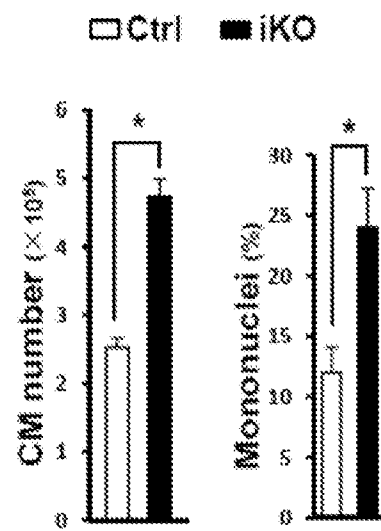
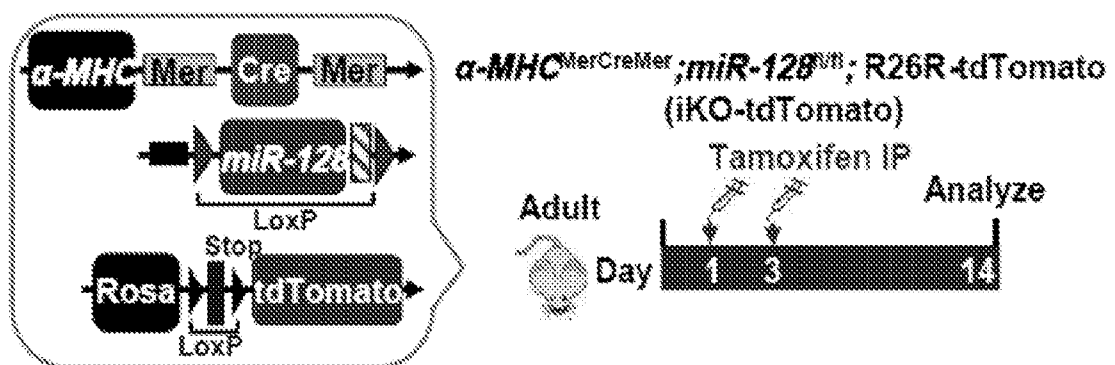


Fig. 7H



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Fig. 7I

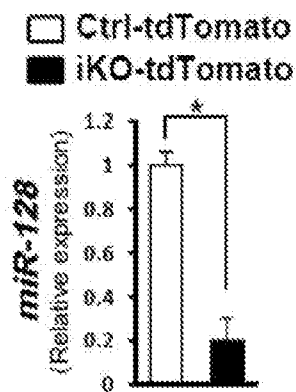


Fig. 7J

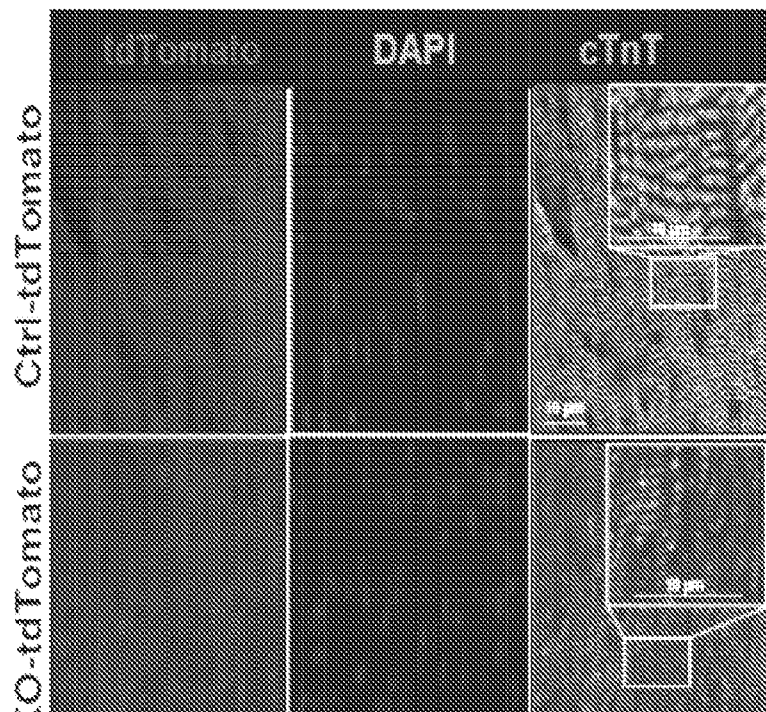
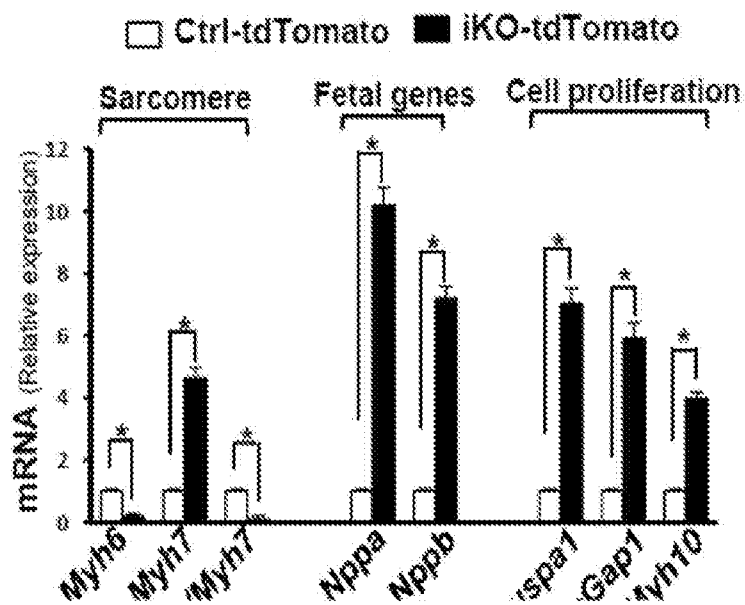


Fig. 7K

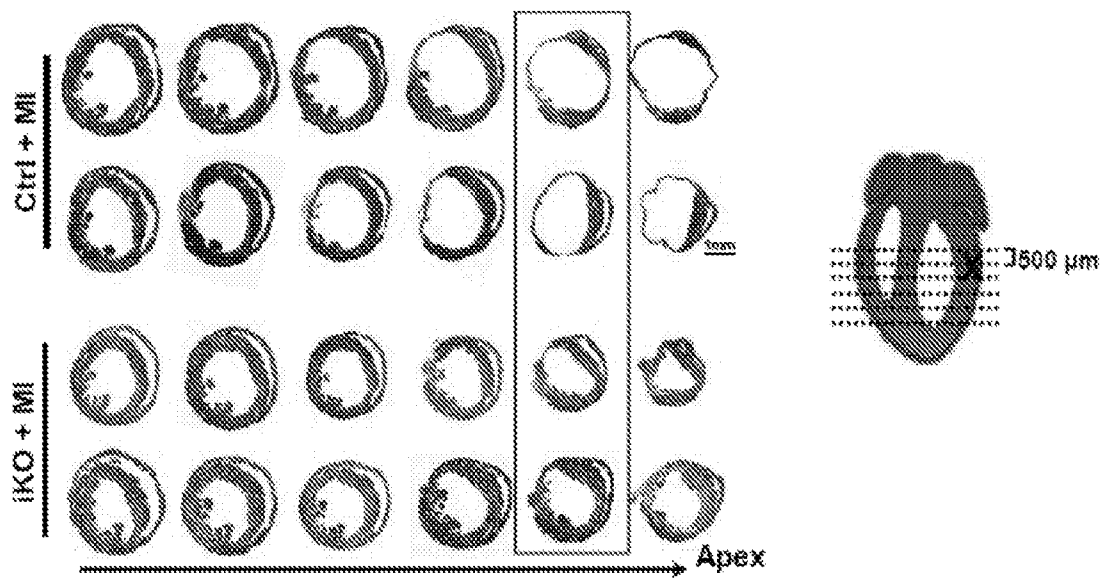


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Fig. 8A



Fig. 8B



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Fig. 8C

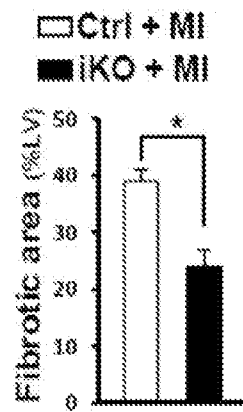
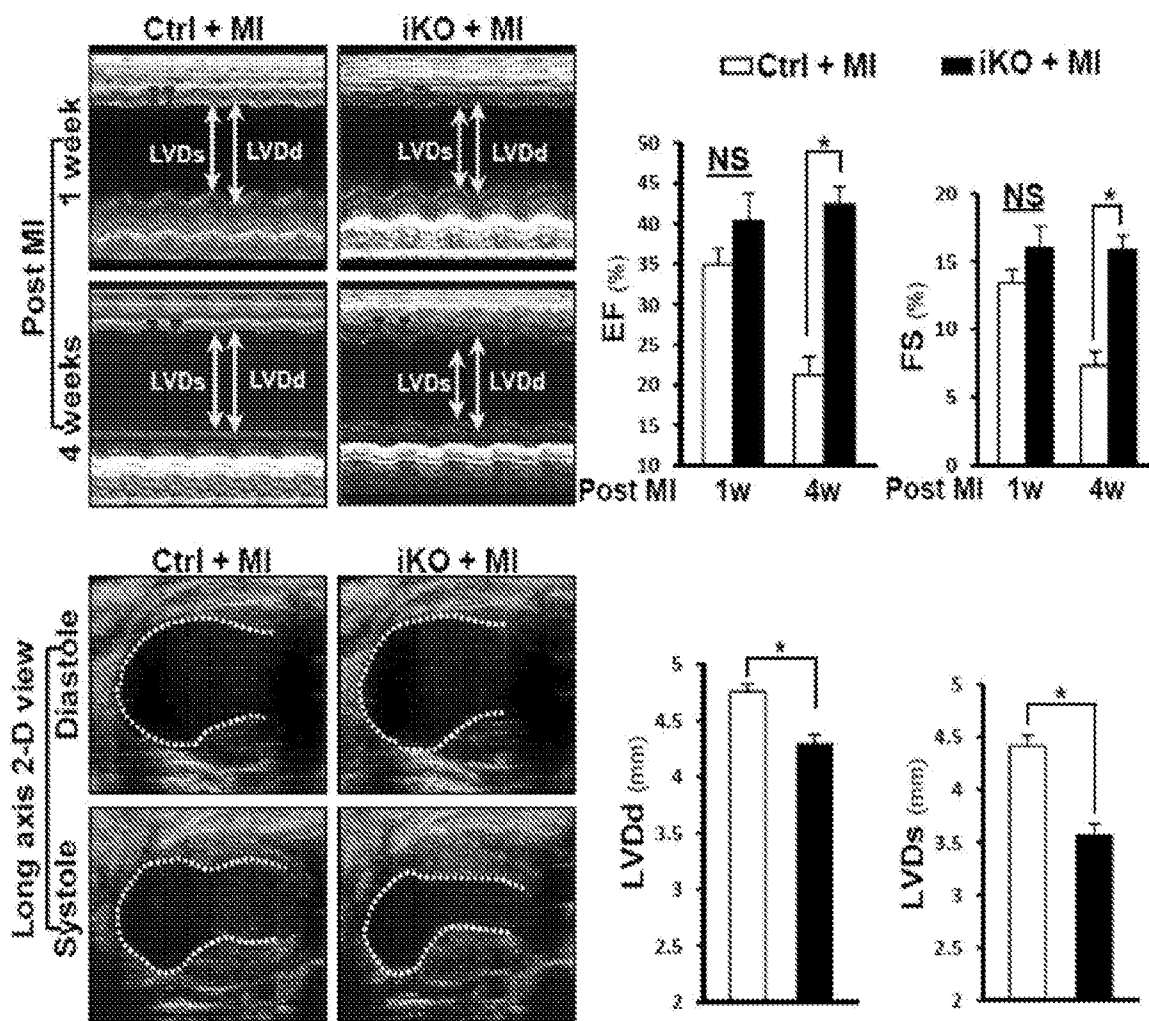


Fig. 8D

Fig. 8E



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Fig. 9

