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(71) Applicant: **THE TRUSTEES OF INDIANA UNIVERSITY** [US/US]; 518 Indiana Avenue, Indianapolis, Indiana 46202 (US).

(72) Inventors: **CHANG, Ching-Pin**; 1431 Yew Street, San Mateo, California 94402 (US). **CHENG, Wei**; 726 Northfield Court, Indianapolis, Indiana 46227 (US).

(74) Agent: **PILCHER, Jessamine G.** et al.; Barnes & Thornburg LLP, 11 South Meridian Street, Indianapolis, Indiana 46204 (US).

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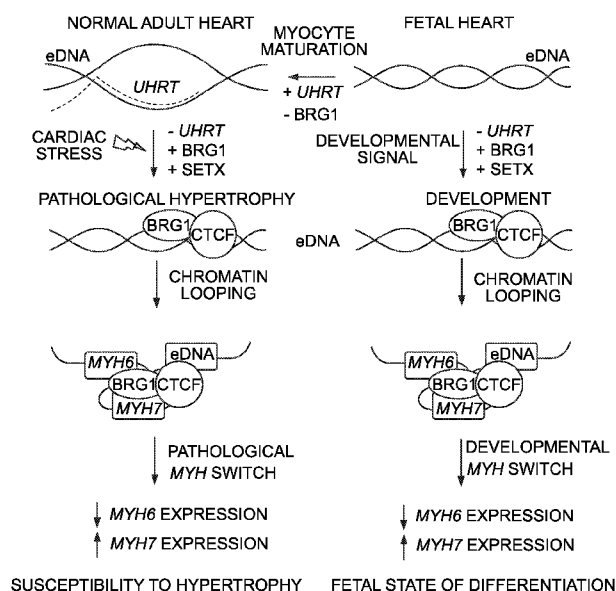


FIG. 22

(57) Abstract: Disclosed are methods of detecting myocardial enhancer RNA levels in mammalian cardiomyocytes. In a further embodiment, a method of disrupting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex, is provided wherein the method comprises providing enhancer RNA to a cardiomyocyte.

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MYOCARDIAL ENHANCER RNA AND METHODS OF USE

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Patent Application No. 62/747,732
5 filed on October 19, 2018. The disclosure of this application is hereby expressly incorporated
by reference in its entirety.

STATEMENT OF GOVERNMENT SUPPORT

This invention was made with government support under HL118087 and HL121197
10 awarded by the National Institutes of Health. The Government has certain rights in the
invention.

INCORPORATION BY REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

15 Incorporated by reference in its entirety is a computer-readable nucleotide/amino acid
sequence listing submitted concurrently herewith and identified as follows: 36 kilobytes ACII
(Text) file named "299852_ST25.txt," created on October 15, 2019.

BACKGROUND OF THE DISCLOSURE

20 Many transcriptional circuits are controlled by enhancer–promoter interactions. An
enhancer is a relatively short (50–1500 bp) region of DNA that can be bound by proteins
(activators) to increase the likelihood that transcription of a particular gene will occur.
Enhancers are cis-acting and can be located up to 1 Mbp (1,000,000 bp) upstream or
downstream from the transcription start site of the gene they regulate. In eukaryotic cells the
25 chromatin complex of DNA is folded so although the enhancer DNA may be far from the gene
in a linear way, it is spatially close to the promoter and gene. This allows it to interact with the
general transcription factors and RNA polymerase II required for expression of the gene. Many
active enhancers transcribe noncoding, enhancer RNAs (eRNAs), capable of facilitating
enhancer–promoter interactions for gene regulation, and levels of eRNAs reflect the degree of
30 enhancer and promoter activation.

SUMMARY

The present disclosure relates generally to the use of noncoding enhancer RNAs
(eRNAs) as therapeutic agents. More specifically, the present disclosure relates to the use of

noncoding myocardial eRNAs to inhibit the formation of a transcriptional complex between the myocardial enhancer DNA (eDNA) and the promoters of the myocardial myosin heavy chain genes (Myh6 and Myh7) in a cardiomyocyte (the eDNA-Myh6 promoter-Myh7 promoter complex). In one embodiment the nonencoding eRNA is a cardioprotective eRNA, named

5 Uheart (Uhrt) for Upstream Myosin Heavy chain RNA Transcript, optionally wherein the Uhrt is an RNA comprising a sequence having at least 95% sequence identity to SEQ ID NO: 1 or SEQ ID NO: 2. A representative listing of relevant sequence identifiers is as follows:

SEQ ID NO: 1 is mouse Uhrt RNA

SEQ ID NO: 2 is human Uhrt RNA

10 SEQ ID NO: 3 is human enhancer DNA

SEQ ID NO: 4 is mouse enhancer DNA

SEQ ID NO: 5 is mouse Uhrt DNA equivalent

SEQ ID NO: 6 is human Uhrt DNA equivalent

In one embodiment, a method of inhibiting the assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex is provided. In some embodiments, the method comprises

15 enhancing the percentage of myocardial enhancer DNA that is bound to Uhrt. In some embodiments, the enhancer DNA comprises a sequence selected from the group of SEQ ID NO: 3 and sequences having at least 95% sequence identity with SEQ ID NO: 3. In one embodiment the method comprises increasing the intracellular concentration of active Uhrt RNA and/or

20 increasing the percentage of myocardial eDNA that has an Uhrt RNA bound to it.

In accordance with one embodiment an isolated nucleic acid comprising a sequence having at least 95% sequence identity to SEQ ID NO: 1 or SEQ ID NO: 2 is provided, or a cDNA derivative of such sequences. In one embodiment the isolated nucleic acid comprises a sequence selected from the group consisting of SEQ ID NO: 1, a cDNA complement of SEQ ID

25 NO: 1, SEQ ID NO: 2, and a cDNA complement of SEQ ID NO:2. In one embodiment a nucleic acid is provided comprising a sequence having at least 95% sequence identity to SEQ ID NO:1, a cDNA complement of SEQ ID NO: 1, SEQ ID NO:2, or a cDNA complement of SEQ ID NO: 2, wherein the nucleic acids are modified to comprise a covalently linked detectable marker. In some embodiments, a nucleic acid sequence is provided comprising SEQ

30 ID NO: 1 coupled to a detectable marker. In some embodiments, a nucleic acid sequence is provided comprising SEQ ID NO: 2 coupled to a detectable marker.

In some embodiments, a method of measuring Uhrt in a patient biological sample is provided. In one embodiment, the method comprises providing an RNA sample recovered from the patient and conducting quantitative reverse transcriptase polymerase chain reaction (rtPCR)

using primers that specifically bind to Uhrt cDNA, and detecting the detecting the resulting amplicon as a measure of the Uhrt in the patient sample.

In some embodiments, a method of identifying a patient at risk for hypertrophy is provided. In one embodiment, the method comprises providing a sample of RNA recovered from cardiomyocytes from the patient, analyzing the levels of Uhrt RNA, and comparing the Uhrt RNA levels in the patient cardiomyocytes to a reference sample. In one illustrative embodiment, if the analysis of the relative concentration of patient Uhrt RNA is lower than the reference sample Uhrt RNA level, then the patient is identified as at risk for hypertrophy. In one embodiment the reference sample is an RNA sample recovered from myocardial cells of one or more healthy individuals that are free of any cardiac disease.

In some embodiments, a method of treating a patient for heart disease is provided. In some embodiment, the method comprises administering an RNA sequence to the patient. In some embodiments the RNA sequence comprises a sequence having at least 95% sequence identity to SEQ ID NO: 2 or its corresponding DNA equivalent thereof.

In some embodiments, a method of switching a cardiomyocyte from a stressed-state to a non-stressed state is provided. In some embodiments, the method comprises decreasing Brg1 activity and increasing Uhrt activity.

In some embodiments, a method of detecting a patient at risk for hypertrophy is provided. The method comprises providing a test sample comprising RNA from the patient, contacting the test sample with a reverse transcriptase primer specific for an enhancer RNA comprising the sequence for Uhrt, reverse transcribing the enhancer RNA to produce a corresponding test cDNA, contacting the test cDNA with PCR primers specific for Uhrt RNA, conducting a PCR reaction on the test cDNA, detecting the amplified product, determining the concentration of the enhancer RNA in the test sample, and obtaining a reference concentration of the corresponding enhancer RNA. In some embodiments, if the enhancer RNA in the test sample is lower in concentration or level than the reference concentration level, then the patient is at risk or may be diagnosed with hypertrophy. In one embodiment the reference sample represents the average concentration of an eRNA having at least 95% sequence identity to SEQ ID NO: 2 as found in the general population.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is an illustration depicting a mouse Myh locus, showing the size of Myh6, Myh7, and eDNA.

Fig. 2 is a graph representing the quantitation of Myh6 and Myh7 mRNAs in E13.5 eDNA-null hearts (Sm22 α -Cre;eDNA^{fl}) verses wild type (wt) fetal hearts.

Fig. 3 is a graph representing the quantitation of Myh6 and Myh7 mRNAs in adult eDNA-null hearts (Tnnt2-rtTA;TRE-Cre;eDNA^{fl}) verses wild type (wt) adult hearts.

5 Fig. 4 is a graph representing the quantitation of Myh6 and Myh7 mRNAs in adult eDNA-null hearts or in wild type (wt) adult hearts 7 days after TAC.

Fig. 5 is a graph representing a ChIP analysis of Brg1-eDNA binding in E13.5 hearts and adult hearts 7 days after sham or TAC operation.

10 Fig. 6 is a graph representing a 3C analysis of Myh6 and Myh7 proximal promoters and eDNA in control (Ctrl) and Brg1-null hearts (KO) of E10.5 embryos.

Fig. 7 is a graph representing a 3C analysis of Myh6 and Myh7 proximal promoters and eDNA in control (Ctrl) and Brg1-null hearts (KO) adult hearts 7 days after sham or TAC operation.

15 Fig. 8 is a graph representing the quantitation of Uhrt and Myh7 RNA in mouse hearts. P: postnatal day.

Fig. 9 is a graph representing the quantification of cardiac Uhrt RNAs 2–56 days (d) after TAC operation.

Fig. 10 is a graph representing the ventricle/body-weight ratio of hearts 2 weeks (w) after TAC.

20 Fig. 11 is a graph representing the quantification of cardiomyocyte cross-sectional areas by wheat germ agglutinin staining in WT and Uhrt KO mice 2 weeks after TAC.

Fig. 12 is an illustration of eDNA reporter mouse lines and quantification of Uhrt 7 days after sham or TAC operation.

25 Fig. 13 is a graph representing the quantification of lacZ RNAs in hearts from eDNA reporter mice 7 days after sham or TAC operation.

Fig. 14 is a graph representing a ChIP quantitation of CTCF-eDNA binding in adult control (Ctrl) and Brg1-null (KO) hearts 7 days after sham or TAC operation.

Fig. 15 is a graph representing a DRIP quantitation of Uhrt-eDNA hybrid in control (Ctrl) and Brg1-null (KO) adult hearts 2 days after sham or TAC operation.

30 Fig. 16 is a graph representing an amylose pull-down assay of MBP-Brg1 D1D2 protein binding to ssDNA (CTCF site), ssRNA (Uhrt sequence at CTCF site) and Uhrt-eDNA hybrid at CTCF site. MBP: maltose binding protein.

Fig. 17 is a graph representing a ChIP analysis of Setx-eDNA binding in adult Ctrl and Brg1-null (KO) hearts 7 days after sham or TAC operation.

Fig. 18 is a graph representing a ChIP-on-ChIP quantitation of Setx on Brg1-immunoprecipitated eDNA 7 days after sham or TAC operation.

Fig. 19 is a graph representing the human Uhrt levels using an X-Gal assay with heart sections.

5 Fig. 20 is a graph representing the human Uhrt levels in heDNA reporter mice 7 days after sham or TAC operation.

Fig. 21 is a graph representing the quantification of Uhrt, Myh6 and Myh7 RNAs of human ventricular tissues with nonfailing and failing hearts.

10 Fig. 22 is an illustration of the molecular interactions between Brg1, Uhrt, and eDNA in cardiac physiology and pathology.

DETAILED DESCRIPTION

DEFINITIONS

15 In describing and claiming the invention, the following terminology will be used in accordance with the definitions set forth below.

As used herein, the term "Uhrt" includes any RNA sequence that binds to an enhancer DNA (eDNA) that participates in an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a mammalian cardiomyocyte. For example this includes both the mouse Uhrt and human Uhrt of SEQ ID NOs: 1 and 2, respectively. In some embodiments human Uhrt is denoted as
20 UHRT.

As used herein, the term "enhancer" refers to a region of DNA that can increase the likelihood that a cis linked gene is transcribed. A myocardial eDNA is an enhancer element located in a patient's cardiomyocyte that helps regulate the expression of Myh7 and Myh6.

25 As used herein, the term "treating" includes prophylaxis of the specific disorder or condition, or alleviation of the symptoms associated with a specific disorder or condition and/or preventing or eliminating said symptoms.

As used herein an "effective" amount or a "therapeutically effective amount" of an enhancer RNA, an interference RNA, or antisense RNA mimetic refers to a nontoxic but sufficient amount of the compound to provide the desired effect. The amount that is "effective"
30 will vary from subject to subject, depending on the age and general condition of the individual, mode of administration, and the like. Thus, it is not always possible to specify an exact "effective amount." However, an appropriate "effective" amount in any individual case may be determined by one of ordinary skill in the art using routine experimentation.

As used herein the term "isolated" describes a polynucleotide, a polypeptide, or a cell that is in an environment different from that in which the polynucleotide, the polypeptide, or the cell naturally occurs.

As used herein the term "detectable marker" describes a molecule conjugated directly or indirectly to a second molecule to facilitate detection of the second molecule. Specific, non-limiting examples of labels include fluorescent tags, enzymatic linkages, and radioactive isotopes.

As used herein, "a reference sample" refers to a sample that is representative of the general population. A test sample is the sample to be analyzed. The reference sample is distinguished from individuals or a subpopulation that displays or expresses a genotypic or phenotypic characteristic that is not present in the majority of a relevant population as a whole. The reference sample may be based on population data (i.e., average concentration of a molecule) or may be a sample recovered from an individual or from a control population known to lack the genotypic or phenotypic characteristic not present in the majority of the relevant population as a whole.

As used herein, "a reference concentration" refers to the concentration of a molecule in the reference sample

As used herein, "Uhr activity" refers to the ability of a Uhr nucleic acid to specifically bind to its corresponding eDNA.

As used herein, "Brg1 activity" refers to the ability of a Brg1 protein to specifically bind to the eDNA-Myh6 promoter-Myh7 promoter complex.

As used herein the term "patient" without further designation is intended to encompass any warm blooded vertebrate domesticated animal (including for example, but not limited to livestock, horses, mice, cats, dogs and other pets) and humans.

EMBODIMENTS

In one embodiment, the present disclosure is directed to the use of noncoding RNAs to inhibit the assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex. In some embodiments, a method of inhibiting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a cell is provided. In some embodiments, the cell is a heart cell. In some embodiments, the cell is a cardiomyocyte.

In some embodiments, a method of inhibiting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte comprising enhancing binding of Uhr to the enhancer DNA is provided. In some embodiments, the enhancer DNA comprises a sequence

selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 4, sequences having at least 95% sequence identity to SEQ ID NO: 3 and sequences having at least 95% sequence identity to SEQ ID NO: 4, and the Uhrt is an RNA sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, sequences having at least 95% sequence identity to SEQ ID NO: 1
5 and sequences having at least 95% sequence identity to SEQ ID NO: 2 or a DNA equivalent of said RNA sequences.

In one embodiment, the method comprises increasing the intracellular concentration of active Uhrt RNA and/or increasing the percentage of myocardial eDNA that is bound to Uhrt RNA. In some embodiments, increasing the intracellular concentration of active Uhrt RNA
10 comprises introducing additional Uhrt RNA into a cardiomyocyte. In an alternative embodiment, a cDNA equivalent of Uhrt may be provided intracellularly to the cardiomyocyte. An active Uhrt RNA or its cDNA equivalent refers to an isolated nucleic acid that is able to bind to eDNA.

In some embodiments, the enhancer DNA comprises a sequence having at least 90%,
15 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 3. In some embodiments, the enhancer DNA consists essentially of a sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 4. In some embodiments, the enhancer DNA consists of a sequence having at least 95% sequence identity to SEQ ID NO: 3. In some embodiments, the enhancer DNA consists of SEQ ID NO:
20 3.

In some embodiments, a method of inhibiting assembly of an eDNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte is provided. The method comprises enhancing binding of Uhrt to said enhancer. In some embodiments, the Uhrt comprises an RNA sequence having at least 95% sequence identity to SEQ ID NO: 2 or its cDNA equivalent thereof. In
25 some embodiments, the Uhrt comprises an RNA sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 2 or its cDNA equivalent thereof. In some embodiments, the Uhrt RNA comprises SEQ ID NO: 2 or its cDNA equivalent thereof. In some embodiments, the enhancer DNA comprises SEQ ID NO: 3 and the Uhrt comprises SEQ ID NO: 2 or its cDNA equivalent.

30 In some embodiments, the method of inhibiting assembly of an eDNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte comprises a step of increasing the amount of Uhrt binding to said enhancer. In some embodiments, the Uhrt comprises an RNA sequence having at least 95% sequence identity to SEQ ID NO: 1 or its cDNA equivalent thereof. In some embodiments, the Uhrt comprises an RNA sequence having at least 90%, 91%, 92%, 93%,

94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 1 or its cDNA equivalent thereof. In some embodiments, the Uhrt RNA comprises SEQ ID NO: 2 or its cDNA equivalent thereof. In some embodiments, the enhancer DNA comprises SEQ ID NO: 3 and the Uhrt comprises SEQ ID NO: 1 or its cDNA equivalent. In some embodiments, the enhancer DNA comprises SEQ ID NO: 4 and the Uhrt comprises SEQ ID NO: 1 or its cDNA equivalent. In one embodiment the enhancer DNA comprises SEQ ID NO: 3 and the Uhrt comprises SEQ ID NO: 2 or its cDNA equivalent.

In some embodiments, the method of inhibiting assembly of an eDNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte comprises a step of decreasing Brg1 activity. In an illustrative embodiment, Brg1 activity is decreased by introducing an interfering RNA (iRNA) to the cardiomyocyte to inhibit the translation of Brg1.

One aspect of the present disclosure is directed to nucleic acids comprising a myocardial eRNA. In one embodiment an isolated RNA comprising a sequence having at least 95% or 99% sequence identity with SEQ ID NO: 1 or 2, or a DNA equivalent is provided. In one embodiment an isolated DNA comprising a sequence having at least 95% or 99% sequence identity with SEQ ID NO: 5 or 6 is provided. In one embodiment the isolated RNA comprises the sequence of SEQ ID NO: 1 or 2, and in a further embodiment the isolated RNA consists of SEQ ID NO: 1 or 2. In one embodiment an isolated DNA is provided comprising the sequence of SEQ ID NO: 5 or 6, and in a further embodiment the isolated DNA consists of SEQ ID NO: 5 or 6.

In accordance with one embodiment, a nucleic acid is provided comprising the sequence of SEQ ID NO: 1 or its cDNA equivalent coupled to a marker. In some embodiments, the nucleic acid comprises a sequence consisting of SEQ ID NO: 1 or its cDNA equivalent coupled to a marker. In some embodiments, the marker is a detectable marker. In some embodiments, detectable the marker is selected from the group consisting of a fluorescent tag, an antibody, and a small peptide. In some embodiments, the detectable marker is coupled to an isolated nucleic acid comprising SEQ ID NO: 1 or its cDNA equivalent by a covalent linkage.

In some embodiments, a nucleic acid comprising a sequence comprising SEQ ID NO: 2 is disclosed. In some embodiments, the nucleic acid comprises a sequence comprising SEQ ID NO: 2 or its cDNA equivalent coupled to a marker. In some embodiments, the nucleic acid comprises a sequence consisting of SEQ ID NO: 2 or its cDNA equivalent coupled to a marker. In some embodiments, the marker is a detectable marker. In some embodiments, the detectable marker is selected from the group consisting of a radionuclide, fluorescent tag, an enzyme, an

antibody, and small peptide. In some embodiments, the detectable marker is coupled to an isolated nucleic acid comprising SEQ ID NO: 2 or its cDNA equivalent by a covalent linkage.

In some embodiments a method of measuring Uhrt in a patient biological sample is provided. The method comprising, providing an RNA sample recovered from said patient,
5 contacting the RNA sample with a nucleic acid that specifically binds to Uhrt, and detecting hybrids formed between the diagnostic nucleic acid and Uhrt as an indication of the presence and quantity of Uhrt in the patient sample. In one embodiment the diagnostic nucleic acid is a nucleic acid that is labeled with a detectable maker. In one embodiment the labeled diagnostic nucleic acid is an RNA sequence having at least 95% or 99% sequence identity with SEQ ID
10 NO: 1 or 2. In one embodiment the labeled diagnostic nucleic acid is an RNA sequence comprising the sequence of SEQ ID NO: 1 or 2, and in a further embodiment the labeled diagnostic nucleic acid is an RNA sequence consisting of SEQ ID NO: 1 or 2. In one embodiment the labeled diagnostic nucleic acid is a DNA sequence comprising a sequence having at least 95% or 99% sequence identity with SEQ ID NO: 5 or 6, or its complement
15 thereof. In one embodiment the labeled diagnostic nucleic acid comprises the sequence of SEQ ID NO: 5 or 6, and in a further embodiment the labeled diagnostic nucleic acid consists of SEQ ID NO: 5 or 6.

In some embodiments, the biological sample is heart tissue, blood, plasma, or a combination thereof, wherein the sample comprises cardiomyocytes RNA. In one embodiment
20 the biological sample is a tissue or blood sample that comprises cardiomyocytes. In some embodiments, the biological sample is biopsy tissue sample comprising cardiomyocytes. In some embodiments, the sample is recovered during an operation, biopsy, or autopsy.

In one embodiment, the method of detecting and/or measuring the relative concentration of eRNA in a patient's cardiomyocytes comprises providing an RNA sample recovered from the
25 patient and conducting quantitative reverse transcriptase polymerase chain reaction (rtPCR) to determined eRNA concentrations. In one embodiment the RNA sample is prepared from a tissue sample isolated from the patient, more particularly from a tissue or blood sample that comprises cardiomyocytes, using techniques known to those skilled in the art. The rtPCR is conducted using standard techniques known to the skilled practitioner, including a first step of
30 converting the RNA present in the RNA sample to cDNA using reverse polymerase and a suitable set of primers. In one embodiment the reverse transcriptase reaction is conducted using a primer that specifically binds to the target eRNA (e.g., an eRNA comprising SEQ ID NO: 1 or 2 or derivative thereof). The generated cDNA is then amplified using standard PCR techniques and primers that specifically bind to Uhrt cDNA. Detection of the resulting amplicon as a

measure of the Uhrt in the patient sample. In some embodiments, the resulting amplicon provides a measure of the relevant concentration of the Uhrt in the patient sample. In some embodiments, the PCR primers each comprise a sequence of at least 10 nucleotides, wherein the continuous primer sequence has at least 95% sequence identity to a corresponding
5 equivalent fragment of SEQ ID NO: 2 or its complement.

In some embodiments, a nucleic acid sequence is provided comprising a sequence of at least 10 nucleotides that has at least 95% sequence identity to a corresponding complementary portion of SEQ ID NO: 2 or its corresponding DNA equivalent or complement thereof. In some
10 embodiments, the nucleic acid is labeled with a detectable marker. In some embodiments, the detectable marker is selected from the group consisting of a fluorophore and radioisotope, and fluorophore. In some embodiments, the term “label” includes a covalent linkage or other known methods in the art of labeling nucleic acids.

In some embodiments, a method of identifying a patient at risk for hypertrophy is provided. The method comprises, providing a sample of RNA recovered from cardiomyocytes
15 from the patient, analyzing the levels of Uhrt, and comparing the relative concentration levels of Uhrt in the patient cardiomyocytes to a reference sample.

In some embodiments, the reference sample comprises a known concentration of Uhrt. In some embodiments, the reference sample is a known concentration of Uhrt representing an amount of Uhrt expected in a patient sample not at risk for hypertrophy. The reference sample
20 may vary depending on age, gender, and species of the patient. In some embodiments, the reference sample comprises an expected concentration of Uhrt in a normal fetal heart from a relevant population. In some embodiments, the reference sample comprises an expected concentration of Uhrt in a normal infant heart from a relevant population. In some
25 embodiments, the reference sample comprises an expected concentration of Uhrt in a normal adolescent heart from a relevant population. In some embodiments, the reference sample comprises an expected concentration of Uhrt in a normal adult heart from a relevant population. In an illustrative embodiment, a low level of Uhrt RNA in the sample RNA recovered from cardiomyocytes compared to the reference sample identifies a patient at risk for hypertrophy.

In some embodiments, the analyzing step is performed using PCR, quantitative real-time
30 PCR, Northern Blot, flow cytometry, mass spectrometry, molecular probes, or a combination thereof.

In some embodiments, a method of treating a patient at risk for heart disease is provided. In some embodiments, the heart disease is hypertrophy. The method comprises administering an isolated RNA sequence to the patient. In some embodiments, the RNA

sequence comprises a sequence having at least 95% sequence identity to SEQ ID NO: 2 or its corresponding DNA equivalent. In some embodiments, the RNA sequence comprises a sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 2 or its DNA equivalent.

5 In some embodiments, the method further comprises decreasing Brg1 activity. In an illustrative embodiment, Brg1 activity can be decreased by administering an iRNA to a cardiomyocyte designed to inhibit the translation of Brg1.

 In some embodiments, the method further comprises analyzing Uhrt levels after the step of administering the RNA. In an illustrative embodiment, the step of analyzing may include
10 performing PCR, rt-qPCR, Northern Blot, flow cytometry, mass spectrometry, the use of molecular probes, or a combination thereof.

 In some embodiments, a method of switching a cardiomyocyte from a stressed-state to a non-stressed state is provided. The method comprising decreasing Brg1 activity and increasing Uhrt activity. In some embodiments, the Brg 1 activity is decreased by providing a Brg1 iRNA.
15 In some embodiments, the Uhrt activity is increased by providing a Uhrt RNA.

 In one embodiment a method of detecting a patient at risk for hypertrophy is provided. The method comprises providing a test sample comprising RNA from the patient, contacting the test sample with a reverse transcriptase primer specific for an enhancer RNA comprising the sequence for Uhrt, reverse transcribing the enhancer RNA to produce a corresponding test
20 cDNA, contacting the test cDNA with PCR primers specific for Uhrt RNA. In some embodiments, the primers comprise a sequence of at least 10 nucleotides having at least a 90% sequence identity to a corresponding complementary portion of SEQ ID NO: 2. In some embodiments, the primers comprise a sequence of at least 10 nucleotides having at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a corresponding
25 complementary portion of SEQ ID NO: 2.

 In some embodiments, the method further comprises conducting a PCR reaction on the test cDNA, and detecting the resulting amplified product. In some embodiments, the method further comprises determining the concentration of the enhancer RNA in the test sample based on the detected test cDNA. In some embodiments, the method further comprises obtaining a
30 reference concentration of the corresponding enhancer RNA from a reference sample. In an illustrative embodiment, a detected low level of the enhancer RNA in the test sample as compared to the reference concentration level of the enhancer RNA indicates hypertrophy.

 In some embodiments, a method of detecting a patient at risk for hypertrophy is provided. The method comprising providing a test sample comprising RNA from the patient;

contacting the test sample with a reverse transcriptase primer specific for an enhancer RNA comprising the sequence for Uhrf; reverse transcribing the enhancer RNA to produce a corresponding test cDNA; contacting the test cDNA with PCR primers specific for Uhrf RNA wherein said primers comprise a sequence of at least 10 nucleotides having at least a 90%
5 sequence identity to a corresponding complementary portion of SEQ ID NO: 2; conducting a PCR reaction on the test cDNA, and detecting the resulting amplified product; determining the concentration of the enhancer RNA in the test sample based on the detected test cDNA; and obtaining a reference concentration of the corresponding enhancer RNA; wherein a detected lower level of the enhancer RNA in the test sample as compared to the reference concentration
10 level of the enhancer RNA indicates hypertrophy.

In accordance with embodiment 1 a method of inhibiting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte cell is provided. The method comprises the step of enhancing binding of Uhrf to said enhancer, wherein said enhancer comprises a sequence having at least 90, 95% or 99% sequence identity with SEQ ID
15 NO: 3.

In accordance with embodiment 2, the method of embodiment 1 is provided wherein the Uhrf comprises an RNA sequence having at least 90, 95% or 99% sequence identity to SEQ ID NO: 2.

In accordance with embodiment 3, the method of embodiment 1 is provided wherein the
20 Uhrf RNA comprises SEQ ID NO: 2 and said enhancer comprises SEQ ID NO: 3.

In accordance with embodiment 4, the method of embodiment 1 is provided wherein the Uhrf comprises an RNA sequence having at least 95% sequence identity to SEQ ID NO: 1.

In accordance with embodiment 5, the method of embodiment 1 is provided wherein the Uhrf RNA comprises SEQ ID NO: 1 and said enhancer comprises SEQ ID NO: 3.

25 In accordance with embodiment 6, the method of any one of embodiments 1-5 is provided wherein the method further comprising a step of decreasing Brg1 activity.

In accordance with embodiment 7, the method of embodiment 6 is provided wherein the Brg1 activity is decreased by introducing an interfering RNA into said cardiomyocyte cell to inhibit translation of Brg1.

30 In accordance with embodiment 8, a nucleic acid comprising an RNA sequence consisting of SEQ ID NO: 1, or its DNA equivalent thereof, coupled to a marker is provided.

In accordance with embodiment 9, a nucleic acid comprising an RNA sequence consisting of SEQ ID NO: 2, or its DNA equivalent thereof, coupled to a marker is provided.

In accordance with embodiment 10, the nucleic acid of embodiment 8 or 9 is provided wherein the marker is selected from the group consisting of a fluorescent tag, an antibody, and a small peptide.

5 In accordance with embodiment 11, a method of measuring Uhrt in a patient biological sample is provided. The method comprises:

providing an RNA sample obtained from said patient;
contacting the RNA sample with a nucleic acid that specifically binds to Uhrt;

and

detecting the Uhrt in the patient sample.

10 In accordance with embodiment 12, the method of embodiment 11 is provided wherein Uhrt is detected by quantitative reverse transcription PCR wherein an amplicon is only produced in the presence of Uhrt.

In accordance with embodiment 13, the method of embodiment 11 or 12 is provided wherein said RNA sample is reverse transcribed into cDNA and said cDNA is contacted with a pair of PCR primers wherein said primers each comprise a sequence of at least 10 nucleotides that each have at least 95% sequence identity to a corresponding DNA equivalent of SEQ ID NO: 2 or a complement thereof.

15 In accordance with embodiment 14, the method of any one of embodiments 11-13 is provided wherein said nucleic acid comprises a sequence of at least 10 nucleotides that has at least 95% sequence identity to a corresponding complementary portion of SEQ ID NO: 2 or its corresponding DNA equivalent or complement thereof, wherein said nucleic acid is labeled with a detectable marker.

20 In accordance with embodiment 15, the method of embodiment 14 is provided wherein the detectable marker is selected from the group consisting of a fluorophore and a radioisotope and a fluorophore.

In accordance with embodiment 16, a method of identifying a patient at risk for hypertrophy is provided. The method comprises:

providing a sample of RNA recovered from cardiomyocytes from the patient;
analyzing the levels of Uhrt RNA in said sample; and

30 comparing the Uhrt RNA levels in the patient cardiomyocytes to a reference sample, wherein a low level of Uhrt RNA compared to the reference sample identifies a patient at risk for hypertrophy.

In accordance with embodiment 17, the method of embodiment 16 is provided wherein the reference sample is either a set of values based on population data (i.e., average

concentration of a molecule in a target population) or the detected eRNA levels in a sample recovered from an individual or from a control population known to lack the relevant genotypic or phenotypic characteristic (e.g., low levels of eRNA, optionally the RNA of SEQ ID NO: 1 or 2) associated with hypertrophy.

5 In accordance with embodiment 18, a method of identifying a patient at risk for heart disease is provided. The method comprises:

administering an RNA sequence to the patient, wherein the RNA sequence comprises a sequence having at least 95% sequence identity to SEQ ID NO: 2 or its corresponding DNA equivalent thereof.

10 In accordance with embodiment 19, the method of embodiment 18 is provided wherein the heart disease is hypertrophy.

In accordance with embodiment 20, the method of embodiment 18 or 19 is provided wherein the method further comprises decreasing Brg1 activity.

15 In accordance with embodiment 21, a method of switching a cardiomyocyte from a stressed-state to a non-stressed state is provided wherein the method comprises:

decreasing Brg1 activity, and

increasing Uhrt activity, wherein the cardiomyocyte is switched from a stressed-state to a non-stressed state.

20 In accordance with embodiment 22, the method of embodiment 21 is provided wherein decreasing the Brg1 activity comprises providing a Brg1 interfering RNA.

In accordance with embodiment 23, the method of embodiment 21 or 22 is provided wherein the step of increasing of Uhrt activity comprises providing a Uhrt RNA.

EXAMPLE 1

25 We identified a cardiac-specific enhancer, situated upstream of its target myosin heavy chain genes (*Myh6* and *Myh7*), that gave rise to a cardioprotective eRNA, which we named *Uheart* (*Uhrt*) for Upstream Myosin Heavy chain RNA Transcript. In fetal mouse hearts, the enhancer produced little *Uhrt* and actively looped to *Myh6* and *Myh7* promoters, forming an enhancer-*Myh6-Myh7* triplex to trigger antithetical *Myh* regulation—*Myh7* up- and *Myh6*
30 down-regulation—to maintain *Myh* in fetal status. As the heart matured, the enhancer robustly transcribed *Uhrt*, which inhibited enhancer's looping to its target *Myh* promoters, switching fetal *Myh* to adult status. Upon cardiac stress, *Uhrt* transcription was shut down, and the enhancer regained its looping to *Myh* loci, triggering *Myh* switch and hypertrophy. Mechanistically, enhancer-*Myh* looping required the chromatin remodeler Brg1 to recruit the

looping regulator CTCF to the enhancer. Binding of CTCF to the enhancer was inhibited by *Uhrt*, which tethered to the enhancer to form RNA-DNA hybrid, preventing CTCF binding. Cardiac stress stimulated Brg1 to bind to *Uhrt*-DNA hybrid and recruit Senataxin—an RNA-DNA helicase—to unwind the hybrid and restore DNA duplex, enabling CTCF to bind and trigger enhancer looping and *Myh* switch. Termination of *Uhrt* transcription unleashed the enhancer and sensitized the hearts to stress-induced hypertrophy. The enhancer-*UHRT* interaction was conserved in human hearts. Our studies thus identify a new cardioprotective eRNA, exemplifying a novel eRNA function in enhancer silencing and disease biology.

Inactive/poised enhancers were excluded from eRNA investigations due to the lack of specific chromatin markers to align with eRNA transcription profiles. The current model indicates that eRNAs are either transcriptional noises that mark activated enhancers or are capable of facilitating enhancer function by enabling enhancer looping to target promoters or by scaffolding enhancer-promoter structure. To the best of our knowledge, there has been no description of eRNAs transcribed from inactive enhancers and capable of keeping the enhancers silent. We found an unconventional eRNA that prevents enhancer-promoter interactions to regulate molecular motor gene expression and cardiac pathophysiology. The molecular motor myosin heavy chain *Myh6* and *Myh7* control the contraction of mammalian hearts. The relative amount of *Myh6* and *Myh7* changes under different pathophysiological conditions, correlating with heart function in animals and in patients with cardiomyopathy. *Myh* genes are regulated antithetically—with up-regulation of one isoform always accompanied by down-regulation of the other—and their ratio governs cardiac resistance to pathological hypertrophy. Hearts expressing more *Myh6* show resistance to pathological stress; those expressing more *Myh7* are susceptible. The new eRNA-enhancer interaction provides a mechanism that coordinates antithetical *Myh* changes to control cardiac contractility and resistance to stress. It also provides a therapeutic strategy to shut down *Myh7*, the mutations of which are the underlying causes of disease in many patients with hypertrophic or dilated cardiomyopathy.

***In vitro* transcription of single guide RNA (sgRNA) for mouse injection**

The 20-bp spacer sequence specific to target locus was designed by deskgen (www.deskgen.com). DNA template for sgRNA *in vitro* transcription was PCR-amplified from pX330 plasmid (42230, Addgene) to acquire a fused DNA template containing the T7 promoter at 5' end, spacer sequence, and transactivating CRISPR RNA (tracrRNA) sequence at 3' end. The PCR product was gel purified (28704, Qiagen) for *in vitro* transcription using MEGAshortscript T7 Kit (AM1354, Thermo Fisher Scientific), and the RNA was purified with miRNeasy Mini Kit (217004, Qiagen) for mouse injection. 20-bp spacer sequences of sgRNAs

for *eDNA^{ff}* mouse line are CAACCCTGAGCACGTGGAGC (SEQ ID NO: 7) and GGCTTAAGAGATCCTCTTGG (SEQ ID NO: 8). Spacer sequence of sgRNA for both *Uhrt* knockout mouse line and *Uhrt* CMV knockin (*Uhrt* KI) is ACACTATGAGATGGACTCGC (SEQ ID NO: 9).

5

Developmental day determination and mouse line generation

The date of observing of a vaginal plug was set as embryonic day E0.5 by convention.

Mouse lines *Sm22α-Cre*, *Brg1^{ff}*, and *Tnnt2-rtTA;Tre-cre* were previously described. CD1 mice were purchased from Charles River (Strain Code: 022). The *eDNA^{ff}* mouse line was generated using the CRISPR/Cas9 system by cytoplasmic injection of mouse embryos with sgRNAs, Cas9 mRNA (L-6129, TriLink Biotechnologies) and single-stranded DNA donors containing loxP sequence (IDT, Ultramer DNA Oligonucleotides). B6D2F1 (C57BL/6 x DBA2, Charles River) female mice and CD1 mouse strains were used as embryo donors and foster mothers, respectively. Superovulated female B6D2F1 mice (4-week-old) were mated to B6D2F1 stud males to collect fertilized embryos. Zygotes were harvested and kept in M16 medium (M7292, Sigma) at 37°C for 1 hr and then transferred in M2 medium (M7167, Sigma) to inject sgRNAs, Cas9 mRNA and single-stranded DNA donors. Injected zygotes were cultured in M16 medium for 1 hr at 37°C before transferred into the oviducts of pseudopregnant CD1 female mice. For *Uhrt* knockout mouse line, the *Uhrt*-tdTO3xpolyA donor vector was generated by cloning homology arms of 2.5-3-kb on either side that is specific to the targeted endogenous locus at the 89-bp from mouse *Uhrt* transcriptional start site into tdTO3xpolyA vector. The donor vector was then mixed with sgRNA and Cas9 mRNA for cytoplasmic injection.

Transgenic mice were derived by pronuclear injection of mouse embryos. For enhancer DNA reporter lines (*eDNA-lacZ* or *heDNA-lacZ*), mouse or human enhancer DNA was subcloned into pENTR/TEV/D-TOPO donor vector (K253520, Thermo Fisher Scientific), and gateway recombination was performed with hsp68-lacZ destination vector (37843, Addgene) to generate eDNA-hsp68-lacZ reporter for mouse injection. For *Uhrt* reporter lines (*CMV-eDNA-lacZ* and *CMV-heDNA-lacZ*), mouse *Uhrt* or human *UHRT* cDNA was subcloned into a modified pcDNA3.1(+) vector whose CMV promoter was surrounded by two loxP sites. A fragment containing both loxP, CMV, *Uhrt/UHRT* cDNA and SV40 polyA terminator (pA) was subcloned into pENTR/TEV/D-TOPO donor vector and recombined into the hsp68-lacZ destination vector by gateway reaction to generate LoxP-CMV-loxP-*Uhrt*-pA-hsp68-lacZ or LoxP-CMV-loxP-*UHRT*-pA-hsp68-lacZ plasmid. These plasmids were then linearized for pronuclear injection.

LacZ reporter assay

Whole-mount X-gal staining was performed using X-gal staining kit (K146501, Thermo Fisher Scientific) following the manufacturer's instruction. E11.5 embryos were fixed in 4% paraformaldehyde/PBS on ice for 30 min. For adult heart tissues, 7- μ m sections were acquired using a Leica cryostat and air-dried for 5 min. 4% paraformaldehyde/PBS was added on the section and fixed for 10 min at room temperature, followed by washing with PBS for 3 times. Embryos or sections were then processed for X-gal staining.

Chromosome conformation capture with quantitative PCR (3C-qPCR)

3C-qPCR was performed following the protocol described with modifications. Briefly, embryonic mouse hearts were collected and cross-linked with 1% formaldehyde immediately. Adult hearts were cut into pieces on ice and homogenized in 1% formaldehyde immediately and incubated at room temperature for 15 min with rotation, followed by standard glycine quenching. After centrifuge (2,000 g x 5 min), pellets were resuspended in ice-cold PBS and pass the tissue strainer (250 μ m) for centrifuge. The pellets were resuspended in cytoplasmic lysis buffer (10 mM HEPES, 60 mM KCl, 1 mM EDTA, 0.1% (v/v) NP40, 1 mM DTT and 1 mM PMSF, pH 7.6) and incubated on ice for 30 min and then centrifuged (2,000 g x 5 min) to collect cross-linked nuclei. Nuclei was washed with restriction enzyme buffer and resuspended in restriction enzyme buffer with 0.3% SDS and incubated with shaking at 1400 rpm overnight at 37 °C. 2x volume of restriction enzyme buffer was added to disperse the aggregations. SDS was sequestered by adding Triton X-100 (1.8% of final concentration) and incubated with shaking at 1400 rpm for 2 hr at 37°C. Restriction enzyme was then added and incubated with shaking at 1400 rpm overnight at 37°C. In the next day, SDS was added into the buffer (1.6% of final concentration) and incubated with shaking at 1400 rpm for 30 min at 65 °C to stop the digestion. A 7-ml ligation reaction system was established with T4 DNA ligase (M0202, New England Biolabs) and DNA at the final concentration less than 1 ng/ μ l to favor intramolecular ligation. Ligation was performed overnight at 16°C with rotation. Reverse-cross-link was performed by adding 5 M NaCl, 1 M EDTA and Proteinase K into the ligation mix overnight at 65 °C followed by phenol/chloroform extraction and ethanol precipitation. The 3C library was amplified in 5-7 PCR cycles using Phusion polymerase (M0530, New England biolabs) and diluted for nested quantitative PCR. For *Myh6*-eDNA and *Myh6-Myh7* interactions, CSP6I (ER0211, Thermo Fisher Scientific) was used for digestion. The genomic area +1192 to -1892 from *Myh6* transcriptional start site generated by CSP6I digestion was used for determining

Myh6-eDNA interaction. The genomic area +1237 to +2911 from *Uhrt* transcriptional start site generated by CSP6I digestion was used for determining *Myh6*-eDNA interaction. The genomic area -147 to -1302 from *Myh7* transcriptional start site generated by CSP6I digestion was used for determining *Myh6-Myh7* interaction. For *Myh7*-eDNA, MSPI (R0106, New England Biolabs) was used for digestion. The genomic area +2263 to -1093 from *Myh7* transcriptional start site generated by MSPI digestion was used for determining *Myh7*-eDNA interaction. The genomic area +528 to +1665 from *Uhrt* transcriptional start site generated by MSPI digestion was used for determining *Myh7*-eDNA interaction.

Chromosome Conformation Capture Carbon Copy (5C)

For 5C library preparation, 3C library was denatured at 95°C for 5 min with salmon testis DNA (Sigma) and 5C oligonucleotides in annealing buffer (20 mM Tris-acetate at pH 7.9, 50 mM potassium acetate, 10 mM magnesium acetate, and 1 mM DTT), followed by annealing for 16 h at 48 °C. Annealed primers were ligated for 1 h at 48 °C by adding 20 µL of ligation buffer (25 mM Tris-HCl at pH 7.6, 31.25 mM potassium acetate, 12.5 mM magnesium acetate, 1.25 mM NAD, 12.5 mM DTT, 0.125% Triton X-100) containing 10 units of Taq DNA ligase (NEB). Unincorporated primers were removed by MinElute Reaction Cleanup Kit (Qiagen). 5C ligation products were amplified by PCR using specific 5C primers for each looping reaction as follow.

Myh7-eDNA 5C-F, TAATACGACTCACTATAGCCTTGTCTTCCC (SEQ ID NO: 10)

Myh7-eDNA 5C-R, TATTAACCCTCACTAAAGGGAAGCCCAGA (SEQ ID NO: 11)

Myh6-eDNA 5C-F, TAATACGACTCACTATAGCCGCTCTTGAG (SEQ ID NO: 12)

Myh6-eDNA 5C-R, TATTAACCCTCACTAAAGGGACCTAAACCTC (SEQ ID NO: 13)

Myh6-Myh7 5C-F, TAATACGACTCACTATAGCCCTTGAGGG (SEQ ID NO: 14)

Myh6-Myh7 5C-R, TATTAACCCTCACTAAAGGGAATGGGCTG (SEQ ID NO: 15).

Chromatin immunoprecipitation quantitative PCR (ChIP-qPCR)

Embryonic mouse hearts were collected and cross-linked immediately. For adult hearts, tissues were cut into pieces on ice, homogenized with 1% formaldehyde immediately and incubated at room temperature for 15 min with rotation. Glycine was then added to quench the cross-link reaction and pass the tissue strainer (250 µm) (87791, Thermo Fisher Scientific). After centrifuge (2,000 g x 5 min), the pellets were resuspended in nuclei lysis buffer (1% SDS, 10 mM EDTA, 50 mM Tris, pH 8.1) for sonication to shear chromatin with Bioruptor (Diagenode) (30 s on, 30 s off, power setting H, 30 min, twice) to generate the fragments at the

range of 100-300 bp. Sonicated chromatin was pre- cleaned by ChIP-Grade Protein G magnetic beads (9006, Cell Signaling Technologies) and immunoprecipitated with anti-Brg1 J1 antibody, anti-CTCF (61311, Active motif), anti-RPA (MABE285, Millipore) or anti-Senataxin (ABN421, Millipore) overnight. ChIP- Grade Protein G magnetic beads were added to collect the immunoprecipitate complex and washed once with low salt wash buffer (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 150 mM NaCl), high salt wash buffer (0.1% SDS, 1% Triton X- 100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 500 mM NaCl), LiCl wash buffer (0.25 M LiCl, 1% IGEPAL-CA630, 1% deoxycholic acid (sodium salt), 1 mM EDTA, 10 mM Tris, pH 8.1) and twice with TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0). Quantitative PCR was then performed with primers as follows. Mouse ChIP-eDNA-F, CTTCGTATCAGGGGGTGTTC (SEQ ID NO: 16) Mouse ChIP-eDNA-R, GAAGGGGTTGGAAGGTCACT (SEQ ID NO: 17).

Transaortic constriction (TAC)

The TAC surgery was performed on adult mice of 8–10 weeks of age and between 20 and 25 g of weight. Mice were fed with doxycycline food pellets (6 g doxycycline per kg of food; Bioserv) 7 days before the TAC operation if needed. Mice were anaesthetized with isoflurane (3%, inhalation) in an induction chamber and endotracheal intubation was performed with a 20-gauge intravenous catheter and ventilated with a mouse ventilator (Minivent, Harvard Apparatus) to maintain anesthesia with haled isoflurane (1–2%). A longitudinal 5 mm incision of the skin was made with scissors at the midline of sternum. The chest cavity was opened by a small incision at the level of the second intercostal space 2–3 mm from the left sternal border and two chest retractors were gently inserted to spread the wound 4–5 mm in width to expose the transverse portion of the aorta. A nonabsorbable 6-0 suture is brought by one ligation aid and moved underneath the transverse aorta between the left common carotid artery and the brachiocephalic trunk to make a loose knot. For aortic constriction, 27-gauge needle was placed directly above and parallel to the aorta. The knot was then tied around the aorta and needle, and secured with a second knot. The needle was removed from the knot carefully to create a lumen with a fixed stenotic diameter. The chest cavity was then closed by 6-0 silk suture. Sham operated mice underwent similar surgical procedures, including isolation of the aorta and looping of the aorta, but without tying of the suture. The TAC was verified and qualified by the pressure gradient across the aortic constriction measured by echocardiography. Only mice with a pressure gradient 30 mmHg were used for further experiments and analysis.

Echocardiography

Transthoracic ultrasonography was performed with a GE Vivid 7 ultrasound platform (GE Health Care) equipped with a 13 MHz transducer to determine aortic pressure gradient and left ventricular function at the time points as indicated. The echocardiographer was blinded to the genotypes and surgical procedure. The isoflurane (inhalational) was adjusted to anaesthetize the mice while maintaining their heart rates at 450–550 beats per minute to minimize its effects on heart rates. The peak aortic pressure gradient was measured by continuous wave Doppler across the aortic constriction. Left ventricular function was assessed by M-mode scanning of the left ventricular chamber, standardized by two-dimensional, short-axis views of the left ventricle at the mid papillary muscle level. Left ventricular chamber size and wall thickness were measured in at least three beats from each projection and averaged. Left ventricular internal dimensions at diastole and systole (LVIDd and LVIDs, respectively) were measured. The fractional shortening (FS) of the left ventricle was defined as $(1 - \text{LVIDs}/\text{LVIDd}) \times 100\%$. The mean FS of the left ventricle was determined by the average of FS measurements of the left ventricular contraction over five beats. *P* values were calculated by Student's *t*-test. Error bars indicate standard error of the mean (SEM).

Rapid amplification of cDNA ends (RACE) and *Uhrt* cloning

The 5' and 3' RACE were performed using the SMARTer® RACE 5'/3' kit (634858, Takara Bio) following the manufacturer's instruction. Total RNA of adult mouse hearts was extracted by TRIzol and used as template. Primers used for 5' RACE (GCCTAGGGGCTGTGGCCTCTTGG; SEQ ID NO: 18) and 3' RACE (CCAAGAGGCCACAGGCCCTAGGC; SEQ ID NO: 19). Once the 5' and 3' cDNA ends were reached, common primers were used to amplify full-length *Uhrt* transcripts, which were subcloned into pCR II TA cloning vector for sequencing. For human *UHRT*, total RNA of adult human hearts was purchased from Takara Bio (636532) as template. Primers used for 5' RACE (TACCTCTCTATCCTCTTGTCCAATGACATTGCC; SEQ ID NO: 20) and 3' RACE (GGAGGGGGGTGGCATGACTCTTGAAGA; SEQ ID NO: 21). Once the 5' and 3' cDNA ends were reached, common primers were used to amplify full-length *UHRT* transcripts, which were subcloned into pCR II TA cloning vector for sequencing.

Northern blot analysis and *in vitro* translation

Northern blot analysis was performed using the DIG Northern Starter Kit (12039672910, Roche) with 5 ug total RNAs from adult mouse hearts. Single-stranded RNA

probe template was generated by PCR with a forward primer containing the T7 promoter. Single-stranded RNA was then *in vitro* transcribed with labeling mix in the kit to label the RNA with digoxigenin. For *in vitro* translation, full-length RNAs were transcribed and performed *in vitro* translation using the PURExpress Kit (E6800, New England Biolabs). To label synthesized protein, Transcend-tRNA (L506A, Promega) was added into the translation reaction system.

Codon substitution frequency (PhyloCSF) and ribosome profiling (Ribo-Seq)

To measure the coding potential of mouse *Uhrt* and human *UHRT*, we used PhyloCSF software to compute the score for how likely each sequence represents a conserved coding region. We used multi-species alignment between human, mouse, rat, rhesus and dog for each gene as input for PhyloSCF. The options used for PhyloSCF are ATGStop for sequences with full ORF, and Asis for other sequences.

Ribosomal profiling was performed using mammalian TruSeq Ribo Profile (RPHMR12126, Illumina) following the manufacture's instruction with modifications described below. Mouse adult hearts were dissected and rinsed in ice-cold PBS with 8 mg/ml cycloheximide (2112, Cell Signaling Technologies) for 5 min. Tissues were then cut into pieces and homogenized with lysis buffer in the kit. Lysates were treated with ARTseq nuclease and the ribosome protected fragments were isolated using MicroSpin S-400 columns (27514001, GE Healthcare). rRNAs were depleted by Ribo-Zero Gold rRNA Removal kit (MRZG126, Illumina) and ribosome-protected fragments were amplified in 9 PCR cycles using Phusion polymerase and purified by 10% Novex™ TBE-Urea Gels (EC6875BOX, Thermo Fisher Scientific). Libraries were sequenced on HiSeqSE50 platform. Reads were mapped to mm10 build of the mouse genome using TopHat2.

Quantitative reverse transcription PCR (RT-qPCR)

Total RNA was extracted by TRIzol, and reverse transcription was performed with PrimeScript™ RT reagent Kit (RR036a, Takara Bio). For strand-specific reverse transcription, SuperScript™ VILO™ cDNA Synthesis Kit (11754050, Thermo Fisher Scientific) was used with specific primers (Mouse: GAGGCATCCGATCCCATTACAGA (SEQ ID NO: 22); human: CTTCCCACTACCTCTCTATC (SEQ ID NO: 23). RT-qPCR was then performed using Power SYBR Green PCR Master Mix (4367659, Thermo Fisher Scientific) with *StepOnePlus* Real-time PCR System (Thermo Fisher Scientific). Transcription factor Iib (*TfIib*) was used as a normalizer. Threshold cycles and melting curve measurements were performed with ABI software. Primers for RT-qPCR of mRNA were as follows. Mouse *TfIib*-F,

CTCTGTGGCGGCAGCAGCTATTT (SEQ ID NO: 24); Mouse *TfIIb*-R,
 CGAGGGTAGATCAGTCTGTAGGA (SEQ ID NO: 25); Mouse *Myh6*-F,
 ACGGTGACCATAAAGGAGGA (SEQ ID NO: 26); Mouse *Myh6*-R,
 TGTCCCTCGATCTTGTGGAAC (SEQ ID NO: 27); Mouse *Myh7*-F,
 5 GCCCTTTGACCTCAAGAAAG (SEQ ID NO: 28); Mouse *Myh7*-R,
 CTTACAGTCACCGTCTTGC (SEQ ID NO: 29); Mouse *Uhrt*-F,
 TCAGTCTGTGGCCTAAGCTC (SEQ ID NO: 30); Mouse *Uhrt*-R,
 TGAACCTCGGCAAGTCCCTC (SEQ ID NO: 31); Human *TfIIb*-F,
 GAGCAGTTCTGATCGGGCAA (SEQ ID NO: 32); Human *TfIIb*-R,
 10 CGAGGGTAGATCAGTCTGTAGGA (SEQ ID NO: 33); Human *Myh6*-F,
 TTCAGGATTCTCCGTGAAGGG (SEQ ID NO: 34); Human *Myh6*-R,
 GTCGAACTTGGGTGGGTTCT (SEQ ID NO: 35); Human *Myh7*-F,
 GAGCTCACCTACCAGACGGA (SEQ ID NO: 36); Human *Myh7*-R,
 CCTCATTCAAGCCCTTCGTG (SEQ ID NO: 37); Human *UHRT*-F,
 15 AGTGGCCCCAAGGTGTTAAG (SEQ ID NO: 38); and Human *UHRT*-R,
 CGCGTGCACCTATTCTCTCT (SEQ ID NO: 39).

Cytoplasmic, nuclear and chromatin-associated RNA fraction

To isolate cytosolic and nuclear RNAs from adult hearts, 10 µg hearts were
 20 homogenized in cell fractionation buffer from PARIS kit (AM1921, Thermo Fisher Scientific),
 followed by centrifuge (500 g x 5 min). The supernatants (set as the cytosolic fraction) and the
 pellets were washed twice and lysed in cell disruption buffer on ice. TRIzol was then added into
 both fractions to extract RNA for RT-qPCR. To isolate chromatin-associated RNAs, nuclei
 pellets were first rinsed in glycerol buffer (20 mM Tris-HCl, pH 7.9, 75 mM NaCl, 0.5 mM
 25 EDTA, 0.85 mM DTT, 0.125 mM PMSF, 50% glycerol) and equal volume of cold nuclei lysis
 buffer (10 mM HEPES, pH 7.6, 1 mM DTT, 7.5 mM MgCl₂, 0.2 mM EDTA, 0.3 M NaCl, 1 M
 UREA, 1% NP-40) was added and incubated for 10 min on ice with vortex for 2 times for each
 5-min interval. After centrifuge (12,000 g x 10 min), the supernatants were collected as
 nucleoplasm, and the pellets as chromatin. Pellets were washed twice with cold nuclei lysis
 30 buffer. TRIzol was then added into both fractions to extract RNA for RT-qPCR.

Cardiomyocyte isolation

Cardiomyocytes were isolated from the ventricles of adult mice using enzymatic
 digestion on a Langendorff system with constant retrograde perfusion and pressure

measurement. Enzyme digestion solution was made with Ca^{2+} (12.5 μM), collagenase type II (300 U/ml, LS004174, Worthington Biochemicals), and protease type XIV (0.04 mg/ml, P5147, Sigma) in Tyrode's solution (133.5 mM NaCl, 4.0 mM KCl, 1.2 mM NaH_2PO_4 , 10 mM HEPES, 1.2 mM MgSO_4 , and 10 mM glucose; pH = 7.4, adjusted with NaOH) Ventricular myocytes were resuspended in Tyrode's solution containing 1 mg/ml BSA and centrifuged at 46 g x 3 min, and the cardiomyocyte pellets were collected. The supernatants were further centrifuged at 46 g x 3 min to discard the pellets, and the cell suspensions were centrifuged at 300 g x 10 min. CD31^+ endothelial cells were then isolated from the pellets using mouse CD31 MicroBeads (130097418, Miltenyi). Remaining cells were collected as cardiac fibroblasts.

Histology, trichrome staining, and morphometric analysis of cardiomyocytes

Adult hearts were dissected and fixed overnight in 4% paraformaldehyde/PBS, followed by dehydration through an ethanol series, treated with xylenes, and embedded in paraffin wax overnight. 7 μm sections were then acquired using a Leica microtome. After re-hydration, the sections were stained with trichrome stain (Masson) kit (HT15-1KT, Sigma) following the manufacturer's instruction. Fluorescein isothiocyanate-conjugated wheat germ agglutinin (WGA) was used to visualize the cell border of cardiomyocytes in paraffin sections. Cardiomyocytes of the papillary muscle at the mid-left ventricular cavity were selected for cardiomyocyte size. The images were acquired by fluorescence microscope (Nikon Eclipse Ni) equipped with HAMAMATSU imaging system.

Strand-specific DNA-RNA immunoprecipitation with quantitative reverse transcription PCR (DRIP-RT-qPCR)

Embryonic or adult hearts were collected and digested with lysis buffer (0.5% SDS, 2 mM EDTA, 10 mM Tris-HCl, pH 8.1, 100 mM NaCl). Genomic DNA was then extracted by phenol/chloroform and precipitated by ethanol. 5 μg genomic DNA was further digested by a combination of BsoB1, NheI, NcoI and StuI overnight at 37 °C with or without RNase H (M0297, New England Biolabs) and followed by phenol/chloroform extraction and ethanol precipitation. Digested DNA was then rinsed in 500 μl binding buffer (1% Triton X-100, 50 mM Tris-HCl, 75 mM KCl, 3 mM MgCl_2 , 10 mM DTT) and pre-cleaned by ChIP-Grade Protein G magnetic beads. Anti-DNA-RNA hybrid S9.6 antibody (ENH001, Kerafast) was then incubated with the digested DNA overnight at 4 °C with rotation. The immunoprecipitated complex was washed once with low salt wash buffer (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 150 mM NaCl), high salt wash buffer (0.1% SDS, 1% Triton

X-100, 2 mM EDTA, 20 mM Tris- HCl, pH 8.1, 500 mM NaCl), LiCl wash buffer (0.25 M LiCl, 1% IGEPAL-CA630, 1% deoxycholic acid (sodium salt), 1 mM EDTA, 10 mM Tris, pH 8.1) and twice with TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) and then treated by proteinase K at 65 °C with agitation. DNA/RNA hybrid was extracted by phenol/chloroform, precipitated by ethanol, and digested with TURBO™ DNase (AM2238, Thermo Fisher Scientific). TRIzol was then added to extract RNA, and strand-specific reverse transcription was performed with SuperScript™ VILO™ cDNA Synthesis Kit.

Western immunoblot analysis

Whole hearts were collected and homogenized in buffer A (25 mM HEPES, pH 7.0, 25 mM KCl, 5 mM MgCl₂, 0.05 mM EDTA, 10% glycerol, 0.1% NP-40). After lysis of heart tissues on ice for 10 min, nuclear pellets were collected and resuspended in buffer B (50 mM Tris-HCl, pH 6.8, 2% SDS, 100 mM DTT, 10% glycerol) and lysed on ice for 30 min. After centrifuge, the supernatants were collected and boiled. The blots were reacted with antibodies for CTCF (61311, Active motif), Senataxin (ABN421, Millipore), and TFIIB (ab109518, Abcam) followed by HRP-conjugated anti-rabbit IgG (211-032-171, Jackson ImmunoResearch Laboratories). Chemiluminescence was detected with Pierce™ ECL Plus Western Blotting Substrate (32134, Thermo Fisher Scientific) and visualized by Odyssey Image System (LI-COR).

Electrophoretic mobility shift assay (EMSA)

EMSA was performed by using LightShift™ Chemiluminescent RNA EMSA Kit (20158, Thermo Fisher Scientific) following the manufacture's instruction. For RNA-DNA hybrid probe, a DNA oligo containing the T7 promoter (lowercase) and a CTCF binding sequence (uppercase) from the mouse eDNA locus with CTCF consensus binding motif (underlined) and surrounding sequences (ttaatacgactcactataggTCAGCCACACAACAGAGGGGGTGGCACAGCTCTTGGGA (SEQ ID NO: 40)), as well as its reverse complementary DNA oligo, were synthesized (Thermo Fisher Scientific) and annealed for *In vitro* transcription with MEGAshortscript T7 Kit. Given the RNA product contains two more guanine nucleotides (lowercase) at 5' end by T7 RNA polymerase (ggTCAGCCACACAACAGAGGGGGTGGCACAGCTCTTGGGA (SEQ ID NO: 41)), its 5' biotin-labeled reverse complementary DNA oligo was introduced 2 more cytosine nucleotides at 3' end to acquire a blunt-ended probe. For double-stranded DNA probe, a DNA oligo with the same sequence as RNA was synthesized and annealed with the biotin-labeled

reverse complementary DNA oligo. A mutant probe was synthesized with a mutated CTCF consensus binding motif (ggTCAGCCACACAACAGAAAAAATGGCACAGCTCTTGGGA (SEQ ID NO: 42)). All these biotin-labelled probes were incubated with 200 ng CTCF recombinant proteins (H00010664-P01, Abnova) in 20 µl 1X binding buffer (10 mM HEPES-KOH, pH 7.3, 10 mM NaCl, 1 mM MgCl₂, 1 mM DTT) with 5 µg tRNA carrier at room temperature for 30 min. The reactions were then loaded onto 6% Novex TBE gels (EC6265BOX, Thermo Fisher Scientific) and transferred to Bright Star-Plus positive charged membrane (AM10110, Thermo Fisher Scientific). Biotin-labeled probes were detected by Chemiluminescent Nucleic Acid Detection Module (89880, Thermo Fisher Scientific) using Odyssey Imaging System (LI-COR).

Amylose pull-down

20 pmol purified Maltose-binding protein (MBP) or MBP-Brg1 D1D2 protein was incubated with Amylose Magnetic Beads (E8035, New England Biolabs) for 2 hr at 4 °C with rotation. After washed three times with MBP column binding buffer (10 mM Tris-HCl, pH7.5, 150 mM NaCl, 1 mM DTT, 0.1% Triton X-100), the beads were resuspended in 500 µl binding buffer. 20 pmol of 200-bp single stranded DNA (ssDNA) probe containing the CTCF binding motif in the eDNA (chr14:55,004,492-55,004,691, mm10), single stranded RNA (ssRNA) probe with the same sequence as the ssDNA, and DNA-RNA hybrid probe annealed from the ssRNA and its complementary DNA were incubated with the beads for 2 hr at 4 °C with rotation and washed three times with low salt wash buffer (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 150 mM NaCl) and three times with high salt wash buffer (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 500 mM NaCl). The beads were then eluted with elution buffer (10 mM Tris-HCl, pH7.5, 150 mM NaCl, 1 mM DTT, 0.1% Triton X-100, 10 mM maltose). Proteinase K was incubated with the elution buffer at 65 °C for 1 hr and the probes were purified by miRNeasy Mini Kit (217004, Qiagen). Reverse transcription was performed for ssRNA samples with SuperScript™ VILO™ Master Mix (11755050, Thermo Fisher Scientific). All samples were then performed with qPCR analysis.

Motif prediction

MEME Suite was used for motif discovery as described. Briefly, all sequences from different species were trimmed to the same size and subjected to MEME-ChIP using JASPAR_CORE_2009.MEME motif database. CentriMo from MEME Suite was used to

calculate different motifs distribution. FindMotif tools from HOMER were used to confirm the results from MEME Suite.

RNA secondary structural prediction and DNA homology score

5 To predict the secondary structure for mouse *Uhrt* and human *UHRT*, their sequences were submitted on Vienna RNA fold web server (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>) with calculation of minimum free energy. To score the sequence homology of mouse and human eDNA, as well as mouse *Uhrt* and human *UHRT*, respective sequences were submitted on T-coffee for analysis (<https://www.ebi.ac.uk/Tools/msa/tcoffee/>).

10

Human heart tissue analysis

Human heart samples were obtained from Duke Human Heart Repository (<https://sites.duke.edu/dhhr/>) and as described. The study of human tissues is in compliance with the regulation of Duke and Indiana University. Human tissues were processed for RT-qPCR. Other human tissue RNAs were purchased from Takara Bio.

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Statistical analysis

Statistical significances were calculated using GraphPad Prism 6 (GraphPad Software, La Jolla, CA) or SPSS 25 (IBM, Armonk, New York). Differences between two groups were compared by student's *t*-test, and differences among multiple groups were compared by one-way ANOVA analysis of variance. All significance levels were computed as 2-tailed and a value of $P < 0.05$ was considered statistically significant.

20

EXAMPLE 2

25 By surveying cardiac chromatin modifications in ENCODE database, we identified a genomic region 7.5-kb upstream of the mouse *Myh7* gene transcriptional start site that spanned a highly conserved 4-kb genomic region (Fig. 1). In embryonic day 14.5 (E14.5) hearts, this genomic region was enriched with chromatin signatures of active enhancers—acetylated histone 3 lysine 27 (H3K27ac) and monomethylated histone 3 lysine 4 (H3K4me1) with low levels of trimethylated histone 3 lysine 4 (H3K4me3)—and the boundaries of this genomic region were well-demarcated by levels of H3K27ac and H3K4me1 (Fig. 1). Also, this genomic region contained consensus binding motifs of transcriptional factor MEF2A and GATA4 that are critical for heart development, and the motifs were conserved between mouse and human. Accordingly, we postulated this 4-kb DNA functioned as a cardiac-specific enhancer and

30

referred to it as eDNA. To test whether eDNA was an enhancer, we fused the eDNA fragment to basal heat shock promoter hsp68 to drive the expression of *lacZ* reporter gene in transgenic mice. We found that eDNA enhanced *lacZ* expression only in the heart but not other tissues of E11.5 embryos, indicating a cardiac-specific enhancer activity. DNase-I footprinting studies (ENCODE database) revealed hypersensitivity sites in eDNA region primarily in the heart, consistent with its cardiac-specific activity. The role of eDNA as a cardiac-specific enhancer was collectively supported by chromatin signatures, *in vivo* reporter studies, DNase-I footprinting, as well as the ability of eDNA to undergo looping to its target promoters, and its bidirectional transcription into cardiac-specific noncoding RNAs.

Given that eDNA was located upstream of *Myh* genes, we asked whether eDNA targeted *Myh* genes. We first examined *Myh* expression in mouse hearts lacking eDNA. To generate eDNA knockout mice, we used Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) technology to introduce two loxP sites flanking eDNA (*eDNA^{ff}*). *eDNA^{ff}* alleles were then deleted in cardiomyocytes by Cre recombinase driven by *Sm22α* promoter, which acted in fetal cardiomyocytes by E8.5 and deleted eDNA efficiently. In E13.5 eDNA-null hearts (*Sm22αCre;eDNA^{ff}*), *Myh7* was decreased by 60%, *Myh6* increased 62%, and *Myh7/6* ratio reduced 75% (Fig. 2), suggesting that eDNA is active in fetal hearts to maintain high *Myh7* and low *Myh6* expression. We then tested whether eDNA was required for pathological *Myh* switch in stressed adult hearts. We crossed *eDNA^{ff}* with the driver *Tnnt2-rtTA;TRE-Cre* to enable doxycycline-inducible, cardiomyocyte-specific deletion of eDNA in adult hearts, with Cre recombinase driven by cardiac-specific troponin (*Tnnt2*) promoter and tetracycline response element (*TRE*). In this mouse line (*Tnnt2-rtTA;TRE-Cre;eDNA^{ff}*), doxycycline treatment effectively deleted eDNA within 7 days. In normal adult hearts, eDNA deletion had no impact on *Myh6* or *Myh7* levels (Fig. 3), suggesting the lack of eDNA activity in mature hearts. However, when the hearts were pressure-overloaded by transaortic constriction (TAC), eDNA deletion prevented stress-induced *Myh6*-to-*Myh7* switch and restored *Myh* isoform expression to pre-stress levels (Fig. 4), indicating that eDNA is active in stressed hearts to trigger pathological *Myh* switch, a return to fetal state. Overall, the results suggest that eDNA is functionally active in fetal and stressed hearts to control *Myh* isoform expression.

We then tested whether eDNA could form a three-dimensional chromatin loop, like an enhancer, to its target *Myh7* and *Myh6* promoters (Fig. 1). We conducted chromosome conformation capture with quantitative PCR (3C-qPCR) to determine the looping between eDNA and *Myh* promoters. In fetal and stressed adult hearts when eDNA was essential for *Myh* expression (Fig. 2 and 4), eDNA was capable of looping to *Myh6* and *Myh7* proximal promoters,

which were previously shown to control *Myh* isoform expression. Conversely, eDNA displayed much diminished looping to *Myh* loci in normal adult hearts, consistent with its lack of activity on *Myh* expression in mature hearts (Fig. 3). The specificity of 3C-qPCR assays was validated by sequencing of the PCR products. Remarkably, *Myh6* and *Myh7* promoters, although 28-kb
 5 apart, were in close proximity in the three-dimensional chromatin space, providing a structural basis for their coordinated changes. Collectively, the results of eDNA reporter, knockout, and chromatin looping studies indicate that eDNA acts as an enhancer to control *Myh* promoters in fetal and stressed hearts. Next, we asked whether eDNA was essential for hypertrophy, given that *Myh* isoform ratio controls cardiac resistance to pathological stress. Indeed, in eDNA-null
 10 hearts (*Tnnt2-rtTA;TRE-Cre;eDNA^{ff}*), TAC-induced hypertrophy was reduced by 55%, with the decline of left ventricular fractional shortening reduced by 42%. These studies demonstrated a pathogenic role of eDNA as an enhancer in stress-induced *Myh* switch and hypertrophy.

We next asked if Brg1, a pro-hypertrophic chromatin remodeler that triggered *Myh* switch, was essential for eDNA looping to *Myh* loci. Chromatin immunoprecipitation (ChIP) of
 15 heart tissues showed that Brg1 was enriched on eDNA in fetal hearts (E13.5), whereas its occupancy of eDNA was reduced by 35% in normal adult hearts (Fig. 5). Upon cardiac stress by TAC, Brg1 was activated and re-accumulated on eDNA with 87% increase of ChIP signals, restoring the occupancy to fetal levels (Fig. 5). The results suggested that Brg1 bound to eDNA to trigger eDNA-*Myh* looping and *Myh* switch. The functional requirement of Brg1 was
 20 revealed by the disruption of eDNA-*Myh* looping in fetal or stressed hearts lacking myocardial Brg1 (*Sm22α-Cre;Brg1^{fl/fl}* or *Tnnt2-rtTA;TRE-Cre;Brg1^{ff}*) (Fig. 6 and 7). Brg1 and eDNA knockout studies showed that both Brg1 and eDNA were essential for eDNA-*Myh* looping to trigger *Myh* switch in response to pathophysiological stimuli (Figs. 2, 3, 4). The formation or disruption of a Brg1-eDNA-*Myh6-Myh7* three-dimensional complex provides a critical spatial
 25 mechanism to orchestrate antithetical *Myh* changes.

We asked whether eDNA activity was regulated by its transcription into RNAs. By 5' and 3' rapid amplification of cDNA ends (RACE) analysis of adult mouse hearts, we identified two RNA species transcribed from the 4-kb eDNA region. A 3.3-kb RNA was transcribed in an opposite direction from *Myh7* gene, and the other 0.75-kb RNA (*Antisense-eRNA*) in *Myh7*
 30 direction. In adult hearts, both RNA species were detectable by northern blot analysis, confirming their length identified by RACE.

We then focused on the 3.3-kb RNA to study its pathophysiological role and named this eRNA *Uheart* (abbreviated as *Uhrt*) for *Upstream Myosin Heavy Chain RNA Transcript*. Strand-specific RT-qPCR showed *Uhrt* levels were minimal in embryonic hearts (Fig. 8), when

eDNA was enriched with chromatin signatures of activity (H3K27ac and H3K4m1) and underwent looping to *Myh* promoters to activate *Myh7* isoform (Fig. 1 and 2). Conversely, as *Uhrt* expression increased from fetal to neonatal and to adult phase (Fig. 8), chromatin signatures of eDNA activity (H3K4m1 and H3K27ac) diminished, along with physiological *Myh* switch and reduced eDNA-*Myh* looping. Remarkably, *Uhrt* increased sharply within the first 24 hours after birth, while *Myh7* levels dropped precipitously in the same period, indicating an abrupt neonatal cessation of eDNA-*Myh* looping. Therefore, *Uhrt* can be transcribed from eDNA only when eDNA is functionally silent with minimal looping to its target *Myh* promoters. This contrasts sharply with known eRNAs, whose levels of expression track activities of enhancers and promoters. The *Uhrt*-eDNA interaction suggests a new mode of eRNA function.

Uhrt was expressed specifically in the heart: its levels were undetectable or minimal in non-cardiac tissues. In adult hearts *Uhrt* was transcribed in cardiomyocytes but not endothelial cells or fibroblasts and was highly enriched in the nuclei, revealed by cell sorting and nuclear/cytoplasmic fractionation studies. Codon substitution frequency suggested a highly negative translation score of *Uhrt* (-1148), which was further confirmed by *in vitro* transcription and translation of *Uhrt* that found no peptide translation. Ribosome profiling of adult hearts showed minimal ribosome binding to *Uhrt*, consistent with *Uhrt* being a nuclear, noncoding RNA. These observations together demonstrated that *Uhrt* is a cardiomyocyte-specific enhancer RNA transcribed from a functionally inactive enhancer in mature hearts.

We predicted that *Uhrt* transcription would be compromised in TAC-stressed hearts where eDNA displayed enhancer activity and *Myh* looping. Indeed, strand-specific RT-qPCR of heart tissues showed that *Uhrt* expression was reduced by 62% within 2 days after TAC, and its levels remained reduced by 62–78% in 7–56 days after TAC (Fig. 9), suggesting a role of *Uhrt* in pathological hypertrophy. To assess its *in vivo* function, we used CRISPR to insert upstream of *Uhrt* a red fluorescent protein variant (*tdTomato*) followed by 3 repeats of polyA transcription termination signals (*tdTO3xpolyA*) to stop *Uhrt*, transcription. This genetic knockout was specific to *Uhrt* since it didn't affect *Antisense-eRNA* transcription from the same eDNA nor did it alter eDNA-dependent *Myh6* and *Myh7* expression in E13.5 hearts that had minimal *Uhrt* transcription. The *Uhrt*-null mice lived to adulthood and appeared grossly normal with normal weight, body size, and left ventricular fractional shortening. The lack of *Uhrt* in adult hearts, however, accelerated cardiac functional decline caused by TAC. Within 2 weeks of TAC, fractional shortening of *Uhrt*-null hearts decreased from 40% to 18%, whereas the control showed a decline from 40% to 30%, showing a 40% excess of functional decline in the absence of *Uhrt*. After 12 weeks of TAC, *Uhrt*-null mice had a mortality of 90%, while control mice

25%, revealing a 3.6-fold excess of mortality. Also, *Uhrt*-null hearts exhibited 114–125% increase of hypertrophy by ventricle/body-weight ratio and by cardiomyocyte cross-sectional area, compared to 71–77% increase of hypertrophy in control hearts (Fig. 10 and 11), indicating 1.6-fold excess hypertrophy. *Uhrt*-null hearts are therefore susceptible to stress-induced

5 pathology, suggesting a cardioprotective role of *Uhrt*, opposite to that of eDNA.

To address whether *Uhrt* transcription blocked eDNA activity in the heart, we generated a stable transgenic reporter mouse line in which *Uhrt* transcription from eDNA was driven by a loxP-floxed *CMV* promoter, followed by *hsp68* basal promoter fused to *lacZ* reporter (*CMV^{fllox}-eDNA-hsp68-lacZ*, abbreviated as *CMV-eDNA-lacZ*) (Fig. 12). The *CMV* promoter, whose

10 activity wasn't inhibited by TAC, allowed *Uhrt* expression under stress conditions to rescue *Uhrt* levels in TAC-stressed hearts. Conversely, transgenic *Uhrt* expression could be shut down by *Sm22 α -Cre* that removed the floxed *CMV* promoter but maintained eDNA in *Sm22 α -Cre;CMV^{fllox}-eDNA-hsp68-lacZ* line (abbreviated as *eDNA-lacZ*). In TAC-stressed hearts, where endogenous *Uhrt* was repressed, *CMV-eDNA-lacZ* transcribed *Uhrt* 3.2-fold higher than *eDNA-lacZ* mice (Fig. 12), showing a rescue of *Uhrt* levels by *CMV* promoter. The *CMV-eDNA-lacZ*

15 line with high *Uhrt* expression displayed low eDNA activity on *hsp68* promoter, whereas *eDNA-lacZ* line that had 3-fold less *Uhrt* showed 6.4-fold stronger eDNA activity (Fig. 13). The rescue of *Uhrt* by *CMV* promoter was therefore sufficient to eliminate TAC-induced eDNA activity (Fig. 13). Conversely, in sham-operated or normal adult hearts, which had abundant

20 endogenous *Uhrt* and minimal Brg1 that's required for eDNA activity, both transgenic reporter lines showed low eDNA activity (Fig. 13). These *in vivo* reporter studies indicate that *Uhrt* inhibits eDNA activity on target promoters.

We then set out to find how *Uhrt* inhibited eDNA activity. We postulated that *Uhrt* might hybridize with its eDNA template to form RNA-DNA hybrid duplex with a unpaired,

25 non-template strand of eDNA—a triplex R loop structure that might prohibit eDNA looping. To test this model, we first examined the distribution of nuclear *Uhrt* between chromatin and nucleoplasm. By strand-specific RT-qPCR and chromatin-nucleoplasm fractionation, we found that 25% of *Uhrt* transcripts existed in the nucleoplasm (nuclei depleted of chromatin), and 75% of *Uhrt* were associated with chromatin, indicating that most *Uhrt* was tethered to chromatin. To

30 test whether *Uhrt* bound to eDNA to form RNA-DNA hybrid, we used the antibody S9.6 that specifically detects RNA-DNA hybrid duplex to conduct DNA-RNA hybrid immunoprecipitation (DRIP) followed by strand-specific RT-qPCR to quantitate *Uhrt*. In E13.5 hearts, we found no enrichment of *Uhrt* in the RNA-DNA hybrid, consistent with low *Uhrt* levels in embryos (Fig. 8). Conversely, in mature adult hearts, DRIP-qPCR showed that *Uhrt*

was enriched by 3.7–4.2-fold in the RNA-DNA hybrid complex, the formation of which, however, was suppressed by TAC. The specificity of RNA-DNA hybrid was confirmed by Rnase H, which specifically degrades RNA-DNA hybrid. Therefore, *Uhrt* predominantly existed in RNA-DNA form tethered to eDNA.

5 These results were further supported by the guanine over cytosine (GC) skew score of *Uhrt*, which measures (G-C)/(G+C) ratio in RNA to predict RNA-DNA hybrid formation. The 5' 1.1-kb of *Uhrt*, which had the lowest score of GC skew score (0.029), exhibited the lowest RNA-DNA enrichment by DRIP, whereas the mid-third 1.1-kb and 3'-third 1.1-kb fragments of *Uhrt*, which had much higher GC skew score (0.16), displayed the highest DRIP enrichment.

10 Therefore, the 3' 2.2-kb fragment of *Uhrt* was tethered to eDNA as an RNA-DNA hybrid duplex. We then tested the presence of an unpaired, non-template strand eDNA in the R-loop triplex. Single-strand DNAs (ssDNAs) are known to be coated by a ssDNA-specific binding protein—replication protein A (RPA). By chromatin-IP using antibodies against RPA coupled with qPCR, we found that RPA-eDNA complex increased by 171% in adult hearts with

15 abundant *Uhrt*-eDNA hybrid, compared to that of E13.5 hearts that had minimal *Uhrt*-eDNA hybrid. In TAC-stressed hearts, as expected, the RPA-eDNA complex was reduced by 42%, along with a reduction of *Uhrt*-eDNA hybrid. Overall, these observations demonstrated that *Uhrt* hybridizes with eDNA to form a triplex R loop structure, consisting of a *Uhrt*-eDNA hybrid duplex with an unpaired strand of eDNA.

20 We next asked whether Brg1 or its associated factor could bind to *Uhrt*-eDNA hybrid. We first investigated the role in eDNA looping of CCCTC-binding factor (CTCF), a regulator protein essential for chromatin looping and three-dimensional structure formation. CTCF contains 11 highly conserved zinc finger domains, capable of binding to specific double-stranded DNA sequence to cause chromatin looping. We found a CTCF consensus binding

25 motif (AGGGGGTGG; SEQ ID NO: 43) on eDNA near the conserved MEF2A and GATA4 sites. ChIP analysis of heart tissues verified CTCF was enriched on eDNA region in E13.5 hearts, whereas its occupancy on eDNA dropped by 42% in normal adult hearts, but was increased by 81% and restored to fetal levels by TAC, while CTCF protein levels remained unchanged. Such dynamic CTCF binding to eDNA coincided with and accounted for the ability

30 of eDNA to loop to *Myh* loci in fetal and stressed hearts. Interestingly, the CTCF binding site on eDNA was guanine-rich with a GC skew score of 0.66, which was highly prone to form RNA-DNA hybrid, and indeed, this site resided within the *Uhrt*-eDNA hybrid zone. Given that CTCF contains zinc finger domains that bind to DNA duplex, we hypothesized that CTCF binding to eDNA was disabled by the formation of *Uhrt*-eDNA hybrid across the binding site. Using

electrophoretic mobility shift assay (EMSA) and probes of CTCF binding site sequence, we found that CTCF proteins were capable of binding to the double-stranded eDNA binding site, but failed to bind *Uhrt*-eDNA duplex in this binding site. Mutation of the double-stranded eDNA probe (AGGGGGTGG (SEQ ID NO: 43) to AAAAAATGG (SEQ ID NO: 44)) disrupted CTCF binding in EMSA, indicating a specificity of the binding site. The *in vivo* ChIP and *in vitro* EMSA studies, together, revealed the ability of *Uhrt* to inhibit CTCF binding to eDNA, thus preventing eDNA looping.

Given that Brg1 was essential for eDNA looping, we tested whether CTCF was recruited by Brg1 to eDNA to trigger the looping. Indeed, loss of Brg1 abolished CTCF binding to eDNA in TAC-stressed hearts of *Tnnt2-rtTA;TRE-Cre;Brg1^{fl/fl}* mice (Fig. 14). The ability of CTCF to bind eDNA duplex but not *Uhrt*-eDNA hybrid brought the next question: how did Brg1 resolve *Uhrt*-eDNA hybrid and restore eDNA duplex to enable CTCF binding? DRIP-qPCR analysis of heart tissues showed that in the absence of myocardial Brg1 (*Tnnt2-rtTA;TRE-Cre;Brg1^{fl/fl}*), *Uhrt*-eDNA hybrid was restored by 60% in TAC-stressed hearts (Fig. 15), suggesting that Brg1 was essential for disrupting *Uhrt*-eDNA hybrid. The persistence of *Uhrt*-eDNA hybrid in Brg1-null hearts, however, wasn't caused by increased *Uhrt* levels in stressed Brg1-null hearts. Therefore, in stressed hearts, there were two factors that contributed to the resolution of *Uhrt*-eDNA hybrid structure—the reduction of *Uhrt* transcription and the activation of Brg1 to resolve that structure.

To test how Brg1 could disrupt *Uhrt*-eDNA hybrid, we first used amylose pulldown experiments to examine Brg1's binding to the following probes: ssDNA (CTCF binding site), ssRNA (*Uhrt* sequence at CTCF binding site), and *Uhrt*-eDNA hybrid (CTCF binding site). We found that Brg1 couldn't bind ssDNA, bound ssRNA modestly, but bound *Uhrt*-eDNA hybrid strongly (Fig. 16). Brg1, unlike CTCF, was capable of binding *Uhrt*-eDNA hybrid. To further determine how Brg1 resolved *Uhrt*-eDNA hybrid, we examined Brg1's interaction with Senataxin (Setx), a major RNA-DNA hybrid helicase that's known to resolve RNA-DNA hybrid *in vivo*. By ChIP analysis, we found that Setx occupied eDNA in TAC-stressed hearts when Brg1 was up-regulated, with 3-fold enrichment compared to normal hearts that had low Brg1 expression (Fig. 17). Such stress-induced Setx binding to eDNA was abolished by myocardial Brg1 knockout (*Tnnt2-rtTA;TRE-Cre;Brg1^{fl/fl}*) in which Setx proteins levels remained unchanged (Fig. 17). Therefore, Brg1 was essential for recruiting Setx to eDNA. This recruitment was further supported by ChIP-on-ChIP analyses that showed co-occupancy of Brg1 and Setx on eDNA of TAC-stressed hearts (Fig. 18). Given the known role of Setx helicase in resolving enhancer RNA-DNA hybrids, these findings indicate that Brg1 recruits

Setx to *Uhrt*-eDNA site to unwind the RNA-DNA hybrid, releasing eDNA strands to form DNA duplex, to enable CTCF binding and the trigger of eDNA-*Myh* looping and *Myh* isoform switch.

To determine the conservation of eDNA and *Uhrt* in human hearts, we searched ENCODE
 5 cardiac chromatin modifications and VISTA enhancer database. In human fetal hearts, 6-kb upstream of *MYH7* transcriptional start site existed a 5.5-kb genomic region that was highly enriched with H3K27ac, a chromatin signature of active enhancers. Sequence alignment showed 50% of homology between this 5.5-kb fragment (termed heDNA) and mouse eDNA. To test heDNA enhancer activity, we generated a mouse line transgenic for *heDNA-hsp68-lacZ* reporter.
 10 The heDNA, indeed, displayed cardiac-specific enhancer activity on *hsp68* promoter in mouse embryos, and such cardiac specificity was consistent with human chromatin studies that showed higher H3K27ac signals in hearts but minimal H3K27ac in aortic tissues. Overall, the results suggest that heDNA is the human homolog of mouse eDNA. We next tested whether heDNA was transcribed into an *Uhrt* homolog by 5' and 3' RACE analysis of adult human hearts. We
 15 identified a single 2.3-kb RNA species transcribed from heDNA in an opposite direction from *MYH7* gene, with 57% sequence homology and similar predicted secondary structure to mouse *Uhrt*. Strand-specific RT-qPCR showed that this human RNA was predominantly expressed in the heart. This human RNA had highly negative coding potential score (-993), and showed no translation of peptides or proteins by *in vitro* translation assay, consistent of its being a
 20 noncoding RNA. These observations together suggest that this enhancer RNA is human *UHRT*.

To test heDNA-*UHRT* interaction, we generated a stable transgenic mouse reporter line in which the transcription of human *UHRT* from heDNA was driven by a floxed *CMV* promoter, followed by *hsp68* basal promoter fused to *lacZ* reporter (*CMV^{fllox}-heDNA-hsp68-lacZ*, abbreviated as *CMV-heDNA-lacZ*). To stop *UHRT* transcription, we used *Sm22 α -Cre* to delete
 25 floxed *CMV* promoter in cardiomyocytes of *Sm22 α -Cre;CMV^{fllox}-heDNA-hsp68-lacZ* (*heDNA-lacZ*) mice (Fig. 19). We found that *lacZ* activity was induced by TAC (2.3-fold) in *heDNA-lacZ* hearts (without *UHRT* expression) but was eliminated by *UHRT* expression in *CMV-heDNA-lacZ* hearts (Fig. 20). In sham hearts, *lacZ* activity was minimal in either reporter mice (Fig. 20) due to the lack in normal adult hearts of Brg1 required for enhancer activity. The *in*
 30 *vivo* interaction of human eDNA and *UHRT* in mice indicates a mechanistic conservation of eDNA-*Uhrt* interaction in humans.

We then asked whether human heDNA and *UHRT* showed antithetical changes in human hearts, like their mouse homologs. Chromatin studies of human tissues (VISTA database) showed that heDNA contained high H3K27ac signals in the hearts with dilated

cardiomyopathy compared to normal hearts, suggesting an increased eDNA enhancer activity in diseased state, similar to that of mouse eDNA in TAC-stressed hearts. Also, human *UHRT* expression was reduced by 52% in failing human hearts that had hypertrophic or dilated cardiomyopathy, accompanied by antithetical *MYH* isoform changes (92% increase of *MYH7* and 85% reduction of *MYH6*) (Fig. 21). Such inverse correlation of eDNA activity and *UHRT* levels suggests an evolutionary conservation of eDNA-*Uhrt* interaction pertinent to the pathogenesis of human heart failure.

Uhrt-eDNA interaction controls the assembly of eDNA-*Myh6*-*Myh7* complex to direct antithetical *Myh* regulation in development and in disease to govern cardiac contractility and resistance to pathological stress (Fig. 22). Those three DNA regulatory elements (eDNA, *Myh6*, *Myh7* promoters) are brought together in the three-dimensional space by Brg1 and CTCF to coordinate *Myh* regulation and cardiac pathophysiology, a process opposed by *Uhrt* (Fig. 22). *Uhrt*, like many eRNAs, arises from a bidirectionally transcribed enhancer, doesn't splice into isoforms, and maintains enhancer-encoded nucleotides for its function. These eRNA features contrast with the known enhancer-associated long noncoding RNAs (lncRNAs) expressed in the heart or fibroblasts for heart development and fibrosis. In those lncRNAs (*Upperhand*, *WISPER*, *CARMEN*), the enhancer-encoded nucleotides are deleted from primary RNAs, which splice into different isoforms. *Uhrt* thus provides a unique example of a cardiomyocyte-specific and protective eRNA, distinct from those and other lncRNAs that affect heart development or function. Using *Uhrt* to silence pathogenic eDNA may provide therapeutic benefits to heart failure patients. Also, identifying cardiac-specific factors essential for eDNA-*Myh* looping will have translational values, especially for patients with *Myh7* mutations causing hypertrophic or dilated cardiomyopathy. Inhibition of such factors by small molecules can disrupt eDNA-*Myh* looping and shut down mutant *Myh7* expression to prevent disease progression.

Transcription of eRNAs is thought to reflect enhancer activation, with many eRNAs known to facilitate interactions between enhancers and promoters. However, *Uhrt* provides a counter example—it is transcribed by an inactive enhancer and physically blocks enhancer activation and looping toward target promoters. Transcription of eRNAs could therefore mark an inactive, rather than active, state of the enhancer. This unusual function of *Uhrt* reveals a new enhancer-eRNA interface in transcriptional circuitry and uncovers a new mechanism of enhancer activation, mediated by a chromatin remodeler Brg1 that recruits an RNA-DNA helicase Setx to unwind eDNA-*Uhrt* and enable looping. Such Brg1- and *Uhrt*-controlled enhancer activation is particularly salient in the disease context, as their dynamic interactions orchestrate different phases of cardiac pathophysiology. The eDNA-*Uhrt* mode of interaction cautions the use of

enhancer transcription as a marker of enhancer activation and emphasizes the importance of studying the transcription of functionally silent enhancers.

WHAT IS CLAIMED IS:

1. A method of inhibiting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte cell, comprising:
enhancing binding of Uhrt to said enhancer, wherein said enhancer comprises a sequence having at least 95% sequence identity with SEQ ID NO: 3.
2. The method of claim 1, wherein the Uhrt comprises an RNA sequence having at least 95% sequence identity to SEQ ID NO: 2.
3. The method of claim 2, wherein the Uhrt RNA comprises SEQ ID NO: 2 and said enhancer comprises SEQ ID NO: 3.
4. The method of claim 1, wherein the Uhrt comprises an RNA sequence having at least 95% sequence identity to SEQ ID NO: 1.
5. The method of claim 4, wherein the Uhrt RNA comprises SEQ ID NO: 1 and said enhancer comprises SEQ ID NO: 3.
6. The method of claim 1 further comprising a step of decreasing Brg1 activity.
7. The method of claim 6, wherein the Brg1 activity is decreased by introducing an interfering RNA into said cardiomyocyte cell to inhibit translation of Brg1.
8. A nucleic acid comprising an RNA sequence consisting of SEQ ID NO: 1, or its DNA equivalent thereof, coupled to a marker.
9. A nucleic acid comprising an RNA sequence consisting of SEQ ID NO: 2, or its DNA equivalent thereof, coupled to a marker.
10. The nucleic acid of claim 8 or 9 wherein the marker is selected from the group consisting of a fluorescent tag, an antibody, and a small peptide.
11. A method of measuring Uhrt in a patient biological sample comprising:

providing an RNA sample recovered from said patient
contacting the RNA sample with a nucleic acid that specifically binds to Uhrt;
and
detecting the Uhrt in the patient sample.

12. The method of claim 11, wherein Uhrt is detected by quantitative reverse transcription PCR wherein an amplicon is only produced in the presence of Uhrt.

13. The method of claim 12, wherein said RNA sample is reverse transcribed into cDNA and said cDNA is contacted with a pair of PCR primers wherein said primers each comprise a sequence of at least 10 nucleotides that each have at least 95% sequence identity to a corresponding DNA equivalent of SEQ ID NO: 2 or a complement thereof.

14. The method of claim 11, wherein said nucleic acid comprises a sequence of at least 10 nucleotides that has at least 95% sequence identity to a corresponding complementary portion of SEQ ID NO: 2 or its corresponding DNA equivalent or complement thereof, wherein said nucleic acid is labeled with a detectable marker.

15. The method of claim 14 wherein the detectable marker is selected from the group consisting of a fluorophore and a radioisotope and a fluorophore.

16. A method of identifying a patient at risk for hypertrophy comprising:
providing a sample of RNA recovered from cardiomyocytes from the patient;
analyzing the levels of Uhrt RNA; and
comparing the Uhrt RNA levels in the patient cardiomyocytes to a reference sample, wherein a low level of Uhrt RNA compared to the reference sample identifies a patient at risk for hypertrophy.

17. A method of treating a patient at risk for heart disease comprising:
administering an RNA sequence to the patient, wherein the RNA sequence comprises a sequence having at least 95% sequence identity to SEQ ID NO: 2 or its corresponding DNA equivalent thereof.

18. The method of claim 17, wherein the heart disease is hypertrophy.

19. The method of claim 17, further comprising decreasing Brg1 activity.
20. The method of claim 19, wherein the Brg1 activity is decreased by administering an interfering RNA to silence the translation of Brg1.
21. The method of claim 17, further comprising analyzing Uhrt levels after the step of administering the RNA.
22. A method of switching a cardiomyocyte from a stressed-state to a non-stressed state comprising:
decreasing Brg1 activity, and
increasing Uhrt activity, wherein the cardiomyocyte is switched from a stressed-state to a non-stressed state.
23. The method of claim 22, wherein decreasing the Brg1 activity comprises providing a Brg1 interfering RNA.
24. The method of claim 22, wherein the increasing of Uhrt activity comprises providing a Uhrt RNA.
25. A method of detecting a patient at risk for hypertrophy, the method comprising:
providing a test sample comprising RNA from the patient;
contacting the test sample with a reverse transcriptase primer specific for an enhancer RNA comprising the sequence for Uhrt;
reverse transcribing the enhancer RNA to produce a corresponding test cDNA;
contacting the test cDNA with PCR primers specific for Uhrt RNA wherein said primers comprise a sequence of at least 10 nucleotides having at least a 90% sequence identity to a corresponding complementary portion of SEQ ID NO: 2;
conducting a PCR reaction on the test cDNA, and detecting the resulting amplified product;
determining the concentration of the enhancer RNA in the test sample based on the detected test cDNA; and

obtaining a reference concentration of the corresponding enhancer RNA; wherein a detected lower level of the enhancer RNA in the test sample as compared to the reference concentration level of the enhancer RNA indicates hypertrophy.

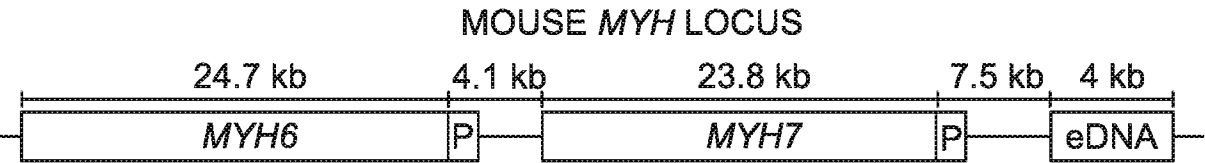


FIG. 1

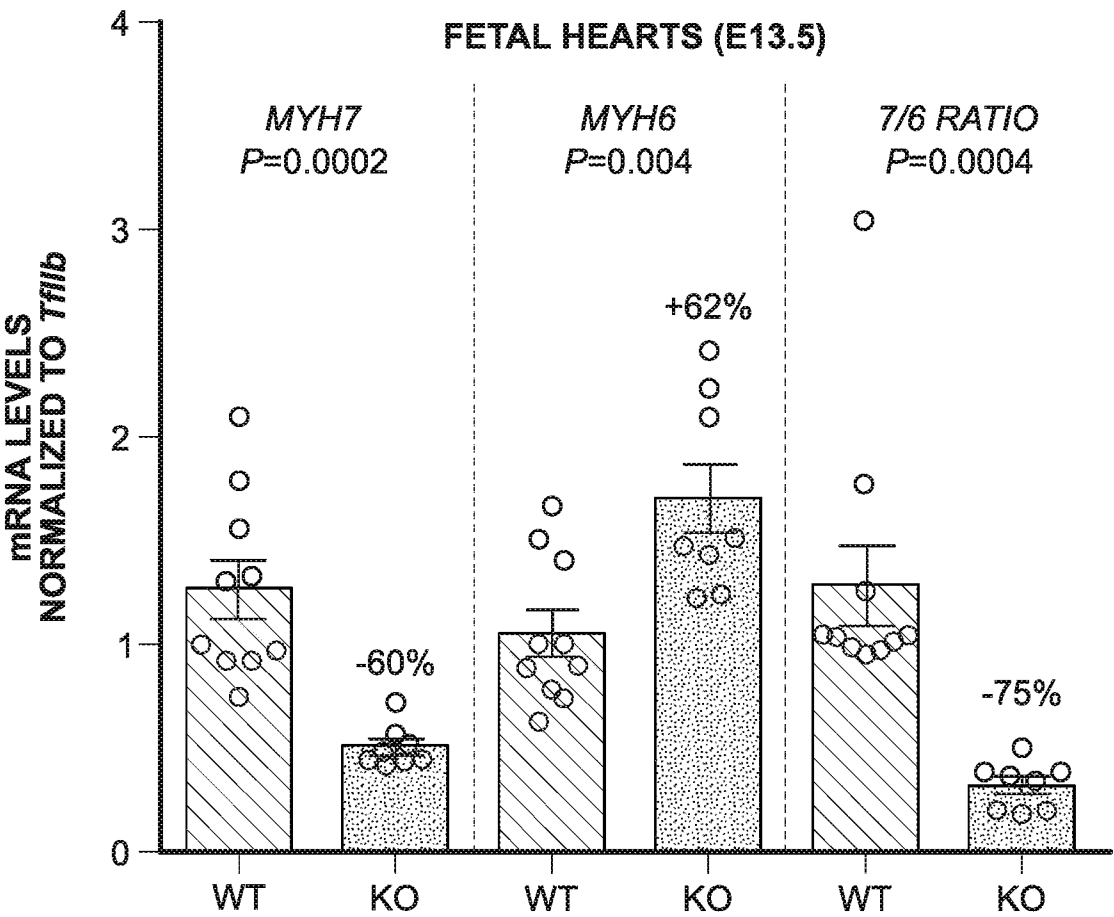


FIG. 2

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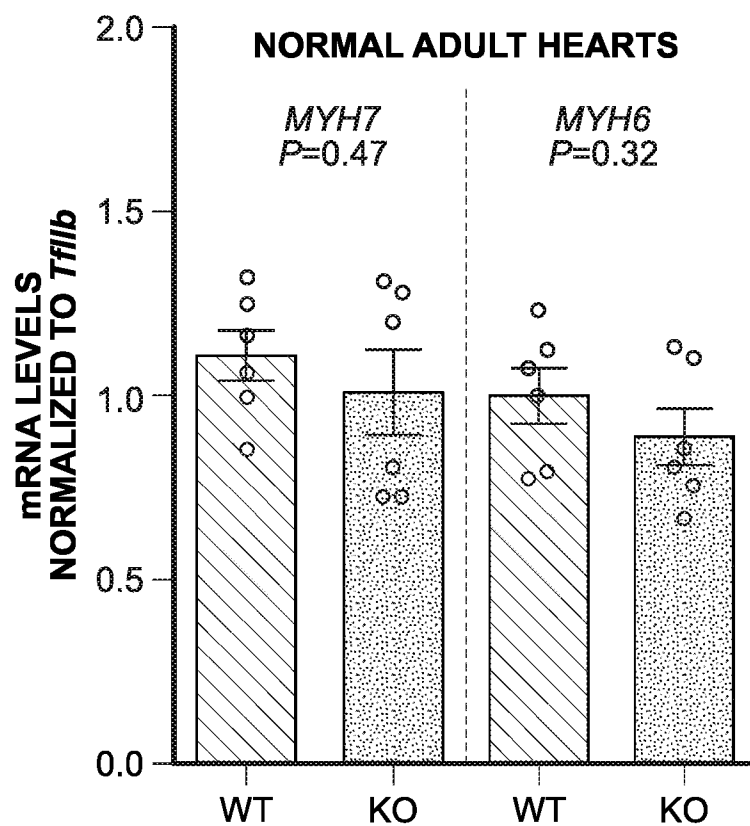


FIG. 3

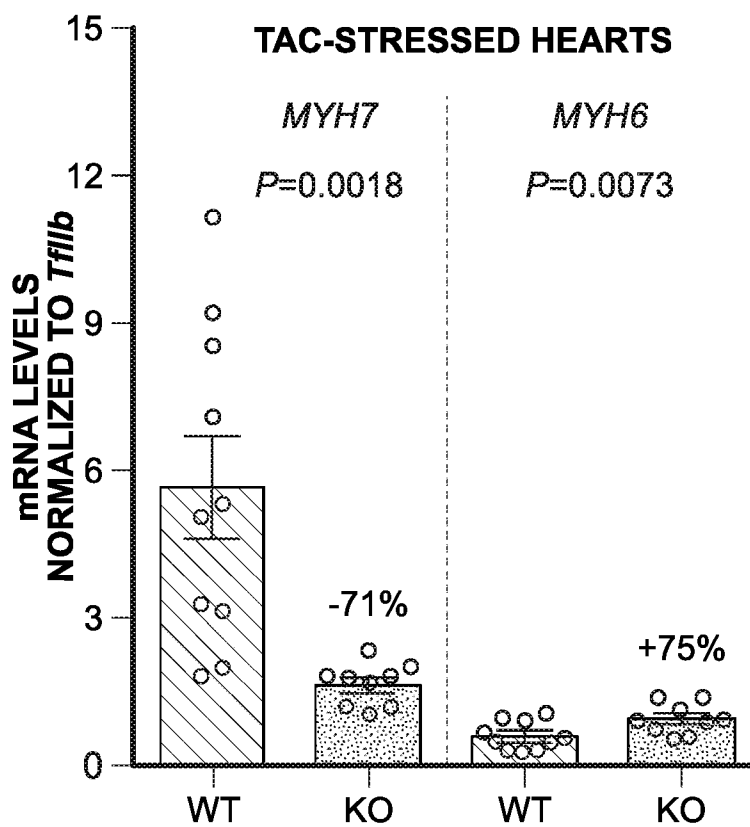


FIG. 4

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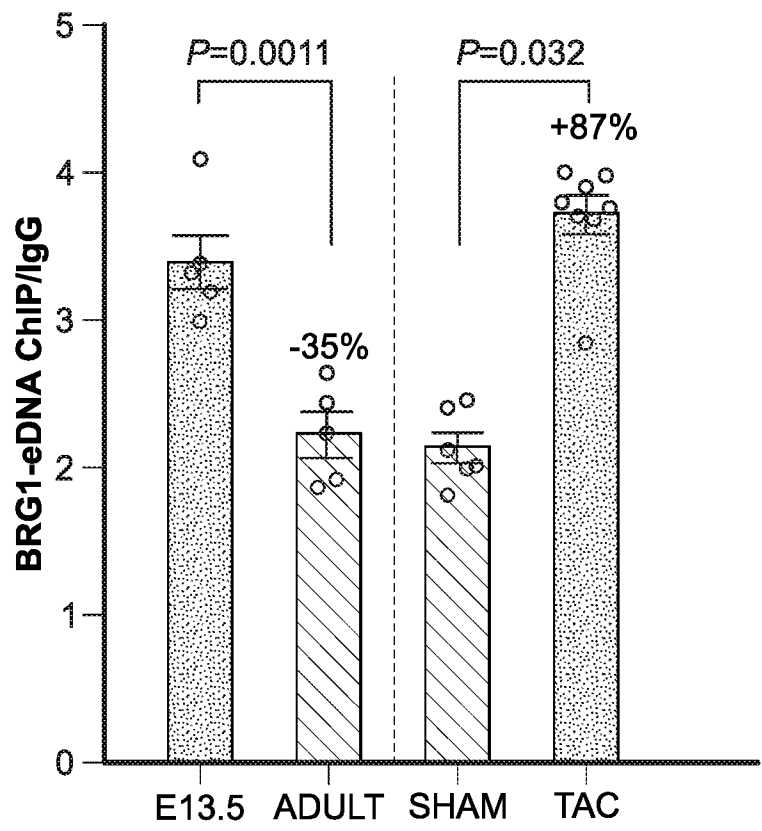


FIG. 5

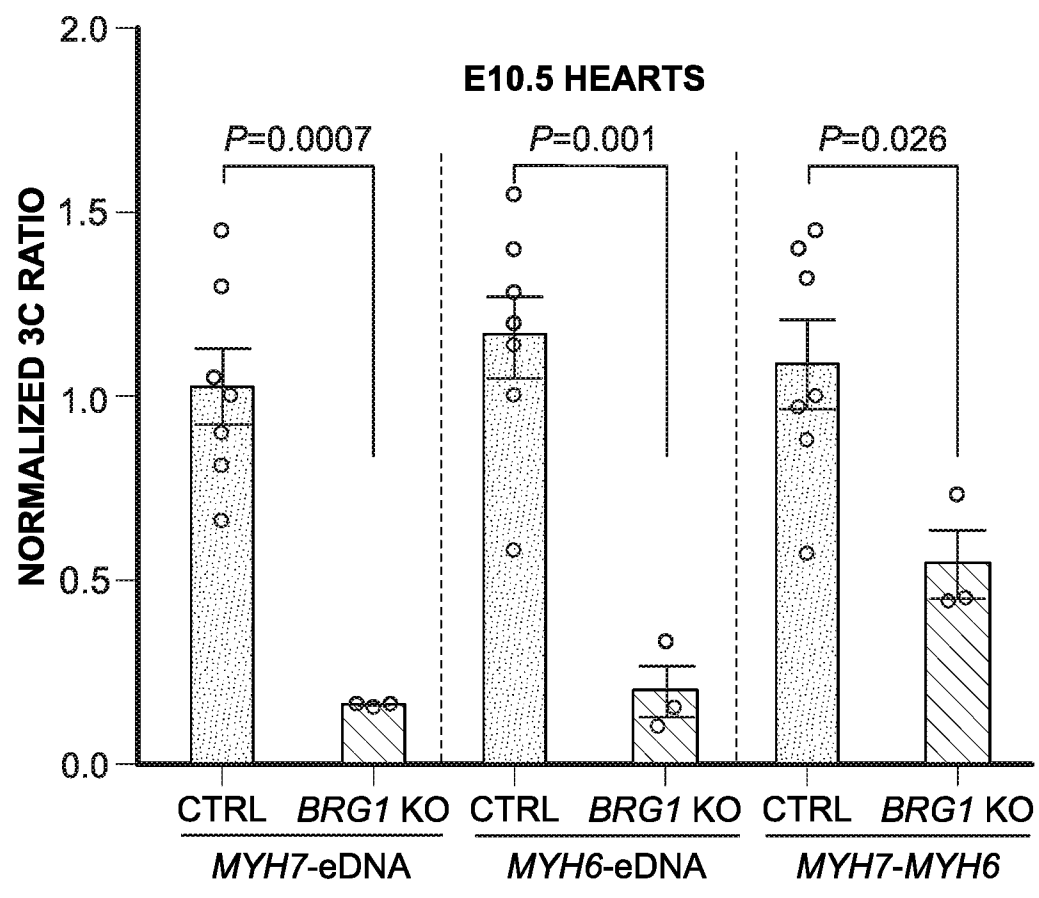
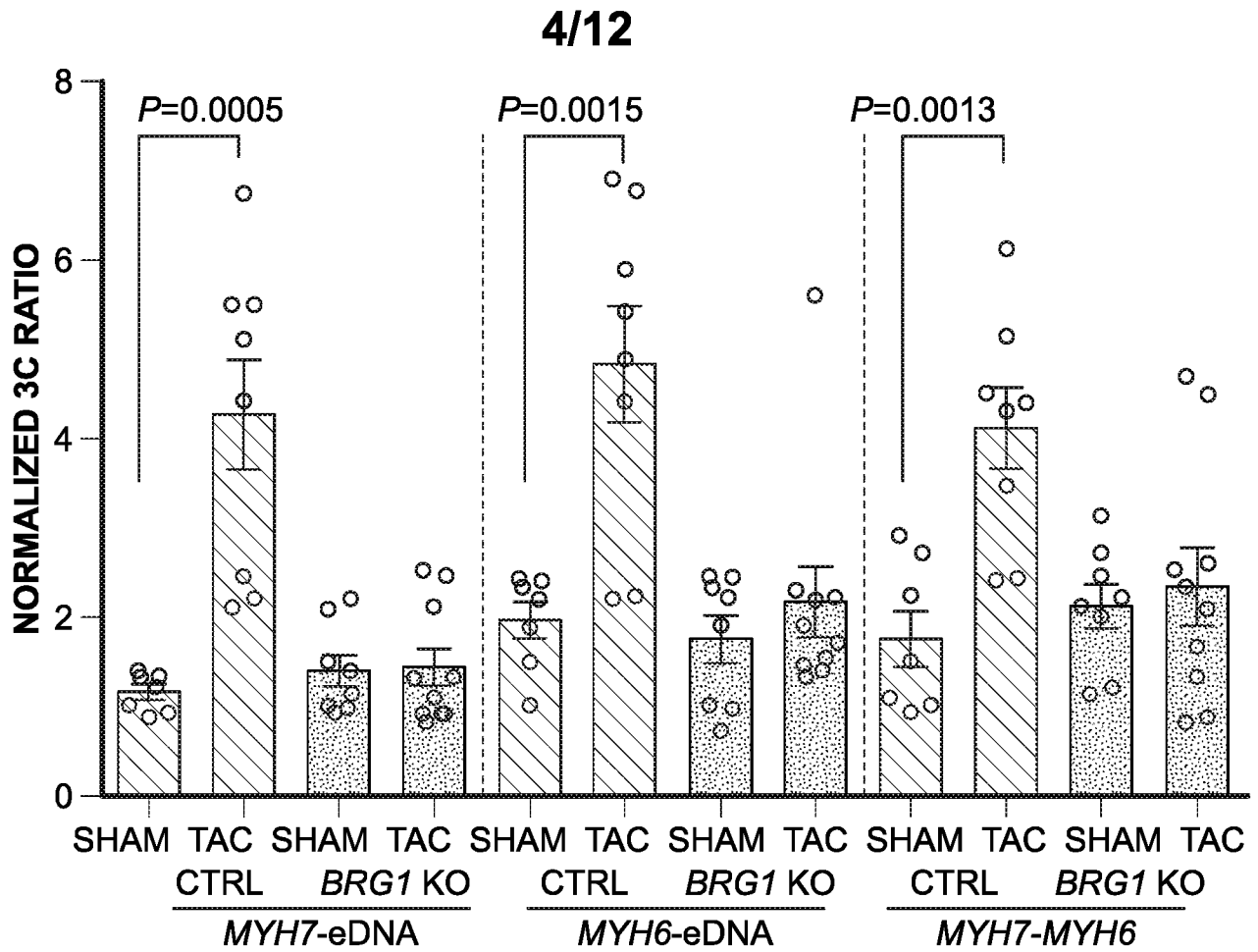
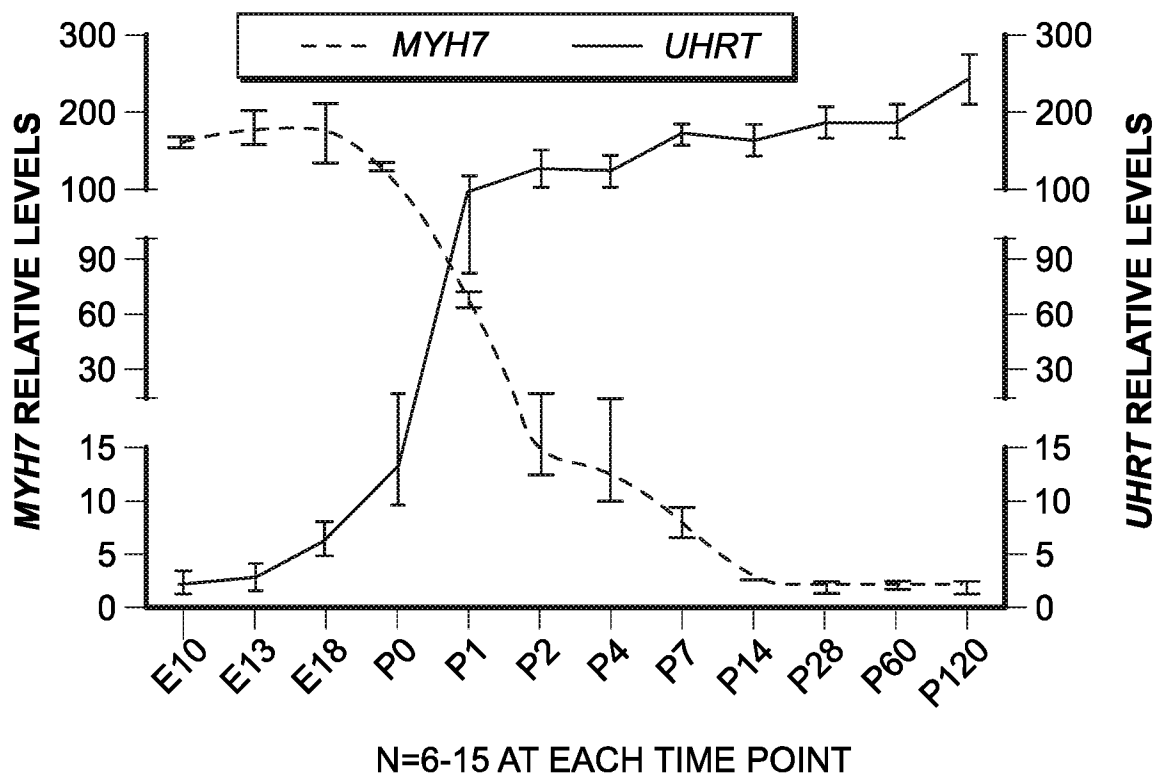
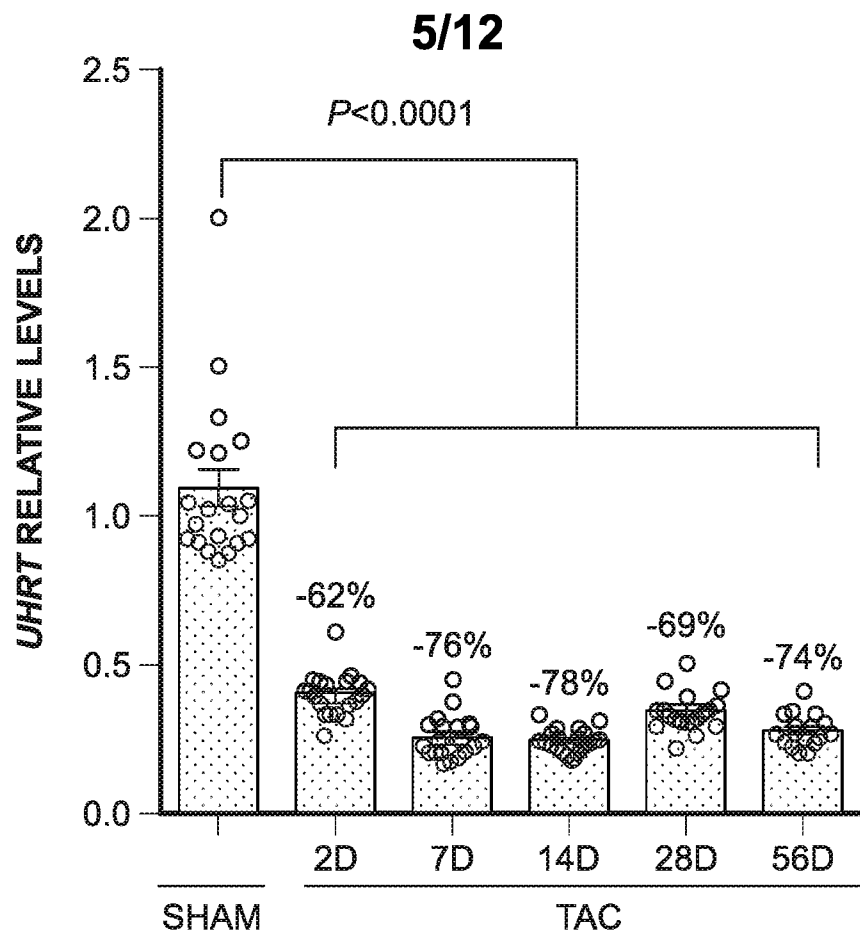
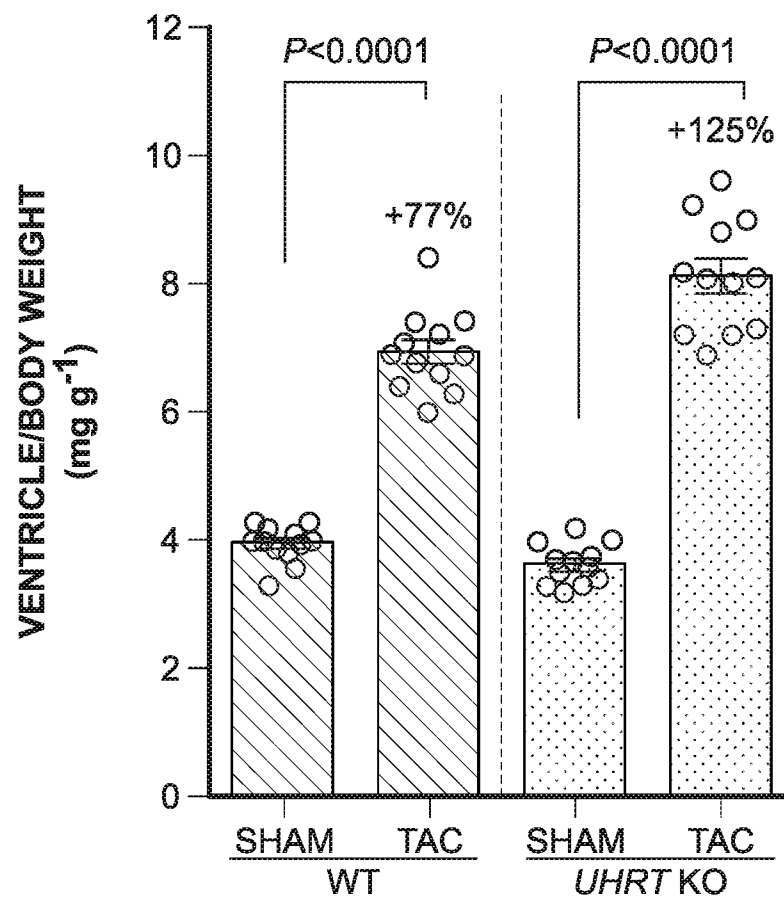


FIG. 6

*FIG. 7**FIG. 8*

*FIG. 9**FIG. 10*

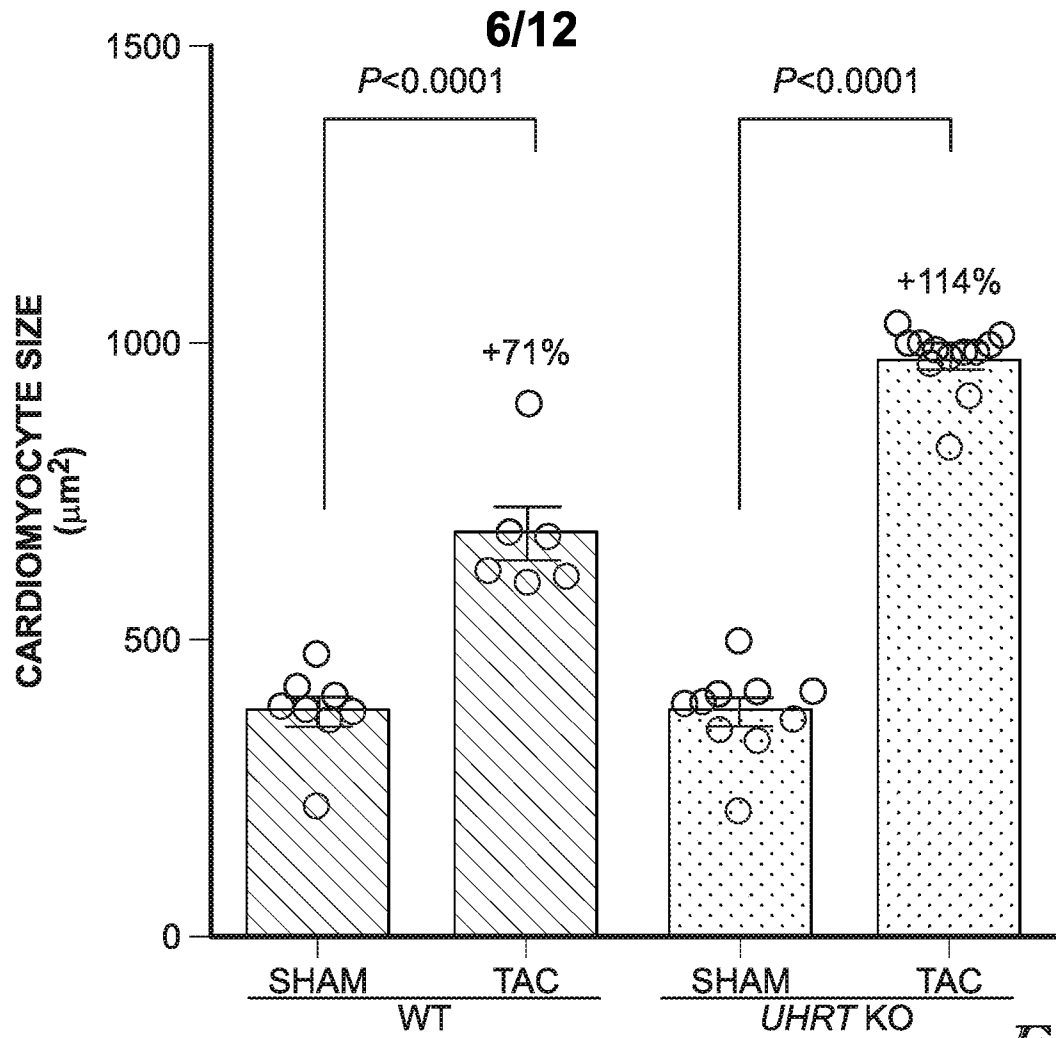


FIG. 11

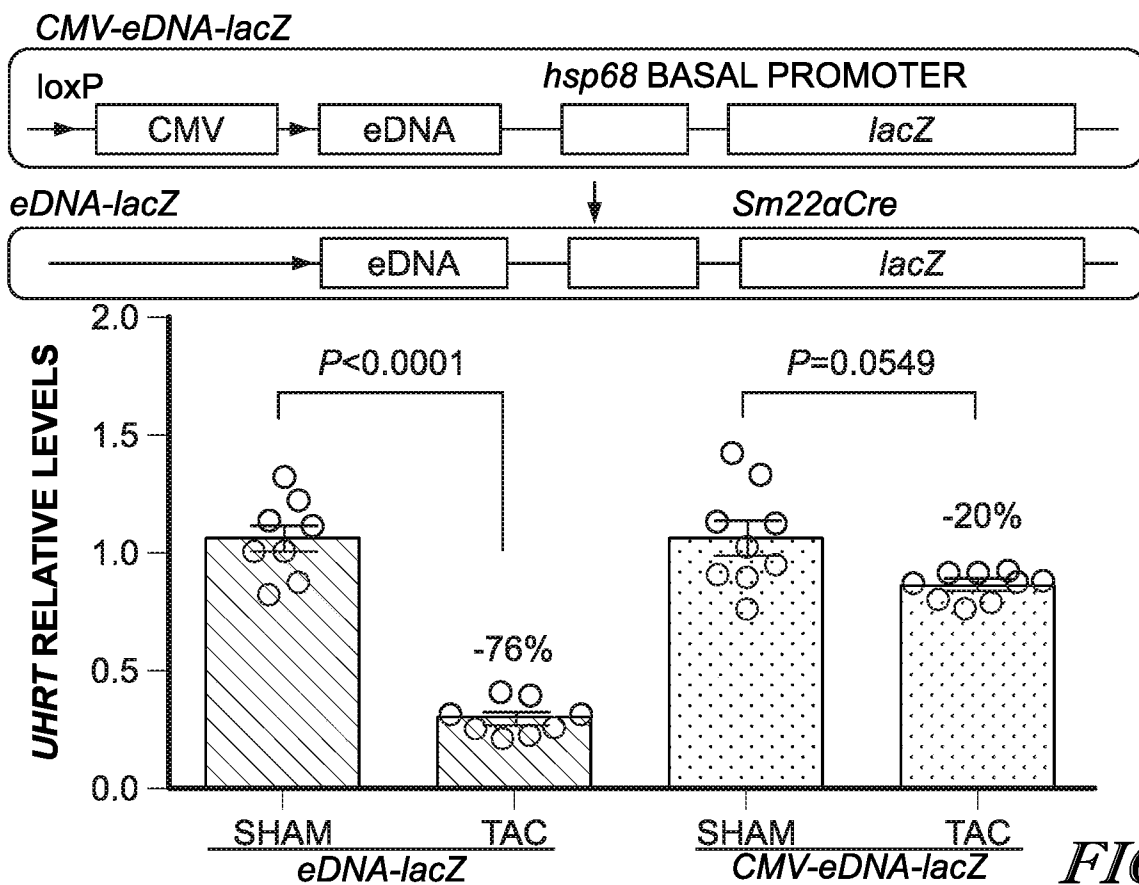


FIG. 12

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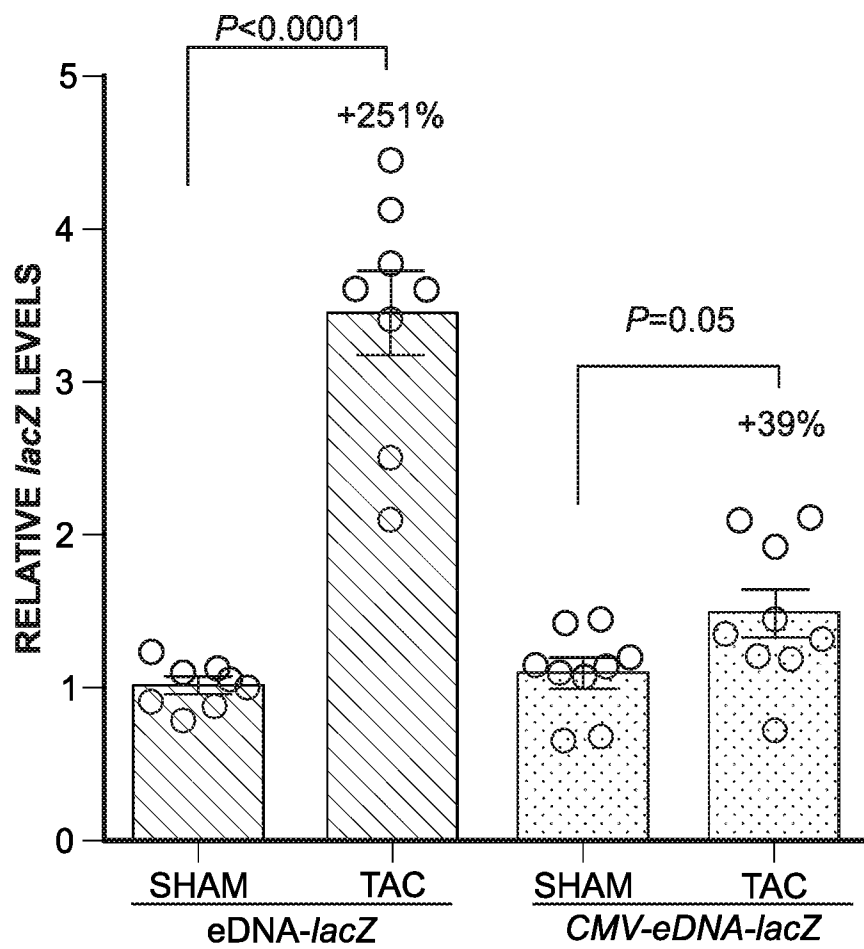


FIG. 13

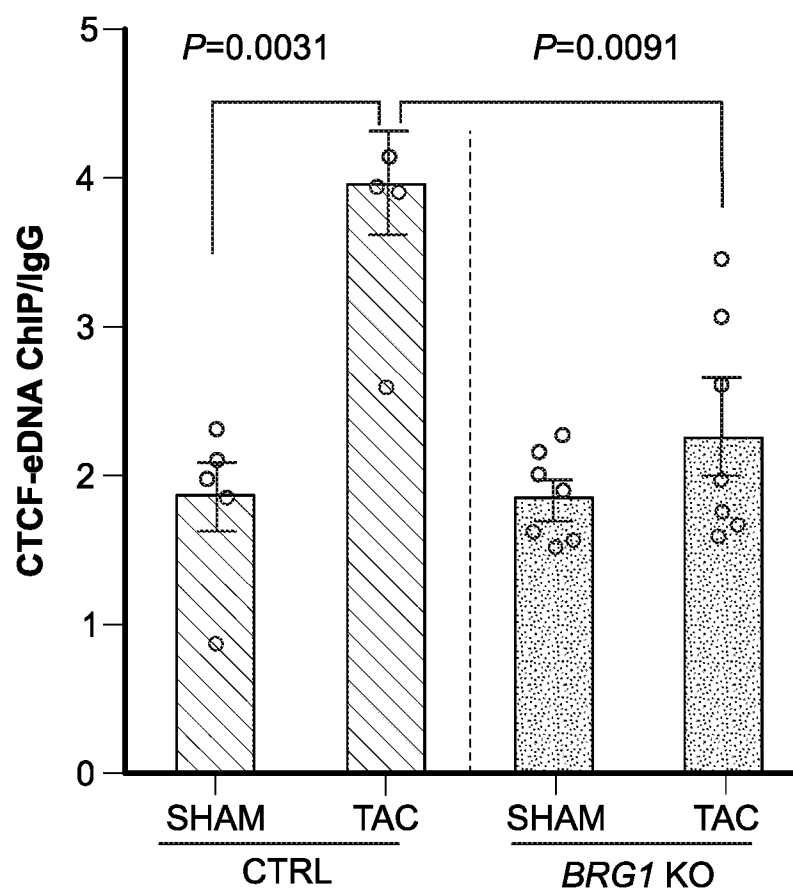


FIG. 14

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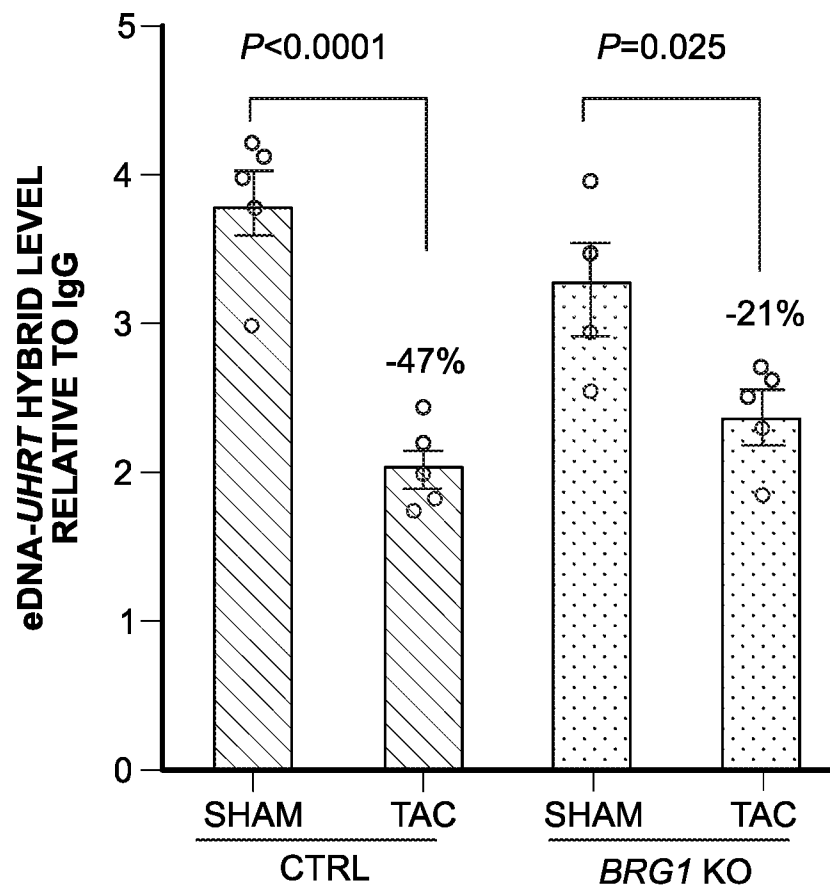


FIG. 15

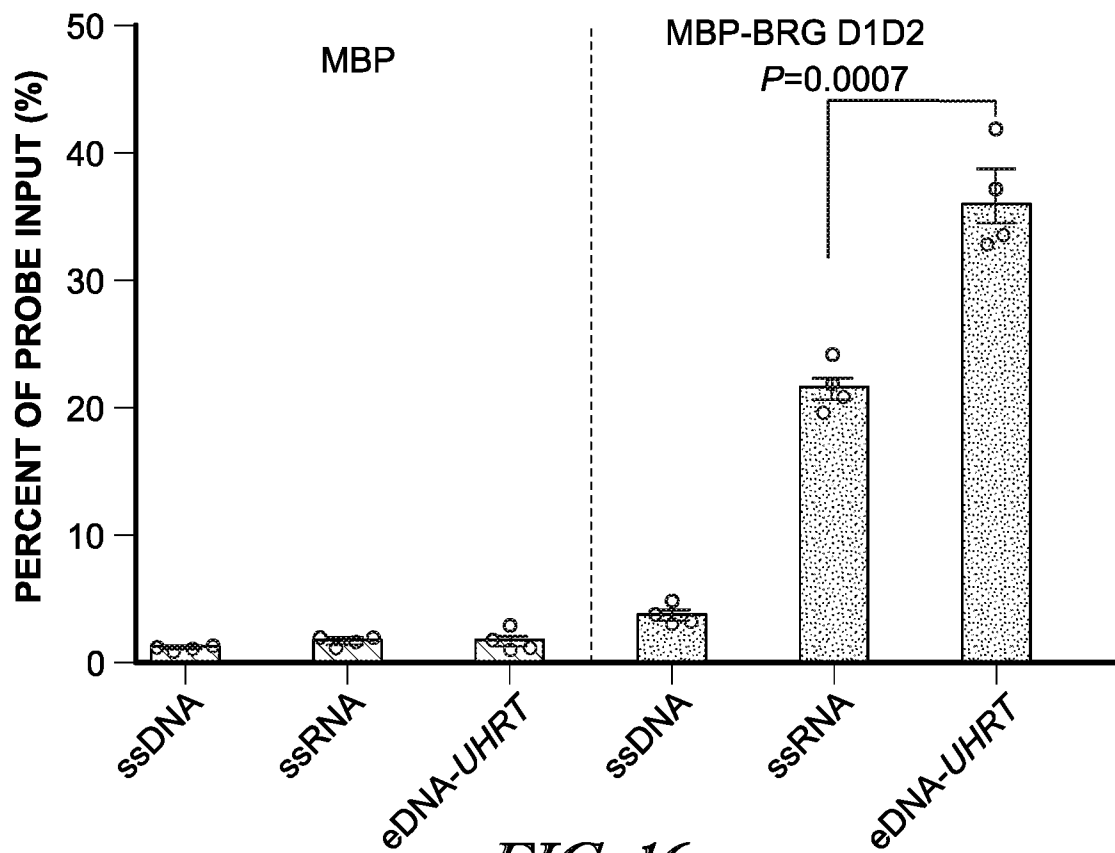


FIG. 16

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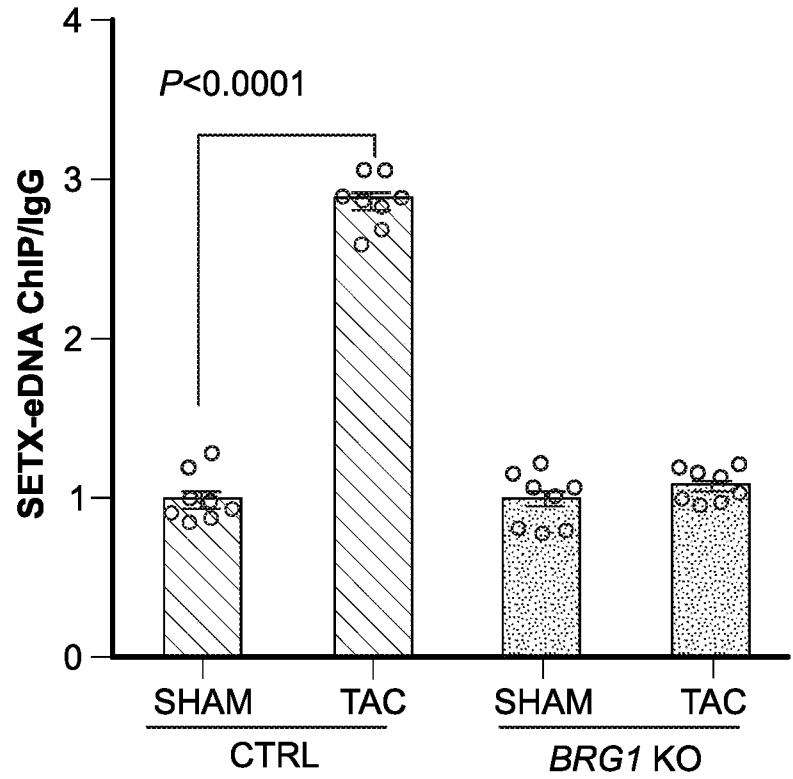


FIG. 17

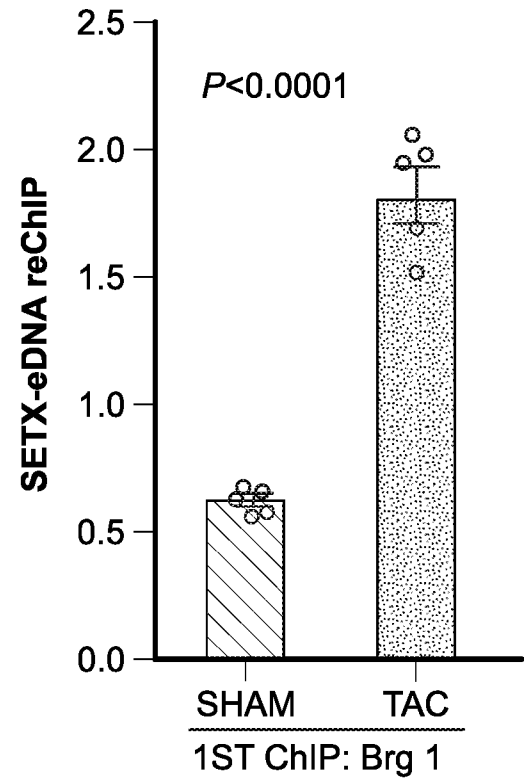


FIG. 18

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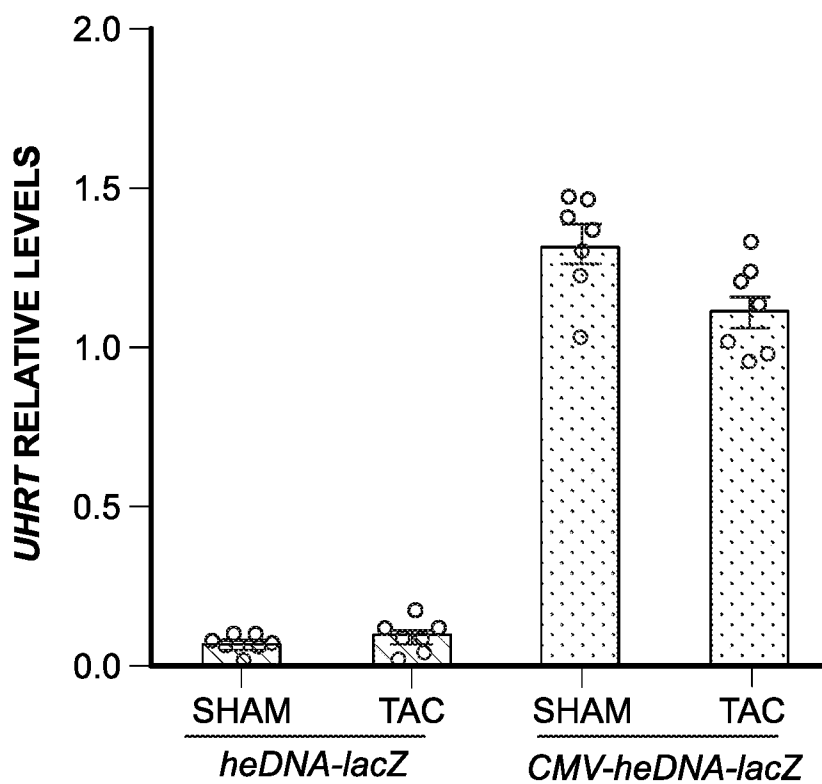


FIG. 19

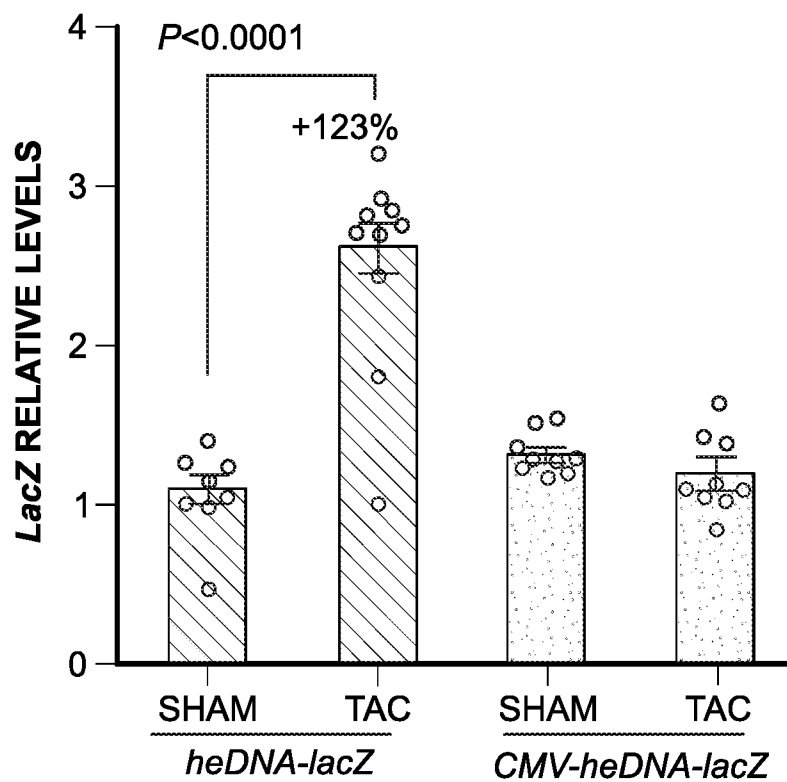


FIG. 20

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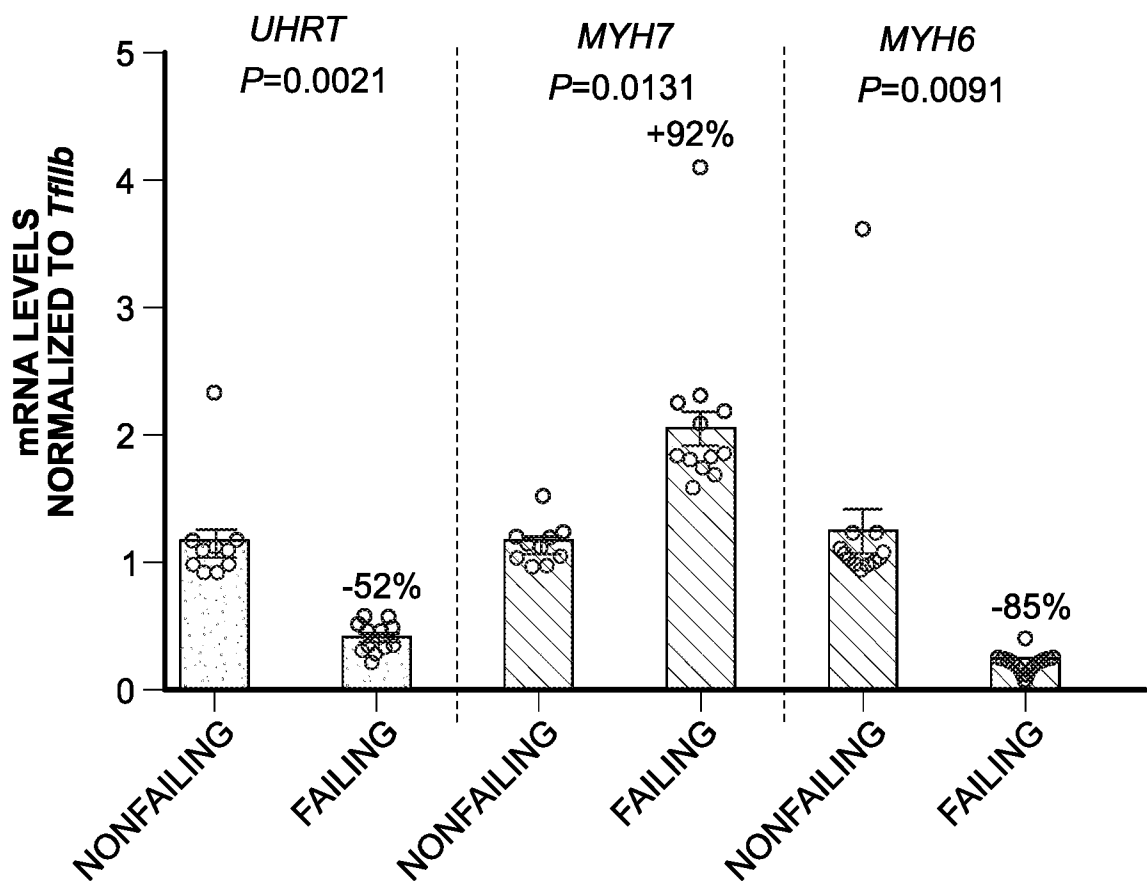


FIG. 21

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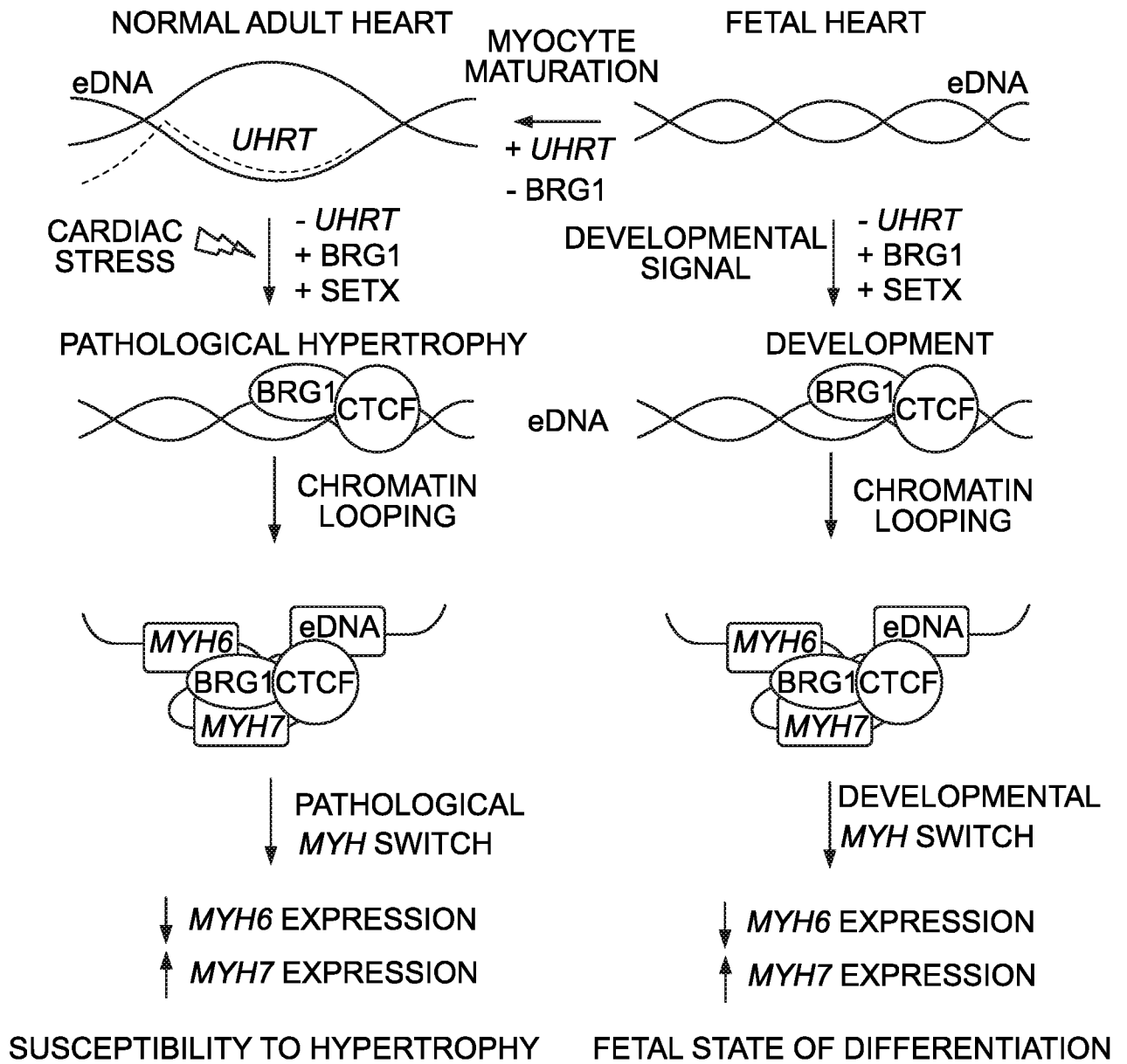


FIG. 22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/56995

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07K 14/47, C12N 9/14, C12N 15/113 (2020.01)

CPC - C07K 14/4716, C12N 9/14, C12N 15/113, C12N 2310/14

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2016/0114004 A1 (INDIANA UNIVERSITY RESEARCH AND TECHNOLOGY CORPORATION) 28 April 2016 (28.04.2016) para [0180], [0188], [0191], [0202], [0205], [0218]	1-7
Y	US 2005/0214835 A1 (BRISTOW et al.) 29 September 2005 (29.09.2005) Claim 47 para [0042], [0048], [0062]	1-7
Y	GenBank AL132855.4, Human chromosome 14 DNA sequence BAC C-2201G16 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence, 14 March 2015 (14.03.2015). [Retrieved on 08 February 2020]. Retrieved from the internet <URL: https://www.ncbi.nlm.nih.gov/nuccore/AL132855 > entire document	1-7
Y	GenBank AC157212, Mus musculus BAC clone RP23-171A13 from chromosome 14, complete sequence, 27 April 2005 (27.04.2005). [Retrieved on 08 February 2020]. Retrieved from the internet <URL: https://www.ncbi.nlm.nih.gov/nuccore/AC157212 > entire document	4, 5
A	Qin et al. "Localization of human cardiac beta-myosin heavy chain gene (MYH7) to chromosome 14q12 by in situ hybridization" Cytogenet Cell Genet, 1990, vol 54, pg 74-76; abstract	1



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

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

"D" document cited by the applicant in the international application

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

08 February 2020

Date of mailing of the international search report

01 APR 2020

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents
P.O. Box 1450, Alexandria, Virginia 22313-1450

Facsimile No. 571-273-8300

Authorized officer

Lee Young

Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/56995

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

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

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

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

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

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

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I: claims 1-7, drawn to a method of inhibiting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte cell.

Group II: claims 8-10, drawn to a nucleic acid comprising an RNA sequence coupled to a marker.

-----Please see Supplemental Sheet-----

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7

Remark on Protest

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

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.

PCT/US 19/56995

Continuation of Box No. III Observations where unity of invention is lacking:

Group III: claims 11-25, drawn to a method of detecting a patient at risk for hypertrophy by measuring Uhrf in a patient biological sample, a method of treating a patient at risk for heart disease, or a method of switching a cardiomyocyte from a stressed-state to a non-stressed state.

The inventions listed as Groups I, II and III do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features

Groups I and III include the special technical feature of a method which differs from the special technical feature of a composition, as disclosed by Group II.

Group I includes the special technical feature of inhibiting assembly of an enhancer DNA-Myh6 promoter-Myh7 promoter complex in a cardiomyocyte cell, not required by Group III.

Group III includes the special technical feature of providing an RNA sample recovered from a patient and contacting the RNA sample with a nucleic acid that specifically binds to Uhrf, not required by Group I.

Group III includes the special technical feature of a method of treating a patient at risk for heart disease, not required by Group I.

Common Technical Features

The inventions of Groups I-III share the technical feature of a nucleic acid encoding Uhrf.

The inventions of Groups I and III share the technical feature of cardiomyocytes, cardiac cells or tissues.

However, these shared technical features do not represent a contribution over prior art in view of WO 2010/006215 A1 to Celera Corporation et al. (hereinafter "Celera").

Celera teaches that Uhrf SNP is a biological marker for subject risk of cardiovascular disease (Claim 1 - "A method of determining whether a human has an altered risk for cardiovascular disease (CVD), ...wherein said polymorphism indicates said human has an altered risk for CVD."; Claim 2 - "The method of claim 1, wherein said CVD is coronary heart disease (CHD)."; SEQ ID NO: 1292 exhibits 100% identity to claimed SEQ ID NO: 2).

As said technical features were known in the art at the time of the invention, these cannot be considered special technical features that would otherwise unify the groups.

Groups I through III therefore lack unity under PCT Rule 13 because they do not share a same or corresponding special technical feature.