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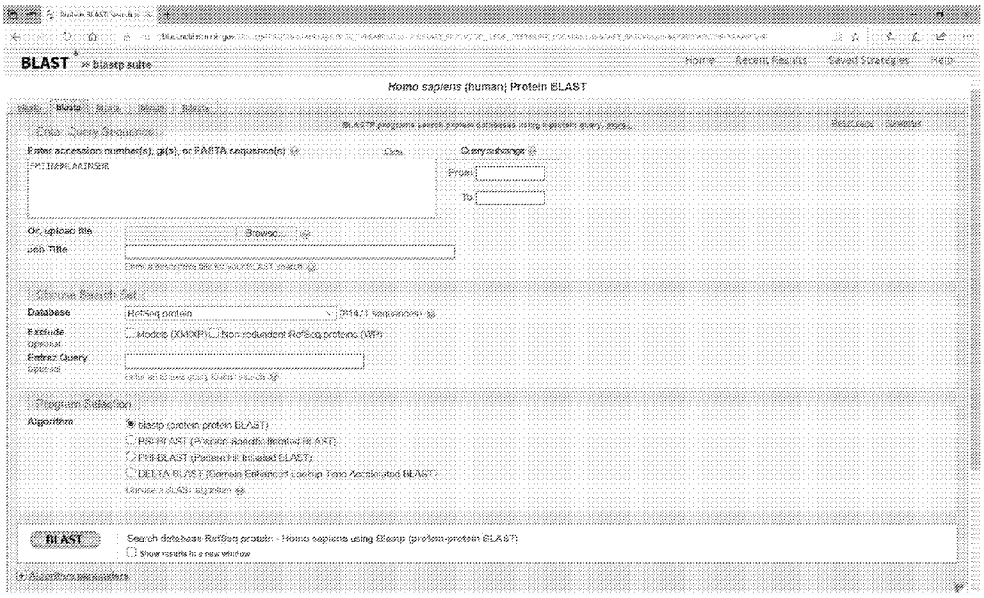

FIG. 1

(57) Abstract: The present invention provides a molecular network, devices, and assays for early diagnosis of ischemic cardiac events in patients experiencing chest pain. The invention allows for the differentiation of chest pain due to ischemic cardiac events and other non-cardiac causes. The invention provides a Nourin- based RNA molecular network composed of IncRNA-CTB89Hl2.4, hsa-miRNA-l37, and FTLH-17 mRNA as an autophagy-related RNA panel linked to each other and to cardiovascular ischemia to specifically diagnose ischemic cardiac events. The invention demonstrates that the down-regulation of RNA-CTB89H12.4 after an AMI event, resulted in the up-regulation of hsa-miRNA-l37 and activation of FTLH-17 mRNA with an increased translation and production of Nourin protein; a cardiac-derived biomarker. These Nourin multiple genes can, therefore, be used alone, and in combination with the protein-based Nourin measured by antibodies comprising of the epitope sequence f-Mll to increase the early diagnosis of ischemic cardiac patients

WO 2020/148589 A1

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EARLY BIOMARKERS FOR CARDIAC PATIENTS

CROSS REFERENCE TO RELATED APPLICATIONS

The current application claims benefit of U.S. Patent Application 16/252,402 filed January 18, 2019.

FIELD OF THE INVENTION:

[001] The present invention generally relates to the fields of medicine, physiology, biomarkers, diagnostics, and biochemistry. The present invention particularly relates to an autophagy-related RNA-based biomarker panel linked to each other and to cardiovascular ischemia. More particularly, the present invention relates to early diagnosis and differentiation between diseases or disorders using a protein and molecular network for the detection of RNAs released as a result of certain events.

BACKGROUND OF THE INVENTION:

[002] Heart disease is the leading cause of death in women and men worldwide according to the World Health Organization and it is predicted to persist as the one of the main causes of illness due to the progressive aging of population. Ischemia of the heart occurs as a result of diminished blood flow to heart tissue. If this reduction is brief (less than 15 minutes), the ischemic injury is *reversible*, as seen in unstable angina (UA) patients. But if reduced blood flow is persistent for an extended period of time (more than 15 minutes), *irreversible* necrotic damage (cell death) occurs which leads to acute myocardial infarction (AMI-heart attack). Currently, no blood test can specifically identify unstable angina patients. Tests for heart attacks cannot be done until several hours (three to six hours) after presentation of symptoms in order to allow enough substances to be released in the blood by dead heart tissue.

[003] The root cause of acute coronary syndromes (ACS) is unstable plaque in the coronary artery. These syndromes represent a continuum of ischemic disease ranging from unstable angina (UA) to heart attack (acute myocardial infarction-AMI) and to large areas of heart cell death. Each year in the U.S., between 6 to 10 million

individuals present annually to Emergency Departments (ED) with clinical signs and symptoms of ACS including chest pain. Of the 6 to 10 million patients presenting annually to the ED with chest pain, up to 90% do *not* have a heart cause for their symptoms. In the U.S., the high rate of chest pain admissions of non-heart origin is as high as 60%. Accordingly, there is an urgent need for an *early* and *accurate* diagnosis of ACS patients to warrant immediate medical care, which would reduce mortality and improve prognosis. A quick blood test is needed that can accurately rule in or out the 10% of ACS heart patients, who are equally divided (50:50) between UA and heart attack. Currently, there is no biomarker to identify patients with unstable angina seen in the ED with chest pain. The misdiagnosis of unstable angina patients in the ED is the highest source of medical malpractice lawsuits in the U.S.

[004] It is known in the art that AMI is associated with the release of proteins and nucleotides (RNAs) as a result of ischemic damage to cardiac tissue. Nourin is a 3 KDa N-formyl peptide rapidly released within 5 minutes by *reversible* ischemic myocardial tissue, such as in the case of UA, and by necrotic myocardial tissue, such as in the case of AMI. The formylated peptide Nourin is a potent inflammatory mediator which stimulates leukocyte chemotaxis, adhesion and activation to release a number of cytokine and chemokine mediators, adhesion molecules, digestive enzymes and free radicals. In vivo, the injection of human cardiac Nourin into rabbit skin resulted in an acute inflammatory response within the first 30 minutes characterized by a significant neutrophil infiltration. Nourin can, thus, be characterized as an *Alarmin* that promotes the innate immune response since it is rapidly released by local myocardial tissues following ischemia and contributes to the initiation and amplification of post-reperfusion myocardial inflammation. As such, Nourin can be an important therapeutic target. Nourin works as a ligand on leukocyte formyl peptide receptors (FPR) that are important potential therapeutic targets to control early and late post-reperfusion inflammation and injury. The cardiac-derived Nourin was purified from cardioplegic solutions collected during cardiac arrest (i.e., reversible ischemia) from patients who underwent cardiopulmonary bypass surgery for coronary revascularization. The amino acid sequence of Nourin released by reversibly ischemic human hearts is

formyl substituted-MIINHNLAAINSHRSPGADGNGGEAMPGGGR (SEQ ID NO:15)

confirmed by mass spectrometry analysis.

[005] Using both the functional leukocyte chemotaxis assay and the ELISA immunoassay, studies demonstrated that the cardiac-derived Nourin peptide is rapidly released by ischemic heart tissue while it is still "*viable*" before cells are dead, as well as by necrotic hearts. Consistent results showing the "*early*" release of Nourin by ischemic hearts were demonstrated using various species (human, dog, rat and cow) as well as several models of ischemic injury to include (1) AMI (necrotic), (2) global cardiac arrest (necrotic), (3) cardiopulmonary bypass surgery (reversible) and (4) heart transplantation (reversible). Unlike Troponin, Nourin was detected in *fresh* blood samples collected from ACS patients as well as from *frozen* samples stored at -70 °C for 3 years.

[006] Currently, Troponin released by necrotic heart tissue is the most widely used biomarker for AMI. However, Troponin is a marker of cell death and have certain drawbacks. For example, the Troponin complex is not highly stable as an extracellular protein, and thus its usefulness as a marker for AMI is diminished in samples that have been stored. Troponin also has low specificity where 50% of the time the elevated levels of Troponin give false positives for non-ischemic heart attack patients such as renal failure and non-ischemic heart failure.

[007] Although the Troponin test is currently the "Gold Standard" for determining if a patient has had a heart attack, it is a marker of "cell death" and requires three to six hours of waiting after the onset of chest pain in order for Troponin to appear in enough quantities to be measured in blood samples. At this stage, however, a delay is a missed treatment to save ischemic heart tissues and that a critical delay could lead to permanent cardiac damage and higher incidence of heart failure or death. Although the cardiac Troponin level is dependent on infarct size following reperfusion therapy, the actual Troponin level can be misleading due to the washout phenomenon. Moreover, truly elevated Troponin levels have also been detected in tachyarrhythmias, hypertension, myocarditis and patients with chronic renal failure (CRF). Therefore, a multi-marker approach incorporating both biomarkers and clinical scores may improve the diagnostic accuracy.

[008] Therefore, a need exists in the art for a better test to diagnose unstable angina and myocardial infarction that is "*earlier*" and more "*specific*" than Troponin. Since AMI is a leading health care threat to human lives, early and accurate diagnosis warrant immediate medical care, which would reduce mortality and improve prognosis.

[009] Additionally, there is a need for a biomarker of ischemic injury without concomitant cell death that can detect subclinical or silent myocardial ischemia without infarction, as well as low-grade myocardial ischemia without cell death. This biomarker could also be used to monitor cardiac disease progression and predict drug therapy response in clinical trials.

SUMMARY OF THE INVENTION:

[010] Generally, in one aspect of the present invention, a novel Nourin gene-based RNA molecular network is disclosed for the early diagnosis of and differentiation between diseases or disorders using molecular network for the detection of RNAs released as a result of certain cardiac events.

[011] In another aspect of the present invention, the novel molecular network has a high stability and is often present in tissue disease's specific expression and can be measured with high sensitivity and specificity.

[012] In yet another aspect of the present invention, the novel Nourin molecular network disclosed therein is composed of lnc-RNACTB89H12.4, hsa-miRNA-137, and FTLH-17 mRNA can be utilized alone, and in combination with the Nourin protein for early diagnosis of acute coronary syndromes (ACS) patients presenting with chest pain to hospital Emergency Departments (ED) and outpatient clinics to allow crucial intervention. Early intervention of ischemic heart patients can abort infarction and save heart muscles. The molecular Nourin RNA network alone and in combination with the Nourin protein can also diagnose AMI patients earlier than Troponin; differentiate cardiac from non-cardiac patients presenting with chest pain to hospital ED and outpatient clinics; monitor disease progression; and predict drug therapy response in clinical trials. The novel Nourin molecular network disclosed therein and Nourin protein have the potential to additionally diagnose subclinical or silent myocardial ischemia without infarction, as well as low-grade myocardial ischemia without cell death; screen CAD patients for risk assessment to predict which patients are at risk for developing AMI; screen heart transplantation patients' blood samples for cardiac allograft inflammation and, thus, reduce heart biopsies; and determine the risk level of heart patients experiencing chest pain who present to hospital ED and outpatient clinics and provide risk stratification of AMI patients.

[013] Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF DRAWING:

[014] The accompanying drawings are included to provide a further understanding of the invention, and are incorporated in and constitute a part of the present invention and, together with the description, serve to explain the principle of the invention. Bioinformatic analysis was done using BLAST program to retrieve relevant gene to the Nourin-1 peptide sequence formyl substituted-MIINHNLAAINSHR (SEQ ID NO:16) that is the N-terminus portion of the Nourin peptide sequence and relevant to AMI based on previous microarray studies.

In the drawings,

[015] Figure 1 indicates a snapshot of expression of Atlas database showing retrieving target gene involved relevant to the Nourin-1 peptide sequence formyl-MIINHNLAAINSHR.

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&BLAST_SPEC=OGP__9606__9558&LINK_LOC=blasttab&LAST_PAGE=blastn&QUERY=FMIINHNLAAINSHR

[016] Figure 2 indicates a print screen showing BLAST alignment of FTLH-17 with Nourin also refer to as Nourin-1 peptide sequence formyl-MIINHNLAAINSHR, available at:

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&BLAST_SPEC=OGP__9606__9558&LINK_LOC=blasttab&LAST_PAGE=blastn&QUERY=FMIINHNLAAINSHR

https://blast.ncbi.nlm.nih.gov/Blast.cgi#300244535

[017] Figure 3 indicates a snapshot showing gene ontology of FTLH17 mRNA.

https://www.ncbi.nlm.nih.gov/gene/53940

[018] Figure 4 indicates a snapshot showing minimal gene expression of FTLH17 mRNA in normal tissues confirming the low level of Nourin FTLH17 mRNA and

Nourin protein detected in serum and plasma samples collected from healthy volunteers.
https://www.genecards.org/cgi-bin/carddisp.pl?gene=FTHL17&keywords=FTHL17

[019] Figure 5 indicates a continuation of the snapshot showing minimal gene expression of FTLH17 mRNA in normal tissues confirming the low level of Nourin FTLH17 mRNA and Nourin protein detected in serum and plasma samples collected from healthy volunteers.
https://www.genecards.org/cgi-bin/carddisp.pl?gene=FTHL17&keywords=FTHL17

[020] Figure 6 indicates a print screen showing miRNA-137 targeting FTLH17 mRNA and it is available at:
http://diana.imis.athenainnovation.gr/DianaTools/index.php?r=microT_CDS/results&keywords=ENSG00000132446&genes=ENSG00000132446%20&mirnas=&descr=&threshold=0.7

[021] Figure 7 indicates a print screen showing the interaction between miRNA-137 and lncRNA-CTB89H12.4. Available at star base database.

[022] Figure 8 indicates the expression pattern and level of the Nourin-based molecular biomarker panel of FTLH-17 mRNA, hsa-miRNA-137 and lncRNA-CTB89H12.4 in comparison to Troponin I measured in the same serum samples collected from AMI patients and healthy volunteers. Results revealed that the two-log analysis of the three RNAs-based biomarker network (long non-coding intergenic RNA-(lncRNA-CTB89H12.4), homo sapiens microRNA-37 (hsa-miRNA-137), and FTLH-17 mRNA, had high sensitivity and specificity for discriminating AMI patients from healthy controls. While the AMI group had a higher expression of FTLH-17 mRNA and hsa-miRNA-137 as well as elevated levels of Troponin I in comparison to the healthy control group, there is concomitant lower expression of lncRNACTB89H12.4 in AMI patients and higher expression in the healthy control group.

[023] Figure 9 indicates the expression level of the Nourin-based molecular biomarker FTLH-17 mRNA in comparison to Troponin I measured in serum samples of AMI patients and healthy volunteers. Highly significant difference by the independent t test ($P<0.001$).

[024] Figure 10 indicates the expression level of the Nourin-based molecular biomarker hsa-miRNA-137 in comparison to Troponin I measured in serum samples

of AMI patients and healthy volunteers. Highly significant difference by the independent t test (P<0.001).

[025] Figure 11 indicates the expression level of the Nourin-based molecular biomarker lncRNA-CTB89H12.4 in comparison to Troponin I measured in serum samples of AMI patients and healthy volunteers. Highly significant difference by the independent t test (P<0.001).

[026] Figure 12 indicates the differential level of the Nourin protein measured with the ELISA immunoassay in Cardiac-AMI patients presenting to hospital ED with chest pain and non-cardiac patients also complaining of chest pain. The ELISA immunoassay measured antibodies (hereinafter referred to as "Nour001-A") developed against Nourin polypeptide comprising of the epitope sequence N-f-MII moiety. Troponin negative (-) samples (labeled "Non-Cardiac) showed an average OD reading of approximately 2.2, whereas the Troponin positive (+) samples (labeled "Cardiac AMI") showed an average OD reading of approximately 2.9, with no overlap between individual samples of the two types. The Nour001-A antibody assay showed a statistical significance difference (P=0.0001) between samples from Cardiac-AMI patients and Non-Cardiac patients with chest pain. When the same samples were stored for one month at -20 °C then thawed and subjected to the same ELISA test procedure, the data was similar to and confirmed the results obtained using *fresh* samples, showing a difference between Troponin (+) samples and Troponin (-) samples. In this repeat frozen-sample study, Troponin (+) samples showed an average OD of approximately 2.4, whereas the Troponin (-) samples showed an average OD of approximately 1.8. The lack of stability of Troponin as a significant drawback to its use as a marker for AMI in stored samples, is overcome by the Nourin assay. Thus, the Nour001-A antibody binding profile correlates well with Troponin level profile. As such, the Nour001-A antibody is well suited as a detection reagent for AMI and can differentiate between patients suffering AMI and patients complaining of chest pain, but not suffering AMI. The Nour001-A antibody, thus, can be used in diagnostic assay to differentiate AMI patients from non-cardiac.

[027] Figure 13 indicates the down-regulation of lncRNA-CTB89H12.4 after an AMI event resulted in up-regulation of hsa-miRNA-137 and activation of FTLH-17 mRNA with an increased translation and production of high levels of Nourin protein. There is none to a minimal gene expression of FTLH17 mRNA in normal non-stressed tissues. lncRNA-CTB89H12.4 is related to cardiomyocyte regeneration and angiogenesis and

it is down-regulated after myocardial injury. Figure 13 also indicates that the clinical application of the Nourin-based molecular biomarker panel composed of FTLH-17 mRNA, hsa-miRNA-137 and lncRNA-CTB89H12.4 can be used individually and in combination with the protein-based biomarker Nourin for better and faster diagnosis of AMI patients presenting with chest pain at the ED and outpatient clinics.

[028] Figure 14 indicates the timeframe under which various assays for UA and AMI are useful. Specifically, the figure indicates that the present Nourin assay *can diagnose UA prior to a heart attack* and it can be detected immediately after the initiation of AMI and up to at least 32 hours after an event. The Nourin protein was not tested beyond 32 hours after the onset of chest pain in AMI patients. The present Nourin assay is capable of diagnosing UA in patients, regardless of whether or not they ultimately suffer a heart attack. The myoglobin assay known in the art cannot detect UA and can detect AMI only between about 2 hours and 8 hours after AMI. The CK-MB assay known in the art likewise cannot detect UA, and is useful only between 6 hours and 36 hours after a heart attack. The Troponin assay is likewise limited to use only after 6 to 8 hours post-heart attack, although it can be detected up to 120 hours or more after an ischemic onset. Recent Troponin assays shortened the early detection time to 3 to 6 hours after the initiation of myocardial injury.

[029] Figure 15A-Figure 15I indicate the sequence listing of the gene sequences for lncRNA-CTB89H12.4 by PatentIn software.

DETAILED DESCRIPTION OF THE INVENTION

[030] The present invention may be understood more readily by reference to the following detailed description of the invention taken in connection with the accompanying drawing figures, which forms a part of this disclosure. It is to be understood that this invention is not limited to the specific devices, systems, conditions or parameters described and/or shown herein and that the terminology used herein is for the example only and is not intended to be limiting of the claimed invention. Also, as used in the specification including the appended claims, the singular forms 'a', 'an', and 'the' include the plural, and references to a particular numerical value includes at least that particular value unless the content clearly directs otherwise. Ranges may be expressed herein as from 'about' or 'approximately' another particular value. When such a range is expressed it is another embodiment.

Also, it will be understood that unless otherwise indicated, dimensions and material characteristics stated herein are by way of example rather than limitation, and are for better understanding of sample embodiment of suitable utility, and variations outside of the stated values may also be within the scope of the invention depending upon the particular application.

[031] Embodiments will now be described in details with reference to the accompanying drawings. To avoid unnecessarily obscuring the present disclosure, well-known features may not be described or substantially the same elements may not be redundantly described, for example. This is for ease of understanding.

[032] The drawings and the following description are provided to enable those skilled in the art to fully understand the present disclosure and are in no way intended to limit the scope of the present disclosure as set forth in the appended claims.

[033] In accordance with one embodiment of the present invention, it discloses a novel AMI-specific Nourin RNA-based integrated competing endogenous molecular network as additional biomarkers for AMI patients. Using the amino acid sequence of Nourin purified from human hearts during *reversible* ischemia, we identified the Nourin gene-based RNA network through *in silico* data analysis after BLAST alignment with the Nourin sequence formyl substituted-MIINHNLAAINSHRSPGADGNGGEAMPGGGR (SEQ ID NO:15). We then investigated the serum Nourin gene-based RNA network expression level and pattern in AMI patients and healthy volunteers and compared them to Troponin I level.

[034] Nourin-based RNA Network is an essential part of central dogma, RNA delivers genetic and regulatory information and reflects cellular states. Based on high-through put sequencing technologies, cumulating data show that various RNA molecules are able to serve as biomarkers for the diagnosis and prognosis of various diseases, for instance, cancer and cardiac ischemia. In particular, detectable in various bio-fluids, such as serum, saliva and urine, extracellular RNAs (exRNAs) are emerging as non-invasive biomarkers for earlier diagnosis, disease progression, monitor, and prediction of drug therapy response in clinical trials. Although RNAs are unstable in alkaline conditions, they are easy to detect and quantify at very low abundance. Compared to protein biomarkers, RNA biomarkers have more sensitivity and specificity. Standard qPCR technique enables traces of RNA sequences to be amplified and thus captured specifically with high sensitivity. Moreover, the cost of RNA biomarker is much lower than protein biomarker because detecting each protein

requires a specific antibody. Additionally, compared with DNA biomarkers, RNA biomarkers have the advantage of providing dynamic insights into cellular states and regulatory processes than DNA biomarkers. Besides, RNA has multiple copies in a cell, which delivers more information than DNA. Moreover, some RNAs with specific structures, such as circular RNA, have the potential to exist stably in plasma and/or serum.

[035] Competing endogenous RNAs (ceRNAs) have been reported to regulate the distribution of miRNA molecules on their targets and thereby impose an additional level of post-transcriptional regulation. In particular, a muscle-specific lncRNA, linc-MD1, sponges miRNA-133 to regulate the expression of MAML1 and MEF2C, transcription factors that activate muscle-specific gene expression. It was found that HuR, which is under the repressive control of miRNA-133, is de-repressed due to the sponging activity of linc-MD1 on miRNA-133. This study, therefore, uncovered a feed forward positive loop involving muscle transcription factors, RNA binding proteins, miRNAs, and a *lncRNA, that controls early phases of myogenesis*. Interestingly, the levels of the muscle-specific lncRNA, linc-MD1 is strongly reduced in muscle cells of patients with Duchenne Muscular Dystrophy. In another study, it was reported that cardiac apoptosis-related lncRNA (CARL) could act as an endogenous miRNA-539 sponge to regulate PHB2 expression, mitochondrial fission and apoptosis. Modulation of their levels may provide a new approach for tackling apoptosis and myocardial infarction. Clearly, understanding this novel RNA crosstalk will lead to significant insight into gene regulatory networks and have implications in human development and disease.

[036] Using both the functional leukocyte chemotaxis assay and the immunoassay ELISA, our studies demonstrated that the cardiac-derived Nourin peptide is rapidly released by ischemic heart tissue while it is still "*viable*" before cells are dead, as well as by necrotic hearts. Consistence results showing the "*early*" release of Nourin by ischemic hearts were demonstrated using various species (human, dog, rat and cow) as well as several models of ischemic injury to include AMI (necrotic), global cardiac arrest (necrotic), cardiopulmonary bypass surgery (reversible) and heart transplantation (reversible). The early release of Nourin by ischemic injury (Figure 14) is clinically significant to abort infarction, save heart muscles and reduce myocardial injury. Unlike Troponin, Nourin was detected in *fresh* blood samples collected from ACS patients, as well as *frozen* samples stored at -70°C for 3 years.

The Nourin-based RNA network is an essential part of central dogma where RNA delivers genetic and regulatory information and reflects cellular states. RNA molecules are able to serve as non-invasive biomarkers for earlier disease diagnosis and level of risk, as well as monitor disease progression and prediction of drug therapy response on heart tissue. Compared to protein-based biomarkers, RNA biomarkers have more sensitivity and specificity as it can be tissue and disease specific.

[037] It is known in the art that autophagy is a process involved in the clearance of damaged proteins and organelles and facilitates cellular health under various stress conditions including hypoxia, ischemia or oxidative stress. Reports indicate that cardiomyocyte autophagy develops in the heart during AMI and it is rapidly activated within 30 minutes after coronary ligation.

[038] In one embodiment of the present invention, the Nourin molecular network composed of lncRNA-CTB89H12.4, hsa-miRNA-137, and FTLH-17 mRNA formyl substituted-MIINHNLAAINSHR (SEQ ID NO:16) as an autophagy-related RNA panel linked to cardiovascular ischemia to specifically identify ischemic cardiac events such as UA and AMI. It is disclosed that autophagy-related Nourin gene-based RNA network may be utilized as an early biomarker for cardiac ischemia. Specifically, there was a down-regulation of RNA-CTB89H12.4 after an AMI event, resulted in the up-regulation of hsa-miRNA-137 and activation of FTLH-17mRNA formyl substituted-MIINHNLAAINSHR (SEQ ID NO:16) with an increased translation and production of high levels of Nourin protein.

[039] In another embodiment of the present invention, Nourin gene regulatory RNA molecular network is disclosed as additional biomarkers for AMI patients. Using the amino acid sequence of Nourin purified from human hearts during *reversible* ischemia, the Applicant has identified the Nourin gene-based RNA network through *in silico* data analysis after BLAST alignment with formyl substituted-MIINHNLAAINSHRSPGADGNGGEAMPGGGR (SEQ ID NO:15)

[040] In another embodiment of the present invention, the Nourin gene-based RNA network expression level and pattern were analyzed in serum samples of AMI patients and healthy volunteers. The novel AMI-specific Nourin RNA-based integrated competing endogenous network is composed of:

(1) Ferritin heavy polypeptide 17 (FTLH-17) formyl substituted-MIINHNLAA INSHR (SEQ ID NO:16) gene for Nourin mRNA;

(2) homo sapiens microRNA-137 (hsa-miRNA-137) gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO:04) as a regulatory gene on FTLH-17; and

(3) long non-coding intergenic RNA-(lncRNA-CTB89H12.4) (SEQ ID NO:19) an autophagy-related gene for cardiac ischemia and regulates hsa-miRNA-137. Please refer to Figure 15A-15I.

[041] In another embodiment of the present invention, the utilization of Nourin integrated genetic epigenetic approach, CTB89H12.4 may be involved in epigenetic activation of miR-137 with subsequent modulation of FTLH-17 mRNA formyl substituted-MIINHNLAA INSHR (SEQ ID NO:16) with potential role in AMI pathogenesis. Standard qPCR-based validation of the network was done in serum from 69 AMI patients collected during the first 8 hours of chest pain and serum from 31 healthy control volunteers. AMI clinical diagnosis was confirmed by angioplasty analysis (presence of a blood clot) and elevation of Troponin I. The relation between the expression of Nourin RNA-based biomarker network and different clinicopathological factors was also explored, as well as the correlation between Nourin RNAs and the level of cardiac Troponin I assessed by Spearman correlation.

[042] Compared with messenger RNAs presenting an average of 2,000 nucleotides long, mature miRNAs have a length of only ~21 to 23 nucleotides. Their subsequent targeting mechanisms show a great deal of complexity because each miRNA can target thousands of transcripts, and one mRNA can contain several target sites for different miRNAs. Currently there are over 2,000 known miRNAs in humans and more are constantly being discovered and added to the miRNA database, “miRBase”. Several microRNAs have been shown to play major roles in myocardial ischemia. A previous study showed that *microRNA-137 was down-regulated as the cardiomyocyte differentiates and proliferates, suggesting that miR-137 may play a critical role in cardiomyocyte regeneration. However, there has been no report yet on whether miRNA-137* gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO:04) *is differentially expressed in pathological cardiomyocytes such as AMI.* miRNA -137 gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga

uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO:04) has an important role in controlling embryonic neural stem cell fate. The down-regulated expression of miR-137 was observed in glioma stem cells and it regulates neuronal maturation. Additionally, miRNA-137 gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO:04) is decreased in Alzheimer disease patients. *The lncRNA-CTB89H12.4 [AC021078.1-201 (ENST00000499521.2)] is located on chromosome 5 and has 2 exons. lncRNA-CTB89H12.4 is also related to cardiomyocyte regeneration and angiogenesis.*

[043] In another embodiment of the present invention, the association of the Nourin gene-based RNA network with FTLH-17, miRNA-137 gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO:04) and lncRNA-CTB89H12.4 is demonstrated along with their expression pattern and level in AMI patients and healthy volunteers.

[044] It is preferred that a biomarker of ACS should fulfill a number of the following criteria; including:

(1) it should be tissue-specific and abundantly expressed in heart tissues;
(2) its expression level in circulation under normal conditions should be extremely low or undetectable;
(3) in ACS patients, it should be quickly released into the circulation from the damaged heart and stably expressed for some time with a long half-life within the sample;
(4) accessible using noninvasive methods;
(5) the capability of rapid and accurate detection with a high degree of sensitivity and specificity to the disease; and
(6) allows early detection with sensitivity to relevant changes in the disease.

[045] Circulating miRNAs fulfill a number of these criteria. They are stable in blood circulation, they are often regulated in a tissue- and pathology-specific manner, and they can be detected with high sensitivity and specificity using sequence-specific amplification.

[046] It has been hypothesized that necrosis of cardiac cells after AMI results in the leakage of miRNAs into the circulation and that miRNAs highly, and preferably, specifically expressed in the heart might be used to diagnose acute coronary events.

The identification of stable circulating miRNAs launches a new generation of potential biomarkers, for which assays can be developed with relative ease, at a relatively low expense, but with potentially better specificity and sensitivity. These assays could easily be designed to combine a large number of circulating miRNAs, which could drastically change the use and interpretation of circulating biomarkers as we know them. At the moment, most studies are investigating the usefulness of individual miRNAs as biomarker for disease, but none of the prior art document has reported that a combination of multiple miRNAs like the Nourin RNA network, which are related to each other and cardiovascular ischemia, would provide greater accuracy with high sensitivity and specificity.

[047] In another embodiment of the present invention, the preclinical study of the invention confirmed the following:

(1) the rapid release of Nourin by reversible ischemic hearts and
(2) necrotic tissues in many animal models of unstable angina and AMI;
(3) the biological activity of Nourin as a potent inflammatory mediator;
(4) purification of Nourin from human reversible ischemic hearts (patients undergoing bypass surgery);
(5) identification of amino acid sequence of Nourin released by human reversible ischemic hearts; and
(6) development of an antibody-based ELISA assay against the amino acid sequence of the Nourin epitope N-f-MII.

[048] In another embodiment, the clinical application of the Nourin functional assay (leukocyte Chemotaxis) and the Nourin ELISA immunoassay (Nourin epitope f-MII) successfully established that:

(1) Nourin released by reversible ischemic hearts was detected in cardioplegic samples collected from patients undergoing open heart surgery and in serum and plasma samples collected from patients experiencing unstable angina while the heart muscles are still alive. A very important finding to permit early crucial therapy and save heart muscles from progressing to necrotic injury;
(2) Nourin is much earlier than the current gold standard Troponin in diagnosing unstable angina and AMI patients;

(3) Nourin can diagnose ACS patients immediately upon arrival to hospital ED without the required 3 to 6 hours wait for Troponin to be released by necrotic hearts at measurable levels in blood samples;
(4) Nourin can differentiate patients presenting to hospital ED with chest pain due to cardiac AMI from non-cardiac patients with also chest pain; and
(5) in comparison to the lack of stability of Troponin, Nourin is stable in ACS patients' samples kept frozen for three years.

[049] The rapid and accurate diagnosis of unstable angina and heart attack patients presenting with chest pain to hospital ED and outpatient clinics play a significant role in saving patients' lives. Therefore, there is a crucial need for biomarkers that can quickly diagnose ACS patients while the myocardial tissue is still *viable* to permit early crucial therapy to save heart muscles and reduce myocardial necrosis and heart failure. Approximately 50% of AMI patients progress to heart failure. Therefore, the Applicants established that the autophagy-related Nourin gene-based RNA network as an early new biomarker for cardiac ischemia to save heart tissue.

[050] In another embodiment of the present invention, an assay for the detection of one or more small molecules that are released as a result of certain heart disorders, including UA and AMI are disclosed. Unlike the Troponin assay currently in use as a marker of necrosis, the Nourin assay according to the invention uses a biomarker for *reversible* ischemia before death. The Nourin assay can be used to diagnose unstable angina patients presenting with chest pain to hospital ED and outpatient clinics, and also can be used to distinguish between cardiac patients (unstable angina and heart attack) and non-heart related symptoms of chest pain.

[051] Therefore, in view of the above the Nourin assay, it can:
(1) identify unstable angina patients and reduce medical malpractice costs associated with missed heart attacks;
(2) complement and enhance the usefulness of the Troponin assay to rule in or out unstable angina and heart attack;
(3) unlike Troponin, it can immediately identify heart attack patients at arrival at hospital ED and eliminates the current required three to six hours of waiting; thus, allows crucial therapy to save heart muscles from dying; and
(4) also reduce unnecessary health care expenses by eliminating unnecessary hospital admissions of chest pain patients.

[052] In another embodiment of the present invention, the aforementioned assay involves the use of at least one, and preferably three Nourin RNAs that are released as a result of cardiac ischemia including UA and AMI. More specifically, the invention provides for the use of the qPCR assay to detect a Nourin molecular network composed of lncRNA-CTB89H12.4 (SEQ ID NO: 19), hsa-miRNA-137 gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO: 04), and FTLH-17 mRNA as an autophagy-related RNA panel linked to each other and to cardiovascular ischemia to specifically identify ischemic cardiac events such as UA and AMI.

[053] In another embodiment of the present invention, the use of one or the three qPCR assays to detect Nourin RNAs that are released from cardiac tissue cells upon an episode of UA and AMI. The aforementioned RNAs, used alone or in combination, can thus be used to detect UA and AMI and to diagnose the cause of chest pain in cardiac patients. It is pertinent to note that, the RNAs can differentiate between patients experiencing or having recently experienced UA and AMI from those having chest pain, but not experiencing of having ACS.

[054] In addition, at least one, and preferably three RNAs can be used to:

(1) detect subclinical or silent myocardial ischemia without infarction as well as low grade myocardial ischemia without cell death;

(2) identify disease risk and monitor progression; and

(3) predict drug therapy response on heart tissues in clinical trials.

[055] In another embodiment of the present invention, it is evidenced that serum Nourin-based FTLH-17 mRNA, hsa-miRNA-137 gguccucuga cucucuucgg ugacggguau ucuugggugg auaauacgga uuacguuguu auugcuuaag aauacgcgua gucgaggaga guaccagcgg ca (SEQ ID NO: 04), and the Nourin protein measured by antibody to the Nourin polypeptide comprising of the epitope sequence N-f-MII are elevated in UA and AMI patients, while the level of lncRNA-CTB89H12.4 (SEQ ID NO: 19) dropped in AMI patients' samples. Based on these results, it is likely that miRNA-137-5p acggguauuc uuggguggau aau (SEQ ID NO:05) and miRNA-137-3p uuauugcuua agaauacgcg uag (SEQ ID NO:06) are also elevated in AMI patients' serum samples. Accordingly, combining the integrated genetic epigenetic approach of Nourin RNAs and the Nourin peptide could be a powerful panel of biomarkers for the early diagnosis of UA and AMI patients. For polygenic diseases such as AMI and a complex human serum, it is expected that a single gene biomarker approach may not

suffice for the high-performance requirement of AMI diagnosis. Therefore, by enlisting multiple Nourin gene network and the Nourin peptide that are functionally linked to each other and to AMI functional networks, it will increase the chance of success than the simpler conventional single-marker approach (e.g., Troponin) as a useful diagnostic and disease monitoring biomarkers to complement protein-based biomarkers and classical risk factors for AMI diagnosis and prognosis.

[056] In another embodiment of the present invention, using the standard chemotaxis functional assay and the ELISA immunoassay, clinical studies demonstrated that the level of Nourin was 3-fold higher in plasmas of ACS (UA and AMI) patients who presented to the ED within 1.5 to 3.5 hours after the onset of symptoms, while the standard cardiac biomarkers Troponin T and CK-MB were not detected. After clinical confirmation of ACS patients, Troponin was detected in AMI patients' samples and lasted for 36 hours. Nourin was also detected in same samples after 32 hours of onset of chest pain. Nourin level was not tested beyond the 32 hours. Additionally, an ELISA assay using antibodies developed specifically against Nourin's epitope N-f-MII moiety (hereinafter referred as "Nour001-A") demonstrated clinically:

(1) the detection of high levels of cardiac Nourin in frozen plasma samples (-70 °C for 3 years) collected from ACS patients within the first 8 hours of chest pain when Troponin I level was below the clinical-decision level (below 0.07 ng/ml) but were later confirmed the diagnosis of ACS; thus, Nourin ELISA distinguished ACS patients from non-cardiac patients with chest pain.

(2) the detection of high levels of cardiac Nourin in AMI patients' fresh plasma samples collected within the first 8 hours of chest pain when Troponin I levels were below the clinical-decision level (below 0.07 ng/ml) but were later confirmed the diagnosis of AMI; thus, Nourin ELISA distinguished AMI patients from non-cardiac patients with chest pain; and

(3) Nourin was not detected in plasma samples collected from non-cardiac patients also presenting to the ED within the first 8 hours of chest pain with negative Troponin I.

[057] It is pertinent to note that a number of studies have indicated that the post transcriptional regulatory RNAs such as circulating non-coding micro RNAs (miRNAs) and long non-coding RNAs (lncRNAs) are potential biomarkers for AMI. Cardiac injury following AMI is known to increase the expression levels of circulating miRNAs such as miRNA-208a ugacgggcga gcuuuuggcc cggguuauac cugaugcuca cguauaagac

gagcaaaaag cuuguugguc a (SEQ ID NO:07) miRNA-208a-5p gagcuuuugg cccggguuau ac (SEQ ID NO:08), miRNA-208a-3p auaagacgag caaaaagcuu gu (SEQ ID NO:09), miRNA-133 acaaugcuuu gcuagagcug guaaaaugga accaaaucgc cucuucaaug gauuuggucccccuucaacca gcuguagcua ugcauuga (SEQ ID NO:01). miRNA-133a-5p agcugguaaa auggaaccaa au (SEQ ID NO:02), miRNA-133a-3p uuuggucccc uucaaccagc ug (SEQ ID NO:04), miRNA-1 ugggaaacau acuucuuuau augcccauau ggaccugcua agcuauggaa uguaaagaag uauguaucuc a (SEQ ID NO:10), miRNA-1-5p acauacuucu uuauaugccc au (SEQ ID NO:11), miRNA-1-3p uggaauguaa agaaguaugu au (SEQ ID NO:12) and miRNA-499-5p uuaagacuug cagugauguu u (SEQ ID NO:13), miRNA-499a-3p aacaucacag caagucugug cu (SEQ ID NO:14). The concentration of miRNA-208a, miRNA-133a, and miRNA-499 is elevated after ACS suggesting that circulating miRNA as diagnostic biomarkers in cardiovascular diseases. The cardiac-specific miR-208a is the most promising STEMI biomarker reported. The first three miRNAs (miRNA-208a, miRNA-133, miRNA-1) peak at 3 hours after AMI and miRNA-499 at 12 hours. Experimentally, the levels of miRNAs in plasma were highly comparable with cardiac Troponin levels in their rat model of isoproterenol-induced myocardial injury. They found miRNA-208 to be undetectable at baseline, increased after 3 hours of isoproterenol treatment, and significantly elevated up to 12 hours. MiRNA-208 was also found to be rapidly induced in rodent models of AMI where it was undetectable in sham-operated animals, increased at 30 minutes, peaked at 3 hours, and disappeared from plasma at 24 hours. In a subgroup of 20 patients with AMI of which blood samples were collected within 4 hours after the onset of symptoms, miRNA-208 was detected in all patients, whereas Troponin I was only detected in 85% of the patients, confirming the superior sensitivity of miRNA-208 at early time points. In a clinical setting the differences in time courses of release between specific miRNAs and Troponin I might be valuable. Especially in the consideration of the fact that the Troponin I levels begin to rise only 3 to 8 hours after AMI, diagnosis via biomarkers with a faster cardiac release, such as miRNA-208, miRNA-1, and miRNA-133, might be beneficial.

[058] The release of miRNAs can be (a) actively secreted and these molecules are referred to as circulating miRNAs, (b) through a jab junction dependent mechanism and (c) as a consequence of cellular content release (macrovesicles, exosomes) following necrosis, for instances during an AMI. MicroRNAs play a pivotal role in a wide range of regulatory processes in the cells and in fact *miRNAs deficiencies or*

excesses have been linked to a number of cardiovascular diseases. The apparent minimal effects of miRNAs under non-stress conditions as compared to their specific involvement during responses to AMI make miRNAs attractive diagnostic targets with little or no effects from normal non-stressed tissues. Similarly, the circulating lncRNA MIAT has been expressed in AMI patients and was able to distinguish STEMI from NSTEMI. However, the circulating lncRNA UCA1 decreased in AMI patients at two hours after the onset of symptoms. At this stage, certain miRNAs individually or in combination may possibly complement protein-based biomarkers and classical risk factors for AMI diagnosis and prognosis.

[059] Circulating miRNAs are emerging as blood-based biomarkers for cardiovascular diseases since they offer many attractive features of biomarkers. They are stable in the circulation, their sequences are evolutionarily conserved, their expression is often tissue or pathology specific, and their detection is based on sequence-specific such as in the case of Nourin, features that are helpful in the development of sensitive and specific assays. In cardiovascular disease, “distinctive patterns” of circulating miRNAs have thus far been found for AMI, coronary artery disease (CAD), hypertension, heart failure (HF), and viral myocarditis (VM). Circulating miRNAs are found to be remarkably stable in plasma even under harsh conditions as boiling, low or high pH, long-term storage at room temperature, and in multiple freeze-thaw cycles. lncRNAs are also found to be present in circulation in a remarkably stable form, which can withdraw multiple freeze-thaw cycles and are resistant against RNase-mediated degradation.

[060] Additional procedures to detect the circulating Nourin RNAs in cardiac patients’ samples are by measuring exosomes and extracellular vesicles. In addition to the use of the standard qPCR, the Nourin-based RNA network can be detected in cardiac patients’ samples using gold coated magnetic nanoparticles as a non-PCR based technique. For this Nanogold assay, the Nourin RNAs will be either extracted or measured directly in patients’ samples without purification or pre-amplification. The Nanogold assay uses magnet beads coated with specific probe and gold nanoparticles to facilitate both RNA extraction and detection of expression using nanoparticles which seems to save time and cost. This assay will measure the Nourin RNA panel of markers in various sera samples. A citrate-capped gold nanoparticles (AuNPs) assay for the direct detection of unamplified Nourin-based RNA network in sera samples for the early diagnosis of AMI patients. The assay employs magnet

nanoparticles (MNPs) functionalized with Nourin-based RNA-specific oligonucleotides for capturing and purifying the target RNA and AuNPs for detection. The method depends on colorimetric determination of unamplified RNA. In addition, Nourin-based RNA panel of markers can be detected in cardiac patients' samples using the technology provided commercially, for example by Multiplex miRNA assays measuring the Nourin-based RNA network via total circulating RNAs, Multiplex miRNA assays with FirePlex® particle technology enable simultaneous profiling of 65 miRNAs directly from small amounts of biofluid or FFPE, without RNA purification or pre-amplification. Assays can be customizable for the Nourin-based RNA panel of markers and suitable for both discovery and verification studies. Readout uses a standard flow cytometer. Additionally, sensor chip procedures can be used to detect the Nourin-based RNA network and the Nourin protein including and not limited to Nourin epitope f-MII.

[061] The invention will be further explained by the following Examples, which are intended to purely exemplary of the invention, and should not be considered as limiting the invention in any way.

EXAMPLES

Example 1

Identify the Nourin Gene-Based RNA Network as Biomarkers for Cardiac Patients.

[062] A combined approach of: (1) bioinformatic analysis (software analysis) using previous microarray studies was conducted and the results were related to our known Nourin peptide sequence to retrieve the Nourin-based RNAs; and (2) biomarker verification was conducted by determining the expression levels and pattern of Nourin RNAs in AMI patients' serum samples and compare them to healthy volunteers using standard qPCR.

[063] To retrieve lncRNA-associated competing endogenous RNAs based on Nourin (Nourin ceRNAs) and to establish their clinical relevance in AMI patients based on previous microarray studies, the following three steps were conducted: (1) biomarker retrieval step to analyze ncRNA gene placement relative to AMI associated genes through public databases and to analyze lncRNA-miRNA interaction databases to lncRNA specific for AMI; (2) bioinformatic validation of the chosen lncRNA-associated

competing endogenous RNAs related to AMI; and (3) using the standard quantitative real time PCR (qPCR) molecular assay to validate the chosen biomarker as a diagnostic marker for early detection of AMI in sera samples in comparison to the gold standard cardiac marker Troponin I.

[064] Nourin RNA analysis was performed on serum samples collected from 69 AMI patients who were diagnosed with documented acute myocardial infarction and ongoing chest pain for 8 hours at the Emergency Department and 31 healthy normal volunteers with matching age and sex to the AMI patients' groups. AMI was diagnosed within the first 8 hours of chest pain on the basis of the presence of a blood clot in the coronary artery confirmed by angiography procedures and elevated serum Troponin I levels, in addition to clinical symptoms & history consistent with cardiac ischemia. The criteria for diagnosing AMI was in accordance with the American College of Cardiology/American Heart Association guidelines and reflected the clinical judgment of two experienced independent cardiologists. Patients were excluded from the study if they have a history of hepatitis, hepatic failure, end-stage renal failure, cardiomyopathy, congenital heart disease, bleeding disorders, previous thoracic irradiation therapy, autoimmune diseases, inflammatory diseases such as inflammatory bowel disease (IBD) and arthritis or malignant disease. Blood samples were obtained once within the first 8 hours of chest pain and were centrifuged and the serum was separated, aliquoted and stored immediately at −80 °C for further processing.

[065] Blood samples were collected from 69 AMI patients and 31 healthy controls in primary blood collection tubes without clot activator and without anticoagulants such as EDTA or citrate (red-topped tubes). These blood samples were left at room temperature for a minimum of 30 min (and a maximum of 60 min) to allow complete blood clotting in the red-topped tubes. The clotted blood samples were then centrifuged at 1300*xg* at 4°C for 20 min. The upper yellow serum was carefully removed, transferred to a polypropylene capped tube in 1 ml aliquots and stored at -80°C until they are assayed by qPCR. All serum samples were labeled with a unique identifier to protect the confidentiality of the patients. None of the serum samples were allowed to thaw before analysis to minimize protein degradation and precipitation.

[066] Biomarker validation using qPCR involved (1) extraction of the total RNA from serum samples (AMI and healthy); (2) generation of cDNA through reverse

transcription; (3) measurement of cDNA using qPCR; and (4) evaluation of results by the plot curve analysis software of Rotor Gene to confirm specificities then amplification plot and data analysis. For the extraction of total RNA, including lncRNA, miRNA and mRNA from sera samples, miRNEasy RNA isolation kit (Qiagen, Hilden, Germany) was used according to manufacturer's instructions. The RNA samples were dissolved in 30 µl of nuclease-free water. The concentration of RNA was determined using a NanoDrop spectrophotometer (Thermo Scientific, USA). Total cDNA including cDNA for miRNA, mRNAs and lncRNA was prepared from sera samples and were loaded to Rotor Gene Thermal cycler (Thermo Electron Waltham, MA) using miScript II RT Kit (Qiagen, Germany) by adding 2ul 10x miScript Nucleics Mix, 4ul 5x miScript HiFlex Buffer, 1ul miScript Reverse Transcriptase Mix and RNase free water to 2ug RNA and the mixture was incubated for 60 minutes at 37 ºC then for 5 minutes at 95 ºC.

[067] Quantification of the expression pattern and levels of Nourin gene-based RNA network panel by qPCR included: lncRNA-CTB89H12.4 and FTLH-17 mRNA expression in sera samples were quantified by adding 10ul 2xRT²SYBR Green ROX qPCR Mastermix and QuantiTect SYBR Green PCR Kit, respectively, RT²lncRNAq PCR Assay for RT² lncRNA qPCR Assay for Human CSNK1A1 (ENST00000499521) and Hs_FTHL17_1_SG QuantiTect Primer Assay (NM_031894), 2ul template cDNA and RNase free water to a final volume of 20ul Hs_ACTB_1_SG QuantiTect Primer Assay (NM_001101) was used as housekeeping gene to normalize our raw data as the invariant control for the samples, and compared with a reference sample. The PCR program for relative lncRNA-CTB89H12.4 quantification was conducted as follow: firstly, denaturation at 95°C for 10 min; followed by 45 cycles of denaturation for 15 seconds at 95°C; then annealing for 30 seconds at 55°C and extension for 30 seconds at 70°C.

[068] To quantify the expression of hsa-miR-137 in the different sera samples, we used miScript SYBR Green PCR Kit (Qiagen/SA Biosciences Corporation, Frederick, MD) by adding 10ul 2x miScript SYBR Green PCR Master Mix, 2ul 10x miScript Universal Primer, 2ul 10x miScript Primer Assay for either Hs_miR-137_1 miScript Primer Assay targets mature miRNA: hsa-miR-137 (MIMAT0000429: 5'UUAUUGCUUAAGAAUACGCGUAG) or RNU6B, 2ul template cDNA and RNase free water to a final volume of 20ul. All the PCR primers were purchased from (Qiagen, Germany MD). The real-time cycler was programmed for relative

quantification of FTLH-17 mRNA and Hsa-miRNA-137 as follows: initial activation step for 15 min at 95ºC to activate HotStarTaq DNA Polymerase. 40 cycle of PCR were performed under the following conditions; 15 seconds at 94 ºC, 30 seconds at 55 ºC and 30 seconds at 72 ºC for denaturation, annealing and extension respectively. Each reaction was carried out in triplicate. Relative quantification of RNA-based biomarker panel expression was calculated using Leviak method RQ= $2^{-\Delta\Delta Ct}$ method. The threshold cycle (Ct) value of each sample was calculated using the Rotor Gene real time PCR detection system (Qiagen, Hilden, Germany). Any Ct value more than 36 was considered negative. The results were analyzed by the plot curve analysis software of Rotor Gene. Amplification plots and Tm values were analyzed to confirm the specificities of the amplicons for SybrGreen-base amplification.

[069] For Nourin RNA's stability in the collected blood samples, we have stored sera samples at -70 for about (4 to 6 months). Sera samples were processed within half an hour after collection and aliquoted to minimize freeze thaw cycle. We have used spin columns with small pore sizes in an attempt to concentrate serum RNA before the precipitation step and have checked the concentration and purity of RNA using U/V spectrophotometer. Real time PCR was done after RNA extraction at the same day. Mean delta CT for housekeeping genes were 24 indicating average RNA expression. In general, RNAs are stable in serum for 2 years. We have investigated miRNA and long non-coding RNA which are already most stable forms of RNA. In general, miRNAs are detected in serum or plasma in a remarkable stable form and can withstand repetitive freezing and thawing cycles. In addition, circulating miRNAs are resistant against RNase-mediated degradation.

[070] Measurement of cardiac Troponin I was conducted in serum samples collected from AMI patients and healthy control samples. The manufacturer of cardiac Troponin I is Siemens (adiva contour). The cardiac Troponin I assay is a 3-site sandwich immunoassay using direct chemillumenscence. The units for the measurements are ng/ml and the 99th percentile upper reference limit of a range 0.04 ng/ml.

[071] All statistical data were executed using SPSS 22 Mann Whitney, independent t test, and chi-square test were used as appropriate to complete comparisons. To characterize the predictive value of the selected RNA-based biomarker panel for AMI, the Receiver Operating Characteristic (ROC) curve was carried out. The Spearman correlation was performed to detect the associations between RNA-based biomarker

network expression and clinicopathological parameters. Two-tailed P value of 0.05 or less was supposed to be statistically significant.

[072] Additional procedures to detect the circulating Nourin RNAs in cardiac patients' samples are by measuring exosomes and extracellular vesicles. Furthermore, in addition to the use of the standard qPCR, the Nourin-based RNA network can be detected in cardiac patients' samples using the gold coated magnetic nanoparticles as a non-PCR based technique. For this Nanogold assay, the Nourin RNAs will be either extracted or measured directly in patients' samples without purification or pre-amplification. This assay will measure the Nourin RNA panel of markers in various sera samples. In addition, Nourin-based RNA panel of markers can be detected in cardiac patients' samples using the technology provided commercially, for example by Multiplex miRNA assays measuring the Nourin-based RNA network via total circulating RNAs, Multiplex miRNA assays with FirePlex® particle technology enable simultaneous profiling of 65 miRNAs directly from small amounts of biofluid or FFPE, without RNA purification or pre-amplification. Assays can be customizable for the Nourin-based RNA panel of markers and suitable for both discovery and verification studies. Readout uses a standard flow cytometer. Additionally, sensor chip procedures can be used to detect the Nourin-based RNA network and the Nourin protein including and not limited to Nourin epitope N-f-MII.

[073] Furthermore, the Point-of-Care (POC) procedures can be used to rapidly within 15 minutes detect in cardiac patients' samples the circulating Nourin RNAs including RNA FTLH-17 mRNA, miRNA-137 and lncRNA-CTB89H12.4 as well as the Nourin epitope N-f-MII. The POC diagnostics has been emerged as a promising real-world application. The POC ecosystem is evolving faster than ever and new technology has to fit into a broader landscape. Some of the main advantages of POC diagnostic device include the use of smaller sample volume, lower test costs and faster turn-around-times i.e., 15 minutes vs, 4 hours to 24 hours for PCR. Beside its rapid and precise response, its portability, low cost and non-requirement of specialized equipment are important advantages. The challenge is that the POC devices use smaller sample volumes to achieve the same detection limit as standardized laboratory equipment. It requires the integration of assay chemistry, fluidics, hardware and software.

[074] A POC device can use a chip-based technology to examine different analytes in various samples including blood, urine and tissue biopsies. Microfluidics and

biosensor can use numerous materials such as glass, silicon, polymer, and paper for the fabrication of microfluidics-based POC devices along with their wide range of biosensor applications. Recent development in nanomaterials, device design, and microfabrication technologies have made it possible to obtain POC devices with enhanced sensing characteristics. Breakthroughs such as the recently published method of 3D printing microfluidics lab-on-a-chip devices could help lead to cheaper mass-production of diagnostic devices. The use of smartphones paired to microfluidics could enable an increased range and ability of POC testing, with the development of devices such as the TRI analyzer on the horizon, it is possible to achieve limits of detection that are comparable to those obtained for the same assay measured with a conventional laboratory microplate reader, demonstrating the flexibility of the system to serve as a platform for rapid, simple translation of existing commercially available bio sensing assays to a POC setting. POC portable devices identification method can be based on microarray platform require extensive testing and validation comparing the outcome with more traditional methods of detection. Thus, the high-performance RNA-detection methods for all types of clinically relevant RNAs (mRNAs, miRNAs and lncRNAs) are based on molecular–biology techniques including and not limited to qPCR, microarrays, nanoparticles, microfluidics and biosensor.

Example 2

Retrieve Molecular Biomarkers Relevant to AMI and Related to the Nourin Peptide Sequence.

[075] Bioinformatic analysis was done to retrieve biomarkers relevant to AMI and related to the Nourin peptide sequence based on previous microarray studies. The bioinformatic analysis included a number of blast programs to retrieve relevant genes to the Nourin peptide sequence. We have retrieved Ferritin heavy polypeptide 17 (FTLH-17) gene after BLAST alignment 100% with the Nourin-1 peptide sequence (US 7659091 B2)

formyl substituted-MIINHNLAAINSHRSPGADGNGGEAMPGGGR (SEQ ID NO:15). Ferritin is the major intracellular iron storage protein in prokaryotes and eukaryotes. It is composed of 24 subunits of the heavy and light ferritin chains. Variation in ferritin subunit composition may affect the rates of iron uptake and release in different tissues. A major function of ferritin is the storage of iron in a soluble and nontoxic

state. We have then identified the Nourin gene-based RNA network through *in silico* data analysis. For clinical validation of the chosen Nourin gene-based RNA network as diagnostic biomarkers for early diagnosis of AMI, we have investigated the serum gene network expression of Nourin FTLH1 mRNA, hsa-miR-137 and long non-coding RNA-*CTB-89H12.4* in AMI patients' serum samples collected within the first 8 hours of chest pain as well as in healthy control samples.

[076] To retrieve the lncRNA-associated competing endogenous RNAs based on Nourin sequence & its relevant to AMI based on previous microarray studies, we conducted the following four blast programs to retrieve the relevant gene to the Nourin peptide sequence: (1) using Atlas database retrieving target gene involved that is relevant to the Nourin peptide. we have selected the FTLH17 gene after BLAST alignment with the Nourin sequence formyl substituted-MIINHNLAAINSHRSPGADGNGGEAMPGGGR (SEQ ID NO:15) corresponding to Nourin-1 (US 7659091 B2) with sequence identity 100% and confirmed by gene ontology which revealed that FTLH17 gene is related to autophagy and cardiac ischemia (reversible and irreversible cardiac ischemia as seen in UA and AMI patients) as illustrated in Figure 1, Figure 2 and Figure 3; (2) we then confirmed the low expression of FTLH17 mRNA in normal tissues (Figure 4 and Figure 5). This low expression of FTLH17 mRNA in normal heart was reported in by two techniques out of three. For normal kidney, one technique proved low expression and other 2 techniques negative. Together, FTLH17mRNA is expressed at low level in normal heart, but more than other tissues (Figure 4 and Figure 5); (3) next, we used Diana database to retrieve miRNA-137 that acts as epigenetic regulator of FTLH-17 mRNA and by performing pathway enrichment analysis we confirmed that miRNA-137 is related to autophagy and cardiac ischemia (Figure 6); and finally, (4) we have selected lncRNA-CTB89H12.4 that acts as miRNA-137 sponge through Starbase database (Figure 7).

Example 3:

Differentiation of AMI Patients with Chest Pain from Healthy Controls using the Nourin FTLH-17 mRNA gene, long non-coding intergenic RNA-(lncRNA-CTB89H12.4) and homo sapiens microRNA-137 (hsa-miRNA-137).

[077] After identification of the Nourin gene-based RNA network retrieved through *in silico* data analysis, we determined the Nourin RNA expression pattern and level in 69

AMI patients presenting to hospital ED with chest pain within 8 hours after onset of symptoms and 31 healthy volunteers as an important first step to determine the biomarker signatures of Nourin that will be effective in AMI detection. Specifically, we investigated the Nourin gene-based RNA network expression as a novel AMI-specific RNA-based integrated competing endogenous network composed of ferritin heavy polypeptide 17 (FTLH-17 mRNA) gene, long non-coding intergenic RNA-(lncRNA-CTB89H12.4) and homo sapiens microRNA-137 (hsa-miRNA-137) selected by *in silico* data analysis. Standard RT-qPCR-based validation of the network was used and the relation between the expression of Nourin RNA-based biomarker network and different clinicopathological factors was explored. The correlation between Nourin RNAs and the level of cardiac Troponin I was assessed by Spearman correlation.

[078] Results revealed that the expression pattern and level of the Nourin-gene RNA network composed of long non-coding intergenic RNA-(lncRNA-CTB89H12.4), homo sapiens microRNA-37 (hsa-miRNA-137), and FTLH-17 mRNA had high sensitivity and specificity for discriminating AMI patients from healthy controls (Figure 8). The recorded average of onset of chest pain is 6.52 hours. There was no significant difference detected between the expression of serum Nourin RNAs and the distribution of sex, smoking, diabetes mellitus, cholesterol, hypertension and the type of treatment in the AMI group. Furthermore, the RNA-based network and Troponin I were detected in clinically documented AMI patients with anterior STEMI, inferior STEMI as well as Non-TEMI (NSTEMI). There was a significant correlation, however, between Nourin FTLH-17 mRNA (Figures 9) and microRNA-37 (hsa-miRNA-137) (Figures 10) and the level of the standard cardiac marker, Troponin I with concomitant negative correlation between lncRNA-CTB89H12.4 (Figures 11) and cardiac Troponin I level in AMI and healthy serum samples. Since there was a correlation between Nourin RNA molecular biomarker panel and cardiac Troponin I level in both AMI serum samples, a combined assay that uses the Nourin protein (e.g., epitope N-f-MII) and the Nourin multiple genes that are functionally linked to each other and to AMI molecular networks, increases the chance of a higher success to accurately diagnose AMI patients than the simpler conventional single-marker approach for Troponin I. The circulating transcriptome of the Nourin gene-based RNA network expression has been revealed as a potential class of non-invasive biomarker with high specificity and sensitivity for early detection of AMI. We proposed an integrative approach between differential FTLH-17 gene expression with the selected epigenetic regulators and this

approach has generated an interesting new Nourin-based molecular biomarker panel (lncRNA-CTB89H12.4, hsa-miRNA-137, and FTLH-17 mRNA) for the early diagnosis of AMI patients presenting with chest pain to hospital ED and outpatient clinics. Since the Nourin RNAs are stable, specific and abundantly expressed in ischemic hearts, they will be an added value to the Nourin protein assays. In general, RNA biomarkers have more sensitivity and specificity with much less interference in serum samples and that the qPCR assay enables traces of RNA sequences to be amplified and thus captured specifically with high sensitivity. Moreover, the cost of RNA biomarker is much lower than protein biomarker because detecting each protein requires a specific antibody. The ROC curves analysis and the area under the curve (AUC) values were used to estimate the diagnostic value of our selected RNAs to differentiate AMI from healthy controls. The results implied that hsa-miRNA-137 and lncRNA-CTB89H12.4 are the most effective biomarkers for differentiating AMI patients from healthy people. The best discriminating cutoff values of hsa-miRNA-137, lncRNACTB89H12.4 and FTLH-17 mRNA were 2.29, 3.36 and 3.83, respectively with sensitivities of 98.6%, 97.1% and 82.6%, respectively. Collectively, we believe that the diagnostic accuracy for AMI detection would be improved by a concurrent measurement of serum lncRNA-CTB89H12.4, miRNA-137, and FTLH-17 mRNA to approximately 100% sensitivity and 98% accuracy in the present study. This result indicates that these thresholds could be used to discriminate AMI patients from healthy subjects.

Example 4

Confirmation of Prior Results Using the Cardiac-Derived Nourin Protein.

[079] Previous studies by the Applicant had shown that the 3 KDa Nourin-1, is released shortly after an ischemic cardiac event, e.g., UA and AMI. Those studies relied on either a leukocyte functional chemotaxis assay or an immunoassay using (a) monoclonal sera raised against the *native full-length* Nourin-1 protein; and (b) polyclonal sera raised against a short peptide sequence derived from the N-terminus of Nourin-1 (Nour001-A) generated in mice. The amino acid sequence formyl substituted-MIINHDDERKC (SEQ ID NO:17) was chemically synthesized and purified using HPLC. This peptide was conjugated to KLH using a proprietary method of Precision Antibody (Columbia, Maryland), and mice were immunized. Tail bleeds were collected for determination of antibody titer at three weeks, and final cardiac bleeds were performed at four weeks to collect final sera. The collected sera were

tested for specificity of binding to the immunogen as follows. Diluted sera were combined with a control peptide (MIINHDDERKC; SEQ ID NO:18) in excess to bind and remove antibodies in the sera that bind to any portion of the immunogen other than a portion that includes the formyl-methionine. The "cleared" sera were tested against a screening antigen having the sequence formyl substituted-MIINHDDERKC (SEQ ID NO:17). From a comparison of the sequences, the screening antigen shows identity to the immunogen only at the N-terminal five residues. Results of an ELISA with the "cleared' sera contained antibodies that specifically bound to the formylated N-terminal sequence.

[080] Using the functional leukocyte chemotaxis assay and the ELISA immunoassay (Nour001-A), clinical studies demonstrated that (1) the level of Nourin was 3-fold higher compared to healthy volunteers in plasmas of ACS (UA and AMI) patients who presented to hospital ED within 1.5 to 3.5 hours after the onset of symptoms, while the standard cardiac biomarkers Troponin T and CK-MB were not detected. After clinical confirmation of ACS patients, Troponin T was detected and it was persistent for 36 hours. Nourin which was also detected in samples after 32 hours; (2) the detection of high levels of cardiac Nourin in frozen plasma samples (-70 °C for 3 years) collected from ACS patients (UA and AMI) within the first 8 hours of chest pain when Troponin I levels were below the clinical-decision level (below the heart attack cut off of 0.07 ng/ml) but were later confirmed the diagnosis. The Nour001-A antibody assay showed a statistical significance difference (P=0.012) between samples from ACS patients and other non-cardiac patients with chest pain; (3) the detection of high levels of cardiac Nourin in AMI patients' fresh plasma samples collected within the first 8 hours of chest pain when Troponin I levels are below the clinical-decision level (below the heart attack cut off of 0.07 ng/ml) but were later confirmed AMI diagnosis demonstrating that Nourin is an *earlier* marker than Troponin I (Figure 12). When the same samples were stored for one month at -20 °C then thawed and subjected to the same ELISA test procedure, the data obtained was similar to the results obtained using fresh samples, showing; (4) Nourin was not detected in plasma samples collected fresh from non-cardiac patients also presented to hospital ED within the first 8 hours of chest pain with negative Troponin I (Figure 12). Thus, the Nour001-A antibody is useful in diagnosing patients suffering cardiac ischemic event and could differentiate between ACS (AMI and UA) samples taken from patients experiencing chest pain from chest pain patients but not suffering AMI or UA. Furthermore, the

Nour001-A antibody assay distinguished AMI patients from non-cardiac patients using *fresh* and *frozen* samples.

Example 5

Up-regulation of Nourin gene-based RNA Network and Protein in AMI.

[081] The present invention of the Nourin gene-based molecular biomarker panel composed of FTLH-17 mRNA, hsa-miRNA-137 and lncRNA-CTB89H12.4 further confirmed the use of the cardiac-derived Nourin protein as a biomarker of AMI patients. The down-regulation of lncRNA-CTB89H12.4 after an AMI event resulted in up-regulation of hsa-miRNA-137 and activation of FTLH-17 mRNA with an increased translation and production of high levels of the cardiac-derived Nourin protein (Figure 13). There is a minimal gene expression of FTLH17 mRNA in normal non-stressed tissues. The Nourin RNA panel can be used individually or in combination with the protein-based biomarker Nourin for better and faster diagnosis of AMI patients presenting with chest pain to hospital ED and outpatient clinics. The Nourin molecular and protein-based assays are significantly earlier than current myoglobin, CK-MB and Troponin assays in detecting UA and AMI in patients presenting to the ED with chest pain (Figure 14). Earlier identification of heart patients allows for early intervention to avoid permanent damage and heart attack that can lead to heart failure and death. In general, about 50% of heart attack patients suffer heart failure.

[082] Although the currently identified circulating miRNA-208a, miRNA-133 and miRNA-1 peak in the blood at 3 hours after AMI, they are still *markers of necrosis similar to Troponin*. Nourin, on the other hand, is much earlier biomarker released by '*viable*' ischemic tissue and, thus, provides fast diagnosis for crucial therapy (Figure 14). Additionally, the low level of Nourin in blood samples collected from healthy individuals, makes Nourin an attractive diagnostic marker with little or no effect from normal non-stressed tissues. Furthermore, the Nourin RNA network will diagnose AMI with anterior STEMI, inferior STEMI as well as Non-STEMI (NSTEMI). Finally, Nourin panel of RNAs may be used to complement the protein-based Nourin and Troponin biomarkers as well as other classical risk factors for AMI diagnosis and prognosis. However, compared to protein-based biomarkers, RNA biomarkers have more sensitivity and specificity as it can be tissue and disease specific.

[083] The Nourin assay using for example and not limited to Nourin including the Nourin panel of RNAs (qPCR, Nanogold, Multiplex, microfluidics and sensor ship) or

Nourin epitope N-f-MII (leukocyte Chemotaxis, ELISA, sensor ship and MALDI-TOF [Matrix Assisted Laser Description Ionization-Time of Flight]) is expected to be used clinically in combination with Troponin for some better sensitive and specific diagnostic tests for acute coronary syndromes. The Nourin assays can identify unstable angina patients and complement and enhance the usefulness of Troponin tests to rule in or out unstable angina and AMI. If the Nourin assay does not detect elevated levels of Nourin RNA network and/or Nourin peptide, then ACS patients can be ruled out and the patients can be released from the hospital ED or a workup can begin to elucidate the true cause of the patients' chest pain syndromes. On the other hand, if the Nourin assay detect elevated levels of Nourin RNA network and/or Nourin peptide, the ACS patients can receive therapies in an earlier timeframe than is presently possible with current Troponin and thus eliminating the required long wait of 3 to 6 hours. Early identification of heart patients allows for early intervention to avoid permanent damage that can lead to ischemic heart failure and death. Specifically, early diagnosis of ischemic heart patients will allow for crucial intervention to avoid permanent damage and, thus, abort infarction, save heart muscles, reduce myocardial injury and the progression of patients to heart failure. In general, 50% of heart attack patients will suffer heart failure. The Nourin protein and its multiple genes that are functionally linked to each other and to AMI functional networks, increase the chance of a higher diagnostic success than the simpler conventional single-marker approach for Troponin. The Nourin assays will also be used to identify patients at risk for coronary artery disease (CDA) since circulating miRNAs were found to have a distinct pattern in cardiovascular disease including: CAD, AMI, hypertension, heart failure (HF) and viral myocarditis (VM). Thus, Nourin can be used not only for early diagnosis and monitoring of ACS patients presented to hospital ED and outpatient clinics with chest pain, but also as a risk predictive biomarker to (1) screen high-risk patients (diabetes, high blood pressure, obesity, aging, smokers, high cholesterol, stress, etc.) for the identification of CAD and allow for crucial intervention to avoid permanent damage, abort infarction, save heart muscles and reduce myocardial injury; (2) screen CAD patients for risk assessment to predict which patients are at risk for developing AMI; (3) predict drug therapy response on heart tissue in clinical trials; (4) monitor the heart health after therapy and disease progression; (5) differentiate cardiac from non-cardiac experiencing chest pain; (6) determine the risk level of heart patients experiencing chest pain; (7) provide risk

stratification of AMI patients.; and (8) diagnose heart failure patients after AMI and determine their risk assessment and prognosis.

[084] It will be apparent to those skilled in the art that various modifications and variations can be made in the practice of the present invention without departing from the scope or spirit of the invention. Other embodiments of the invention will be apparent to those skilled in the art from considering of the specification and practice of the invention. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

CLAIMS:

1. A novel autophagy-related Nourin gene-based RNA network as early biomarkers for cardiac diagnosis comprises:
    a) ferritin heavy polypeptide 17 (FTLH-17) gene for Nourin mRNA related to autophagy and cardiac ischemia;
    b) homo sapiens micro RNA-137 (hsa-miRNA-137), an autophagy-related gene for cardiac ischemia as a regulatory gene on FTLH-17;
    c) long non-coding intergenic RNA (lnc-RNA-CTB89H12.4), an autophagy-related gene for cardiac ischemia and regulates hsa-miRNA-137;
    wherein, the Nourin molecular network composed of lncRNA-CTB89H12.4, hsa-miRNA-137, and FTLH-17 mRNA are the first differential expression in pathological cardiomyocytes such as AMI as an autophagy-related RNA panel linked to each other and to cardiovascular ischemia to specifically identify ischemic cardiac events including unstable angina (UA) and acute myocardial infarction (AMI).
2. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein the down-regulation of RNA-CTB89H12.4 after an AMI event resulted in the up-regulation of hsa-miRNA-137 and activation of FTLH-17 mRNA with an increased translation and production of high levels of Nourin protein, and wherein there is extremely low or no gene expression of FTLH-17 mRNA in normal non-stressed tissues.
3. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein a significant correlation between the high expression of Nourin microRNA-37 (hsa-miRNA-137), FTLH-17 mRNA, and the standard cardiac marker, Troponin in AMI serum samples in comparison to the low expression of the three in healthy control serum samples, and wherein a concomitant negative correlation between Nourin lncRNA-CTB89H12.4 and Troponin in AMI and normal serum samples, where there is a lower expression of lncRNACTB89H12.4 in AMI patients and a higher expression in the healthy control group.
4. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein the correlation between Nourin RNA molecular biomarker panel and cardiac Troponin level in AMI and healthy serum samples and by using a combined assay of the Nourin protein (e.g., epitope f-MII) and the Nourin multiple genes that are functionally linked to each other and to AMI molecular networks,

increase the chance of a higher success than the simpler conventional single-marker approach for Troponin.

5. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein the Nourin protein may be measured by antibodies against Nourin polypeptide comprising of the epitope sequence f-MII alone or in combination with Nourin FTLH-17 mRNA, microRNA-37 (hsa-miRNA-137), and lncRNA-CTB89H12.4, are elevated in ischemic cardiac patients.
6. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network is tissue-specific and abundantly expressed in heart tissues.
7. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network is quickly released into the circulation from damaged heart and stably expressed with half-life time range between 3 to 5 years.
8. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecule network is capable of rapid and accurate diagnosis with high degree of sensitivity and specificity to the disease.
9. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network allows early diagnosis with sensitivity to relevant changes in the disease.
10. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network is stable for the period in the range between 2 to 4 years after processing of the sample.
11. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network is clinically detected among AMI patients with anterior STEMI, inferior STEMI, as well as Non-STEMI (NSTEMI).
12. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network possesses a discriminating cut-off value in the range of 2.29 to 3.38.
13. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein measuring serum lncRNA-CTB89H12.4, miRNA-137, and FTLH-17 mRNA is approximately 100% sensitivity and 98% accuracy.
14. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network measured through the Nourin peptide

has been found to be 3-fold higher in plasma of ACS patients compared to healthy volunteers.

15. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network measured through the Nourin peptide has been detectable in ACS patients within 1.5 to 3.5 hours of the onset of the symptom, which is much earlier than Troponin.

16. The novel autophagy-related Nourin gene-based RNA network as claimed in claim 1, wherein said molecular network measured through the Nourin peptide was absent in the non-cardiac patients in fresh and frozen samples which leads to differentiation between ACS patients experiencing chest pain from chest pain patients who are not suffering from UA or AMI.

17. A method for the early diagnosis and differentiation of ischemic cardiac events by the Nourin-gene based RNA molecular network as claimed in claim 1, comprising the steps of:

    a) identifying the Nourin gene-based RNA network as biomarkers;
    b) retrieving molecular biomarkers relevant to AMI and related to Nourin peptide sequence;
    c) differentiating the AMI patient sample from healthy control using Nourin RNA molecular network;
    d) confirming the retrieved output;
    e) up-regulation of Nourin-gene RNA network and protein in AMI.

18. The method as claimed in claim 17 wherein the identification of the Nourin gene in step (a) is performed by following steps consisting of:

    a) bioinformatic analysis using previous microarray and relating it to the Nourin peptide sequence to retrieve Nourin-based RNAs;
    b) verifying biomarkers by determining the expression level and pattern of Nourin-based RNAs in AMI patients' serum (or plasma) samples and comparing it to healthy volunteers using qPCR technique.

19. The method as claimed in claim 17, wherein the identification of the Nourin gene is performed alone or in combination of an antibody to Nourin polypeptide comprising of the epitope sequence f-MII with the sample under conditions where the antibody can specifically bind to the epitope and detecting:

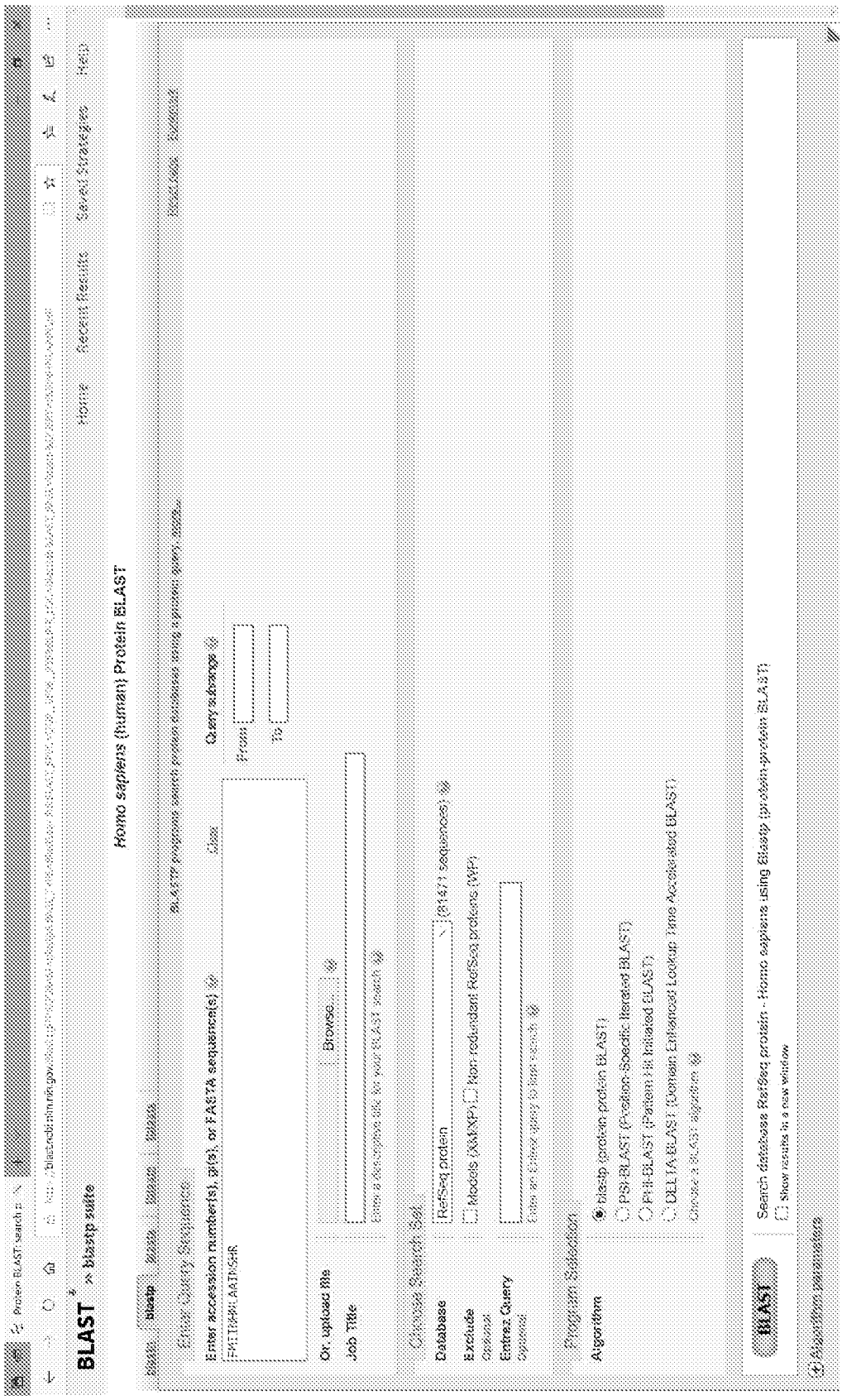
    a) binding of the antibody to the polypeptide;

b) binding that indicates the sample is from a subject who experienced unstable angina or acute myocardial infarction;

c) a subject who is experiencing unstable angina or acute myocardial infarction earlier than Troponin;

d) a subject who is experiencing unstable angina or acute myocardial infarction in various bio-fluids samples including freshor frozen blood, serum, plasma, saliva and urine as well as tissue biopsies.

20. The method as claimed in claim 17, wherein the assay method can early diagnose ischemic heart patients and allow for crucial intervention to avoid permanent damage and, thus, abort infarction, save heart muscles, reduce myocardial injury and the progression of patients to heart failure; complement and enhance the usefulness of Troponin tests to rule in or out unstable angina and AMI; provide risk stratification for AMI patients; identify at-risk patients for coronary artery disease (CAD) since miRNAs were found to have distinct patterns in cardiovascular disease including AMI, hypertension, heart failure, and viral myocarditis; diagnose heart failure patients after AMI and determine their risk assessment and prognosis; diagnose subclinical or silent myocardial ischemia without infarction as well as low-grade myocardial ischemia without cell death; screen heart transplantation patients‘ blood samples for cardiac allograft inflammation, and thus reduce heart biopsies; screen CAD patients for risk assessment to predict which patients are at risk for developing AMI; predict drug therapy response on heart tissue in clinical trials; monitor heart health after therapy and disease progression; and differentiate cardiac from non-cardiac patients presenting with chest pain to outpatient clinics and hospital Emergency Departments and determine the risk level of heart patients.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Help
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Clear
Query subrange
From
To
Or, upload file
Browse...
Job Title
Choose Search Set
Database
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Exclude
Models (XM/XP)
Non-redundant RefSeq proteins (WP)
Entrez Query
Program Selection
Algorithm
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PSI-BLAST (Position-Specific Iterated BLAST)
PHI-BLAST (Pattern Hit Initiated BLAST)
DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)
BLAST
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Show results in a new window
Algorithm parameters

FIG. 1

ferritin heavy polypeptide-like 17 [HOMO Sapiens]

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Range 1: 19 to 24 Genpept Graphics

▽ Next Match △ Previous Match

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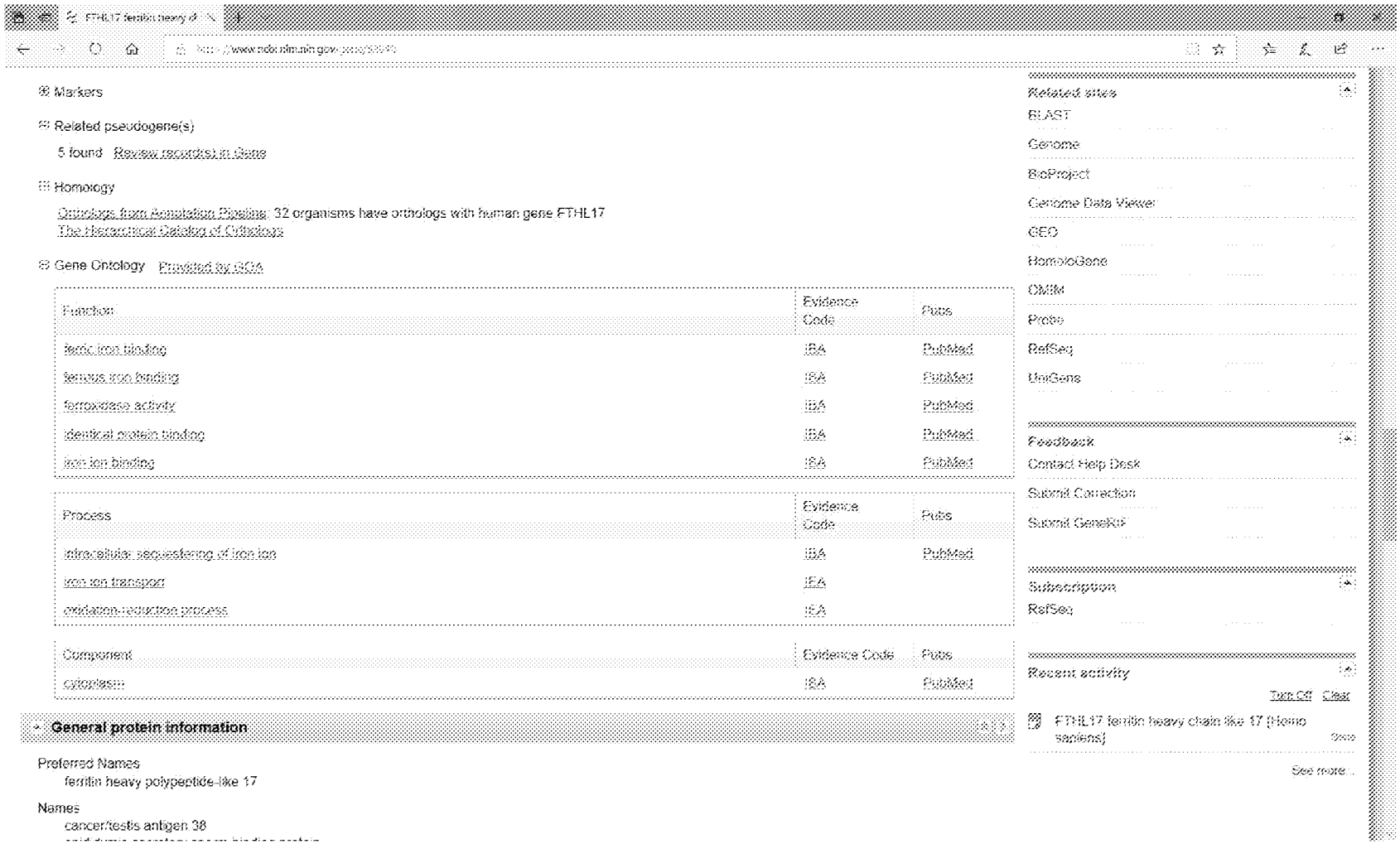
Query 9 AAINSH 14
AAINSH
Sbjct 19 AAINSH 24

FIG. 2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5 found Review record(s) in Gene
Homology
Orthologs from Annotation Pipeline 32 organisms have orthologs with human gene FTHL17
The Hierarchical Catalog of Orthologs
Gene Ontology Provided by GOA
Function
Evidence Code
Pubs
ferric iron binding
IBA
PubMed
ferrous iron binding
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GEO
HomoloGene
OMIM
Probe
RefSeq
UniGene
Feedback
Contact Help Desk
Submit Correction
Submit GeneRIF
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Turn Off
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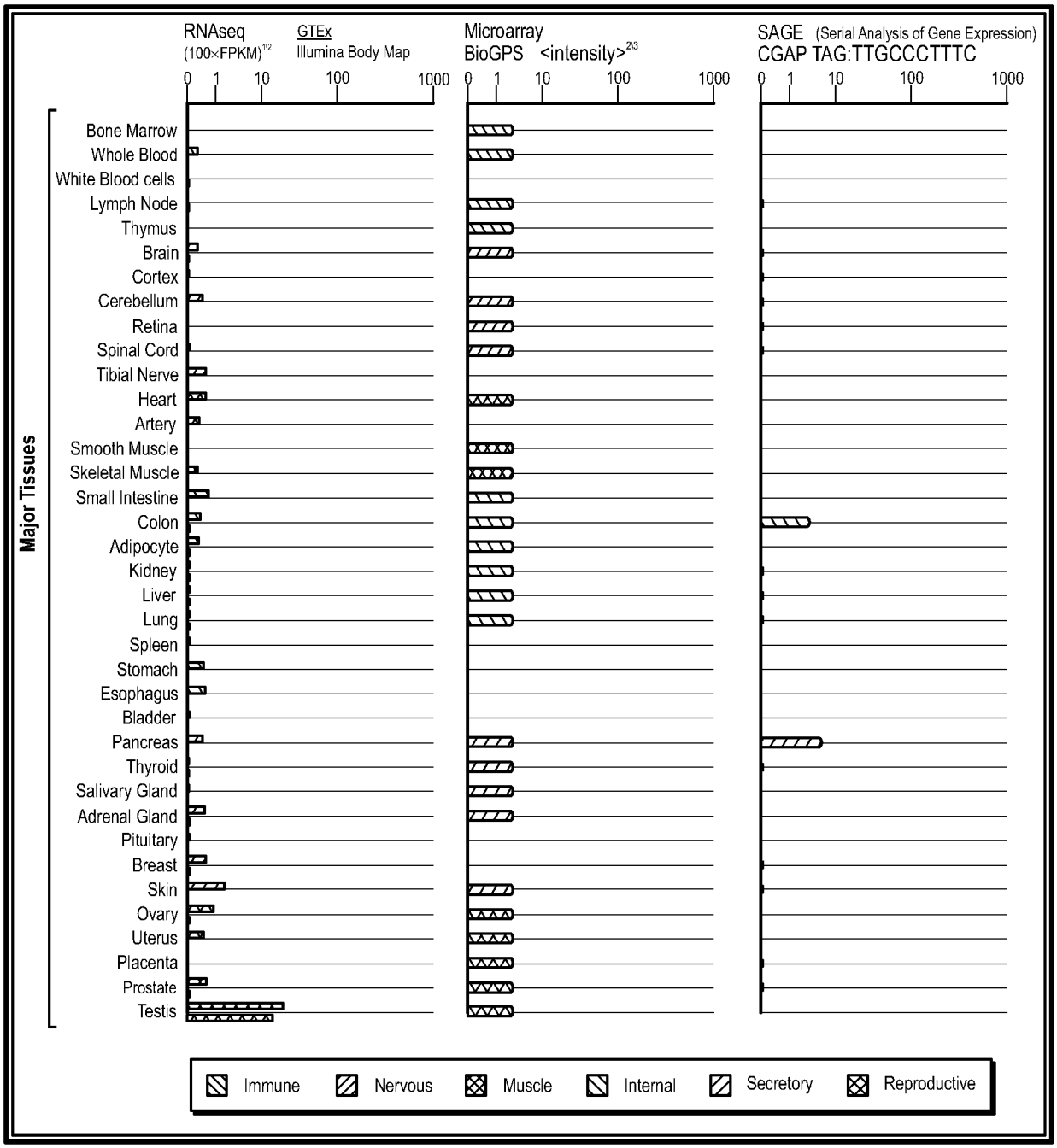
Gene
See more...

FIG. 3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White Blood cells
Lymph Node
Thymus
Brain
Cortex
Cerebellum
Retina
Spinal Cord
Tibial Nerve
Heart
Artery
Smooth Muscle
Skeletal Muscle
Small Intestine
Colon
Adipocyte
Kidney
Liver
Lung
Spleen
Stomach
Esophagus
Bladder
Pancreas
Thyroid
Salivary Gland
Adrenal Gland
Pituitary
Breast
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Uterus
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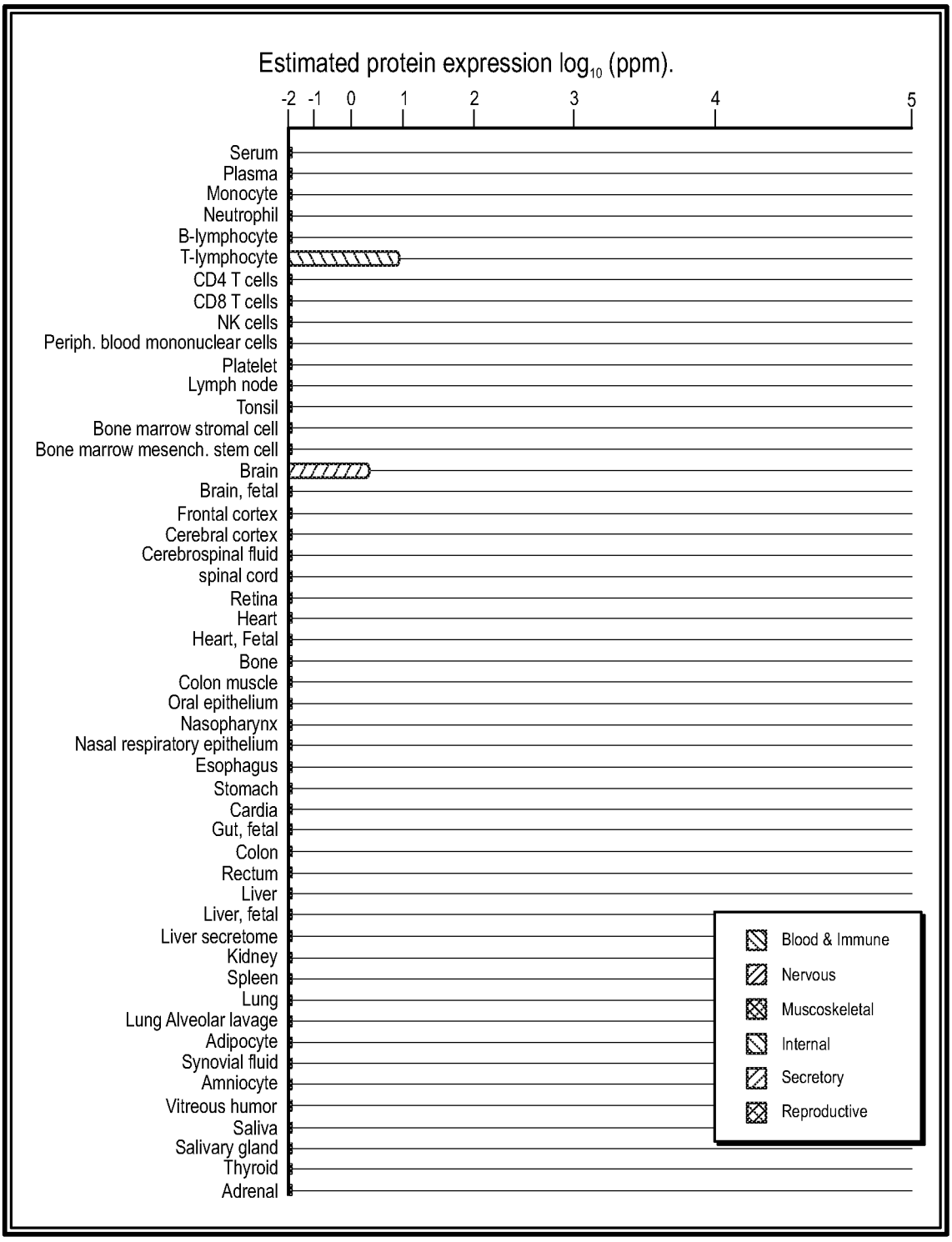
Nervous
Muscle
Internal
Secretory
Reproductive

FIG. 4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Plasma
Monocyte
Neutrophil
B-lymphocyte
T-lymphocyte
CD4 T cells
CD8 T cells
NK cells
Periph. blood mononuclear cells
Platelet
Lymph node
Tonsil
Bone marrow stromal cell
Bone marrow mesench. stem cell
Brain
Brain, fetal
Frontal cortex
Cerebral cortex
Cerebrospinal fluid
spinal cord
Retina
Heart
Heart, Fetal
Bone
Colon muscle
Oral epithelium
Nasopharynx
Nasal respiratory epithelium
Esophagus
Stomach
Cardia
Gut, fetal
Colon
Rectum
Liver
Liver, fetal
Liver secretome
Kidney
Spleen
Lung
Lung Alveolar lavage
Adipocyte
Synovial fluid
Amniocyte
Vitreous humor
Saliva
Salivary gland
Thyroid
Adrenal
Blood & Immune
Nervous
Muscoskeletal
Internal
Secretory
Reproductive

FIG. 5

	Ensembl Gene Id	miRNA name	miTG score	Also Predicted
1	ENSG00000132445 (FTHL17)	hsa-miR-548ar-3p	0.97769557050703	
2	ENSG00000132445 (FTHL17)	hsa-miR-589-5p	0.977113273205747	
3	ENSG00000132445 (FTHL17)	hsa-miR-548e-3p	0.958778553040087	
4	ENSG00000132445 (FTHL17)	hsa-miR-4766-5p	0.953774408116615	
5	ENSG00000132445 (FTHL17)	hsa-miR-137	0.916733991921927	
6	ENSG00000132445 (FTHL17)	hsa-miR-548a-3p	0.858381214044193	
7	ENSG00000132445 (FTHL17)	hsa-miR-548az-3p	0.84514951953714	
8	ENSG00000132445 (FTHL17)	hsa-miR-548f-3p	0.837928897852551	
9	ENSG00000132445 (FTHL17)	hsa-miR-4639-5p	0.816317602779086	

FIG. 6

name	mirAccession	geneName	targetSites	bioComplex	clipReadNum	CancerNum
hsa-miR-137	MIMAT0000429	RP11-206L10.11	1	1	6	NoData
hsa-miR-137	MIMAT0000429	RP11-3782.1	1	1	99	NoData
hsa-miR-137	MIMAT0000429	RP11-14886.1	1	1	9	NoData
hsa-miR-137	MIMAT0000429	OIP5-AS1	3	13	836	NoData
hsa-miR-137	MIMAT0000429	AF127936.7	1	1	12	NoData
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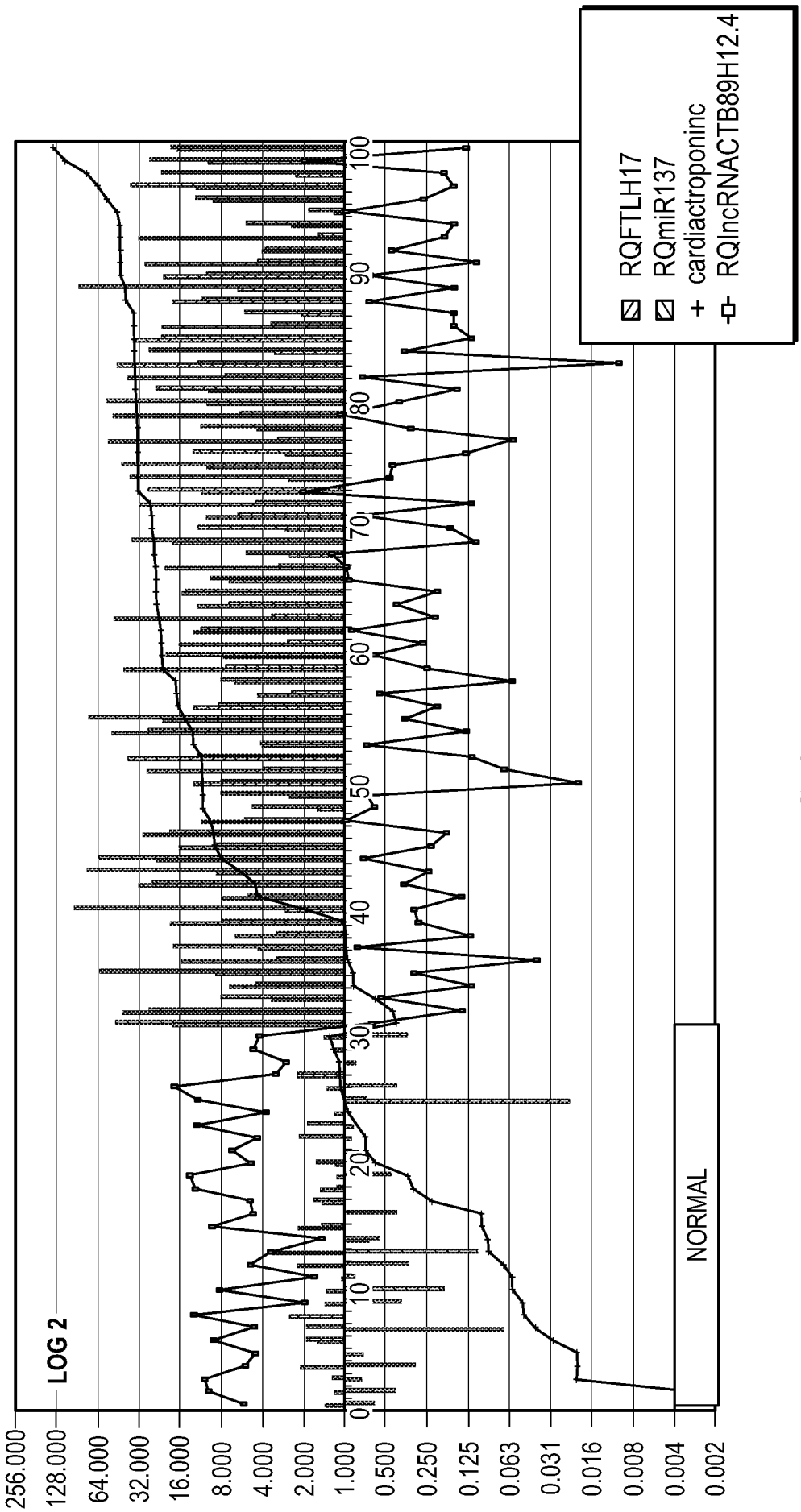
FIG. 7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4.000
2.000
1.000
0.500
0.250
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0.063
0.031
0.016
0.008
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0.002
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10
20
30
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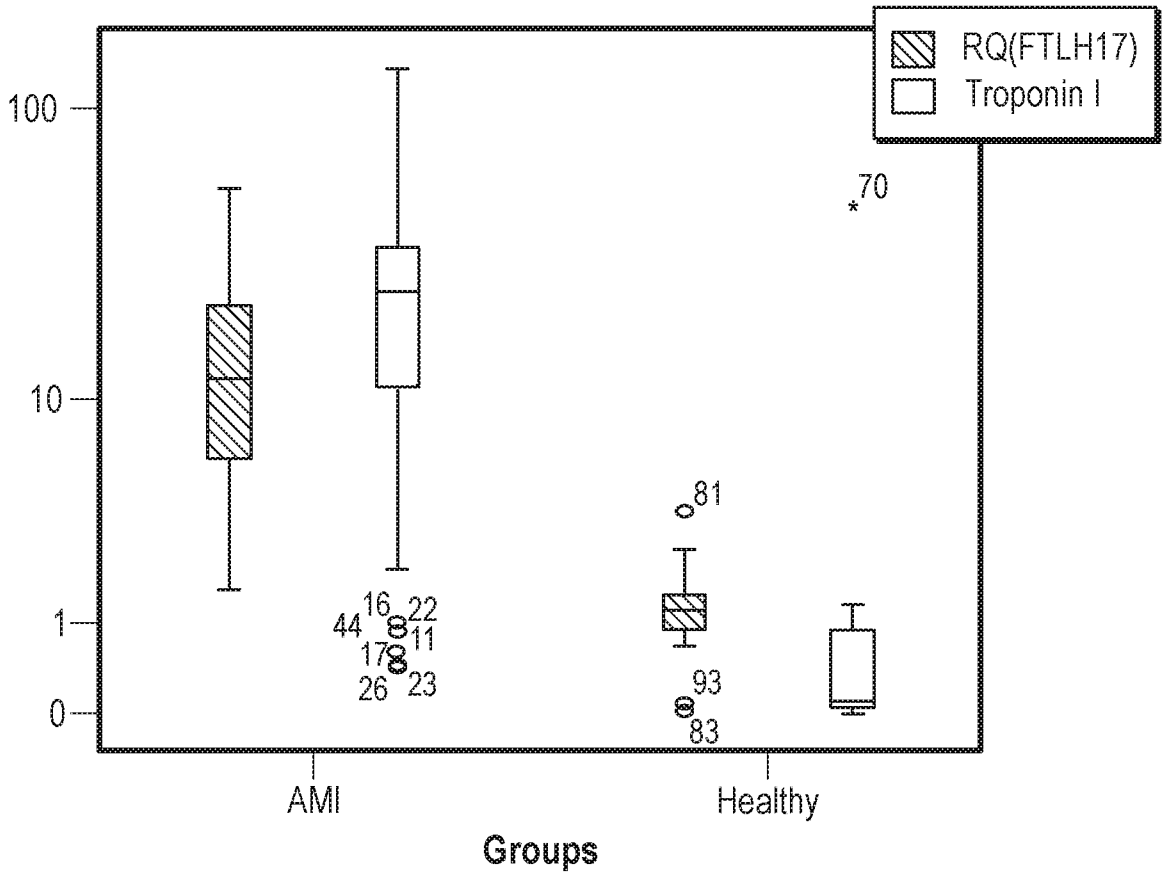
50
60
70
80
90
100
NORMAL

FIG. 8


RQ(FTLH17)
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100
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0
70
81
93
83
16
22
44
11
17
8
26
23
AMI
Healthy
Groups

FIG. 9

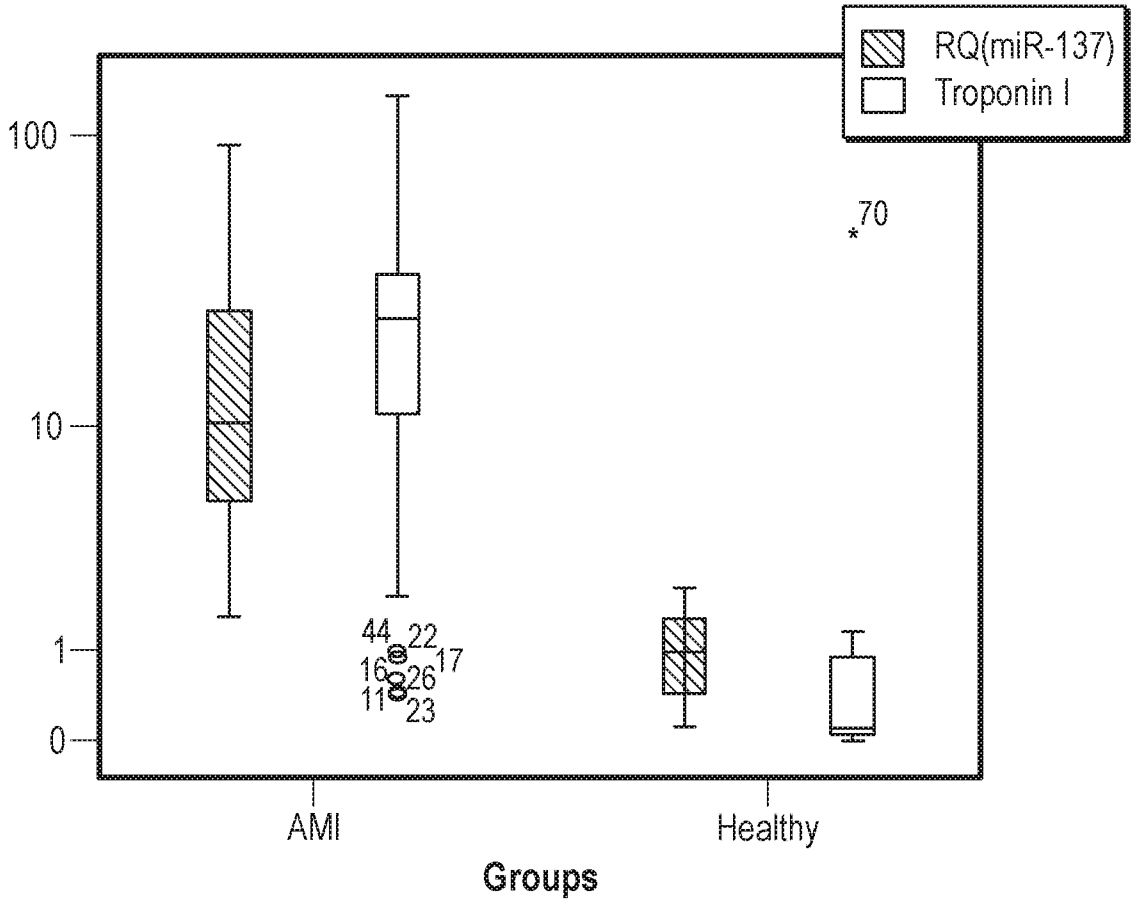
RQ(miR-137)
Troponin I
100
10
1
0
70
44
22
16
26
17
11
23
AMI
Healthy
Groups

FIG. 10

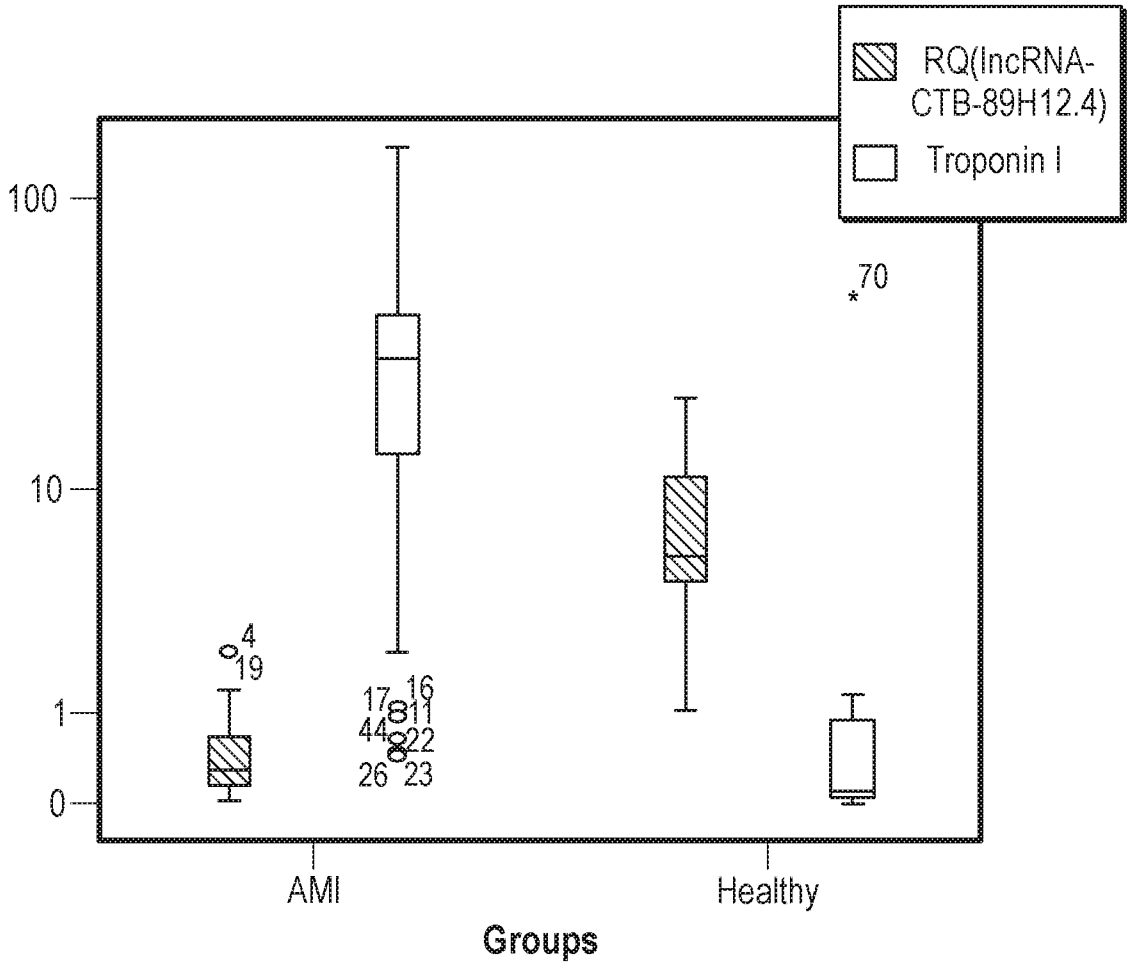
RQ(lncRNA-CTB-89H12.4)
Troponin I
100
10
1
0
4
19
17
16
11
44
22
26
23
70
AMI
Healthy
Groups

FIG. 11

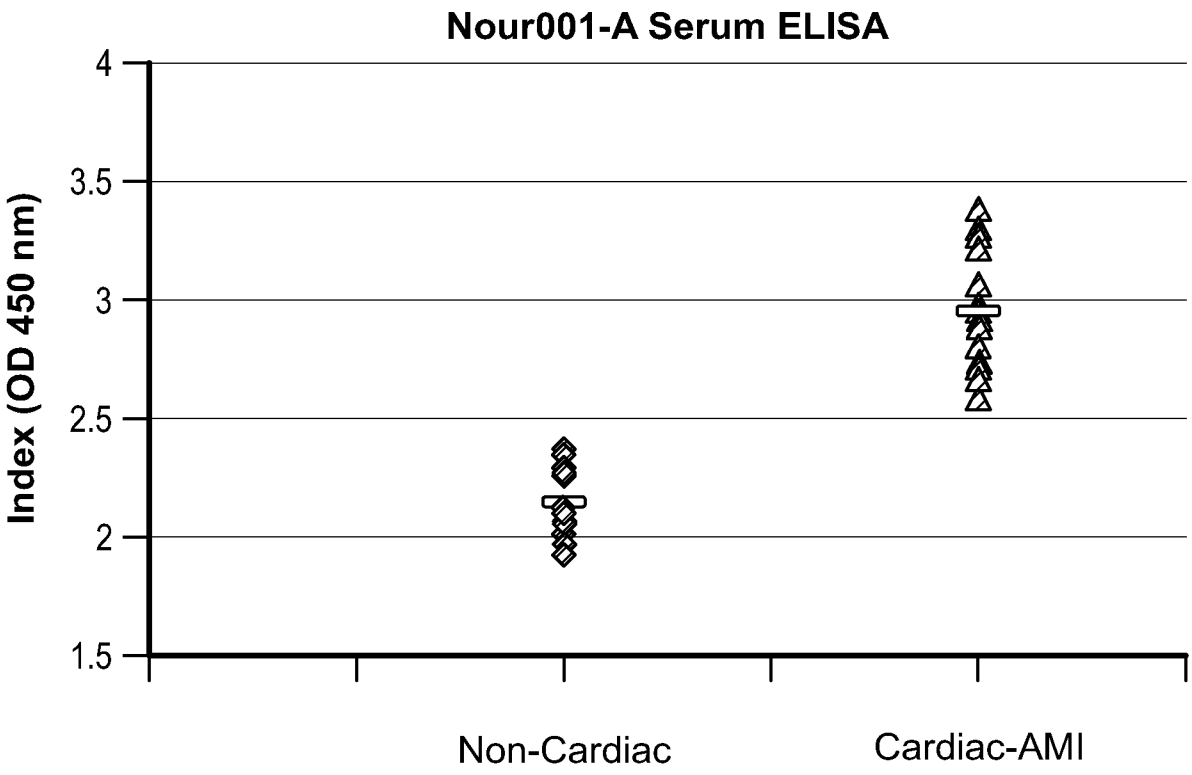
Nour001-A Serum ELISA
Index (OD 450 nm)
4
3.5
3
2.5
2
1.5
Non-Cardiac
Cardiac-AMI

FIG. 12

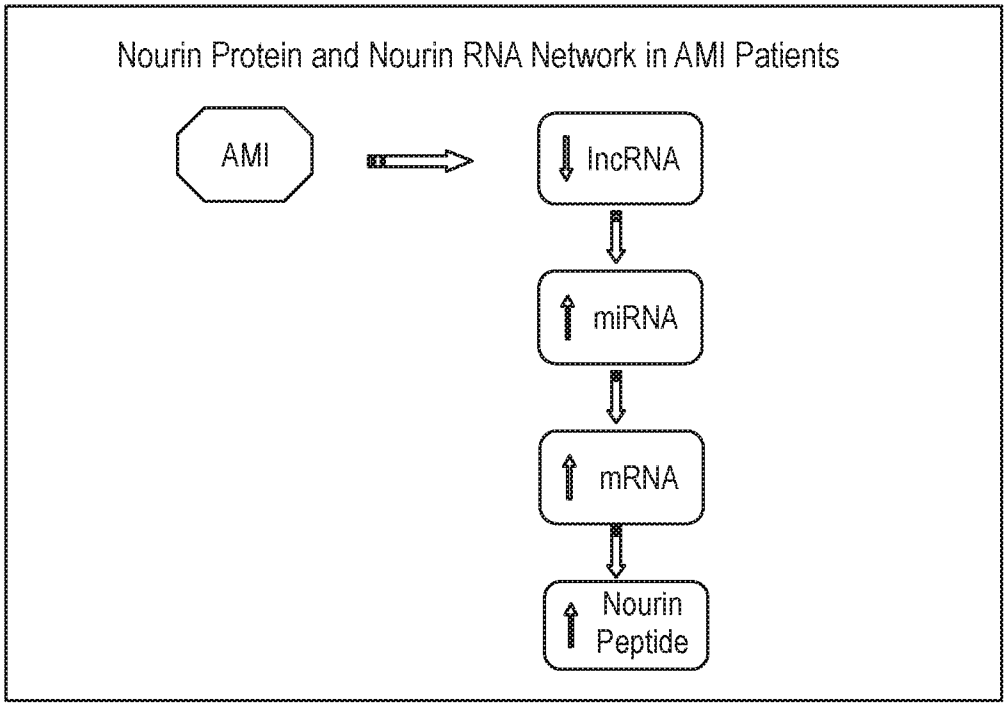
Nourin Protein and Nourin RNA Network in AMI Patients
AMI
lncRNA
miRNA
mRNA
Nourin Peptide

FIG. 13

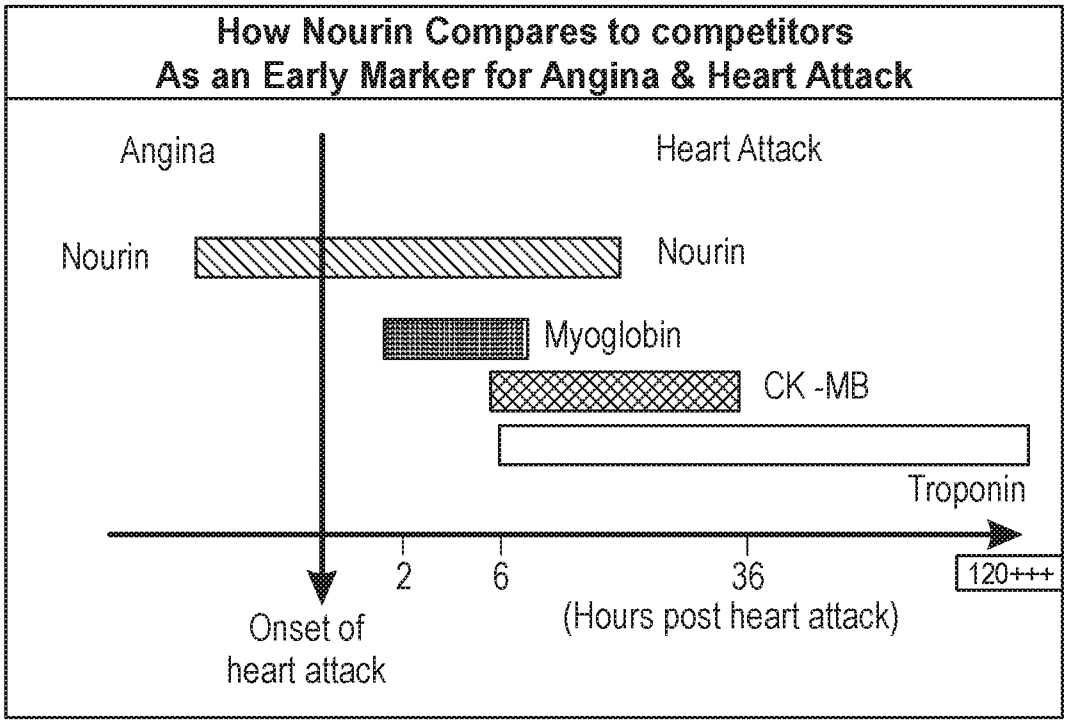
How Nourin Compares to competitors
As an Early Marker for Angina & Heart Attack
Angina
Heart Attack
Nourin
Nourin
Myoglobin
CK -MB
Troponin
2
6
36
120+++
Onset of heart attack
(Hours post heart attack)

FIG. 14

caaatgccat tgaaaccgct agtcttattt cctttctact tttctttggc actcttactg 60

cctgtaagga gtagaactgt tagggcacac tgttgctata cagtttaact cccattttca 120

tgttttgtct ttcttttccc atttctgggg cttacctcct gatacctgct tactttctgg 180

aagtagtggg caagtaagat ttggctcttg gtttctaatt tttaaatttc tgaatactgc 240

cctagtctga acttggcctt tatagattaa tctttgcttc acatttttag tgttgtattt 300

aaactatttt ataatttaaa aatagattct aatctgaaga tacttttcaa gaaatattat 360

taactgatgt catcctcatc ccagcagctc atctgttagg aatgaagttg agatgcttct 420

attccatgtt tttgtatttg ggaaggattc aaagttgaag gtttattgtc gttgggtttt 480

tcagatggtg acatgtaaac tcaggatagc aaaccctaat gttcacacag tgctctgcct 540

ctgcatctca gttgggatag ttgctccttt tgagtgtttt aatcatcgta taactaatca 600

tagtgccaag aagttcataa tgtgttatgt agctaatgtc actgaaaaac agtcctacca 660

ttttaggtaa gaccaaacag agtctctaac ccaaggactt gttacacctg acaacctata 720

gtatatttgc tttttctcac aaaatgaaac caattttgcc gaaagctagc tgggataata 780

ggatcatcac aagttgcagt ttctataact aaaattagat tgaaatctct tctgacctag 840

aacattttac ttcaggcatt cagcagattt cagaaagaat taccttattt taagttagtt 900

tctttgttag tttactgtgt gtctcttatt caataaacaa gcagaatttg tgtcctgccc 960

FIG. 15A

tatccatgtc ttaaagatga gaagttggat ccactgagtt agtttcattg gggcggggga 1020

aagaactgta attaaacttg tttaatcctt attttgtatt gtagctattt tttgtaaaag 1080

caacttaaaa tcttttaaaa attttatagt gacattagag acaatggtca tacaaattat 1140

cacataaaca tggacttgaa aaattaggct tttcataaaa cacatcacat gtcattgact 1200

gctttttaga aatacacttc caaggcagta catctgtatt gctactgaaa agtgccattt 1260

cacagaacac agacttcttt ttgctctttg acatcttgaa aacatctgtt tttctttttt 1320

aatacaaaac tttgtgctca agacaaatct tacatgaaac tctcataaac catgaaaatg 1380

tagctggcct tcgggcctta ggcatgaaat aagcatgagg aacatattcc cctaacttct 1440

acccccagcc cagcaagtta tcctttaaga aatctcctag gaattctgga gtttgaaaac 1500

aattgctcta tgttattcct gcttccagtc tctaagtaac aagggcattt aaaagcatag 1560

tctcttaagg tccactatag tggttcttta tttaaggaat aactcagctg ggtgcagtgg 1620

ctcacgcctg ttatcccagc actttgagag gctgaggcaa gcagatcact tgaggccagg 1680

agttcgagag tctggccaac atggtggaaa cccatctcta caaaaaatac aaaaattagc 1740

caggtgtggt ggcgtgcacc tatggtccca gctatttggg aggctgaggc aggagaattg 1800

cttgaacctg ggaggtggag gttgcagtga gccaagattg tgccgctgca ctccagcctg 1860

ggtgacagag tgagactctg tctcaaaaaa aaaaaaaaaa ggaactcata cagctcaatg 1920

FIG. 15B

attcattgat cccaataata aatcgtttta ataatgatga aaacatccta ctggggtttt 1980

cttgttaaaa actttaggac aggcgcagtg gctcatgcct gttattccaa cacatttggg 2040

aggctgaggt gggagaattg cttgacccta ggagttctag acttgcctgg gccacatagt 2100

aagaccctgt cccagctccc tccaacatcg tccccaaccc cccccccccc aaaaaaaaaa 2160

agcgccaggc gcagtagtga gtgcctgtga tcccagctgt gttgggaggc tgaggtggga 2220

gtatcacctg agccctggag gttgaggctg caatgagagc tgtgatcatg ccactgcact 2280

ccagcctggg caacagatga gaccctgtgt cacaacaagg aatttttaga aggtgctttt 2340

tatattactc ttcacagagt taaattttca gaggatttag tattattgaa ctaagtttca 2400

taagtgtatt ttaagcaagt aaatctctaa tgtaggaaaa tccccaaaat ggtagcattt 2460

actaatgttt tatatggtaa tttttgaaaa atatatctga tatttcttca gtaaaaatgg 2520

tgttgtttta ataacttaat aagaatgttt aaagattctt taagtctggc ttatctagct 2580

aatgtgggcc tattaaataa taggcagact tctgccttcc ttatattctt tagatctttt 2640

caaatactcc attccaatat ccatcaaaag acttctcttt atgccactta ttatctatac 2700

tagtttttaa tgttcaatta ctacaagatt ataattactg tttttattca tgttcccaag 2760

aaaaatacat aagattcaca cccaacacac ttcgaaattt atttcactcc ctttgactat 2820

atgtgattat caaaaaagta tttttcaaga tattaaaaat aagtaaagga aaatgaaata 2880

FIG. 15C

```
tttttaggac attcaaaatc taatgaagtt cagtgtttct ttaattgagg gcaggcagag     2940

gtgggggaga atttcagaag gtagtgaacc caaaggtgga ttcttggata attctactat     3000

tctgtactct catcatctta acccatctgt ttactaccct aaccatagtt actaagcaga     3060

gttttatcat aataatatag acagctctca aagtattgac attcagaggg gattacaaat     3120

attatttttc tatcatattg acctaccatg tccacagtct tccttgaatt accttccagt     3180

tttactgggc tgcatctacc gtttatgtct agtttgactt tttctgagtt caccaattgc     3240

tgctaggaat gtgctggtca ctcagcagca cacccacatc acaggggaag attttgaaat     3300

acctggacag tctgaacaca ctgctctgaa tacactcaat tctaagaagt accagggaac     3360

cgcatcttct tgctgaaatc ttgaatttttt gtcagctttt ttttttactg tggacagtaa     3420

agctggaaag atctaaataa cccaacagga aatgcggatg aaagtgcaag agttggtttg     3480

tggtcatctg gagtccatgt ctccaagact gctggacctt caaattctgc aacttgttag     3540

atcatctgga tgatagcaca actgttagaa gacctagaag aatacagcgt tgctatgact     3600

cagtggtgtt gaatgcagac catctaccag ctggggaaag aatcaattat aaacaggaat     3660

aaagggattc attcctcatt ttaactgatg ttacagtgaa gatgggttct tgaactcttg     3720

gaagcctgga tgagccacct aatctgcaag ataaaaacca aagaccaatg cgtattgggg     3780

aaaagaatgc ttagtactgc aagactgttg aatacctgtt gaatattcct attgaggttt     3840
```

FIG. 15D

tttcctaaac atacttcagt aacatcttag gacaattcac tggagaaatg ttgatccctg 3900

gctggaatgt cataccattg acccatttga agagttaaag ctggatttga ctgctctatt 3960

ctaccaggaa tattgttagg gtagcctttt accagtttct aaacaattgt aatcatttat 4020

tgactcagca attcctcaga taacaggtca aaagatgtac agatacattc tgaagttttc 4080

ttgctattaa aggcacaaga gtttccttgt attttgactg acaatgtagc atgtttccat 4140

tttagtttgt tagtgatggt ggttttccct ttgaaagcca tttggtatat tcaccataac 4200

aattagttta atatgattac ataagaaaac tatgataaaa cccagcaatt ttagtagttg 4260

tgaaaatacg ttttttaaat catgtttaag aagaattgca agacttgaaa ccaaatcctg 4320

atgggggaat tctgtttaat cctgtttaat ctgtttaatt tctgtttaat ccttagtttc 4380

ttaacctgca tagcttatcc tgtattgtac tttttttctt ttttaaactc ccaaacaaga 4440

agcttgaaac ttttcctgta ttttaaaatt gaaatttggt cacagggtat agtcagattt 4500

ttattaaggt ttggtttgac aacctttaaa agaaaggttt acctcgctaa tacttcttaa 4560

taacatgcat caaatgatat tccctatggt gaagtatatt ctcaaagtta tgttatcttt 4620

catttttggc atttggtgct tatggactta gtacccaggc aacaaagatc tattatgcac 4680

ctactctctt gtatgttcgc tattatttcc caaaaaaaaa aaggggcata tatgcataag 4740

aaataaatat tagaattatt ttgtttctcc cacaaagccc atgggagatg gcccaacaaa 4800

FIG. 15E

tgtttaaaaa gtaaaagaag ctgggcacgg tggctcccac ctgtaacccc cacactttgg 4860

gaggccatgg cgggtggatc acgaggtcag gagtttgaga ccagcctggc caacacagtg 4920

aaactgtgtc tctactataa atacaaaaat tagccaggca tggtggcagg cacctatagt 4980

cccagctact caggaggctg aggcaggaga atcgcttgaa cccaggaggc agaggttgcg 5040

gtgagccaag atcatgccac tgccctccag cctgggtgac agagcgagac tgtctccaaa 5100

aaaaaagaaa aaagaactaa aagaaaagga gcagtttatg attgaagaaa acatgacctg 5160

ggctgaagaa gtgaggattg attggagtgg gctagaatga gctatagttt ctagctcatt 5220

tgtaaggagg tagacaaagg agcattggtg cctcagagtg ggtgtctggt gagaggaaaa 5280

acggtgctta agagattttc aggctattgc tgtgggacag gcatattttc tccctttgcc 5340

tttagctgta gataaagtgt ggttatgacc tgaggcttct tgtattcaaa cttggcctag 5400

ggcctatgta gaggccctag ggtctacttg tggtggagga gggaagtatt tgtagaatgt 5460

gtaggcttga gaagtaaata aagccaaaaa agcatcactt gcttacattt ttaaatgagt 5520

cacaaaacaa tctttctaat gcggccggta aagaagtttt aaaggtctaa ggtttctcta 5580

cagaaattac atgcttctca ggtctttgtt tagtaaaata atacagataa ttatgctttg 5640

aatgcattta ttattaaagc taaccgtttt aatttgtgtc agaaataatt tgtgcctatg 5700

gtaggattaa aattgtattc tttagttaaa gcaaagcaat ctgtttttca ttgatttgat 5760

FIG. 15F

aaatatgtga atgcctaata tgttctgcat atgtaaaaat gcagaaacat gctcatttga 5820

attactaata attatttttag tatgctgaga ggctttgaat tcactgtacc actccttcct 5880

agagtcattc aaaacagaaa aaattagttt taagtataga ttcatgtttt tctgttttaa 5940

aaagttgagc taatactttt cacaagagac gaaataacat gagccactat aattattggc 6000

tcagttccac ccaatttcca tattttgggt gtaatttaaa atttttgact tggaatttta 6060

actttttttt tgttttgatt ttttaccagg tttctaagca tgaattgagg aacagaagaa 6120

gcagagcaga tgatcggagc agcatttgtt tctccccaaa tctagaaatt ttagttcata 6180

tgtacactag ccagtggttg tggacaacca tttacttggt gtaaagaact taatttcagt 6240

ataaactgac tctgggcagc attggtgatg ctgtatcctg agttgtagcc tctgtaattg 6300

tgaatattaa ctgagatagt gaaacatggt gtccggtttt ctattgcatt ttttcaagtg 6360

gaaaagttaa ctaaatggtt gacacacaaa aattggtgga gaaattgtgc atatgccaat 6420

tttttgttaa aacctttttgt tttgaactat actgctttga gatctcattt cagaagaacg 6480

gcatgaacag tcttcagcca cagttgtgat ggttgttaaa tgctcacaat tgtgcattct 6540

tagggttttt ccatccctgg ggtttgcaag ttgttcactt aaaacattct taaaatggtt 6600

ggcttcttgt ctgcaagcca gctgatatgg tagcaaccaa agattccagt gtttgagcat 6660

atgaaagact ctgcctgctt aattgtgcta gaaataacag catctaaagt gaagacttaa 6720

FIG. 15G

gaaaaactta gtgactacta gattatcctt aggactctgc attaactcta taatgttctt 6780

ggtattaaaa aaaaagcata tttgtcacag aaatttagtt aacatcttac aactgaacat 6840

gtatgtatgt tgcttagata aatgtaatca ctgtaaacat ctatatgatc tgggattttg 6900

tttttatttt gaaatgggag ctttttttgtt tacaagttca ttaaaaacta aaaactgttt 6960

ctgtaaggaa atgagatttt ttttaaacaa caaaaaatgc cttgctgact cactattaaa 7020

taaaaatctc cccaattttt tgatagacta cttcaagcca tttgttacat ggtattcctt 7080

tgcaagtcaa tttaggtttc gtgttataac ttttcctctt ttttaagaa aaatgaaaaa 7140

agtaattctt ttgtctgaag gggaaaggca ttctttcatt ttttttctttt ttttttttt 7200

tttttatgac ttgcaggcac aatatctagt actgcaactg ccagaacttg gtattgtagc 7260

tgctgcccgc tgactagcag ctggactgat tttgaataaa aatgaaagca ttaaagggtt 7320

tccctacaaa acatttttct ttaaaatact tttgaaatgg ctataagcag ttgactttca 7380

cccttggaga gcatcacact gtgtgaggtt cagtgattgt tgaccctccc cagcccctcc 7440

tgcttcttta agttatctgt gtgcgtgcgc ttcctctcaa tcttctttgc acgctcattt 7500

ctttttctct gacccatgag aaaggaaaac ttactgatga taatttttaa atagtgtaat 7560

ttattcattt atagcatgtc aggataaatt aaaagaacat ttgtctggaa atgctgccgg 7620

gagcctattg tgtaaatgta ggtattttgt aaaataacct tgaaattgta aattgacacg 7680

FIG. 15H

tgtttggtca gattgtgtca agtttaattt gttttgtttt ctttttttctt ttttttattt 7740

gaaaactact ttagcaataa ttaattccat gattatcaca ttctgccatt aagggatatt 7800

agtaccgtaa tactgaagaa attttattaa gtctgaactt ctggggtagg cagcttcttt 7860

gtttcttttc tatccaccct tgtcggttga ggtatttgtt tcttgactaa taaacccttt 7920

gatactttta gccagaaatc agtctcataa agctattttt gagtatagtt tgtgtaaaat 7980

aaaaatgttt agctttggta ataacttcca agctgaactc cctctagcaa gatatttttc 8040

agtgctttta tttactatgc acttagacta tgcacttttt ctgaaatatt tttgtaacac 8100

ttttttgtat ttttgccatt tgaaaaggtt gtggtgtagt tggtctgtaa ttaagttgca 8160

gatttaaaac tgctgttagc tttgtaaatc aaaatatagg tgtttttttgt cctggtatat 8220

cgtcattcca tctgcagctg gagctggaat cccattgatc ttctagctac cattcatttt 8280

cttcactgtt cacaaaagaa gagtgtgaaa ttcagtgaat gctgttacta atcctgttac 8340

gagatgaatc tcatttcacc aaaattaaat tatgtttttc cgctaaaatg atgatacaag 8400

ttgaagacac atcactctga aattggaaga cctcaccact taaggctcca cagtggctta 8460

ctcagctgaa ctctaggtta ctactcttta ctttgttcac ccattggggg gtgcagtttt 8520

tttaaaatgt tgggagatgg ccattctaac tactgttgaa tgtctctgtt ttgggaaggt 8580

ataacaagaa ataaaaaaga atatatatga agggagagac tggttatctc ctccca 8636

FIG. 15I

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 2019/061055

A. CLASSIFICATION OF SUBJECT MATTER

G01N 33/96 *(2006.01)*
C12N 15/10 *(2006.01)*
C12Q 1/686 *(2018.01)*

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)

G01N 33/50, G01N 33/53, G01N 33/96, C12N 15/10, C12Q 1/68, C12Q 1/686

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

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

EAPATIS, ESPACENET, PatSearch (RUPTO internal), Information Retrieval System of FIPS, USPTO, PATENTSCOPE, PubMed, Embase, e-Library

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2006/0063199 A1 (SALWA A. ELGEBALY et al.) 23.03.2006, paragraphs [0010]-[0011], [0039], [0041]-[0046], [0069]-[0070]	1-20
A	KUMARSWAMY Regalla et al. Circulating Long Noncoding RNA, LIPCAR, Predicts Survival in Patients With Heart Failure. Circulation Research, 2014, Volume 114, Issue 10, pp. 1569-1575, doi: 10.1161/CIRCRESAHA.114.303915	1-20
A	WANG Chen et al. Non-coding RNAs as biomarkers for acute myocardial infarction. Acta Pharmacologica Sinica, 2018, Volume 39, Issue 7, pp. 1110-1119, doi: 10.1038/aps.2017.205	1-20

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

☐ See patent family annex.

* Special categories of cited documents:

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

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

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

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

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

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

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

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 March 2020 (13.03.2020)	09 April 2020 (09.04.2020)

Name and mailing address of the ISA/RU:	Authorized officer
Federal Institute of Industrial Property, Berezhkovskaya nab., 30-1, Moscow, G-59, GSP-3, Russia, 125993 Facsimile No: (8-495) 531-63-18, (8-499) 243-33-37	O. Tulinova Telephone No. +7 (495) 531-64-81