(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
18 December 2014 (18.12.2014)

WIPO | PCT

(10) International Publication Number
WO 2014/201301 A1

(51) International Patent Classification:
A61K 31/7105 (2006.01)

(21) International Application Number:
PCT/US2014/042196

(22) International Filing Date:
12 June 2014 (12.06.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/834,389 12 June 2013 (12.06.2013) US

(71) Applicant: **NEW YORK UNIVERSITY** [US/US]; 70 Washington Square South, New York, NY 10012 (US).

(72) Inventors: **FERNANDEZ-HERNANDO, Carlos**; 37 Governors Way, Madison, CT 06443 (US). **GOEDEKE, Leigh**; 4111 Cremson Drive, Phoenix, MD 21131 (US).

(74) Agents: **VAINBERG, Irina, E.** et al.; Troutman Sanders LLP, 405 Lexington Avenue, New York, NY 10174 (US).

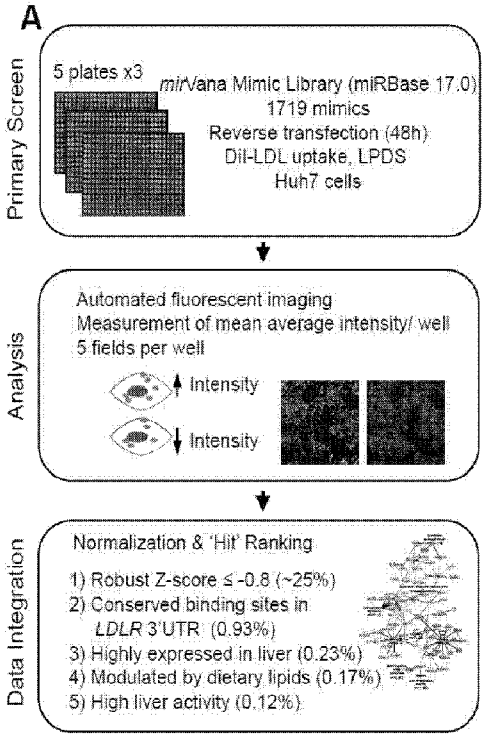
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: ANTI-MIR-27B AND ANTI-MIR-148A OLIGONUCLEOTIDES AS THERAPEUTIC TOOLS FOR TREATING DYSLIPIDEMIAS AND CARDIOVASCULAR DISEASES

Figure 1



(57) Abstract: The present invention relates to anti-miR-27b and anti-miR-148a oligonucleotides that are capable of decreasing the level and/or activity of miR-27b and miR-148a, respectively. In conjunction with the oligonucleotide molecules of the present invention, the invention also provides a method for decreasing the level and/or activity of miR-27b and/or miR-148a in a cell. In a further embodiment, the invention provides a method for treating a disease, especially dyslipidemias and cardiovascular diseases.

WO 2014/201301 A1

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

ANTI-miR-27b AND ANTI-miR-148a OLIGONUCLEOTIDES AS THERAPEUTIC TOOLS FOR TREATING DYSLIPIDEMIAS AND CARDIOVASCULAR DISEASES

CROSS-REFERENCE TO RELATED APPLICATIONS

[001] This application claims priority to U.S. Provisional Application Serial No., 61/834,389, filed June 12, 2013, which are herein incorporated by reference in their entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[002] The research leading to the present invention was supported, in part, by National Institutes of Health grants R01HL107953, R01HL106063, and 1F31AG043318. Accordingly, the U.S. government has certain rights in the invention.

FIELD OF THE INVENTION

[003] The present invention relates to anti-miR-27b and anti-miR-148a oligonucleotides and their use as therapeutic tools for treating dyslipidemias and cardiovascular diseases.

BACKGROUND OF THE INVENTION

[004] Cellular and plasma cholesterol levels are maintained through tightly controlled mechanisms, which regulate the expression and activity of key metabolic genes at both the transcriptional and post-transcriptional level. Alterations in the control of cholesterol homeostasis can lead to pathological processes, including atherosclerosis, the most common cause of mortality in Western societies (Lusis 2000, Glass and Witztum 2001). Epidemiological studies have identified many environmental and genetic factors that contribute to atherogenesis. In particular, high levels of low-density lipoprotein (LDL) cholesterol and low levels of high-density lipoprotein (HDL) cholesterol are associated with increased cardiovascular disease (CVD) risk (Lusis 2000, Glass and Witztum 2001). As a result, substantial therapeutic progress has resulted from the widespread use of statins (Gould, Rossouw et al. 1998) and other lipid-lowering drugs aimed at lowering plasma LDL-cholesterol (LDL-C). Despite this, statins are not sufficient to prevent the progression of atherosclerosis in many individuals and there is

considerable evidence that quantitatively important determinants of disease susceptibility remain to be identified (Hennekens 1998, Sjouke, Kusters et al. 2011).

[005] In humans, the majority of serum cholesterol is transported as cholesterol esters in LDL particles. To ensure that blood cholesterol levels are balanced, LDL is constantly internalized. The uptake of LDL and other ApoE/ApoB containing lipoproteins occurs through the LDL receptor (LDLR) and is a classic example of receptor-mediated endocytosis (Brown and Goldstein 1976, Brown and Goldstein 1986). The circulating level of LDL is determined in large part by its rate of uptake through this pathway, as evidenced by mutations in *Ldlr* or *ApoB,* which lead to the massive accumulation of LDL in patients with familial hypercholesterolemia (FH) (Brown and Goldstein 1974, Maxfield and Tabas 2005). The expression of the LDLR is tightly controlled by feedback mechanisms that operate at both transcriptional and post-transcriptional levels. One of the classical transcriptional regulators of the LDLR is the ER-bound sterol regulatory element-binding protein (SREBP). SREBPs are members of the basic helix-loop-helix leucine zipper (bHLH-Zip) family that bind to sterol response elements (SREs) and promote gene expression (Goldstein and Brown 1990, Brown and Goldstein 1997). In mammals there are three isoforms: SREBP1a and SREBP1c, encoded by the *Srebp1* gene, and SREBP2, encoded by the *Srebp2* gene. While SREBP1c is regulated by insulin and oxysterols and preferentially enhances the transcription of genes involved in fatty acid synthesis, SREBP2 is regulated by intracellular cholesterol concentrations and is the main regulator of *de novo* cholesterol biosynthesis (Goldstein and Brown 1990, Brown and Goldstein 1997). When intracellular levels of cholesterol are high, the ER-bound sterol regulatory element-binding proteins (SREBPs), such as SREBP2, coordinate the down-regulation of the LDLR, as well as 3-hydroxy-3methylglutaryl coenzyme A reductase (HMGCR), the rate-limiting enzyme of cholesterol biosynthesis (Goldstein and Brown 1990, Brown and Goldstein 1997). Conversely, when sterol concentrations are low, SREBPs, such as SREBP2, upregulate HMGCR and the LDLR, thereby enhancing LDL clearance from the plasma and ensuring that intracellular cholesterol levels are maintained (Goldstein and Brown 1990, Brown and Goldstein 1997). Additionally, the LDLR is also subject to post-transcriptional regulation such as its proprotein convertase sutilisin/kexin type 9 (PCSK9)- dependent degradation and inducible degrader of idol (IDOL)-dependent ubiquitination (Park, Moon et al. 2004, Zelcer, Hong et al. 2009)

[006] While several key transcriptional regulators of cellular and systemic lipid levels have been identified, post-transcriptional mediators of cholesterol metabolism, including microRNAs, are less well-characterized and just beginning to emerge. MicroRNAs (miRNAs) are short (~22 nt), evolutionary conserved, single-stranded RNAs that control the expression of complementary target mRNAs, leading to their transcript destabilization, translational inhibition, or both (Ambros 2004, Filipowicz, Bhattacharyya et al. 2008, Bartel 2009). As such, they are crucial for the development and maintenance of tissues, both in health and disease states. Recently, it has been suggested that miR-122, miR-33, miR-758, miR-106b, and miR-144 are involved in control of lipid metabolism (Krutzfeldt, Rajewsky et al. 2005, Esau, Davis et al. 2006, Najafi-Shoushtari, Kristo et al. 2010, Ramirez, Davalos et al. 2011, Rayner, Esau et al. 2011, Kim, Yoon et al. 2012, de Aguiar Vallim, Tarling et al. 2013, Ramirez, Rotllan et al. 2013). However, the effect of miRNAs on LDLR activity has not been described.

[007] miRNAs typically control the expression of their target transcripts by binding to the 3'-UTR of mRNAs. In mammals, the most consistent requirement of miRNA:target interaction, although not always essential, is the contiguous and perfect base pairing of nucleotides 2-8 (the 'seed') at the 5' end of the miRNA (Ambros 2004, Bartel 2004, Filipowicz, Bhattacharyya et al. 2008, Bartel 2009). Given the shortness of the seed region, it is no surprise that a single miRNA can potentially regulate hundreds of genes that are involved in multiple signaling cascades or cellular mechanisms (Bartel 2004). While these numbers emphasize the regulatory potential of miRNAs, they also reflect how difficult it is to determine the function of a given miRNA, as not all predicted targets will contribute to a phenotype. Ascertaining the biological function of miRNAs in regulating a physiological process, therefore, is complex and relies on systematic, unbiased experiments in living cells or organisms.

SUMMARY OF THE INVENTION

[008] As specified in the Background Section, above, there is a great need in the art to develop new therapeutic tools for treating dyslipidemias and cardiovascular diseases. The present invention addresses this and other needs by providing novel antisense oligonucleotides which are specific inhibitors of miR-27b or miR-148a.

[009] In one embodiment, the invention provides an isolated oligonucleotide, wherein said oligonucleotide is capable of decreasing the level and/or activity of miR-27b. In one

specific embodiment, miR-27b comprises the sequence 5'- UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NOS: 1, 58-59). In one specific embodiment, miR-27b consists of the sequence 5'- UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NOS: 1, 58-59). In another specific embodiment, miR-27b consists of the sequence

5'- ACCUCUCUAACAAGGUGCAGAGCUUAGCUGAUUGGUGAACAGUGAUUGGUU UCCGCUUUGUUCACAGUGGCUAAGUUCUGCACCUGAAGAGAAGGUG-3' (SEQ ID NO: 2).

[0010] In one embodiment, the invention provides an isolated oligonucleotide, which oligonucleotide comprises the sequence complimentary to nucleotides 2-8 at the 5' end of the mature miRNA sequence of miR-27b. In one specific embodiment, such mature miRNA sequence of miR-27b is 5'- UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NOS: 1, 58-59). In one specific embodiment, said oligonucleotide comprises the sequence 5'-AC(T/U)G(T/U)GA-3' (SEQ ID NO: 114). In another specific embodiment, said oligonucleotide comprises the sequence 5'-ACTGTGA-3' (SEQ ID NO: 115). In yet another specific embodiment, said oligonucleotide comprises the sequence 5'-ACUGUGA-3' (SEQ ID NO: 116). In one specific embodiment, said oligonucleotide ranges from 7 to 40 nucleotides in length. In another specific embodiment, said oligonucleotide ranges from 8 to 21 nucleotides in length. In one specific embodiment, said oligonucleotide is capable of decreasing the level and/or activity of miR-27b.

[0011] In one embodiment, the invention provides an isolated oligonucleotide, wherein said oligonucleotide is capable of decreasing the level and/or activity of miR-148a. In one specific embodiment, miR-148a comprises the sequence 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NOS: 6, 60-61). In one specific embodiment, miR-148a consists of the sequence 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NOS: 6, 60-61). In another specific embodiment, miR-148a consists of the sequence

5'-GAGGCAAAGUUCUGAGACACUCCGACUCUGAGUAUGAUAGAAGUCAGUGCA CUACAGAACUUUGUCUC-3' (SEQ ID NO: 7).

[0012] In one embodiment, the invention provides an isolated oligonucleotide, which oligonucleotide comprises the sequence complimentary to nucleotides 2-8 at the 5' end of the mature miRNA sequence of miR-148a. In one specific embodiment, such mature miRNA

sequence of miR-148a is 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NOS: 6, 60-61). In one specific embodiment, said oligonucleotide comprises the sequence 5'-(T/U)GCAC(T/U)G-3' (SEQ ID NO: 117). In another specific embodiment, said oligonucleotide comprises the sequence 5'-TGCACTG-3' (SEQ ID NO: 118). In yet another specific embodiment, said oligonucleotide comprises the sequence 5'-UGCACUG-3' (SEQ ID NO: 119). In one specific embodiment, said oligonucleotide ranges from 7 to 40 nucleotides in length. In another specific embodiment, said oligonucleotide ranges from 8 to 22 nucleotides in length. In one specific embodiment, said oligonucleotide is capable of decreasing the level and/or activity of miR-148a.

[0013] In one embodiment, the oligonucleotide of the invention is a modified oligonucleotide. In one specific embodiment of the invention, the oligonucleotide modification is selected from the group consisting of locked nucleic acids (LNA), 2'-fluoro (2'-F) modified nucleotides, 2'-O-methoxyethyl (2'-MOE) modified nucleotides, 2'-O-methyl (2'O-Me) modified nucleotides, and phosphorothiate (PS) nucleotides.

[0014] The invention also provides pharmaceutical compositions comprising one or more oligonucleotides of the invention and a pharmaceutically acceptable carrier or excipient. In one specific embodiment, the composition comprises one or more oligonucleotides targeting miR-27b. In another specific embodiment, the composition comprises one or more oligonucleotides targeting miR-148a. In yet another specific embodiment, the composition comprises (i) one or more oligonucleotides targeting miR-27b and (ii) one or more oligonucleotides targeting miR-148a.

[0015] In conjunction with the oligonucleotide molecules of the present invention, the invention also provides a method for decreasing the level and/or activity of miR-27b and/or miR-148a in a cell, which method comprises administering to the cell one or more oligonucleotides of the invention or a composition comprising such one or more oligonucleotide(s). In one specific embodiment, the cell to which the oligonucleotide(s) or composition is administered is a hepatic cell.

[0016] In another embodiment, invention provides a method for increasing plasma high-density lipoprotein cholesterol (HDL-C) level and/or reducing plasma low-density lipoprotein cholesterol (LDL-C) level in a subject in need thereof, which method comprises administering to

the subject a therapeutically effective amount of one or more oligonucleotides of the invention or a composition comprising such one or more oligonucleotide(s). In a preferred embodiment, the subject is human.

[0017] In a further embodiment, the invention provides a method for treating a disease in a subject in need thereof, which method comprises administering to the subject a therapeutically effective amount of one or more oligonucleotides of the invention or a composition comprising such one or more oligonucleotide(s). Non-limiting examples of the diseases treatable by the method of the invention include dyslipidemias (such as, e.g., hyperlipidemia [elevated lipid levels], hypercholesterolemia [elevated cholesterol levels], low HDL/LDL ratio) and cardiovascular diseases (such as, e.g., atherosclerosis, coronary artery disease, coronary heart disease, conditions associated with coronary artery disease or coronary heart disease [e.g., angina, myocardial infarction], transient ischemic attack, stroke). In a preferred embodiment, the subject is human.

[0018] In one embodiment of any of the above methods of the invention, the oligonucleotide is a modified or unmodified oligonucleotide selected from the group consisting of 5'-TTCTGTAGTGCACTG-3' (SEQ ID NO: 52; anti-miR-148a), 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33; anti-miR-148a), 5'-AACTTAGCCACTGTGA-3' (SEQ ID NO: 54; anti-miR-27b), and 5'-AGAACTTAGCCACTGTGA-3' (SEQ ID NO: 34; anti-miR-27b). In one specific embodiment, the oligonucleotide is selected from the group consisting of LNA oligonucleotide 5'-TTCTGTAGTGCACTG-3' (SEQ ID NO: 52; anti-miR-148a), LNA oligonucleotide 5'-AACTTAGCCACTGTGA-3' (SEQ ID NO: 54; anti-miR-27b), miRCURY LNA™ microRNA inhibitor 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33; anti-miR-148a), miRCURY LNA™ microRNA inhibitor 5'- AGAACTTAGCCACTGTGA- 3' (SEQ ID NO: 34; anti-miR-27b), miRCURY LNA™ microRNA Power inhibitor 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33; anti-miR-148a), and miRCURY LNA™ microRNA Power inhibitor 5'-AGAACTTAGCCACTGTGA- 3' (SEQ ID NO: 34; anti-miR-27b).

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] **Figures 1A-F.** Genome-wide miRNA screen identifies novel regulators of LDLR activity. (**A**) Schematic workflow of primary screen and bioinformatic procedures. (**B-D**) Linear

regression analysis between DiI-LDL mean average intensity for plate set 1 and 2 (**B**), plate set 2 and 3 (**C**) and plate set 1 and 3 (**D**). The goodness of fit (r2) and regression line (indicative of overall reproducibility of the screen) is indicated on each graph. (**E**) DiI-LDL mean average intensity (MAI, open bars) and robust Z-score (dots) comparison for cells transfected with the negative control siRNA (non-silencing, NS) or positive control siRNA (siRNA LDLR, siLDLR). (**F**) Distribution of average robust Z-scores for individual miRNAs in the primary screen. Controls are represented by the grey (NS siRNA) and black (siLDLR) dots. miR-27b and miR-148a, highlighted in dark grey and light grey, respectively, were chosen for further validation based on predefined criteria (**A**, lower panel). All other miRNAs are shown in black.

[0020] **Figures 2A-Q.** miR-27b and miR-148a are regulated by hepatic lipid content. (**A**) Schematic diagram of the human APO gene locus, showing the localization of the miR-23b~miR-27b~miR-24-1 cluster and its conservation among species. (**B**) Schematic diagram of human chromosome 7, showing the localization of miR-148a and its conservation among species. (**C-E**) qRT-PCR analysis of pri-miR-27b (**C**), pre-miR-27b (**D**) and miR-27b (**E**) in human hepatic cells (Huh7) left untreated (FBS) or loaded with 120 μg/ml native LDL (nLDL) in 10% LPDS. (**F-H**) qRT-PCR analysis of pri-miR-148a (**F**), pre-miR-148a (**G**) and miR-148a (**H**) in human hepatic cells (Huh7) left untreated (FBS) or loaded with 120 μg/ml nLDL in 10% LPDS. (**I-K**) qRT-PCR analysis of pri-miR-27b (**I**), pre-miR-27b (**J**) and miR-27b (**K**) in the livers of C57BL/6 mice (n=3 per group) fed a chow or high-fat diet (HFD). (**L-N**) qRT-PCR analysis of pri-miR-148a (**L**), pre-miR-148a (**M**) and miR-148a (**N**) in the livers of C57BL/6 mice (n=3 per group) fed a chow or high-fat diet (HFD). (**O**) qRT-PCR analysis of miR-27b in the livers of rhesus monkeys (n=5 per group) fed a chow or high-fat diet (HFD). (**P**) qRT-PCR analysis of miR-148a in the livers of rhesus monkeys (n=5 per group) fed a chow or high-fat diet (HFD). (**Q**) qRT-PCR analysis of miR-148a in the livers of wild-type or *ob/ob* mice (*n*=3 per group). In panels (**C**) through (**Q**), the data are the mean ±SEM and representative of ≥3 experiments in duplicate. *, P≤ 0.05 compared to cells cultured in FBS (**C-H**). *, P≤ 0.05 compared to chow diet-fed animals (**I-P**) or wild-type animals (**Q**).

[0021] **Figure 3A-D.** miR-27b specifically targets the 3'UTR of human LDLR, LDLRAP1, and ABCA1, while miR-148a specifically targets the 3'UTR of human LDLR and ABCA1. (**A** and **B**) Human LDLR, LDLRAP1, and ABCA1 3'UTR sequences. Underlined sequences indicate predicted miR-27b binding sites (**A**) and predicted miR-148a binding sites

(**B**). Nucleotides highlighted in grey indicate respective point mutations (PM) in the miR-27b and miR-148a binding sites. (**C**) Luciferase reporter activity in COS7 cells transfected with control mimic (CM) or miR-27b mimic (miR-27b) and the human 3'UTR of LDLR, LDLRAP1, and ABCA1 containing the indicated point mutations (PM) in the miR-27b target sites. Double mutation (DM) indicates that two miR-27b binding sites were mutated in the same 3'UTR construct. (**D**) Luciferase reporter activity in COS7 cells transfected with control mimic (CM) or miR-148a mimic (miR-148a) and the human 3'UTR of LDLR and ABCA1 containing the indicated point mutations (PM) in the miR-148a target sites. Double mutation (DM) indicates that two miR-148a binding sites were mutated in the same 3'UTR construct. In panels (**C**) and (**D**), the data are the mean ±SEM and representative of ≥2 experiments in triplicate. *, P≤ 0.05 compared to cells transfected with CM. #, P≤ 0.05 compared to cells transfected with miR-27b or miR-148a and the control 3'UTR (WT).

[0022] **Figures 4A-S.** Post-transcriptional regulation of LDLR expression and activity by miR-27b and miR-148a in human hepatic cells. (**A**) qRT-PCR analysis of LDLR in Huh7 cells transfected with a control mimic (CM), miR-27b mimic, or miR-148a mimic. (**B**) Western blot analysis of LDLR in Huh7 cells transfected with a control mimic (CM), miR-27b mimic (left panel) or miR-148a mimic (right panel). HSP90 was used as a loading control. (**C**) qRT-PCR analysis of LDLRAP1 in Huh7 cells transfected with a control mimic (CM) or miR-27b mimic. (**D**) qRT-PCR analysis of LDLR in Huh7 cells transfected with a control inhibitor (CI), miR-27b inhibitior (Inh-27b), or miR-148a inhibitor (Inh-148a). (**E**) Western blot analysis of LDLR in Huh7 cells transfected with a control inhibitor (CI), miR-27b inhibitor (Inh-27b, left panel) or miR-148a inhibitor (Inh-148a, right panel). HSP90 was used as a loading control. (**F**) qRT-PCR analysis of LDLRAP1 in Huh7 cells transfected with a control inhibitor (CI) or miR-27b inhibitior (Inh-27b) (**G** and **H**) Flow cytometry analysis of DiI-LDL uptake in Huh7 cells transfected with a control mimic (CM), miR-27b mimic (**G**) or miR-148a mimic (**H**) and incubated with 30 μg/ml DiI-LDL for 2h at 37°C. (**I** and **J**) Flow cytometry analysis of DiI-LDL binding in Huh7 cells transfected with a control mimic (CM), miR-27b mimic (**I**) or miR-148a mimic (**J**) and incubated with 30 μg/ml DiI-LDL for 30 min at 4°C. (**K** and **L**) Intracellular cholesterol content in Huh7 cells transfected with a control mimic (CM), miR-27b mimc (**K**), or miR-148a mimic (**L**) and incubated with 30 μg/ml native LDL (nLDL) for 2h at 37°C. (**M** and **N**) Flow cytometry analysis of DiI-LDL uptake in Huh7 cells transfected with a control inhibitor

(CI), inhibitor of miR-27b (Inh-27b, **M**) or inhibitor of miR-148a (Inh-148a, **N**) and incubated with 30 μg/ml DiI-LDL for 2h at 37°C. (**O** and **P**) Flow cytometry analysis of DiI-LDL binding in Huh7 cells transfected with a control inhibitor (CI), inhibitor of miR-27b (Inh-27b, **O**) or inhibitor of miR-148a (Inh-148a, **P**) and incubated with 30 μg/ml DiI-LDL for 30 min at 4°C. (**Q-R**) Intracellular cholesterol content in Huh7 cells transfected with a control inhibitor (CI), miR-27b inhibitor (Inh-27b, **Q**), or miR-148a inhibitor (Inh-148a, **R**) and incubated with 30 μg/ml native LDL (nLDL) for 2h at 37°C. (**S**) LDLR antibody internalization in Huh7 cells transfected with a control mimic (CM, upper panel), miR-27b mimic (middle panel), or miR-148a mimic (lower panel) and incubated with anti-LDLR and 30 μg/ml DiI-LDL for 40 min at 4°C. Following internalization for 30 or 60 min at 37°C, cells were washed, fixed and stained with Alexa Fluor® 488 and TOPRO. Representative confocal images are shown; LDLR staining is represented by light grey, DiI-LDL staining is represented by darker grey, and stained nuclei are in darkest grey. Scale bar, 5μm. In panels (**A**) through (**R**), the data are the mean ±SEM and representative of ≥3.

[0023] **Figure 5A-R**. LDLR-GFP overexpression rescues LDLR activity in miR-27b- and miR-148a-transfected cells. (**A-I**) Huh7 cells were cotransfected with LDLR-GFP and a control mimic (CM, A-C), miR-27b mimic (**D-F**), or miR-148a mimic (**G-I**) and incubated with 30 μg/ml DiILDL for 2h at 37°C. Following incubation, cells were washed, fixed and stained with TOPRO. In all panels, LDLR staining is represented by light grey, DiI-LDL staining is represented by darker grey, and stained nuclei are in darkest grey. . Scale bar, 10μm. (**J-R**) Huh7 cells were co-transfected with LDLR-GFP and a control mimic (CM, **J-L**), miR-27b mimic (**M-O**), or miR-148a mimic (PR) and incubated with 30 μg/ml DiI-LDL for 90 min at 4°C. Following incubation, cells were washed, fixed and stained with TOPRO.. Scale bar, 10μm. In panels (**A**) through (**R**), images are representative of ≥3 experiments that gave similar results.

[0024] **Figures 6A-E.** miR-27b represses ABCA1 expression and regulates cholesterol efflux in human hepatic cells. (**A**) qRT-PCR analysis of ABCA1 expression in Huh7 cells transfected with a control mimic (CM) or miR-27b mimic in the absence or presence of T0901317 (T090). (**B**) Western blot analysis of ABCA1 expression in Huh7 cells transfected with a control mimic (CM) or miR-27b mimic in the absence or presence of T0901317 (T090). HSP90 was used as a loading control (**C**) qRT-PCR analysis of ABCA1 expression in Huh7 cells transfected with a control inhibitor (CI) or miR-27b inhibitor (Inh-27b) in the absence or

presence of T0901317 (T090). (**D**) Western blot analysis of ABCA1 expression in Huh7 cells transfected with a control inhibitor (CI) or miR-27b inhibitor (Inh-27b) in the absence or presence of T0901317 (T090). HSP90 was used as a loading control. (**E**) Cholesterol efflux to ApoA1 in Huh7 cells transfected with a control mimic (CM) or miR-27b mimic and stimulated with T0901317 (T090). In panels (**A**) through (**E**) data are the mean ±SEM and representative of ≥2 experiments in triplicate. *, P≤ 0.05 compared to cells transfected with CM within each treatment group (**A, E**). *, P≤ 0.05 compared to cells transfected with CI within each treatment group (**C**).

[0025] **Figures 7A-T.** miR-27b regulates plasma LDL and HDL levels in vivo. (**A**) Experimental outline of AAV-Null and AAV-pre-miR-27b (AAV-27b) treated mice (n=5 per group) fed a chow diet. (**B** and **C**) qRT-PCR analysis of pre-miR-27b (**B**) and miR-27b (**C**) levels in the livers of mice following 4 weeks treatment. *, P≤ 0.05 compared to AAV-Null treated mice. (**D** and **E**) qRT-PCR analysis of LDLR expression (**D**) and ABCA1 expression (**E**) in the livers of mice following 4 weeks treatment. *, P≤ 0.05 compared to AAV-Null treated mice. (**F** and **G**) Western blot analysis of LDLR and ABCA1 expression in the livers of mice following 4 weeks treatment. HSP90 was used as a loading control. Quantification of blot relative to HSP90 is shown in (**G**). Numbers are represented as fold-change compared to AAV-Null treated mice, *, P≤ 0.05. (H and I) Levels of total cholesterol (**H**) and HDL cholesterol (**I**) in the plasma of mice treated with AAV-Null or AAV-27b for 0, 2, and 4 weeks. *, P≤ 0.05 compared to AAV-Null treated mice within each treatment week. (**J** and **K**) Cholesterol content of FPLC-fractionated lipoproteins following 2 (**J**) and 4 weeks (**K**) of treatment with AAV-Null or AAV-27b. (**L**) Experimental outline of AAV-Null and AAV-pre-miR-27b (AAV-27b) treated mice (n= 5 per group). Four weeks after the initial treatment, mice were injected a second time with AAV-Null or AAV-27b and challenged with a Western diet (WD) for the following 2 weeks. (**M** and **N**) qRT-PCR analysis of pre-miR-27b (**M**) and miR-27b (**N**) levels in the livers of mice following 6 weeks treatment. *, P≤ 0.05 compared to AAV-Null treated mice. (**O** and **P**) qRT-PCR analysis of LDLR expression (**O**) and ABCA1 expression (**P**) in the livers of mice following 6 weeks treatment. *, P≤ 0.05 compared to AAV-Null treated mice. (**Q** and **R**) Western blot analysis of LDLR and ABCA1 expression in the livers of mice following 6 weeks treatment. HSP90 was used as a loading control. Quantification of blot relative to HSP90 is shown in (**R**). Numbers are represented as fold-change compared to AAV-Null treated mice, *,

P≤ 0.05. (**S** and **T**) Post-prandial (fed) and fasting (3h) cholesterol content of FPLC-fractionated lipoproteins following 6 weeks treatment. In panels (**B**) through (**E**), (**G**) through (**I**), (**M** through **P**) and (**R**) data are the mean ±SEM.

[0026] **Figures 8A-J.** Optimization of primary miRNA screen, Related to Figure 1. (**A**) Flow cytometry analysis of DiI-LDL uptake in Huh7 cells incubated with varying concentrations of DiI-LDL (2-100 μg/ml) for 8h at 37°C. (**B-D**) Representative images of DiI-LDL uptake in Huh7 cells incubated with 10 μg/ml (**B**), 20 μg/ml (**C**) and 40 μg/ml (**D**) DiI-LDL. Following 8h incubation at 37°C, cells were washed, fixed, and stained with Hoechst; DiI-LDL staining is represented by darker grey, and stained nuclei are in darkest grey . (**E** and **F**) Representative images of cell segmentation used to quantify DiI-LDL uptake in a high-throughput format. Huh7 cells were incubated with 30 μg/ml DiI-LDL for 8h at 37°C. Following this, cells were washed, fixed, counterstained with Hoechst, and imaged using the Cellomics ArrayScan. DiI-LDL uptake was quantified using the Cellomics Target Activation BioApplication. (**G**) Mean average intensity of DiI-LDL in Huh7 cells incubated with varying concentrations of DiI-LDL (2-40 μg/ml) in 384-well plates. Following incubation for 8h at 37°C, cells were washed, fixed, stained, and imaged using the Cellomics ArrayScan. In certain wells, cells were incubated with 40 μg/ml DiI-LDL + 30x unlabeled native LDL (nLDL) to show specificity of DiI-LDL uptake/quantification. (**H**) Western blot analysis of LDLR in Huh7 cells transfected with nonsilencing (NS) control siRNA or siRNA LDLR (siLDLR). HSP90 was used as a loading control. (**I**) Mean average intensity of DiI-LDL in Huh7 cells transfected with non-silencing (NS) control siRNA or siRNA LDLR (siLDLR) and incubated with 30 μg/ml DiI-LDL for 8h at 37°C. Following incubation, cells were washed, fixed, stained and imaged using the Cellomics ArrayScan. Z' factor was calculated based on DiILDL mean average intensity (MAI) in cells transfected with NS siRNA or siLDLR. Representative images are shown in panel (**J**). DiI-LDL staining is represented by darker grey, and stained nuclei are in darkest grey. In panels (**A**), (**G**), and (**I**) data are the mean ±SEM and representative of ≥2 experiments in triplicate. *, P≤ 0.05 compared to cells transfected with NS siRNA (**I**). In panels (**B**) through (**D**), (**E**) through (**F**), and (**J**) images are representative of ≥3 experiments that gave similar results.

[0027] **Figures 9A-B.** Bioinformatic analysis of predicted target genes for miR-27b and miR-148a, related to Figure 2 and 3. Predicted targets for miR-27b (**A**) or miR-148a (**B**) in functional clusters that interact and are enriched in lipid metabolism are shown. Targets for miR-

27b or miR-148a that are predicted in Targetscan, miRWalk, and miRanda were uploaded into DAVID for functional annotation cluster analysis. Functional clusters with an enrichment score of ≥1.0 are depicted in diamonds. n represents the number of genes within each cluster, while bracketed numbers represent each cluster number. Grey lines between genes of different clusters indicate STRING interaction score. Genes not found within a functional annotation cluster are indicated by white inverted arrowheads. Predicted gene targets in bold are validated herein.

[0028] **Figures 10A-B.** Predicted binding sites for miR-27b and miR-148a in the 3'UTR of LDLR, ABCA1, and LDLRAP1, related to Figure 3. (**A**) Location of predicted binding sites for miR-27b in the 3'UTR of LDLR, ABCA1, and LDLRAP1. Site conservation between species is shown below each 3'UTR. (**B**) Location of predicted binding sites for miR-148a in the 3'UTR of LDLR and ABCA1. Site conservation between species is shown below each 3'UTR. In panels (**A**) and (**B**), site prediction was based on the target prediction algorithm, Targetscan. Seed sequences are in grey font for miR-27b and miR-148a on the 3' to 5' strand of each 3'UTR. Binding sites on the 5' to 3' strand are outlined in grey. Hsa, human; ptr, chimpanzee; mmu, mouse; rno, rat; ocu, rabbit.

[0029] **Figures 11A-G.** miR-27b and miR-148a regulate LDLR expression and activity in mouse hepatic cells, related to Figure 4. (**A** and **B**) qRT-PCR analysis of LDLR in Hepa cells transfected with a control inhibitor (CI), inhibitor of miR-27b (Inh-27b, **A**) or inhibitor of miR-148a (Inh-148a, **B**). (**C**) Western blot analysis of LDLR in Hepa cells transfected with a control inhibitor (CI), inhibitor of miR-27b (Inh-27b, left panel) or inhibitor of miR-148a (Inh-148a, right panel). HSP90 was used as a loading control. (**D** and **E**) Flow cytometry analysis of DiI-LDL uptake in Hepa cells transfected with a control inhibitor (CI), inhibitor of miR-27b (Inh-27b, **D**), or inhibitor of miR-148a (Inh-148a, **E**) and incubated with 30 μg/ml DiI-LDL for 2h at 37°C. (**F** and **G**) Flow cytometry analysis of DiI-LDL binding in Hepa cells transfected with a (CI), inhibitor of miR-27b (Inh-27b, **F**), or inhibitor of miR-148a (Inh-148a, **G**) and incubated with 30 μg/ml DiILDL for 30 min at 4°C. In panels (**A**) through (**G**), data are the mean ±SEM and representative of ≥2 experiments in triplicate. *, P≤ 0.05 comapred to CI transfected cells (**A-B, D-G**).

[0030] **Figures 12A-N**. Transcriptional regulation of miR-148a by SREBP1c. (**A**) Schematic diagram of human chromosome 7, showing the localization of miR-148a. The active

promoter region of miR-148a is shown (HepG2 ChromHMM) and correlates with CpG islands and enriched H3K4Me3 histone marks. Transcription factor binding sites (as assayed by ChIP-seq) are shown below. Data was compiled using the UCSC Genome Browser (NCBI36/hg18). (**B**) Western blot analysis of nuclear SREBP1c in Huh7 cells transfected with an empty vector control (Empty) or nuclear SREBP1c-FLAG vector (nSREBP1c). p84 was used as a loading control. (**C** and **D**) qRT-PCR analysis of FASN (**C**), pre-miR-148a (**D**) and miR-148a (**D**) in Huh7 cells transfected with an empty vector control (Empty) or nuclear SREBP1c-FLAG vector (nSREBP1c). (**E**) qRT-PCR analysis of miR-148a in the livers of wild-type (WT) or SREBP1c-Tg mice. *n*=4 per group. (**F** through **G**) qRT-PCR analysis of *SREBP1c* responsive genes (**F**) and pre-miR-148a/miR-148a (**G**) in mouse primary hepatocytes treated with vehicle or T090137 (T090). *ABCA1* expression was measured as a positive control for T090 treatment (**G**). (**H**) Northern blot analysis of pre-miR-148a (precursor form) and miR-148a (mature form) in mouse primary hepatocytes treated with 3μM vehicle or T090 for 12h. 5s was used as a loading control. (**I** through **J**) qRT-PCR analysis of *SREBP1c* responsive genes (**I**) and pre-miR-148a/miR-148a (**J**) in mouse primary hepatocytes treated with vehicle or 30 nM insulin for 6h. (**K**) Northern blot analysis of pre-miR-148a (precursor form) and miR-148a (mature form) in mouse primary hepatocytes treated with vehicle or insulin for 6h. 5s was used as a loading control. (**L**) Promoter activity of miR-148a in Hela cells transfected with nuclear SREBP1c (nSREBP1c) or empty vector control. (**M-N**) Promoter activity of miR-148a in Huh7 cells stimulated with 100 nM insulin (**M**) or 3μM T090 (**N**) for 8h and 12h, respectively. In panels (**B**) through (**N**), the data are the mean ±SEM and representative of ≥2 experiments in triplicate. *, $P \leq 0.05$ compared to cells treated with vehicle (**F-G, I-J, M-N**). *, $P \leq 0.05$ compared to cells treated with empty vector (**C, D, L**). , $P \leq 0.05$ compared to WT mice (**E**).

[0031] **Figures 13A-E**. Inhibition of miR-148a increases LDLR expression *in vivo*. (**A**) Experimental outline of LNA control or LNA anti-miR-148a treated *ApoBTg;LDLR*$^{-/+}$ mice (*n*=7 per group). Sequences highlighted are complementary to the seed region of mmu-miR-148a (underlined). (**B**) Northern blot analysis of pre-miR-148a (precursor form) and miR-148a (mature form) in the livers of *ApoBTg;LDLR*$^{-/+}$ mice after two weeks of treatment with LNA control (LNA CON) or LNA anti-miR-148a (LNA 148a). 5s was used as a loading control. (**C**) qRT-PCR analysis of miR-148a levels in the livers of mice following 2 weeks of treatment. *, $P \leq 0.05$ compared to LNA control (LNA CON) treated mice. (**D**) Western blot analysis of

LDLR expression in the livers of mice following 2 weeks of treatment. HSP90 was used as a loading control. Quantification of LDLR relative to HSP90 is shown in (**E**). Numbers are represented as fold-change compared to LNA control (LNA CON) treated mice, *, $P \leq 0.05$. (**F**) Schematic representation of miR-148a-mediated regulation of LDLR. In panels (**B**) through (**E**) data are the mean ±SEM and representative of each treatment group.

[0032] **Figures 14A-D**. Inhibition of miR-27b increases LDLR expression in vivo. (**A**) Experimental outline of LNA control or LNA anti-miR-27b treated *ApoBTg;LDLR*$^{-/+}$ mice (n=7 per group). Sequences highlighted are complementary to the seed region of mmu-miR-27b (underlined). (**B**) qRT-PCR analysis of miR-27b levels in the livers of mice following 2 weeks of treatment. *, $P \leq 0.05$ compared to LNA control (LNA CON) treated mice. (**C**) Western blot analysis of LDLR expression in the livers of mice following 2 weeks of treatment. HSP90 was used as a loading control. Quantification of LDLR relative to HSP90 is shown in (**D**). Numbers are represented as fold-change compared to LNA control (LNA CON) treated mice, *, $P \leq 0.05$. In panels (**B**) through (**D**) data are the mean ±SEM and representative of each treatment group.

DETAILED DESCRIPTION OF THE INVENTION

[0033] The present invention is based on the identification of miRNAs involved in regulating LDLR activity in a high-throughput microscope-based screening assay that monitored the effect of over 1700 miRNAs on the cellular internalization of fluorescently labeled LDL (DiI-LDL) in human hepatic cells. From this initial screen, the present inventors identified 423 miRNAs that decreased LDLR activity; of these miRNAs, 14 were predicted to target the LDLR and highly expressed in the liver or previously described to be regulated by dietary lipids. Among them, gain and loss-of function experiments established the importance of miR-27b and miR-148a in regulating LDLR activity through direct targeting of the LDLR. In addition, a SREBP1 binding site in the miR-148a promoter region was identified by the inventors; overexpression of nSREBP1c and activation of endogenous SREBP1c by T090 and insulin was shown to increase the promoter activity and expression of miR-148a, thus defining a novel feedback loop for maintaining cholesterol uptake. Furthermore, inhibition of miR-148a with locked nucleic acid (LNA) antisense oligonucleotides significantly increased the expression of LDLR in the livers of mice.

[0034] As described in detail in the Examples section below, miR-27b was selected for further characterization and shown to directly target ABCA1 and reduce cellular cholesterol efflux to ApoA1 in human hepatic cells. Importantly, hepatic-specific over expression of miR-27b in mice repressed ABCA1 and LDLR expression in the liver, reducing circulating HDL levels and increasing plasma LDL-C. In addition, inhibition of miR-27b with LNA antisense oligonucleotides significantly upregulated hepatic LDLR expression in mice. Taken together, the data provided herein highlights the role of miRNAs in regulating LDLR activity and demonstrates the therapeutic potential of inhibiting miRNAs to simultaneously contest two of the main risk factors of cardiovascular diseases, namely high levels of LDL-C and low levels of HDL-C.

[0035] The present invention provides novel compounds which are specific inhibitors of miR-27b or miR-148a.

Definitions

[0036] As used herein, the term "oligonucleotide" refers to a nucleic acid consisting of from 2 to 200 nucleotides, which may be DNA, RNA, a DNA-RNA chimera, or a derivative thereof (see the Oligonucleotide Modifications section, below).

[0037] The antisense oligonucleotides of the invention can target both mature miRNAs amd miRNA precursors. As used herein, the term "miRNA precursor" is used to encompass, without limitation, primary miRNA transcripts (also known as pri-pre-miRNAs), pri-miRNAs, and pre-miRNAs.

[0038] As used herein, the term "complementary sequence," refers to a nucleic acid base sequence that can form a double-stranded structure with another DNA/RNA fragment to which it is complementary, by following base-pairing rules (e.g., A pairs with T/U, and C with G).

[0039] Within the meaning of the present invention, the terms "an activity" or "a function" when used in connection with miR-27b or miR-148a are interchangeable and encompasses all possible structural and functional interactions of miR-27b and miR-148a, respectively, including changes in their secondary and/or tertiary structure as well as interactions with various molecules (*e.g.*, nucleic acids, proteins, etc.).

[0040] In the context of the present invention insofar as it relates to any of the disease conditions recited herein, the terms "treat", "treatment", and the like mean:

(1) preventing or delaying the appearance of at least one clinical or sub-clinical symptom of the state, disorder or condition developing in a subject that may be afflicted with or predisposed to the state, disorder or condition but does not yet experience or display clinical or subclinical symptoms of the state, disorder or condition; or

(2) inhibiting the state, disorder or condition, i.e., arresting, reducing or delaying the development of the disease or a relapse thereof (in case of maintenance treatment) or at least one clinical or sub-clinical symptom thereof; or

(3) relieving the disease, i.e., causing regression of the state, disorder or condition or at least one of its clinical or sub-clinical symptoms.

[0041] As used herein the term "therapeutically effective" applied to dose or amount refers to that quantity of a compound (*e.g.*, oligonucleotide) or pharmaceutical composition that is sufficient to result in a desired activity upon administration to an animal in need thereof. Within the context of the present invention, the term "therapeutically effective" refers to that quantity of a compound or pharmaceutical composition that is sufficient to reduce or eliminate at least one symptom of a disease specified above. Note that when a combination of active ingredients is administered (e.g., anti-miR-27b and anti-miR-148a), the effective amount of the combination may or may not include amounts of each ingredient that would have been effective if administered individually. Therapeutically effective dosages according to the present invention can be determined stepwise by combinations of approaches such as, *e.g.*, (i) characterization in cell cultures using miR-27b and/or miR-148a levels as a readout followed by (ii) characterization in animal studies using plasma high-density lipoprotein cholesterol (HDL-C) and/or low-density lipoprotein cholesterol (LDL-C) levels as a readout, followed by (iii) characterization in human trials using plasma HDL-cholesterol (HDL-C) and/or LDL-cholesterol (LDL-C) levels and/or disease symptoms releief as a readout.

[0042] The phrase "pharmaceutically acceptable", as used in connection with the compositions of the invention, refers to molecular entities and other ingredients of such

compositions that are physiologically tolerable and do not typically produce untoward reactions when administered to a mammal (*e.g.*, a human). Preferably, as used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in mammals, and more particularly in humans.

[0043] The term "about" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, *i.e.*, the limitations of the measurement system. For example, "about" can mean within an acceptable standard deviation, per the practice in the art. Alternatively, "about" can mean a range of up to ±20%, preferably up to ±10%, more preferably up to ±5%, and more preferably still up to ±1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 2-fold, of a value. Where particular values are described in the application and claims, unless otherwise stated, the term "about" is implicit and in this context means within an acceptable error range for the particular value.

[0044] The term "subject" means any animal, including mammals and, in particular, humans.

[0045] As used in this specification and the appended claims, the singular forms "a," "an," and "the" include plural references unless the context clearly dictates otherwise.

[0046] In accordance with the present invention, there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. See, *e.g.*, Sambrook, Fritsch and Maniatis, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989 (herein "Sambrook *et al.*, 1989"); DNA Cloning: A Practical Approach, Volumes I and II (Glover ed. 1985); Oligonucleotide Synthesis (Gait ed. 1984); Nucleic Acid Hybridization (Hames and Higgins eds. 1985); Transcription And Translation (Hames and Higgins eds. 1984); Animal Cell Culture (Freshney ed. 1986); Immobilized Cells And Enzymes (IRL Press, 1986); B. Perbal, A Practical Guide To Molecular Cloning (1984); Ausubel *et al.* eds., Current Protocols in Molecular Biology, John Wiley and Sons, Inc. 1994; among others.

Antisense Oligonucleotides of the Invention

[0047] The antisense oligonucleotides of the invention encompass all antisense oligonucleotides which are capable of inhibiting expression and/or function of miR-27b or miR-148a. To successfully inhibit expression and/or function of miR-27b or miR-148a, such antisense oligonucleotides need to be complementary to at least the 'seed region' of the target mature miRNA sequence (nt 2-8 at the 5' end of the mature miRNA sequence). Perfect complementarity is not required for other parts of the antisense oligonucleotide and can be, for example, at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% complementary to a target miRNA sequence.

[0048] Sequences for hsa-miR-27b-3p

Mature: MIMAT0000419 5'- UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NO: 1)

Precursor: MI0000440

5'- ACCUCUCUAACAAGGUGCAGAGCUUAGCUGAUUGGUGAACAGUGAUUGGUU UCCGCUUUGUUCACAGUGGCUAAGUUCUGCACCUGAAGAGAAGGUG-3' (SEQ ID NO: 2)

[0049] Sequences for hsa-miR-148a-3p

Mature: MIMAT0000243 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NO: 6)

Precursor: MI0000253

5'-GAGGCAAAGUUCUGAGACACUCCGACUCUGAGUAUGAUAGAAGUCAGUGCA CUACAGAACUUUGUCUC-3' (SEQ ID NO: 7)

[0050] The antisense oligonucleotides of the present invention include ribonucleotides or deoxyribonucleotides or combinations thereof. The antisense oligonucleotides of the present invention include various oligonucleotide analogs and derivatives, which analogs and derivatives are also capable of inhibiting expression and/or function of miR-27b or miR-148a. Such analogs and derivatives may have increased *in vivo* stability, particularly nuclease resistance, and/or reduced non-specific binding, and/or increased bioavailability as compared to unmodified oligonucleotides. The oligonucleotides may be modified at the backbone, the sugar moiety, or the bases themselves.

[0051] For instance, suitable antisense oligonucleotides may be comprised of one or more "conformationally constrained" or bicyclic sugar nucleoside modifications (BSN) that confer enhanced thermal stability to complexes formed between the oligonucleotide containing BSN and their complementary miRNA target strand. For example, in one embodiment, the antisense oligonucleotides contain at least one "locked nucleic acid." Locked nucleic acids (LNAs) contain the 2'-O, 4'-C-methylene ribonucleoside wherein the ribose sugar moiety is in a "locked" conformation. In another embodiment, the antisense oligonucleotides contain at least one 2', 4'-C-bridged 2' deoxyribonucleoside (CDNA). See, e.g., U.S. Patent No. 6,403,566 and Wang et al. (1999) Bioorganic and Medicinal Chemistry Letters, Vol. 9: 1147-1150. The antisense oligonucleotides of the invention can also contain combinations of BSN (LNA, CDNA and the like) or other modified nucleotides, and ribonucleotides or deoxyribonucleotides. The antisense oligonucleotides of the invention can comprise peptide nucleic acids (PNAs), which contain a peptide-based backbone rather than a sugar-phosphate backbone. Other modified sugar or phosphodiester modifications to the antisense oligonucleotide are also contemplated. Non-limiting examples of other chemical modifications that the antisense oligonucleotides of the invention can contain include sugar modifications, such as 2'-O-alkyl (e.g., 2'-O-methyl, 2'-O-methoxyethyl), 2'-fluoro, and 4'-thio modifications, and backbone modifications, such as one or more phosphorothioate, morpholino, or phosphonocarboxylate linkages (see, for example, U.S. Patent Nos. 6,693,187 and 7,067,641). In some embodiments, suitable antisense oligonucleotides are 2'-O-methoxyethyl "gapmers" which contain 2'-O-methoxyethyl-modified ribonucleotides on both 5' and 3' ends with at least ten deoxyribonucleotides in the center. These "gapmers" are capable of triggering RNase H-dependent degradation mechanisms of RNA targets.

[0052] Examples of oligonucleotide backbone modifications include, without limitation, oligonucleotides that contain phosphorus group in the backbone, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates comprising 3'alkylene phosphonates and chiral phosphonates as well as short chain alkyl, or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar linkages, phosphinates, phosphoramidates comprising 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-

5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included. Specific examples include, among others, oligonucleotides with CH_2-NH-O-CH_2, CH_2-N(CH_3)-O-CH_2, CH_2-O-N(CH_3)-CH_2, CH_2-N(CH_3)-N(CH_3)-CH_2 and O-N(CH_3)-CH_2-CH_2 backbones (where phosphodiester is O-PO_2-O-CH_2).

[0053] Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These comprise those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH2 component parts. U.S. Patent No. 5,034,506 describes oligonucleotides having morpholino backbone structures. U.S. Patent No. 5,677,437 describes heteroaromatic oligonucleoside linkages. U.S. Patents Nos. 5,792,844 and 5,783,682 describe nitrogen linkers or groups containing nitrogen. U.S. Patent No. 5,637,684 describes phosphoramidate and phosphorothioamidate oligomeric compounds. Further examples include oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular-CH_2-NH-O-CH_2-,-CH_2-N (CH_3)-O-CH_2-known as a methylene (methylimino) or MMI backbone,-CH_2-O-N (CH_3)-CH_2-,-CH_2N(CH_3)-N(CH_3) CH_2-and-O-N(CH_3)-CH_2-CH_2- wherein the native phosphodiester backbone is represented as-O-P-O-CH_2-. See, *e.g.*, US Patents Nos. 5,489,677 and 5,602,240.

[0054] In other oligonucleotide modifications encompassed by the present invention, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. Example of such modification is a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. See, *e.g.*, Nielsen *et al.*, Science 1991; 254:1497.

[0055] Modified oligonucleotides encompassed by the present invention may also contain one or more substituted sugar moieties. Examples include oligonucleotides containing substituted sugar moieties comprising one of the following at the 2' position: OH, SH, SCH_3, F, OCN, $O(CH_2)_nO_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_{2n}ON(CH_2)_nCH_3)_2$ where n and m can be from 1 to about 10; C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl or aralkyl; O-alkaryl or O-aralkyl; Cl; Br; CN; CF_3; OCF_3; O-; S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S-or N-alkynyl; or O alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C to C_0 alkyl or C_2 to C_0 alkenyl and alkynyl; $SOCH_3$; SO_2CH_3; ONO_2; NO_2; N_3; NH_2; heterocycloalkyl; heterocycloalkaryl; aminoalkylamino; polyalkylamino; substituted sialyl; a fluorescein moiety; an RNA cleaving group; a reporter group; an intercalator; a group for improving the pharmacokinetic properties of an oligonucleotide; or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. See, *e.g.*, Martin et al., Helv. Chim. Acta, 1995, 78, 486-504 which describes a modification comprising 2'-methoxyethoxy (2'-O-$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE), i.e., an alkoxyalkoxy group. Another specific modification comprises 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O-CH_2-O-CH_2-N $(CH_2)_2$. Other preferred modifications comprise 2'-methoxy (2'-O CH_3), 2'-aminopropoxy (2'-O $CH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyls or other carbocyclics in place of the pentofuranosyl group.

[0056] Oligonucleotides of the invention may also include, additionally or alternatively, nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include adenine (A), guanine (G), thymine (T), cytosine (C) and uracil (U). Modified nucleobases include nucleobases other synthetic and natural nucleobases such as xanthine, hypoxanthine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 5-Me pyrimidines, particularly 5-methylcytosine (also referred to as 5-methyl-2' deoxycytosine and often referred to in the art as 5-Me-C), 5-hydroxymethylcytosine (HMC), glycosyl HMC and

gentobiosyl HMC, 2-aminoadenine, 2-(methylamino)adenine, 2-(imidazolylalkyl)adenine, 2-(aminoalklyamino)adenine or other heterosubstituted alkyladenines, 2-thiouracil, 2-thiothymine, 2-thiocytosine, 5-halouracil and cytosine (*e.g.*, 5-bromouracil), 5-hydroxymethyluracil, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudo-uracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylquanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine, N_6 (6-aminohexyl)adenine and 2,6-diaminopurine. A "universal" base known in the art, *e.g.*, inosine, may be also included. See, *e.g.*, Kornberg, A., DNA Replication, W. H. Freeman & Co., San Francisco, 1980, pp75-77; Gebeyehu, G., et al. Nucl. Acids Res. 1987, 15:4513). Further modified nucleobases comprise those disclosed in US Patent No. 3,687,808, those disclosed in "The Concise Encyclopaedia of Polymer Science And Engineering", pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, 1990, those disclosed by Englisch et al., 'Angewandle Chemie, International Edition', 1991, 30, page 613, and those disclosed by Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds, 'Antisense Research and Applications', CRC Press, Boca Raton, 1993, pp. 276-302 and Crooke, S.T. and Lebleu, B. ea., CRC Press, 1993.

[0057] A further class of oligonucleotide modifications used in the present invention is referred to as cyclohexenyl nucleic acids (CeNA). The furanose ring normally present in a DNA or RNA molecule is replaced with a cyclohenyl ring. CeNA DMT protected phosphoramidite monomers have been prepared and used for oligomeric compound synthesis following classical phosphoramidite chemistry. Fully modified CeNA oligomeric compounds and oligonucleotides having specific positions modified with CeNA have been prepared and studied (see Wang *et al., J. Am. Chem. Soc.*, 2000, 122, 8595-8602).

[0058] In other embodiments, locked nucleic acids (LNA) can be used (reviewed in, *e.g.*, Jepsen and Wengel, Curr. Opin. Drug Discov. Devel. 2004; 7:188-194; Crinelli *et al.*, Curr. Drug Targets 2004; 5:745-752). LNA are nucleic acid analog(s) in which the 2'-hydroxyl group of the ribosyl sugar ring is linked to the 4' carbon atom of the sugar ring thereby forming a 2'-O,4'-C-oxymethylene linkage to form the bicyclic sugar moiety (reviewed in Elayadi *et al., Curr. Opinion Invens. Drugs*, 2001, 2, 558-561; Braasch *et al., Chem. Biol.*, 2001, 8 1-7; and Orum *et al., Curr. Opinion Mol. Ther.*, 2001, 3, 239-243; see also U.S. Patents Nos.: 6,268,490

and 6,670,461). This bridge restricts the flexibility of the ribofuranose ring and locks the structure into a rigid C3-endo conformation, conferring enhanced hybridization performance and exceptional biostability (see, *e.g.*, Uhlman, Current Opinions in Drug Discovery & Development 2000, Vol. 3 No. 2; Frieden et al., Nucleic Acids Research, 2003, 21, 6365-6372; Wahlestedt et al., Proc. Natl. Acad. Sci. U.S.A., 2000, 97, 5633-5638). The linkage can be a methylene ($-CH_2-$) group bridging the 2' oxygen atom and the 4' carbon atom, for which the term LNA is used for the bicyclic moiety; in the case of an ethylene group in this position, the term ENA is used (Singh et al., Chem. Commun., 1998, 4, 455-456; ENA™: Morita et al., Bioorganic Medicinal Chemistry, 2003, 11, 2211-2226). Another similar bicyclic sugar moiety that has been prepared and studied has the bridge going from the 3'-hydroxyl group via a single methylene group to the 4' carbon atom of the sugar ring thereby forming a 3'-C,4'-C-oxymethylene linkage (see U.S. Pat. No. 6,043,060). LNA and other bicyclic sugar analogs display very high duplex thermal stabilities with complementary DNA and RNA (Tm= +3 to +10 °C), stability towards 3'-exonucleolytic degradation and good solubility properties. LNAs are commercially available from, *e.g.*, ProLigo (Paris, France and Boulder, Colo., USA).

[0059] Another oligonucleotide modification encompassed by the present invention is threose nucleic acid (TNA) which contains threose nucleosides instead of ribose nucleosides. See, *e.g.*, Chaput et al., J. Am. Chem. Soc., 2003, 125, 856-857; Wu et al., Organic Letters, 2002, 4(8), 1279-1282.

[0060] Further oligonucleotide mimetics have been prepared to include bicyclic and tricyclic nucleoside analogs (see Steffens *et al., Helv. Chim. Acta*, 1997, 80, 2426-2439; Steffens *et al., J. Am. Chem. Soc.*, 1999, 121, 3249-3255; Renneberg *et al., J. Am. Chem. Soc.*, 2002, 124, 5993-6002; and Renneberg *et al., Nucleic Acids Res.*, 2002, 30, 2751-2757). These modified nucleoside analogs have been oligomerized using the phosphoramidite approach and the resulting oligomeric compounds containing tricyclic nucleoside analogs have shown increased thermal stabilities (Tms) when hybridized to DNA, RNA and itself.

[0061] Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more heterologous moieties which enhance the activity or cellular uptake of the oligonucleotide. Such heterologous moieties include but are not limited to lipid moieties such as a cholesterol moiety, a cholesteryl moiety (Letsinger et al., Proc.

Natl. Acad. Sci. USA 1989, 86, 6553), cholic acid (Manoharan et al. Bioorg. Med. Chem. Let. 1994, 4, 1053), a thioether, *e.g.*, hexyl-S-tritylthiol (Manoharan et al. Ann. N.Y. Acad. Sci. 1992, 660, 306; Manoharan et al. Bioorg. Med. Chem. Let. 1993, 3, 2765), a thiocholesterol (Oberhauser et al., Nucl. Acids Res. 1992, 20, 533), an aliphatic chain, *e.g.*, dodecandiol or undecyl residues (Saison-Behmoaras et al. EMBO J. 1991, 10, 111; Kabanov et al. FEBS Lett. 1990, 259, 327; Svinarchuk et al. Biochimie 1993, 75, 49), a phospholipid, *e.g.*, di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al. Tetrahedron Lett. 1995, 36, 3651; Shea et al. Nucl. Acids Res. 1990, 18, 3777), a polyamine or a polyethylene glycol chain (Manoharan et al. Nucleosides & Nucleotides 1995, 14, 969), or adamantane acetic acid (Manoharan et al. Tetrahedron Lett. 1995, 36, 3651), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-t oxycholesterol moiety (Crooke et al., J. Pharmacol. Exp. Ther. , 1996, 277, 923-937). Oligonucleotides comprising lipophilic moieties, and methods for preparing such oligonucleotides are known in the art, for example, from U.S. Patent Nos. 5,138,045, 5,218,105 and 5,459,255. Other covalently linked moieties may include, for example, proteins, intercalators, chelators, or alkylators. The oligonucleotides herein may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

[0062] Examples of modified phosphate groups which can be used in antisense oligonucleotides of the invention include phosphorothioate, phosphoroselenates, borano phosphates, borano phosphate esters, hydrogen phosphonates, phosphoroamidates, alkyl or aryl phosphonates and phosphotriesters. Phosphorodithioates have both non-linking oxygens replaced by sulfur. The phosphate linker can also be modified by replacement of a linking oxygen with nitrogen (bridged phosphoroamidates), sulfur (bridged phosphorothioates) and carbon (bridged methylenephosphonates). The replacement can occur at a terminal oxygen. The phosphate group can be replaced by non-phosphorus containing connectors. Examples of moieties which can replace the phosphate group include siloxane, carbonate, carboxymethyl, carbamate, amide, thioether, ethylene oxide linker, sulfonate, sulfonamide, thioformacetal, formacetal, oxime, methyleneimino, methylenemethylimino, methylenehydrazo, methylenedimethylhydrazo and methyleneoxymethylimino.

[0063] The antisense oligonucleotides of the invention can include a 2′-deoxy, 2′-deoxy-2′-fluoro, 2′-β-methyl, 2′-O-methoxyethyl (2′-O-MOE), 2′-O-aminopropyl (2′-O-AP), 2′-O-dimethylaminoethyl (2′-O-DMAOE), 2′-O-dimethylaminopropyl (2′-O-DMAP), 2′-O-dimethylaminoethyloxyethyl (2′-O-DMAEOE), or 2′-O-N-methylacetamido (2′-O-NMA). The 3′ and 5′ ends of an antisense oligonucleotide can be conjugated to other functional molecular entities such as labeling moieties, e.g., fluorophores (e.g., pyrene, TAMRA, fluorescein, Cy3 or Cy5 dyes) or protecting groups (based e.g., on sulfur, silicon, boron or ester).

[0064] The sugar group can also contain one or more carbons that possess the opposite stereochemical configuration than that of the corresponding carbon in ribose. Thus, a modified RNA can include nucleotides containing e.g., arabinose, as the sugar. Modified RNAs can also include "abasic" sugars, which lack a nucleobase at C-1′. These abasic sugars can also further contain modifications at one or more of the constituent sugar atoms. The modification can also entail the wholesale replacement of a ribose structure with another entity (an SRMS) at one or more sites in the oligonucleotide agent.

[0065] Terminal modifications can include the addition of a methylphosphonate at the 3′-most terminal linkage; a 3′ C5-aminoalkyl-dT; 3′ cationic group; or another 3′ conjugate to inhibit 3′-5′ exonucleolytic degradation. Non-limiting examples of 5′-phosphate modifications include: 5′-monophosphate ((HO)2(O)P—O-5′); 5′-diphosphate ((HO)2(O)P—O—P(HO)(O)—O-5′); 5′-triphosphate ((HO)2(O)P—O—(HO)(O)P—O—P(HO)(O)—O-5′); 5′-guanosine cap (7-methylated or non-methylated) (7m-G-O-5′-(HO)(O)P—O—(HO)(O)P—O—P(HO)(O)—O-5′); 5′-adenosine cap (Appp), and any modified or unmodified nucleotide cap structure (N—O-5′-(HO)(O)P—O—(HO)(O)P—O—P(HO)(O)—O-5′); 5′-monothiophosphate (phosphorothioate; (HO)2(S)P—O-5′); 5′-monodithiophosphate (phosphorodithioate; (HO)2(HS)(S)P—O-5′), 5′-phosphorothiolate ((HO)2(O)P—S-5′); any additional combination of oxygen/sulfur replaced monophosphate, diphosphate and triphosphates (e.g. 5′-alpha-thiotriphosphate, 5′-gamma-thiotriphosphate, etc.), 5′-phosphoramidates ((HO)2(O)P—NH-5′, (HO)(NH2)(O)P—O-5′), 5′-alkylphosphonates (R=alkyl-methyl, ethyl, isopropyl, propyl, etc., e.g. RP(OH)(O)—O-5′-, (OH)2(O)P-5′-CH2—), 5′-alkyletherphosphonates (R=alkylether=methoxymethyl (MeOCH2—), ethoxymethyl, etc., e.g. RP(OH)(O)—O-5′-).

[0066] Nuclease resistant antisense oligonucleotides can be prepared with nucleobases such as, e.g., inosine, thymine, xanthine, hypoxanthine, nubularine, isoguanisine, or tubercidine. Non-limiting examples of other substitute bases that can be used include 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 5-halouracil, 5-(2-aminopropyl)uracil, 5-amino allyl uracil, 8-halo, amino, thiol, thioalkyl, hydroxyl and other 8-substituted adenines and guanines, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine, 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine, dihydrouracil, 3-deaza-5-azacytosine, 2-aminopurine, 5-alkyluracil, 7-alkylguanine, 5-alkyl cytosine, 7-deazaadenine, N6, N6-dimethyladenine, 2,6-diaminopurine, 5-amino-allyl-uracil, N3-methyluracil, substituted 1,2,4-triazoles, 2-pyridinone, 5-nitroindole, 3-nitropyrrole, 5-methoxyuracil, uracil-5-oxyacetic acid, 5-methoxycarbonylmethyluracil, 5-methyl-2-thiouracil, 5-methoxycarbonylmethyl-2-thiouracil, 5-methylaminomethyl-2-thiouracil, 3-(3-amino-3-carboxypropyl)uracil, 3-methylcytosine, 5-methylcytosine, N.sup.4-acetyl cytosine, 2-thiocytosine, N6-methyladenine, N6-isopentyladenine, 2-methylthio-N-6-isopentenyladenine, N-methylguanines, or O-alkylated bases.

[0067] To facilitate in vivo delivery and stability, the antisense oligonucleotide may be linked to a steroid, such as cholesterol moiety, a vitamin, a fatty acid, a carbohydrate or glycoside, a peptide, or other small molecule ligand at its 3' end.

[0068] Other modifications of antisense oligonucleotides are known in the art and are suitable for use in the present invention.

[0069] It is not necessary for all positions in a given oligonucleotide to be uniformly modified. More than one of the aforementioned modifications may be incorporated in a single oligonucleotide or even within a single nucleoside within an oligonucleotide. The present invention also includes “chimeric” oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one nucleotide. These chimeric oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding

affinity for the target nucleic acid or protein. An additional region of the oligonucleotide may serve as a substrate for enzymes or as a means for oligonucleotide detection.

[0070] Useful modifications of miRNA inhibitory oligonucleotides of the invention also include miRCURY LNA™ microRNA inhibitors and miRCURY LNA™ microRNA Power inhibitors (Exiqon). miRCURY LNA™ microRNA inhibitors are DNA/LNA™ mixmer antisense oligonucleotides (a combination of LNA monomers and DNA monomers) with normal phosphodiester nucleotide bonds. miRCURY LNA™ microRNA Power inhibitors have a fully phosphorothioate (PS) modified backbone which makes them highly resistant to enzymatic degradation.

[0071] In one specific embodiment of the invention, oligonucleotide modification is selected from the group consisting of locked nucleic acids (LNA), 2'-fluoro (2'-F) modified nucleotides, 2'-O-methoxyethyl (2'-MOE) modified nucleotides, 2'-O-methyl (2'O-Me) modified nucleotides, and phosphorothiate (PS) nucleotides.

[0072] In one specific embodiment, the miRNA inhibitory oligonucleotide is selected from the group consisting of LNA oligonucleotides 5'-TTCTGTAGTGCACTG-3' (SEQ ID NO: 52; anti-miR-148a) and 5'-AACTTAGCCACTGTGA-3' (SEQ ID NO: 54; anti-miR-27b), miRCURY LNA™ microRNA inhibitors 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33; anti-miR-148a) and 5'- AGAACTTAGCCACTGTGA- 3' (SEQ ID NO: 34; anti-miR-27b), and miRCURY LNA™ microRNA Power inhibitors 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33; anti-miR-148a) and 5'- AGAACTTAGCCACTGTGA- 3' (SEQ ID NO: 34; anti-miR-27b).

Oligonucleotide Preparation

[0073] The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including Applied Biosystems. Any other means for such synthesis may also be employed; the actual synthesis of the oligonucleotides is well within the talents of one of ordinary skill in the art. It is also well known to use similar techniques to prepare other oligonucleotides such as the phosphorothioates and alkylated derivatives. It is also well known to use similar techniques and commercially available modified amidites and controlled-pore glass (CPG) products such as biotin, fluorescein, acridine or psoralen-modified

amidites and/or CPG (available from Glen Research, Sterling VA) to synthesize fluorescently labeled, biotinylated or other modified oligonucleotides such as cholesterol-modified oligonucleotides. Preparation of LNA and derivatives has been described, for example, in PCT Publications Nos. WO 98/39352 and WO 99/14226; Koshkin et al., Tetrahedron, 1998, 54, 3607-3630; Kumar et al., Bioorg. Med. Chem. Lett., 1998, 8, 2219-2222; Singh et al., J. Org. Chem., 1998, 63, 10035-10039. Representative patents that teach the preparation of the phosphorus-containing linkages comprise, but are not limited to, US Patents Nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5, 177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455, 233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563, 253; 5,571,799; 5,587,361; and 5,625,050.

[0074] Representative patents that teach the preparation of the oligonucleotides having backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages comprise, but are not limited to, US Patents Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264, 562; 5, 264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596, 086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623, 070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439. Representative patents that teach the preparation of PNA compounds comprise, but are not limited to, US Patent Nos. 5,539,082; 5,714,331; and 5,719,262. See also Nielsen et al., Science, 1991, 254, 1497-1500. Representative patents that teach the preparation of modified sugar structures comprise, but are not limited to, US Patent Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514, 785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646, 265; 5,658,873; 5,670,633; and 5,700,920. Representative patents that teach the preparation of the modified nucleobases comprise, but are not limited to, US Patent Nos. 3,687,808; 4,845,205; 5,130,302; 5,134,066; 5,175, 273; 5, 367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,596,091; 5,614,617; 5,750,692, and 5,681,941. Representative patents that teach the preparation of oligonucleotide conjugates comprise, but are not limited to, US Patent Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552, 538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486, 603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735;

4,667,025; 4,762, 779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082, 830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5, 245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391, 723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599, 928 and 5,688,941. Representative patents that teach the preparation of chimeric oligonucleotides comprise, but are not limited to, US Patents Nos. 5,013,830; 5,149,797; 5, 220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922.

Pharmaceutical Compositions of the Invention

[0075] For administration to human and animal patients, the oligonucleotides of the present invention can be formulated in pharmaceutical compositions in combination with one or more pharmaceutically acceptable carriers and/or excipients such as, *e.g.*, lubricants, diluents, flavorants, colorants, buffers, and disintegrants. Suitable pharmaceutically acceptable carriers include any and all conventional solvents (such as, *e.g.*, water, physiological solution, dextrose, glycerol, ethanol, and the like, as well as combinations thereof), wetting agents, emulgators, buffers, conservants, dispersion media, fillers, solid carriers, aqueous solutions, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, as well as other well-known agents which enhance the shelf life or effectiveness of one or more of the active components of the composition. Examples of such useful substances can be found in "Remington's Pharmaceutical Sciences" by E. W. Martin. Except insofar as any conventional media or agent is incompatible with the active ingredient, use thereof in compositions of the present invention is contemplated. The term "pharmaceutically acceptable" refers to a carrier or excipient that does not cause an allergic reaction or other untoward effect in patients to whom it is administered.

[0076] The pharmaceutical compositions of the invention can be produced in useful dosage units for administration by various routes including, among others, topical, oral, subcutaneous, intravenous, and intranasal administration.

[0077] The pharmaceutical compositions of the invention can also include other biologically active substances in combination with the oligonucleotides of the invention. Such additional biologically active substances can be also formulated as separate compositions and

can be administered simultaneously or sequentially with the oligonucleotides of the invention. Non-limiting examples of useful biologically active substances include statins, niacin, bile-acid resins, fibric acid derivatives, cholesterol absorption inhibitors, and other lipid-lowering drugs.

Oligonucleotide Administration

[0078] With the aid of present disclosure, those of skill in the art should be able to derive suitable dosages and schedules of administration for any of a number of suitable compositions that contain the oligonucleotides of the invention. Thus, pharmaceutical compositions within the scope of the present invention include compositions where the active ingredient(s) is contained in an effective amount to increase plasma high-density lipoprotein cholesterol (HDL-C) level and/or reduce plasma low-density lipoprotein cholesterol (LDL-C) level.

[0079] The formulation and dose for therapeutic administration of the oligonucleotides of the invention will depend on the severity of the disease condition being treated, whether other drugs are being administered, whether other actions are taken, the weight, age, and sex of the subject, and other criteria. The skilled medical practitioner will be able to select the appropriate formulation and dose in view of these criteria and based on the results of published clinical trials. The dosage and administration regimen can be further adjusted for an individual patient by monitoring the level of HDL-C and/or LDL-C.

[0080] The optimal therapeutically effective amount of an oligonucleotide or composition of this invention may be determined experimentally, taking into consideration the exact mode of administration, the form in which the drug is administered, the indication toward which the administration is directed, the subject involved (*e.g.*, body weight, health, age, sex, etc.), and the preference and experience of the physician or veterinarian in charge.

[0081] As disclosed herein, the concentrations of the oligonucleotides administered in the present invention are both therapeutically effective and pharmaceutically acceptable. The oligonucleotides of the present invention are preferably used *in vivo* at 0.1-5 mg/kg of body weight, most preferably at 0.5-2 mg/kg of body weight.

[0082] Following methodologies which are well-established in the art, effective doses and toxicity of the oligonucleotides and compositions of the present invention, which performed well in *in vitro* tests, can be determined in studies using small animal models (*e.g.*, mice, rats) in

which they have been found to be therapeutically effective and in which these drugs can be administered by the same route proposed for the human trials.

[0083] For any pharmaceutical composition used in the methods of the invention, dose-response curves derived from animal systems can be used to determine testing doses for administration to humans. In safety determinations for each composition, the dose and frequency of administration should meet or exceed those anticipated for use in any clinical trial.

[0084] As disclosed herein, the dose of the oligonucleotide in the compositions of the present invention is determined to ensure that the dose administered continuously or intermittently will not exceed an amount determined after consideration of the results in test animals and the individual conditions of a patient. A specific dose naturally varies (and is ultimately decided according to the judgment of the practitioner and each patient's circumstances) depending on the dosage procedure, the conditions of a patient or a subject animal such as age, body weight, sex, sensitivity, feed, dosage period, drugs used in combination, seriousness of the disease, etc.

[0085] Toxicity and therapeutic efficacy of the compositions of the invention can be determined by standard pharmaceutical procedures in experimental animals, *e.g.*, by determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic index and it can be expressed as the ratio ED_{50}/LD_{50}.

[0086] The oligonucleotides of the invention can be formulated for parenteral, oral, topical, transdermal, transmucosal, intranasal, buccal administration, or by any other standard route of administration. Parenteral administration includes, among others, intravenous (i.v.), subcutaneous (s.c.), intraperitoneal (i.p.), intramuscular (i.m.), subdermal (s.d.), intradermal (i.d.), intra-articular, intra-synovial, intra-arteriole, intraventricular, intrathecal, intrasternal, intrahepatic, intralesional, or intracranial administration, by direct injection, via, for example, bolus injection, continuous infusion, or gene gun. A preferred route of administration according to the present invention will depend primarily on the indication being treated and includes, among others, topical, oral, subcutaneous, intravenous, and intranasal administration.

[0087] Formulations for injection can be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The compositions can take such forms

as suspensions, solutions or emulsions in oily or aqueous vehicles, and can contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient can be in powder form for reconstitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use. Suitable formulations for parenteral administration may contain substances which increase viscosity, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the formulation may also contain stabilizers. Additionally, the oligonucleotides of the present invention may also be administered encapsulated in liposomes. The oligonucleotide, depending upon its solubility, may be present both in the aqueous layer and in the lipidic layer, or in what is generally termed a liposomic suspension. The hydrophobic layer, generally but not exclusively, comprises phospholipids such as lecithin and sphingomyelin, steroids such as cholesterol, more or less ionic surfactants such a diacetylphosphate, stearylamine, or phosphatidic acid, and/or other materials of a hydrophobic nature.

[0088] For oral administration, the formulations of the invention can take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets can be coated by methods well known in the art. The compositions of the invention can be also introduced in microspheres or microcapsules, *e.g.*, fabricated from poly glycolic acid/lactic acid (PGLA) (see, U.S. Patent Nos. 5,814,344; 5,100,669 and 4,849,222; PCT Publication Nos. WO 95/11010 and WO 93/07861). Liquid preparations for oral administration can take the form of, for example, solutions, syrups, emulsions or suspensions, or they can be presented as a dry product for reconstitution with water or other suitable vehicle before use. Such liquid preparations can be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations can also contain buffer

salts, flavoring, coloring and sweetening agents as appropriate. Preparations for oral administration can be suitably formulated to give controlled release of the active compound.

[0089] For administration by inhalation, the therapeutics according to the present invention can be conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, *e.g.*, dichlorodifluoro-methane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit can be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator can be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

[0090] In addition to the formulations described previously, the compositions can also be formulated as a depot preparation. Such long acting formulations can be administered by implantation (for example, subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds can be formulated with suitable polymeric or hydrophobic materials (for example, as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Oligonucleotide Delivery

[0091] Compositions of the present invention can be delivered systemically or locally. If targeted delivery to a particular cell or tissue is desirable (e.g, liver), oligonucleotide conjugates or oligonucleotide delivery vectors containing antibodies to cell- or tissue-specific antigens can be used.

[0092] As specified above, some of the oligonucleotides of the present invention (*e.g.*, 15-mers and smaller) are small enough to enter cells without transfection or other methods of facilitating cell entry. Other oligonucleotides can be chemically modified (*e.g.*, by chemically linking them to a lipophilic moiety or other heterologous moiety) to enhance their cellular uptake. However, even these oligonucleotides may require specific delivery methods and delivery systems to ensure their efficient and targeted delivery to the tissue to be treated. Oligonucleotide delivery methods of the present invention include both local and systemic administration of stabilized nucleic acids, oligonucleotides incorporated into delivery vectors, and/or oligonucleotides conjugated to peptides or small molecules that are subsequently

transported into cells. Mechanical and electrical strategies for targeted oligonucleotide delivery include microinjection, particle bombardment, the use of pressure, and electroporation.

[0093] Nanoparticles, miRNA sponges and vector-mediated delivery approaches can be used. Vector-assisted oligonucleotide delivery systems include biological viral delivery systems and chemical non-viral delivery systems. Viral delivery systems include without limitation retroviruses, parvoviruses, adenoviruses, lentiviruses, adeno-associated viruses, herpes simplex virus, pseudovirions, etc. Non-viral delivery systems (which are clinically preferable due to lack of immune response and ease of formulation and assembly) include (i) polymeric delivery systems (oligonucleotide-polymer complexes) and (ii) liposomal delivery systems (oligonucleotides entrapped in and/or complexed to liposomes). Commonly used polymers in polymeric delivery systems include, for example, polyethylenimine (PEI), poly(L-lysine) (PLL), chitosans, and polyamidoamine (PANAM) dendrimers (*e.g.*, commercially available Superfect and Polyfect [Qiagen, Valencia, CA]). Agents such as folates, transferrin, antibodies, or sugars such as galactose and mannose can be also incorporated for tissue targeting.

[0094] Liposomal delivery systems include systems that deliver oligonucleotides either by entrapping them inside an aqueous core or complexing them to the phospholipid lamellae. Similarly to viral vectors, liposomes offer substantial protection to the oligonucleotide therapeutics from nucleases and improve their biological stability. Liposomes may also offer significant advantages over viral delivery options for the delivery of oligonucleotide therapeutics due to much lower immunogenicity (because they lack proteinaceous components) and their versatility. Since the phospholipid composition in the liposome bilayers can be varied, liposomal delivery systems can be easily engineered to yield a desired size, surface charge, composition, and morphology. Liposomes for oligonucleotide delivery according to the present invention can include a variety of cationic, anionic, synthetically modified lipids, and combinations thereof.

[0095] Examples of cationic lipids include without limitation 3β[N-(N',N'-dimethylaminoethane)-carbamoyl] cholesterol (DC-chol)/DOPE, 1,2-dioleoyl-3-trimethylammonium propane (DOTAP), N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride (DOTMA), 2,3-dioleoyloxy-N-[2-(sperminecarboxamido)ethyl]-N,N-dimethyl-1-propanaminium (DOSPA), dioctadecyl amido glycil spermine (DOGS), 3,[N-(N1,N-dimethylethylenediamine)-carbamoyl]cholesterol (DC-chol), polyethyleneimine (PEI),

polyamidoamine (PAMAM) dendrimers, and poly-L-lysine (PLL). Commonly used zwitterionic lipids, also known as helper lipids, are DOPE, 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC), and cholesterol. The cationic lipids in the liposomal formulation serve as an oligonucleotide complexation and condensation agents during the formation of the lipoplex. The positive charge also helps in cellular association. The zwitterionic lipids help in membrane perturbation and fusion. Proprietary formulations of cationic lipids such as Lipofectamine (Invitrogen, Carlsbad, CA), Effectene (Qiagen, Valencia, CA), and Tranfectam (Promega, Madison, WI) are commercially available.

[0096] Examples of anionic lipids include without limitation DPPC and 1,2-dimyristoyl-sn-glycero-3-[phospho-rac-(1-glycerol)] (DMPG). LPDII vectors can be also used for delivery of the oligonucleotides of the present invention. These are non-viral delivery vehicles that consist of a complex between anionic pH-sensitive liposomes and polycation-condensed oligonucleotides (polyplexes). Another useful delivery vehicle can be composed of a mixture of anionic lipid 1,2-dioleoyl-sn-glycero-3-[phospho-rac-(1-glycerol)] (sodium salt) (DOPG) and zwitterionic lipid DOPE.

[0097] Other useful specialized liposomal delivery platforms include pH-sensitive liposomes, immunoliposomes, and stealth liposomes. pH-sensitive liposomes can be generated by the inclusion of DOPE or citraconyl-DOPE or phosphatidylcholine/glycyrrhizin combination into liposomes composed of acidic lipids such as cholesterylhemisuccinate or oleic acid. At the neutral cellular pH 7, these lipids have the typical bilayer structure; however, upon endosomal compartmentalization they undergo protonation and collapse into a non-bilayer structure, thereby leading to the disruption and destabilization of the endosomal bilayer, which in turn helps in the rapid release of the oligonucleotide into the cytoplasm. Immunoliposomes incorporate functionalized antibodies attached to lipid bilayers and thus target specific receptors and facilitate receptor-mediated endocytosis for the uptake of the lipoplex. Stealth liposomes are sterically stabilized liposomal formulations that include polyethylene glycol (PEG)-conjugated lipids. Pegylation prevents the opsonization and recognition of the liposomal vesicles by the reticuloendothelial system. Consequently, stealth liposomes have long circulating times in the systemic circulation.

[0098] Liposomes useful for oligonucleotide delivery according to the present invention can take a shape of multilamellar vesicles (MLV) formed by reconstituting thin lipid films in buffer. Small unilamellar vesicles (SUV) of specific size (100-500 nm) can be produced by extruding MLV through polycarbonate membranes. SUV (50-90 nm) can also be produced by sonication of MLV or larger SUV.

[0099] Transmembrane permeation of the oligonucleotides of the invention can be also enhanced by inclusion of cell penetrating peptides (CPPs; also termed "peptide transduction domain" (PTD)) in the delivery vehicles or covalent oligonucleotide conjugation to such peptides. Conjugated CPPs are also contemplated for use as a heterologous moiety of the present invention. CPPs/PTDs are a class of small cationic peptides of approximately 10-30 amino acids in length that have been shown to engage the anionic cell surface through electrostatic interactions and rapidly induce their own cellular internalization through various forms of endocytosis. Examples of useful CPPs/PTDs include TAT peptide, penetratin, an Antennepedia domain, transportan, poly-arginine, and MPG.

[00100] Other compounds useful in delivery of the oligonucleotides of the present invention include cyclodextrins (CyDs), porphyrin derivatives, branched chain dendrimers, polyethylenimine polymers, nanoparticles, microspheres, and polylysine conjugates with vector proteins such as asialofetuin or transferrin.

[00101] Preferred methods of oligonucleotide delivery according to the present invention include Lipofectamine 2000 or Lipofectamine RNAiMAX (Invitrogen) (used to transfect oligonucleotides into cells), antibodies, peptides, liposomes, and nanoparticles. Other methods include addition of naked oligonucleotides.

[00102] More information on useful delivery vehicles and methods can be obtained from recent reviews such as, *e.g.*, Meade and Dowdy, Adv Drug Deliv Rev., 2008, 60(4-5): 530-6; Juliano et al., Nucleic Acids Res., 2008, 36(12): 4158-71; Lysik and Wu-Pong, J. Pharmaceutical Sciences, 2003, 92: 1559; Dass, J., Pharmacy Pharmacol., 2002, 54 (1): 3-27, and references cited therein. See also Lorenz et al., Bioorg Med Chem Lett., 2004, 14(19): 4975-7; Dalby et al., Methods, 2004 33(2): 95-103; Hassani et al., J. Gene Med., 2005, 7(2): 198-207; Pirollo et al., Hum Gene Ther., 2006, 17(1): 117-24; Jaaskelainen et al., Eur J Pharm Sci., 2000,

10(3): 187-93; Urban-Klein et al., Gene Ther., 2005, 12(5): 461-6; Zhou et al., Chem. Commun. (Camb), 2006. 22: 2362-4; Leng et al., J. Gene Med., 2005, 7(7): 977-86.

[00103] *In vivo* nuclease degradation of oligonucleotides of the invention can be circumvented by chemical derivatization of the backbone and/or by the protection and stability offered by the above-described vector delivery systems. As discussed above, various chemical modifications to the backbone can be used to improve oligonucleotide stability. The most common modifications include the introduction of phosphorothioate and/or methyl phosphonate linkages in the backbone. Phosphorothioate analogs are chosen for their stability against nucleases and the methylphosphonate backbone for its relative hydrophobicity and ease of diffusion across membranes. Mixed-backbone oligonucleotides can also be used. To ensure protection of the oligonucleotides of the invention from the endosomal degradation upon intracellular delivery, viral delivery vectors or pH-sensitive and cationic liposome delivery systems (*e.g.*, including fusogenic lipids such as 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE)). Lysosomatropic agents such as monensin and chloroquine, which raise the endosomal pH, block acidification, and thus inhibit lysozyme activity, can also be used to facilitate endosomal release of the oligonucleotides of the invention. In addition, endosomal degradation of oligonucleotides can be circumvented by the incorporation of viral peptides such as hemagglutinin HA2 and those derived from adenoviruses in their delivery systems or by using fusogenic peptides such as poly(L-lysine) (PLL) and cationic polymers such as polyethylenimine (PEI) and dendrimers. See the review by Patil et al., AAPS J., 2005, 7(1): E61-E77 and references cited therein.

Therapeutic Methods of the Invention

[00104] In conjunction with the novel oligonucleotides of the present invention, provided herein are methods of treatment using such oligonucleotides. Specifically, the invention provides a method for treating a disease in a subject in need thereof, which method comprises administering to the subject a therapeutically effective amount of one or more oligonucleotides of the invention or a composition comprising such one or more oligonucleotide(s). Non-limiting examples of the diseases treatable by the method of the invention include dyslipidemias (such as, e.g., hyperlipidemia [elevated lipid levels], hypercholesterolemia [elevated cholesterol levels], low HDL/LDL ratio) and cardiovascular diseases (such as, e.g., atherosclerosis, coronary artery

disease, coronary heart disease, conditions associated with coronary artery disease or coronary heart disease [e.g., angina, myocardial infarction], transient ischemic attack, stroke). In a preferred embodiment, the subject is human.

EXAMPLES

[00105] The present invention is further described by way of the following particular examples. However, the use of such examples is illustrative only and is not intended to limit the scope or meaning of this invention or of any exemplified term. Nor is the invention limited to any particular preferred embodiment(s) described herein. Indeed, many modifications and variations of the invention will be apparent to those skilled in the art upon reading this specification, and such "equivalents" can be made without departing from the invention in spirit or scope. The invention is therefore limited only by the terms of the appended claims, along with the full scope of equivalents to which the claims are entitled.

EXAMPLE 1

Materials and Methods

[00106] The LDLR-GFP plasmid was provided by Dr. Peter Tontonoz (UCLA, Los Angeles, CA). Chemicals were obtained from Sigma-Aldrich unless otherwise noted. The synthetic LXR ligand T0901217 (T090) was purchased from Cayman Chemical. Human ApoA1 was obtained from Meridian Life Sciences. Lipoprotein-deficient serum (LPDS) was prepared from FBS delipidated with 4% fumed silica. 1,1'-Dioctadecyl-3,3,3,3'-tetramethylindocarbocyanineperclorate (DiI) was purchased from Molecular Probes (Invitrogen). A mouse monoclonal antibody against ABCA1 was purchased from Abcam. A rabbit polyclonal antibody against LDLR was obtained from Cayman Chemical and a mouse monoclonal antibody against HSP90 was purchased from BD Bioscience. A mouse monoclonal antibody against LDLR was obtained from Santa Cruz. Secondary fluorescently labeled antibodies were from Molecular Probes (Invitrogen). miRNA mimics and inhibitors were obtained from Life Technologies. siRNAs were purchased from Dharmacon and locked nucleic acid (LNA) miRNA detection probes were purchased from Exiqon (Woburn, MA). For in vivo experiments, in vivo locked nucleic acid (LNA)^{TM} miRNA inhibitors against mmu-miR-148a-3p (5'-TTCTGTAGTGCACTG-3'; SEQ ID NO: 52), mmu-miR-27b-3p (5'-

AACTTAGCCACTGTGA-3'); SEQ ID NO: 54) or scrambled control (5'-ACGTCTATACGCCCA-3'; SEQ ID NO: 51) were purchased from Exiqon.

Cell Culture

[00107] Human (Huh7) and mouse (Hepa) hepatic cells and monkey kidney fibroblast (COS7) and Hela cells were obtained from American Type Tissue Collection. Huh7, Hepa and COS7 cells were maintained in Dulbecco's Modified Eagle Medium (DMEM) containing 10% fetal bovine serum (FBS) and 2% penicillin-streptomycin in 10 cm^2 dishes at 37°C and 5% CO_2. For DiI-LDL uptake and binding experiments, Huh7 cells were cultured in DMEM containing 10% LPDS and incubated with 30 μg/ml DiI-LDL cholesterol. For analysis of miR-27b and miR-148a expression, Huh7 cells were cultured in DMEM containing 10% LPDS and left untreated or treated with nLDL (120 μg/ml) for 24h. For analysis of miR-148a expression, Huh7 cells were cultured in DMEM 10% FBS and transfected with 1 μg pcDNA3.1-2xFLAG-SREBP-1c (Addgene) or 1 μg pcDNA empty vector for 24h using Lipofectamine LTX (Invitrogen).

[00108] Hepatocytes were isolated from 8-week old male mice by isopynic centrifugation as previously described (Gao, 2013and Birmingham 2009). On day zero, isolated hepatocytes were plated on six-well collagen-I-coated dishes (400,000 cells/well) in 2 ml Adherence culture medium (William's E medium supplemented with 5% fetal bovine serum, 10 mM HEPES buffer, 2 mM L-glutamine, 8 μg/ml Gentamicin, 1 μM Dexamethasone and 1 nM insulin). After incubation at 37°C and 5% CO_2 for 4-6h, the attached cells were washed once in 1x PBS and then incubated at 37°C and 5% for 14-16h in 2 ml Basal maintenance media (William's E medium supplemented with 5% LPDS, 2 mM L-glutamine, 8 μg/ml Gentamicin, 1 μM Dexamethasone and 1 nM insulin). On day one, cells in each well were washed once with 1x PBS, and supplemented with 2 ml fresh maintenance media without insulin with or without 3 μM T090 or 30 nM insulin. After incubation for 6h (insulin experiments) or 12h (T090 experiments) at 37°C, cells were harvested for RNA extraction, immunobloting and northern blotting.

miRNA Screen

[00109] All steps of the genome-wide miRNA screen, including reverse transfection and im age acquisition and analysis, were performed at the NYU RNAi Core Facility (NYU School of Medicine).

[00110] Reverse Transfection, Fixation and Staining. Huh7 cells were reverse transfected in triplicate with a library of 1719 miRNA mimics (Life Technologies *mir*Vana Mimic Library, miRBase release 17.0) in Corning 384-well flat clear-bottom black plates (Fisher Scientific) using a standard reverse transfection protocol. Briefly, Huh7 cells (5,000 cells/well in 30 µl of DMEM media containing 10% LPDS) were seeded into a well containing 30 µl of transfection mix (25 µl of Optimem, 0.07 µl RNAi Max (Invitrogen), and 5 µl of 0.3 µM miRNA or control siRNA). 20 µl of fresh LPDS media was added to all wells 12h post transfection, giving a final mimic concentration of 18 nM. 48h later, cells were incubated with 10 µl of fresh LPDS containing 30 µg/ml of DiI-LDL for 8h at 37°C. Following incubation, cells were washed twice with 1x PBS and fixed with 4% PFA for 15 min. After three subsequent washes with 1x PBS, cells were incubated with PBS containing 1 µg/ml Hoechst (Molecular Probes) for 25 min. Before scanning, a final wash with 1xPBS was performed and plates were spun down to minimize contaminants when imaging with the automated microscope. All liquid handling steps, including seeding, diI-LDL incubation, fixation, washing, and Hoechst incubation were performed using a Wellmate Microplate Dispenser (Matrix Technologies) and BioTek Plate Washer (PerkinElmer). The triplicate screen consisted of fifteen 384-well plates and was completed over the course of four days.

[00111] Image Acquisition and Analysis. Automated high content and throughput images were acquired using an Arrayscan VTI HCS Reader (Thermo Scientific) with a Zeiss 10x objective. 384-well plates were loaded onto the microscope using a Catalyst Express robotic arm and imaged overnight. In each well, cell nuclei and DiI-LDL intensities were imaged in 5 pre-defined fields. Image data was analyzed using BioApplication's Target Activation V3 image analysis software (Thermo Scientific). Briefly, nuclei were first identified on the Hoechst stain (Channel 1). Following this, cell boundaries were estimated using the geometric segmentation method and used to calculate DiI intensity (Channel 2) within each cell. In total, valid object count, mean average intensity, and total average intensity of DiI were recorded for each field. For the primary screen, 57,600 images, consisting of on average 533,528 objects/plate, were analyzed.

[00112] Hit Classification. miRNAs were scored based on their ability to significantly increase or decrease DiI intensity compared to negative controls. Cytotoxic miRNA overexpression phenotypes were filtered for hit classification by excluding wells in which fewer then 500 cells were identified as valid objects. In addition, 32 validated internal controls, including non-silencing (NS) siRNA and siLDLR (**Figure 1**), as well as the negative control miRNAs and siRNA KIF11 (Life Technolgogies) were used on each plate to monitor transfection efficiency. After confirming efficient transfection efficiency, mean average intensities of each well were normalized to plate medians and converted to robust Z-scores using Matlab, as previously described(Birmingham, Selfors et al. 2009). Robust Z-scores were compared between each plate replicate and the mean of each score was calculated and used to rank potential candidates. Those miRNAs that had a robust Z-score of $\leq$-0.8 (423, 25% of miRNAs screened) were chosen for further characterization. To narrow down candidate miRNA genes, hits were subjected to several screening passes (**Figure 1A,** *lower panel*). Briefly, these candidates were filtered based on whether they were predicted to target the LDLR (40 miRNAs, 2% of miRNAs screen), the binding sites were conserved (16 miRNAs, 0.93% of miRNAs screened), they were highly expressed in mouse or human liver (4 miRNAs, 0.23% of miRNAs screened), they responded to dietary cholesterol (3 miRNAs, 0.16% of miRNAs screened), and had high liver activity (2 miRNAs, 0.12% of miRNAs screened).

Bioinformatic Analysis of miRNA Target Genes.

[00113] Target genes for hsa-miR-27b and hsa-miR-148a were identified and compared using the online target prediction algorithm, miRWalk (http://www.umm.uni-heidelberg.de/apps/zmf/mirwalk/), which provides target interaction information from eight different prediction algorithms. Specifically, the programs miRanda, miRWalk and TargetScan were used. Putative targets produced by all three of these algorithms for miR-27b (2,929 targets) and miR-148a (2,217 targets) were uploaded into DAVID v6.7 for functional annotation clustering (Huang da, 2009a and Huang da, 2009b). "High" classification stringency settings yielded 447 functional annotation clusters for miR-27b and 398 functional annotation clusters for miR-148a, of which 78 clusters (miR-148a) and 77 clusters (miR-27b) were highly enriched ($E \geq 1.0$). In another set of analyses, the present inventors took the putative targets for miR-27b and miR-148a identified above and uploaded them into the gene classification system,

PANTHER v8.0 (Thomas, 2003 and Mi 2010) to identify gene targets that were mapped to the lipid metabolic process (GO:0006629). The functional interactions of these predicted targets (150 for miR-27b and 110 for miR-148a) described in STRING v9.05 (Franceschini, 2013) were then combined with the functional annotation groups described in DAVID. Matlab and Cytoscape v2.8.3 were used to create the visualization networks, as previously described(Mercer, Snijder et al. 2012). STRING interactions with a confidence score of 0.4 or higher were added and highlighted in grey (**Figure 9**). Smaller annotation clusters and unconnected genes were left out of the visualization due to space constraints.

siRNA and miRNA Mimic/Inhibitor Transfections

[00114] For siRNA transfections, Huh7 cells were transfected with 60 nM of SMARTpool ON-TARGETplus LDLR siRNA or 60 nM of ON-TARGETplus Non-Targeting pool (Dharmacon) for 48h in LPDS medium. Verification of LDLR knockdown was assessed by Western blotting, as described below. For mimic and inhibitor transfections, Huh7 and Hepa cells were transfected with 40 nM *mirVana*™ miRNA mimics (miR-27b and miR-148a) or with 60 nM *mirVana*™ miRNA inhibitors (Inh-27b and Inh-148a) (Life Technologies) utilizing RNAimax (Invitrogen) or Lipofectamine 2000 (Invitrogen). All experimental control samples were treated with an equal concentration of a non-targeting control mimic sequence (CM) or inhibitor negative control sequence (CI) for use as controls for non-sequence-specific effects in miRNA experiments. Verification of miR-27b and miR-148a over-expression and inhibition was determined using qRT-PCR, as described below.

RNA isolation and Quantitative Real-Time PCR

[00115] Total RNA was isolated using TRIzol reagent (Invitrogen) according to the manufacturer's protocol. For mRNA quantification, cDNA was synthesized using iScript RT Supermix (Bio-Rad), following the manufacturer's protocol. Quantitative real-time PCR (qRT-PCR) analysis was performed in triplicate using iQ SYBR green Supermix (BioRad) on an iCycler Real-Time Detection System (Eppendorf). The mRNA level was normalized to GAPDH or 18S as a house keeping gene. The human primer sequences used were: GAPDH, 5'-TTGATTTTGGAGGGATCTCG-3' (SEQ ID NO: 11) and 5'-CAATGACCCCTTCATTGACC-3' (SEQ ID NO: 12); LDLR, 5'-TGATGGGTTCATCTGACCAGT-3' (SEQ ID NO: 13) and 5'-AGTTGGCTGCGTTAATGTGAC-3' (SEQ ID NO: 14); LDLRAP1 5'-

ATCGTGGCTACAGCTAAGGC-3' (SEQ ID NO: 15) and 5'-CAAACACCTTGTCGTGCATC-3' (SEQ ID NO: 16); and ABCA1, 5'-TGTCCTCATACCAGTTGAGAGAC-3' (SEQ ID NO: 17) and 5'-GGTGATGTTTCTGACCAATGTGA-3' (SEQ ID NO: 18); The mouse primers sequences used were: LDLR, 5'-GGTACTGGCAACCACCATTGGG-3' (SEQ ID NO: 19) and 5'-GCCAATCGACTCACGGGTTCAG-3' (SEQ ID NO: 20); 18S, 5'-TTCCGATAACGAACGAGACTCT-3' (SEQ ID NO: 21) and 5'-TGGCTGAACGCCACTTGTC-3' (SEQ ID NO: 22); ABCA1, 5'-GGTTTGGAGATGGTTATACAATAGTTGT-3' and 5'-CCCGGAAACGCAAGTCC-3'; SREBP1c, 5'-GGAGCCATGGATTGCACATT-3' and 5'-ACAAAGTTGCTCTGAAAACAAATCA-3'; and FASN, 5'-GGAGGTGGTGATAGCCGGTAT-3' and 5'-TGGGTAATCCATAGAGCCCAG-3'. For miRNA quantification, total RNA was reverse transcribed using the miScript II RT Kit (Qiagen). Primers specific for human and mouse pre-miR-27b, pre-miR-148a, miR-27b and miR148a (Qiagen) were used and values normalized to SNORD68 (Qiagen) as a housekeeping gene. For pri-miRNA quantification, cDNA was synthesized using TaqMan® reverse transcription reagents (Applied Biosystems), following the manufacturer's protocol. For pri-miR-148a, quantitative real-time PCR was performed in triplicate using TaqMan Universal Master Mix (Applied Biosystems) on a Real-Time PCR System (Applied Biosystems). Primers for human and mouse miR-148a were obtained from Applied Biosystems. For pri-miR-27b quantification, quantitative real-time PCR was performed in triplicate using SYBR Green Master Mix (SA Biosciences) on an iCycler Real-Time Detection System (Eppendorf). Primer sequences used for human pri-miR-27b were: 5'-GTTCCTGGCATGCTGATTTG-3' (SEQ ID NO: 23) and 5'-CTAAGCTCTGCACCTTGTTAGA-3' (SEQ ID NO: 24) and primer sequences for mouse pri-miR-27b were: 5'-GTTCCTGGCATGCTGATTTG-3' (SEQ ID NO: 25) and 5'-CTAAGCTCTGCACCTTGTTAGA-3' (SEQ ID NO: 26). The pri-miRNA levels were normalized to 18S (Applied Biosystems) as a housekeeping gene.

[00116] For mouse tissues, total liver RNA from C57BL/6 mice (fed a chow or Western diet), from *LDLR-/+; ApoB* Tg mice, from *ob/ob* mice, or from *Tg-SREBP1c* mice was isolated using the Bullet Blender Homogenizer (Next Advance) in TRIzol. 1 μg of total RNA was reverse transcribed and gene/miRNA expression assessed as above.

Western blot analysis

[00117] Cells were lysed in ice-cold buffer containing 50 mM Tris-HCl, pH 7.5, 125 mM NaCl, 1% NP-40, 5.3 mM NaF, 1.5 mM NaP, 1 mM orthovanadate and 1 mg/ml of protease inhibitor cocktail (Roche) and 0.25 mg/ml AEBSF (Roche). Cell lysates were rotated at 4°C for 1h before the insoluble material was removed by centrifugation at 12000 x *g* for 10 min. After normalizing for equal protein concentration, cell lysates were resuspended in SDS sample buffer before separation by SDS-PAGE. Following overnight transfer of the proteins onto nitrocellulose membranes, the membranes were probed with the following antibodies: ABCA1 (1:1000), LDLR (1:500), and HSP90 (1:1000). Protein bands were visualized using the Odyssey Infrared Imaging System (LI-COR Biotechnology). Densitometry analysis of the gels was carried out using ImageJ software from the NIH (Schneider, 2012 #219).

Northern blot analysis

[00118] miRNA expression was assessed by Northern blot analysis as previously described (Chamorro-Jorganes, 2014 #218). Briefly, total RNA (5 ug) was separated on a 15% acrylamide TBE 8M urea gel and blotted onto a Hybond N+ nylon filter (Amersham Biosciences). DNA oligonucleotides complementary to mature miR-148a-3p (5'-ACAAAGTTCTGTAGTGCACTGA-3' [SEQ ID NO: 56]) were end-labeled with [a-^{32}P] ATP and T_4 polynucleotide kinase (New England Biolabs) to generate high-specific activity probes. Hybridization was carried out according to the ExpressHyb (Clontech) protocol. Following overnight membrane hybridization with specific radiolabeled probes, membranes were washed once for 30 min at 42°C in 4x SSC/0.5% SDS and subjected to autoradiography. Blots were reprobed for 5s rRNA (5'-CAGGCCCGACCCTGCTTAGCTTCCGAGAGATCAGACGAGAT-3' [SEQ ID NO: 57]) to control for equal loading.

LDL receptor activity assays

[00119] Human LDL was isolated and labeled with the fluorescent probe DiI as previously reported (Calvo, Gomez-Coronado et al. 1998). Huh7 cells were transfected in 6- or 12-well plates with miRNA mimics and inhibitors in DMEM containing 10% LPDS for 48h. Then, cells were washed once in 1x PBS and incubated in fresh media containing DiI-LDL (30 µg cholesterol/ml). Non-specific uptake was determined in extra wells containing a 50-fold

excess of unlabeled native LDL (nLDL). Cells were incubated for 8h at 37°C to allow for DiI-LDL uptake in screening optimization experiments and for 2h at 37°C for subsequent validation experiments. In other instances, cells were incubated for 30 min at 4°C to assess DiI-LDL binding. At the end of the incubation period, cells were washed, resuspended in 1 ml of PBS and analyzed by flow cytometry (FACScalibur, Becton Dickinson), as previously described(Suarez, Fernandez et al. 2004). The results are expressed in terms of specific median intensity of fluorescence (M.I.F.) after subtracting autofluorescence of cells incubated in the absence of DiI-LDL.

Fluorescence Microscopy

[00120] For LDLR-Ab internalization and DiI-LDL uptake assays, Huh7 cells were grown on coverslips and transfected with a miR-27b mimic, miR-148a mimic or negative control mimic (CM) in DMEM containing 10% LPDS. 48h post transfection, cells were cooled to 4°C for 20 min to stop membrane internalization. Cells were then incubated with LDLR mAb (C7) (Santa Cruz) and 30 μg/ml DiI-LDL for 40 min at 4°C. Following incubation, cells were gently washed twice with cold medium and shifted to 37°C to allow for internalization of both LDLR-Ab complexes and DiI-LDL for the indicated times and fixed with 4% PFA. After 5 min of Triton X-100 0.2% permeabilization and 15 min of blocking (PBS BSA 3%), cells were stained with anti-mouse Alexa 488 (Molecular Probes) and TO-PRO 3 (Life Technologies) for 1h at room temperature. After this, cells were washed twice with 1x PBS and mounted on glass slides with Prolong-Gold (Life Technologies).

[00121] For LDLR-GFP rescue experiments, Huh7 cells were grown on coverslips and co-transfected with 1 μg LDLR-GFP and 40 nM of a control mimic CM, miR-27b mimic or miR-148a mimic. 48h post transfection cells were incubated with 30 μg/ml DiI-LDL for 2h at 37°C (uptake) or with 30 μg/ml DiI-LDL for 90 min at 4°C (binding). Then, cells were washed twice with 1x PBS, fixed with 4% PFA, and blocked (3% BSA in 1x PBS) for 15 min. Following this, cells were washed twice and mounted on glass slides with Prolong-Gold (Life Technologies). All images were analyzed using confocal microscopy (Leica SP5 II) equipped with a 63X Plan Apo Lenses. All gains for the acquisition of comparable images were maintained constant. Analysis of different images was performed using ImageJ (NIH) and Adobe Photoshop CS5.

3'UTR Luciferase Reporter Assays

[00122] cDNA fragments corresponding to the entire 3'UTR of human *LDLR*, *ABCA1* and *LDLRAP1* were amplified by RT-PCR from total RNA extracted from HepG2 cells with XhoI and NotI linkers. The PCR product was directionally cloned downstream of the *Renilla* luciferase open reading frame of the psiCHECK2™ vector (Promega) that also contains a constitutively expressed firefly luciferase gene, which is used to normalize transfections. Point mutations in the seed region of the predicted miR-27b and miR-148a binding sites within the 3'UTR of *LDLR*, *ABCA1* and *LDLRAP1* were generated using the Multisite-Quickchange Kit (Stratagene), according to the manufacturer's protocol. All constructs were confirmed by sequencing. COS7 cells were plated into 12-well plates and co-transfected with 1 μg of the indicated 3'UTR luciferase reporter vectors and miR-27b mimics , miR-148a mimics, or control mimics (CM) (Life Technologies) utilizing Lipofectamine 2000 (Invitrogen). Luciferase activity was measured using the Dual-Glo Luciferase Assay System (Promega). *Renilla* luciferase activity was normalized to the corresponding firefly luciferase activity and plotted as a percentage of the control (cells co-transfected with the corresponding concentration of control mimic). Experiments were performed in triplicate wells of a 12-well plate and repeated at least three times.

miR-148a promoter assays

[00123] The promoter region (2.3 kb) of miR-148a was amplified by PCR from BAC clone RPCI-11-184C17 and cloned into a PGL3 promoter vector (Promega) using KpnI and HindIII linkers. The primers were: 5'-TGATGGCAGACAATAACTCC-3' and 5'-AAAGTGCTTTCCCATCTTCC-3'. All constructs were confirmed by sequencing. For some experiments, Hela cells were plated into 12-well plates and co-transfected with 0.5 μg of miR-148a promoter and 0.01 μg of *Renilla* luciferase reporter plasmid and 0.5 μg of pcDNA3.1-2xFLAG-SREBP1c or pcDNA3.1 empty control using Lipofectamine 2000. Cells were collected 24h later. In another set of experiments, Huh7 cells were transfected with 0.5 μg of miR-148a promoter and 0.01 μg of Renilla luciferase reporter plasmid using Lipofectamine LTX. Following 24h transfection, cells were stimulated with 3 μM T090 (12h) or 100 nM insulin (8h). Luciferase activity was measured using the Dual-Glo Luciferase Assay System (Promega). *Renilla* luciferase activity was normalized to the corresponding firefly luciferase activity and

plotted as a percentage of the control (cells co-transfected with the corresponding concentration of empty control or vehicle treated cells). Experiments were performed in triplicate wells of a 12-well plate and repeated at least three times.

Cholesterol Efflux Assays

[00124] Huh7 cells were seeded at a density of 2 x 10^5 cells per well and transfected with either a control mimic (CM) or miR-27b mimic or miR-148a mimic or a control inhibitor (CI) or miR-148a inhibitor (Inh-148a). Following 48h of transfection, cells were either loaded with 0.5 μCi/ml ^{3}H-cholesterol for 24h. 12h after loading, cells were incubated with 3 μM T090 to increase the expression of ABCA1. Then, cells were washed twice with PBS and incubated in DMEM supplemented with 2 mg/ml fatty-acid free BSA (FAFA-media) in the presence of an ACAT inhibitor (2 μmol/L) for 4h prior to the addition of 50 μg/ml human ApoA1 in FAFA-media with or without the indicated treatments. Supernatants were collected after 6h and expressed as a percentage of total cell ^{3}H-cholesterol content (total effluxed ^{3}H-cholesterol+cell-associated ^{3}H-cholesterol).

Cellular Cholesterol Measurements

[00125] Huh7 cells were seeded at a density of 5 x 10^5 cells/well and transfected with either a control mimic (CM), miR-27b mimic, miR-148a mimic or a control inhibitor (CI), miR-27b inhibitor (Inh-27b), or miR-148a inhibitor (Inh-148a). Following 48h transfection, cells were incubated with 30 μg/ml nLDL for 2h. Intracellular cholesterol content was measured using the Amplex Red Cholesterol Assay Kit (Molecular Probes, Invitrogen), according to the manufacturer's instructions.

AAV8-Pre-miR-27b Vector

[00126] mmu-pre-miR-27 (accession MI000142) was subcloned into an AAV8 vector and its expression was regulated under the control of a liver-specific thyroxine-binding globulin (TBG) promoter, as previously described (Kassim, Li et al. 2013). The AAV8 particles (AAV8.TBG.PI.mir27b.rBG) were generated at the University of Pennsylvania's Penn Vector Core. An empty AAV8 (AAV8.TBG.PI.Null.bGH), also provided by the Penn Vector Core, was used as a control in all experiments.

Mouse Studies

[00127] Eight-week-old male C57BL/6 mice were purchased from Jackson Laboratories (Bar Harbor, ME, USA) and kept under constant temperature and humidity in a 12h controlled dark/light cycle. For miR-27b overexpression studies, mice were randomized into 2 groups: non-targeting AAV8 (AAV-Null, *n*=10) and pre-miR-27b AAV8 (AAV- 27b, *n*=10). In one set of experiments (see **Figure 7A**), mice fed a chow diet were treated once with $5X10^{12}$ GC/kg AAV-Null (*n=5*) or $5X10^{12}$ GC/kg (*n*=5) in PBS by retro-orbital injection. Blood samples were collected at 0, 2 and 4 weeks after treatment for lipid analysis and lipoprotein profile measurements (see below). Then mice were sacrificed, and hepatic gene expression and liver histology were analyzed (see above). In another set of experiments, mice were challenged with a Western diet [(WD) 9.5% casein, 0.3% DL-Methionine, 15% cornstarch, 40% sucrose, 5% cellulose, 21% anhydrous milk fat, 3.5% mineral mix, 1% vitamin mix, 0.4% calcium carbonate and 0.3% cholesterol] after 4 weeks of treatment with AAV-Null or AAV-27b, as outlined in **Figure 7L**. Following 2 weeks of diet, blood was collected for lipid analysis and lipoprotein measurements. Mice were then sacrificed for gene expression analysis and liver histology. All animal experiments were approved by the Institutional Animal Care Use Committee of New York University Medical Center.

[00128] For miR-148a inhibition experiments, 8-week old male *LDLR-/+;ApoB* Tg mice (Taconic) were randomized into 3 groups: LNA control (*n*=7), LNA anti-miR-148a (*n*=7) or LNA-anti-miR-27b. Mice received i.p. injections of 5 mg/kg LNA control (5'-ACGTGTATACGCCCA-3'; SEQ ID NO: 51), LNA anti-miR-148a (5'-TTCTGTAGTGCACTG-3'; SEQ ID NO: 52), or LNA anti-miR-27b (5'-AACTTAGCCACTGTGA-3'); SEQ ID NO: 54) oligonucleotides every three days for a total of two weeks (see **Figure 12A**). Twenty-four hours after the final injection, mice were sacrificed and hepatic gene expression analyzed (see above). Blood samples were collected at day 1 and day 14 for lipid analysis (see below).

[00129] "Obese" (C57BL/6J-*ob/ob*) mice were purchased from Jackson Laboraties. In one set of experiments 5 male wild-type and 5 *ob/ob* mice were studied at 13 weeks of age. In another set of experiments, transgenic mice that overexpress the truncated form of human SREBP1c (amino acids 1-436) in the liver under the control of the PEPCK promoter were used (Shimano, 1997 #222). For these experiments 5 male wild-type and 5 male *Tg-SREBP1c* were

studied at 12-weeks of age. Mice were maintained and sacrificed as previously described(Shimomura, 1999 #221).

[00130] For HFD studies, six-week old male C57BL6 (Jackson Laboratories) were placed on a chow diet or HFD containing cholesterol and 21% (wt/wt) fat (from Dyets Inc) for 12 weeks. At sacrifice, mice were fasted for 12-14h before blood samples were collected by retro-orbital venous plexus puncture. Liver samples were collected and stored at -80°C and total RNA was harvested for miRNA and gene expression analysis.

Plasma Lipid Analysis and Lipoprotein Profile Measurements

[00131] In the chow diet studies, mice were fasted for 12-14h before blood samples were collected by retro-orbital venous plexus puncture. Plasma was separated by centrifugation and stored at -80°C. Total plasma cholesterol and HDL-cholesterol were enzymatically measured with the Cholesterol Assay Kit (Wako Diagnostics), according to the manufacturer's instructions. Total triglycerides were measured with the Wako Diagnostics Triglycerides Reagent. The lipid distribution in plasma lipoprotein fractions was assessed by fast-performance liquid chromatography (FPLC) gel filtration with 2 Superose 6 HR 10/30 columns (Pharmacia). Cholesterol in each fraction was enzymatically measured using the Amplex Red Cholesterol Assay Kit (Molecular Probes, Invitrogen). In another set of experiments, mice were fed with a WD for 2 weeks and blood samples were collected in non-fasting and fasting (3h) conditions. Lipid analysis and lipoprotein fractionation were performed as described above.

Statistics

[00132] All data are expressed as mean ±SEM. Statistical differences were measured using either an unpaired Student's *t* test or 2-way ANOVA with Bonferroni correction for multiple comparisons when appropriate. A value of $P \leq 0.05$ was considered statistically significant. Data analysis was performed using GraphPad Prism Software Version 5.0a (GraphPad, San Diego, CA). $*P \leq 0.05$.

RESULTS

Primary miRNA screen design and optimization

[00133] To systematically identify miRNAs that regulate LDLR activity, the present inventors developed an automated, high-throughput microscope-based screening assay that

monitored the effect of miRNA overexpression on DiI-LDL uptake in human hepatic (Huh7) cells. In order to avoid confounding effects of lipoproteins in the media, the present inventors initially characterized the specific uptake of DiI-LDL in Huh7 cells incubated in 10% lipoprotein deficient serum (LPDS). To this end, the changes in LDLR activity were analyzed in Huh7 cells treated with increasing concentrations of DiI-LDL for 8h. The cell-associated DiI-fluorescence was determined at the end of the incubation period by flow cytometry. As seen in **Figures 8A-D**, DiI-LDL uptake kinetics were saturable and showed complete saturation at approximately 20-40 μg/ml DiI-LDL cholesterol, which is in accordance with the well-known kinetic properties of the LDLR (Brown, Dana et al. 1973, Goldstein, Basu et al. 1976). Similar results were observed when cells were cultured in 384-well plates and fluorescence intensity was measured with automated fluorescent microscopy (**Figures 8E-G**). Importantly, LDL uptake was specific, as DiI accumulation was displaced when cells were incubated in the presence of 30x unlabeled LDL (**Figure 8G**). The inventors further analyzed whether this system was suitable for functional genomic studies by assessing LDLR gene inactivation by RNA interference (RNAi). As expected, treatment of Huh7 cells with siRNA LDLR (siLDLR) significantly reduced LDLR expression at the protein level (**Figure 8E**). Consistent with this, DiI-LDL uptake was also diminished in siLDLR-treated Huh7 cells compared to cells transfected with a non-silencing (NS) control siRNA (**Figure 8I-J**). Importantly, the z-factor was determined to be greater than 0.5 (**Figure 8I,** *inset),* indicative of a robust setup for our screen (Zhang, Chung et al. 1999).

Identification of miRNAs that regulate LDLR activity in human hepatic cells

[00134] For the genome-wide miRNA screen, Huh7 cells were reverse transfected in triplicate with a library of 1719 distinct miRNAs (Life Technologies *mir*Vana Mimic Library, miRBase release 17.0) and incubated with 30 μg/ml DiI-LDL cholesterol. Following 8h of incubation, cells were washed, fixed and stained with Hoechst to distinguish nuclei (**Figure 1A**, *upper panel*). In addition to internal controls on each screening replicate (see Methods), previously validated siRNAs against the LDLR and a non-silencing (NS) control siRNA were used as positive and negative controls, respectively (**Figures 8H-J**). Mean average intensity of DiI-LDL was determined on an individual cell basis (**Figure 1A,** *middle panel*) using automated high-content image analysis software. To standardize measurements from different plates, phenotypic effects of each miRNA (i.e. those that increased or decreased average DiI intensity) were converted to robust Z-scores (Birmingham, Selfors et al. 2009) based on the median

average intensity of each array plate. Notably, comparison of plate replicates (**Figure 1B-D**) and internal plate controls (**Figure 1E**) suggested high reproducibility of the screen. Upon normalization, robust Z-scores for each individual miRNA were ranked and compared to their respective plate replicates (**Table 2**). While our screen identified miRNAs that both increased and decreased LDL uptake, the present inventors chose to focus on those miRNAs whose overexpression decreased receptor activity, as pharmalogical inhibitors of this miRNA subset represent potential therapeutic targets to lower LDL-cholesterol levels.

[00135] Given the propensity for off-target effects in high-throughput screening assays, a multi-step system was designed in order to narrow down candidates; specifically, miRNAs were subjected to five screening passes before chosen for further validation (**Figure 1A,** *lower panel*). In the first pass, miRNAs were considered putative regulators of LDLR activity for which two or more replicate miRNAs yielded activities smaller than 0.8 median absolute deviations (MAD) away from plate medians (deviation ≤-0.8) (**Figure 1F**). Although this criterion is less stringent than most cut-offs for high-throughput screenings (Birmingham, Selfors et al. 2009), this pass was designed to yield a significantly higher hit rate (423 miRNAs, ~25% of miRNAs screened) to allow for subsequent passes (**Table 2**). To minimize the risk of identifying false positives, the selection of miRNAs for follow-up evaluation in the ensuing passes was based on several criteria. Specifically, miRNAs were chosen for further validation if they: 1) had conserved predicted binding sites in the 3'UTR of the *LDLR*, 2) were highly expressed in human and mouse liver, 3) were modulated by dietary lipids, and 4) had high liver activity (i.e. high miRNA expression versus reduced target gene expression) (**Figure 1A,** *bottom panel* and **Table 1**). Out of the 423 miRNAs indentified from the initial pass, miR-27b and miR-148a (~0.1% of miRNAs screened) emerged as the most obvious and strongest positive hits, showing reduced LDLR activity (TargetScan v6.2, www.targetscan.org), conserved predicted binding sites in the 3'UTR of the *LDLR*, medium to high expression in human and mouse hepatic tissue(Barad, Meiri et al. 2004, Landgraf, Rusu et al. 2007, Vickers, Shoucri et al. 2013) and high liver activity(Arora and Simpson 2008). In addition, both of these miRNAs have previously been shown to be upregulated in the livers of mice fed a high fat diet (HFD) [(Vickers, Shoucri et al. 2013) **Table 1**], suggesting a possible physiological role for miR-27b and miR-148a in regulating lipid metabolism and therefore, highlighting them for further validation.

miR-27b and miR-148a are regulated by hepatic lipid content and enriched in lipid metabolism target genes

[00136] miR-27b is a member of the miR-23b~27b~24-1 miRNA cluster encoded within the intron of the alanine aminopeptidase gene (*APO*) on human chromosome 9 (**Figure 2A**). The mature miRNA sequences of miR-23b, miR-27b and miR-24 are conserved among vertebrate species (**Figure 2A**, *lower panels*). miR-148a is also highly conserved in vertebrates, however it is encoded within an intergenic region of human chromosome 7 (**Figure 2B**). Dietary lipids regulate the hepatic expression of both miRNAs (**Figure 2C-P**). Specifically, the expression levels of the mature and precursor forms of miR-27b and miR-148a (pri-, pre- and mature) were increased in mice and non-human primates fed a high-fat diet (HFD) compared to those fed a chow diet (**Figure 2I-P**). Consistent with our *in vivo* observations, the mature and precursor forms of miR-27b and miR-148a were also significantly upregulated in Huh7 cells treated with 120 μg/ml native LDL (nLDL) (**Figure 2C-H**). Furthermore, the mature form of miR-148a was also significantly upregulated in the livers of *ob/ob* mice (**Figure 2Q**). Taken together, these results demonstrate the regulation of the miR-148a and miR-27b transcript by dietary lipids.

[00137] To gain insight into the function of miR-27b and miR-148a in regulating cholesterol homeostatsis (and more specifically, LDLR activity), their potential targets were analyzed using a rigorous bioinformatic algorithm (Mercer, Snijder et al. 2012). For this, predicted targets identified in three target-prediction websites (Targetscan, miRWalk, and miRanda) were assigned to functional annotation clusters using the public database, DAVID [http://david.abbc.ncifcrf.gov (Huang da, Sherman et al. 2009)]. As shown, miR-27b and miR-148a target genes were enriched (E≥1.0) within 77 and 78 clusters, respectively, and several annotation networks. The functional cluster analysis was combined with data on protein-protein interactions between individual target genes enriched in lipid metabolism using the STRING v9 (Szklarczyk, Franceschini et al. 2011) and PANTHER databases (Thomas, Campbell et al. 2003). The results of this bioinformatic analysis are visually shown in **Figure 9** and indicate that both miRNAs target a vast network of lipid metabolism regulators, including *LDLR, LDLRAP1,* and *ABCA1*.

[00138] Further characterization of the aforementioned target genes revealed that miR-27b has one predicted binding site in the 3'UTR of *LDLR* and two predicted binding sites in the

3'UTR of *LDLRAP1* and *ABCA1* (**Figure 3A**). miR-148a has two predicted binding sites in the 3'UTR of *LDLR* and one predicted binding site in the 3'UTR of *ABCA1* (**Figure 3B**). Notably, most of the miR-27b and miR-148a predicted binding sites are conserved between mammals (**Figures 10A** and **10B**). As expected, 3'-UTR luciferase reporter assays revealed that the *LDLR*, *LRLRAP1* and *ABCA1* are directly regulated by miR-27b (**Figure 3C**). Importantly, mutations of miR-27b target sites relieved miR-27b repression of *LDLR*, *LRLRAP1* and *ABCA1* 3'UTR activity, consistent with a direct interaction of miR-27b with these sites (**Figure 3C**). Similar to miR-27b, overexpression of miR-148a inhibited *LDLR* and *ABCA1* 3'UTR activity and specific point mutations in the predicted binding sites abolished this inhibitory effect (**Figure 3D**). Together, these experiments identify the LDLR and ABCA1 as direct targets for both miR-27b and miR-148a, whereas ABCA1 and LDLRAP1 are direct targets of miR-27b only. As such, both of these miRNAs represent particularly useful targets to alter plasma levels of LDL and HDL cholesterol.

miR-27b and miR-148a inhibit LDLR expression and regulate LDLR activity

[00139] The effect of miR-27b and miR-148a overexpression and inhibition on LDLR mRNA and protein expression was determined next. Transfection of Huh7 cells with miR-27b and miR-148a, but not a control mimic (CM) significantly decreased LDLR mRNA and protein levels (**Figure 4A** and **4B**). Conversely, inhibition of endogenous miR-27b and miR-148a increased the expression of the LDLR (**Figure 4D** and **4E**). Similar results were observed in mouse hepatic cells (Hepa) transfected with antisense inhibitors of miR-27b (Inh-27b) and miR148a (Inh-148a) (**Figures 11A-C**). In addition, miR-27b also regulated the expression of LDLRAP1 in Huh7 cells (**Figure 4C** and **4F**), suggesting that this miRNA might control LDLR activity by direct targeting of the LDLR and by regulating its endocytosis.

[00140] Defective hepatic LDLR activity results in elevated levels of LDL in the blood and is associated with an increased risk of atherosclerosis and coronary heart disease (Lusis 2000, Glass and Witztum 2001). To assess the role of miR-27b and miR-148a in regulating LDL uptake in human hepatic cells and to confirm findings from the primary screen, miR-27b and miR-148a were overexpressed or inhibited and DiI-LDL uptake and binding were assessed by flow cytometry. Transfection of Huh7 cells with miR-27b and miR-148b attenuated LDL specific uptake (**Figure 4G-H**) and binding (**Figure 4I-J**). Consistent with the inhibitory effect

of miR-27b and miR-148a on LDLR activity, transfection of both miRNAs significantly reduced intracellular cholesterol concentration after incubation with nLDL (**Figure 4K-L**). Importantly, antagonists of endogenous miR-27b (Inh-27b) and miR-148a (Inh-148a) increased LDL uptake and binding in Huh7 (**Figures 4M-P**) and Hepa cells (**Figures 11D-G**). Intracellular cholesterol levels were also slightly, but significantly, increased in Huh7 cells overexpressing inhibitors of miR-27b (Inh-27b) and miR-148a (Inh-148a) (**Figures 4Q-R**). Additionally, when LDLR-antibody internalization and DiI-LDL uptake were analyzed by immunofluorescence, reduced LDLR internalization and a concomitant decrease in DiI-LDL uptake were observed in cells overexpressing miR-27b and miR-148a compared to controls (**Figure 4S**). The inventors next determined whether the effect of miR-27b and miR-148a in regulating LDL uptake was rescued by overexpressing a LDLR-GFP cDNA construct that lacked the 3'UTR, thereby resistant to miR-27b and miR-148a inhibitory action. As previously shown in **Figure 4S**, Huh7 cells transfected with miR-27b or miR-148a have a significant reduction in DiI-LDL uptake and binding when analyzed by immunofluresecnce (**Figure 5A-R**). However, this effect was abrogated in cells that expressed the LDLR-GFP construct, suggesting that miR-27b and miR-148a regulate DiI-LDL uptake and binding by direct down-regulation of the LDLR (**Figure 5A-R**). Thus, manipulation of cellular miR-27b and miR-148a alters LDLR activity, a critical step in controlling the levels of atherogenic lipoproteins in the blood.

miR-27b regulates ABCA1 expression and cholesterol efflux in human hepatic cells

[00141] ABCA1 plays a major role in regulating cholesterol efflux from macrophages to ApoA1 and in the biogenesis of HDL in the liver, thereby controlling reverse cholesterol transport (RCT), a process that mediates the clearance of cholesterol from peripheral cells to the liver for excretion to the bile and feces (Oram and Vaughan 2000). To assess whether miR-27b regulates ABCA1 expression and cholesterol efflux from human hepatic cells, Huh7 cells were transfected with miR-27 mimics (miR-27b) or miR-27 antisense oligonucleotides (Inh-27b) and analyzed ABCA1 mRNA and protein levels and cholesterol efflux to ApoA1. As seen in **Figure 6A**, miR-27 overexpression strongly reduced ABCA1 mRNA expression in basal conditions (control) and when cells were pre-treated with the LXR ligand T0901317 [(T090) (to directly stimulate ABCA1 expression)]. Similar effects were observed at the protein level (**Figure 6B**). Most importantly, endogenous inhibition of miR-27b in human hepatic cells increased ABCA1 mRNA and protein levels (**Figure 6C and 7D**). In agreement with the known cellular functions

of ABCA1, transfection of Huh7 cells with miR-27b significantly attenuated cholesterol efflux to ApoA1 (**Figure 6E**).

miR-27b levels regulate circulating LDL and HDL cholesterol in mice

[00142] Because miR-27b alters both LDL uptake and cholesterol efflux in human hepatic cells, the functional contribution of increased miR-27b levels on plasma lipids were next assessed in mice fed a chow or Western Diet (WD). To specifically alter miRNA expression in the liver, an adeno-associated virus serotype 8 (AAV8) vector encoding pre-miR-27b (AAV-27b) or a control vector (AAV-Null) were used. AAV8 vectors have previously been evaluated for liver directed gene transfer in murine models and show no signs of liver toxicity (Wang, Wang et al. 2010, Kassim, Li et al. 2013). For the chow diet studies, AAV-Null or AAV-27b vectors (5×10^{12} GC/kg) were delivered to 8-week old male C57BL/6 mice (n= 5 per group) via retro-orbital injection; plasma lipids were measured after two and four weeks (**Figure 7A**). To determine the efficacy of miR-27b over-expression, the expression of hepatic miR-27b and its target genes were measured after four weeks of treatment. As expected, pre-miR-27b expression levels were significantly higher in mice treated with AAV-27b compared to mice treated with AAV-Null (**Figure 7B**). Similarly, the expression levels of mature miR-27b were also upregulated in mice injected with AAV-27b, but modestly when compared to pre-miR-27b levels (**Figure 7C**). Consistent with our *in vitro* results, hepatic *LDLR* expression was significantly decreased in mice treated with AAV-27b (**Figure 7D**), however no significant changes in *ABCA1* mRNA were observed (**Figure 7E**). Notably, both LDLR and ABCA1 protein levels were significantly reduced in the livers of mice treated with AAV-27b compared to those treated with AAV-Null (**Figure 7F-G**). Given that decreased hepatic expression of ABCA1 would be predicted to reduce HDL biogenesis, circulating total and HDL-C levels were next measured in mice treated with AAV-Null or AAV-27b after over-night fasting. As expected, *in vivo* over-expression of miR-27b resulted in a progressive decline of total plasma HDL and cholesterol compared to controls (**Figure 7H-I**). Consistent with this, analysis of lipoproteins by FPLC showed a prominent decrease in cholesterol content of the HDL fractions in mice treated with miR-27b for two and four weeks (**Figure 7J-K**). Surprisingly, hepatic over-expression of miR-27b did not alter cholesterol content in the IDL/LDL fractions, despite decreased levels of the LDLR (**Figure 7J-K**). Moreover, no significant differences in plasma triglycerides were observed (*data not shown*).

[00143] Because the rate of hepatic LDL-clearance is 40-fold greater in C57BL/6 mice than in humans(Dietschy, Turley et al. 1993), the efficacy of miR-27b over-expression on plasma lipids were further determined in mice challenged with a WD after four weeks of miR-27b treatment (**Figure 7L**). Similar to mice fed a chow diet, hepatic levels of pre-miR-27b and mature miR-27b were significantly increased (**Figure 7M-N**), while ABCA1 and LDLR protein expression were decreased (**Figure 7Q-R**). No significant differences were observed in *ABCA1* and *LDLR* mRNA levels (**Figure 7O-P**). Next, post-prandial and fasting (3h) plasma lipid levels were analyzed in mice treated with AAV-27b or AAV-Null. Fractionation of plasma lipoproteins revealed that IDL/LDL cholesterol was markedly increased in mice over-expressing miR-27b (**Figure 7S-T**). Interestingly, no differences were observed in the HDL-cholesterol fraction in either the fed or fasted state (**Figure 7S-T**), despite a striking down-regulation of ABCA1 in AAV-miR-27b treated mice. Taken together, these results suggest that manipulation of miR-27b levels *in vivo* alters LDLR and ABCA1 expression and plasma LDL and HDL cholesterol levels.

Modulation of miR-27b and miR-148a expression regulates LDLR expression *in vivo*

[00144] To ascertain the endogenous role of miR-27b and miR-148a in regulating LDLR expression and activity *in vivo*, miR-148a expression was inhibited using locked nucleic acid (LNA) miRNA inhibitors (primer sequences were 5'-TTCTGTAGTGCACTG-3' [SEQ ID NO: 52] and 5'-AACTTAGCCACTGTGA-3' [SEQ ID NO: 54]) (Exiqon). Because LDL levels in wild-type mice plasma are low (Dietschy, Turley et al. 1993), "humanized" mice (*LDLR-/+;*ApoBTg background) were used for the studies (Purcell-Huynh 1995). To inhibit hepatic miR-27b and miR-148a expression, mice were intraperitoneally injected every three days for a period of two weeks with 5 mg/kg of DNA/LNA mixmer antisense oligonucleotides against miR-148a (LNA 148a) or miR-27b (LNA 27b) (**Figure 13A and 14A**). A scrambled LNA oligonucleotide (LNA CON, 5'- ACGTGTATACGCCCA-3'; SEQ ID NO: 51) was used as a control. Twenty-four hours following the last injection, mice were sacrificed and serum and livers collected for plasma cholesterol and gene expression analysis, respectively. As expected, treatment with LNA anti-miR-148a (LNA 148a, 5'- TTCTGTAGTGCACTG-3'; SEQ ID NO: 52) and LNA anti-miR-27b (LNA 27b, 5'-AACTTAGCCACTGTCA-3'; SEQ ID NO: 54) significantly reduced levels of hepatic miR-148a and miR-27b (**Figure 13B-C and 14B**). Importantly, and consistent with this, hepatic protein levels of *LDLR* were significantly increased in LNA 148a and LNA 27b treated mice compared to controls (**Figure 13D-E and**

14C-D). Further experiments are necessary to determine whether the anti- miR-27b or anti-miR-148a-induced expression of LDLR plays a functional role in decreasing levels of LDL-cholesterol. Nevertheless, taken together, these results suggest a physiological role for miR-148a in controlling hepatic LDLR expression *in vivo*.

Transcriptional regulation of miR-148a by SREBP1c

[00145] Given that miR-148a is upregulated in the livers of *ob/ob* and high-fat-diet (HFD) fed mice, the present inventors next sought to determine how this intergenic miRNA is transcriptionally regulated. Previous reports have identified several transcriptional start sites (TSSs) located ~1.1 to ~1.6 kb upstream of the miR-148a sequence (Eponine, miRstart source) (Saini 2007). Importantly, these TSSs correlate with CpG islands and H3K4Me3 marks (Ernst 2010, Monteys 2010). Furthermore, upstream regions adjacent to the putative TSSs revealed active and weak promoter and enhancer regions involved in the regulation of miR-148a expression (**Figure 12A**) (Ernst 2010). Intriguingly, a SREBP1 binding site was previously identified in this active promoter region using ChIP-seq (Gerstein 2012). The present inventors reasoned that SREBP1c, the predominant isoform of SREBP1 in the liver (Horton 2002), might be a transcriptional regulator of miR-148a expression. Therefore, to test whether SREBP1c could modulate miR-148a expression *in vitro,* Huh7 cells were transfected with a vector expressing FLAG-tagged nuclear SREBP1c (nSREPB1c) and miR-148a expression was measured by qRT-PCR. As shown in **Figure 12B-D**, overexpression of nSREBP1c significantly increased the expression of miR-148a (mature and precursor forms), as well as the SREBP1c target gene, *FASN,* thereby suggesting that SREBP1c may regulate miR-148a expression by binding to its promoter. To further explore the *in vivo* relevance of SREBP1c-dependent regulation of miR-148a, the mature form of miR-148a was next measured in the livers of mice overexpressing a truncated form of human SREBP1c (Shimano 1997). qRT-PCR analysis showed that miR-148a was increased in the livers of SREBP1c transgenic (SREBP1c-Tg) mice compared to controls (**Figure 12E**), corroborating the above *in vitro* findings that miR-148a is regulated by nSREBP1c.

[00146] The induction of hepatic SREBP1c is dependent on LXR agonists (Bobard 2005). Therefore, to determine whether miR-148a expression is affected by modulation of endogenous SREBP1c, mouse primary hepatocytes were treated with T090, a synthetic LXR-ligand, and

miR-148a expression was assessed by qRT-PCR and Northern blotting. As shown in **Figure 12F**, the expression of several LXR-regulated genes, including *ABCA1, SREBP1c,* and *FASN* were all significantly upregulated upon LXR-activation compared to vehicle-treated cells. Importantly, the precursor and mature forms of miR-148a were also induced by T090 treatment (**Figure 12G-H**). As insulin is the major activator of SREBP1c in the liver, the present inventors further validated whether miR-148a expression is affected by the insulin-mediated induction of SREBP1c. As seen in **Figure 12I,** insulin treatment significantly upregulated *FASN* and *SREBP1c* expression in primary mouse hepatoctytes. Importantly, pre-miR-148a and miR-148a expression were also significantly increased in insulin-treated cells (**Figure 12J-K**). Furthermore, the inventors found that miR-148a promoter activity was induced in Hela cells overexpressing nuclear SREBP1c and Huh7 cells treated with insulin or T090 (**Figure 12L-N).** Collectively, these results demonstrate that activation of hepatic SREBP1c by LXR and insulin correlates with endogenous miR-148a expression. Thus, miR-148a may define a novel SREBP1c-dependent axis for regulating LDLR expression.

DISCUSSION

[00147] This example provides the identification of miRNAs that control LDLR activity. Amongst them, the inventors have characterized the role of miR-27b and miR-148a in regulating LDLR expression and activity. Both miRNAs are highly expressed in the liver and are regulated by hepatic lipid content. Mechanistically, it is disclosed herein that the aforementioned miRNAs directly target and inhibit the expression of the LDLR, thereby reducing LDL uptake in human hepatic cell lines. Moreover, miR-27b also regulates ABCA1 expression and cellular cholesterol export. Importantly, overexpression of miR-27b in mice increases plasma LDL-C and reduces circulating HDL-C, thus suggesting that antagonists of endogenous miR-27b may be useful as a therapeutic strategy for enhancing LDLR and ABCA1 expression. Indeed, when the inventors inhibited miR-27b expression using LNA antisense oligonucleotides, hepatic LDLR expression was significantly increased. In addition, miR-148a contains a SREBP1 binding site in its promoter region. Accordingly, induction of SREBP1c by overexpression constructs and by the LXR agonist, T090, and insulin increases miR-148a promoter activity and expression, thus defining a complementary pathway for controlling cholesterol uptake. Importantly, inhibition of miR-148a in mice increases hepatic LDLR expression, suggesting that antagonists of

endogenous miR-148a may be useful as a therapeutic strategy for increasing LDLR activity and ultimately reducing levels of LDL-C.

[00148] Although several miRNAs, including miR-33, miR-144, miR-758 and miR-106b, have been shown to regulate ABCA1 and plasma HDL-C levels (Krutzfeldt, Rajewsky et al. 2005, Esau, Davis et al. 2006, Najafi-Shoushtari, Kristo et al. 2010, Ramirez, Davalos et al. 2011, Rayner, Esau et al. 2011, Kim, Yoon et al. 2012, de Aguiar Vallim, Tarling et al. 2013, Ramirez, Rotllan et al. 2013), little is known about miRNAs that control the expression of the LDLR and modulate LDL-C levels. To date, only the liver-restricted miR-122 has been shown to play a direct role in LDL cholesterol metabolism. Specifically, studies by Esau *et al.* and Elmen *et al.* have shown that antisense targeting of miR-122 in mice significantly reduces total plasma cholesterol and triglyceride levels, as well as hepatic steatosis (Esau, Davis et al. 2006, Elmen, Lindow et al. 2008). While these studies paved the way for the first experiments of miRNA targeting in non-human primates and shed light on the use of miR-122 inhibitors to treat dyslipidemias (Elmen, Lindow et al. 2008, Elmen, Lindow et al. 2008, Lanford, Hildebrandt-Eriksen et al. 2010), the mechanistic understanding by which anti-miR-122 mediates its effects on lipid homeostasis is still unclear. Unfortunately, this incomprehension, combined with adverse consequences of reduced HDL-C and increased risk of developing hepatocellar carcinomas, have challenged the fervent development of miR-122 antisense technologies (Esau, Davis et al. 2006, Elmen, Lindow et al. 2008)

[00149] Functional genomic screens can provide a direct and powerful approach to identify gene and/or miRNA functions in mammalian biology. Indeed, several *in vitro* screens based on miRNA expression libraries have proven to be highly useful (Voorhoeve, le Sage et al. 2006, Huang, Gumireddy et al. 2008, Izumiya, Okamoto et al. 2010, Poell, van Haastert et al. 2011). Although these types of screens circumvent the problem of identifying functionally relevant miRNA target genes, they inherently give rise to high rates of false positives and negatives. Furthermore, high-throughput identification of miRNA function relies on unnaturally high expression levels of miRNAs, which may cause artifacts and thwart the tissue-specific functional roles of certain miRNA genes. To address these problems, the present inventors integrated results from genome-wide screen with computational predictions from TargetScan, as well as pre-existing deep sequencing data on miRNA expression and activity. With this method, the present inventors were able to narrow down our hit list from 25% of miRNAs screened to

0.12%, which is well within the range of acceptable 'hit' rates for genome-wide screens (Malo, Hanley et al. 2006). Nevertheless, it cannot be completely ruled out that some candidates have been discarded that may play a functional role in controlling LDL levels, as the present screen only focused on miRNAs that effect LDLR activity by direct repression of the LDLR. Furthermore, many miRNAs were found to significantly increase DiI-LDL uptake. Given the complex regulatory mechanisms governing the expression of the LDLR, it is likely that some of these miRNAs regulate LDLR activity by targeting post-transcriptional regulators of the LDLR, such as PCSK9 and IDOL (Benjannet, Rhainds et al. 2004, Zelcer, Hong et al. 2009).

[00150] Out of the 423 miRNAs identified to negatively regulate LDLR activity, miR-148a and miR-27b were selected for follow-up studies. miR-148a is an intergenic miRNA located on human chromosome 7 and has previously been shown to modulate cell transformation and tumor angiogenesis (Yu, Li et al. 2011, Xu, Jiang et al. 2013). Additionally, miR-148a is aberrantly expressed in several types of cancers, with its down-regulation well described in various solid tumors, such as gastric, colorectal, esophageal, and pancreatic carcinomas (Lujambio, Calin et al. 2008, Hummel, Watson et al. 2011, Zhang, Li et al. 2011, Zheng, Liang et al. 2011). Interestingly, miR-148a was recently described to be upregulated in differentiating liver progenitors and shown to play a role in the fate of the liver by inducing hepatospecific gene expression and suppressing tumor cell invasion (Gailhouste, Gomez-Santos et al. 2013). This study demonstrates the role of miR-148a in regulating LDLR activity indicating that miR-148a plays an important role in the liver. In addition to identifying miR-148a, the present screen also identified miR-148b, the second member of the miR-148 family, as a negative regulator of LDLR activity. Like miR-148a, miR-148b is predicted to target the LDLR, is highly expressed in human liver tissue, and is upregulated with dietary cholesterol. Several studies have also demonstrated a similar tumor suppressive function for this miRNA in ovarian cancer (Chang, Zhou et al. 2012).

[00151] As demonstrated herein, miR-148a controls LDLR activity and appears to be regulated by SREBP1c. LXR-mediated induction of SREBP1c results in increased expression of miR-148a and a resultant decrease in LDLR expression. While these results suggest that LDLR expression is regulated by the LXR-SREBP1c-dependent induction of miR-148a (**Figure 13F**), one cannot rule out that the decrease in LDLR after T090 treatment is due to an increase in miR-185 or the LXR-Idol axis (Zelcer 2009, Yang 2014). Experiments using miR-148a inhibitors

and LXR agonists can elucidate the mechanism by which miR-148a contributes to the post-transcriptional regulation of LDLR. Nevertheless, as miR-148a controls LDLR activity by directly binding to and repressing LDLR expression, these results may define a complementary LXR-SREBP1c-mediated mechanism for post-transcriptionally controlling the expression of LDLR, and thus, fine-tuning cholesterol homeostasis (**Figure 13E**).

[00152] In the present example, the miRNA that has been characterized the most, miR-27b, is a member of the miR-27 family, of which there are two isoforms, miR-27a and miR-27b. While miR-27a is an intergenic miRNA, miR-27b is located within the 14th intron of the *APO* gene on human chromosome 9 and is a member of the miR-23b~27b~24-1 cluster. Unlike miR-148, miR-27 has been implicated in numerous cellular processes that regulate atherosclerosis, including angiogenesis, adipogenesis, inflammation, lipid metabolism, oxidative stress, insulin resistance and type-2 diabetes (Chen, Yin et al. 2012). Additionally, miR-27 levels correlate with clinical pathological factors and the prognosis of patients with atherosclerosis (Chen, Yin et al. 2012). Moreover, aberrant expression of miR-27 has been shown to be a predictor for unstable atherosclerotic plaques (Li, Cao et al. 2011, Staszel, Zapala et al. 2011).

[00153] In particular, miR-27 has been shown to directly target many lipid-metabolism transcription factors, including RXRα, PPARα, and PPARγ (Karbiener, Fischer et al. 2009, Kim, Kim et al. 2010, Kida, Nakajima et al. 2011, Shirasaki, Honda et al. 2013). In addition to these, here, identified and described herein are three novel targets for miR-27b, namely LDLR, LDLRAP1 and ABCA1. By inhibiting the expression of LDLR and LDLRAP1, miR-27b reduces DiI-LDL uptake and binding, and concomitantly decreases intracellular cholesterol concentrations in human hepatic cells. The decreased expression of hepatic LDLR and LDLRAP1 would be expected to augment circulating plasma LDL-C levels *in vivo*. Indeed, when miR-27b was over-expressed in the livers of mice fed a WD, a marked increase in IDL/LDL cholesterol was found. This increase in LDL-C suggests that miR-27b treatment either, 1) increases VLDL secretion or, 2) reduces lipoprotein clearance from the circulation. As the major route of clearance of ApoE- and ApoB-containing lipoproteins is by means of LDLR-mediated enodcytosis in the liver (Dietschy, Turley et al. 1993), the present results suggest that the reduction in LDL-C is mainly due to miR-27b-mediated repression of hepatic LDLR. While this does not rule out the possibility that miR-27b could be affecting VLDL secretion, it may establish a key role for miR-27b in regulating LDLR activity *in vivo*, thereby giving confidence

that other miRNAs identified in this genome-wide screen also play functionally relevant roles in controlling LDL uptake. Recently, Shirasaki *et al.* reported that ABCA1 was a direct target of miR-27a in human hepatoma cells (Shirasaki, Honda et al. 2013). It is shown herein that the second member of the miR-27 family, miR-27b, also directly targets the 3'UTR of *ABCA1* and represses ABCA1 mRNA and protein levels. In addition, this example demonstrates a role for miR-27b in regulating cholesterol efflux to ApoA1. Consistent with this result, mice fed a chow diet and treated with miR-27b show a progressive decline in HDL and total cholesterol levels.

[00154] Augmented expression of LDLR would be expected to decrease circulating plasma LDL-C levels *in vivo*, and thus reduce the burden of cardiovascular disease. Given the role of miR-148a and miR-27b in negatively regulating LDLR expression and activity, one would predict that inhibitors of these miRNAs would represent a novel therapeutic strategy for increasing hepatic LDLR expression and decreasing plasma LDL. Indeed, when the inventors inhibited miR-148a and miR-27b expression using LNA oligonucleotides in mice, they found a marked increase in hepatic LDLR expression, thus suggesting that the endogenous levels of miR-148a and miR-27b are important for regulating LDLR expression *in vivo*. Experiments using non-human primates and/or "humanized" mouse models that exhibit LDL-dominant lipoprotein profiles, such as *Apobec-/-;* CETPTg mice, should help characterize the endogenous role of miR-148a and miR-27b in regulating levels of LDL-C.

[00155] While the inventors cannot completely rule out the possibility that miR-27b and miR-148a may alter other pathways that contribute to LDL-C metabolism, the present study unequivocally establishes a key role for both miRNAs in regulating LDLR expression *in vivo*, thereby giving confidence that other miRNAs identified in this genome-wide screen also play functionally relevant roles in controlling LDL uptake. Indeed, single-nucleotide polymorphisms (SNPs) in the promoter region of miR-148a contribute to altered LDL-C and triglyceride levels in humans (**Figure 12A**) (Do 2013, Global Lipids Genetics 2013). These genetic polymorphisms may affect the expression of miR-148a. For example, the T allele at rs472251 in the *miR-148a* gene was strongly associated with reduced LDL-C. While the mechanism by which this SNP contributes to altered LDL-C remains unknown, one can imagine a scenario where the SNP leads to decreased expression of miR-148a, thereby increasing LDLR expression and reducing levels of LDL-C. Experiments are therefore warranted to dissect the contribution of this variant to altered lipid levels and cardiovascular disease risk.

[00156] Altogether, these results underscore the importance of miRNAs in regulating LDLR expression. Specifically, this data highlights the therapeutic potential of suppressing miR-27b and miR-148a activity to simultaneously reduce circulating levels of LDL-C and increase levels of HDL-C, beneficial outcomes for reducing the global burden of atherosclerosis and related dyslipidemias.

REFERENCES

Ambros, V. (2004). "The functions of animal microRNAs." Nature **431**(7006): 350-355.

Arora, A. and D. A. Simpson (2008). "Individual mRNA expression profiles reveal the effects of specific microRNAs." Genome Biol **9**(5): R82.

Barad, O., et al. (2004). "MicroRNA expression detected by oligonucleotide microarrays: system establishment and expression profiling in human tissues." Genome Res **14**(12): 2486-2494.

Bartel, D. P. (2004). "MicroRNAs: genomics, biogenesis, mechanism, and function." Cell **116**(2): 281-297.

Bartel, D. P. (2009). "MicroRNAs: target recognition and regulatory functions." Cell **136**(2): 215-233.

Benjannet, S., et al. (2004). "NARC-1/PCSK9 and its natural mutants: zymogen cleavage and effects on the low density lipoprotein (LDL) receptor and LDL cholesterol." J Biol Chem **279**(47): 48865-48875.

Birmingham, A., et al. (2009). "Statistical methods for analysis of high-throughput RNA interference screens." Nat Methods **6**(8): 569-575.

Bobard, A., Hainault, I., Ferre, P., Foufelle, F. & Bossard, P. Differential regulation of sterol regulatory element-binding protein 1c transcriptional activity by insulin and liver X receptor during liver development. *The Journal of biological chemistry* **280**, 199-206, doi:10.1074/jbc.M406522200 (2005)

Brown, M. S., et al. (1973). "Regulation of 3-hydroxy-3-methylglutaryl coenzyme A reductase activity in human fibroblasts by lipoproteins." Proc Natl Acad Sci U S A **70**(7): 2162-2166.

Brown, M. S. and J. L. Goldstein (1974). "Familial hypercholesterolemia: defective binding of lipoproteins to cultured fibroblasts associated with impaired regulation of 3-hydroxy-3-methylglutaryl coenzyme A reductase activity." Proceedings of the National Academy of Sciences of the United States of America **71**(3): 788-792.

Brown, M. S. and J. L. Goldstein (1976). "Receptor-mediated control of cholesterol metabolism." Science **191**(4223): 150-154.

Brown, M. S. and J. L. Goldstein (1986). "A receptor-mediated pathway for cholesterol homeostasis." Science **232**(4746): 34-47.

Brown, M. S. and J. L. Goldstein (1997). "The SREBP pathway: regulation of cholesterol metabolism by proteolysis of a membrane-bound transcription factor." Cell **89**(3): 331-340.

Calvo, D., et al. (1998). "Human CD36 is a high affinity receptor for the native lipoproteins HDL, LDL, and VLDL." J Lipid Res **39**(4): 777-788.

Chang, H., et al. (2012). "Increased expression of miR-148b in ovarian carcinoma and its clinical significance." Mol Med Rep **5**(5): 1277-1280.

Chen, W. J., et al. (2012). "The magic and mystery of microRNA-27 in atherosclerosis." Atherosclerosis **222**(2): 314-323.

de Aguiar Vallim, T., et al. (2013). "MicroRNA-144 Regulates Hepatic ABCA1 and Plasma HDL Following Activation of the Nuclear Receptor FXR." Circ Res.

Dietschy, J. M., et al. (1993). "Role of liver in the maintenance of cholesterol and low density lipoprotein homeostasis in different animal species, including humans." J Lipid Res **34**(10): 1637-1659.

Do, R. *et al.* Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature genetics* **45**, 1345-1352, doi:10.1038/ng.2795 (2013).

Global Lipids Genetics, C. *et al.* Discovery and refinement of loci associated with lipid levels. *Nature genetics* **45**, 1274-1283, doi:10.1038/ng.2797 (2013).

Elmen, J., et al. (2008). "LNA-mediated microRNA silencing in non-human primates." Nature **452**(7189): 896-899.

Elmen, J., et al. (2008). "Antagonism of microRNA-122 in mice by systemically administered LNA-antimiR leads to up-regulation of a large set of predicted target mRNAs in the liver." Nucleic Acids Res **36**(4): 1153-1162.

Ernst, J. & Kellis, M. Discovery and characterization of chromatin states for systematic annotation of the human genome. *Nature biotechnology* **28**, 817-825, doi:10.1038/nbt.1662 (2010).

Esau, C., et al. (2006). "miR-122 regulation of lipid metabolism revealed by in vivo antisense targeting." Cell Metab **3**(2): 87-98.

Filipowicz, W., et al. (2008). "Mechanisms of post-transcriptional regulation by microRNAs: are the answers in sight?" Nature reviews. Genetics **9**(2): 102-114.

Gailhouste, L., et al. (2013). "MiR-148a plays a pivotal role in the liver by promoting the hepatospecific phenotype and suppressing the invasiveness of transformed cells." Hepatology.

Gerstein, M. B. *et al.* Architecture of the human regulatory network derived from ENCODE data. *Nature* **489**, 91-100, doi:10.1038/nature11245 (2012).

Glass, C. K. and J. L. Witztum (2001). "Atherosclerosis. the road ahead." Cell **104**(4): 503-516.

Goldstein, J. L., et al. (1976). "Release of low density lipoprotein from its cell surface receptor by sulfated glycosaminoglycans." Cell **7**(1): 85-95.

Goldstein, J. L. and M. S. Brown (1990). "Regulation of the mevalonate pathway." Nature **343**(6257): 425-430.

Gould, A. L., et al. (1998). "Cholesterol reduction yields clinical benefit: impact of statin trials." Circulation **97**(10): 946-952.

Hennekens, C. H. (1998). "Increasing burden of cardiovascular disease: current knowledge and future directions for research on risk factors." Circulation **97**(11): 1095-1102.

Horton, J. D., Goldstein, J. L. & Brown, M. S. SREBPs: activators of the complete program of cholesterol and fatty acid synthesis in the liver. *The Journal of clinical investigation* **109**, 1125-1131, doi:10.1172/JCI15593 (2002).

Huang da, W., et al. (2009a). "Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources." Nat Protoc **4**(1): 44-57.

Huang da, W., Sherman, B. T. & Lempicki, R. A. Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. *Nucleic acids research* **37**, 1-13, doi:10.1093/nar/gkn923 (2009b).

Huang, Q., et al. (2008). "The microRNAs miR-373 and miR-520c promote tumour invasion and metastasis." Nat Cell Biol **10**(2): 202-210.

Hummel, R., et al. (2011). "Mir-148a improves response to chemotherapy in sensitive and resistant oesophageal adenocarcinoma and squamous cell carcinoma cells." J Gastrointest Surg **15**(3): 429-438.

Izumiya, M., et al. (2010). "Functional screening using a microRNA virus library and microarrays: a new high-throughput assay to identify tumor-suppressive microRNAs." Carcinogenesis **31**(8): 1354-1359.

Karbiener, M., et al. (2009). "microRNA miR-27b impairs human adipocyte differentiation and targets PPARgamma." Biochem Biophys Res Commun **390**(2): 247-251.

Kassim, S. H., et al. (2013). "Adeno-associated virus serotype 8 gene therapy leads to significant lowering of plasma cholesterol levels in humanized mouse models of homozygous and heterozygous familial hypercholesterolemia." Hum Gene Ther **24**(1): 19-26.

Kida, K., et al. (2011). "PPARalpha is regulated by miR-21 and miR-27b in human liver." Pharm Res **28**(10): 2467-2476.

Kim, J., et al. (2012). "MiR-106b impairs cholesterol efflux and increases Abeta levels by repressing ABCA1 expression." Exp Neurol **235**(2): 476-483.

Kim, S. Y., et al. (2010). "miR-27a is a negative regulator of adipocyte differentiation via suppressing PPARgamma expression." Biochem Biophys Res Commun **392**(3): 323-328.

Krutzfeldt, J., et al. (2005). "Silencing of microRNAs in vivo with 'antagomirs'." Nature **438**(7068): 685-689.

Landgraf, P., et al. (2007). "A mammalian microRNA expression atlas based on small RNA library sequencing." Cell **129**(7): 1401-1414.

Lanford, R. E., et al. (2010). "Therapeutic silencing of microRNA-122 in primates with chronic hepatitis C virus infection." Science **327**(5962): 198-201.

Li, T., et al. (2011). "Identification of miR-130a, miR-27b and miR-210 as serum biomarkers for atherosclerosis obliterans." Clin Chim Acta **412**(1-2): 66-70.

Lujambio, A., et al. (2008). "A microRNA DNA methylation signature for human cancer metastasis." Proc Natl Acad Sci U S A **105**(36): 13556-13561.

Lusis, A. J. (2000). "Atherosclerosis." Nature **407**(6801): 233-241.

Malo, N., et al. (2006). "Statistical practice in high-throughput screening data analysis." Nat Biotechnol **24**(2): 167-175.

Maxfield, F. R. and I. Tabas (2005). "Role of cholesterol and lipid organization in disease." Nature **438**(7068): 612-621.

Mercer, J., et al. (2012). "RNAi screening reveals proteasome- and Cullin3-dependent stages in vaccinia virus infection." Cell Rep **2**(4): 1036-1047.

Mi, H. *et al.* PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. *Nucleic acids research* **38**, D204-210, doi:10.1093/nar/gkp1019 (2010).

Monteys, A. M. *et al.* Structure and activity of putative intronic miRNA promoters. *Rna* **16**, 495-505, doi:10.1261/rna.1731910 (2010).

Najafi-Shoushtari, S. H., et al. (2010). "MicroRNA-33 and the SREBP host genes cooperate to control cholesterol homeostasis." Science **328**(5985): 1566-1569.

Oram, J. F. and A. M. Vaughan (2000). "ABCA1-mediated transport of cellular cholesterol and phospholipids to HDL apolipoproteins." Curr Opin Lipidol **11**(3): 253-260.

Park, S. W., et al. (2004). "Post-transcriptional regulation of low density lipoprotein receptor protein by proprotein convertase subtilisin/kexin type 9a in mouse liver." J Biol Chem **279**(48): 50630-50638.

Poell, J. B., et al. (2011). "Functional microRNA screening using a comprehensive lentiviral human microRNA expression library." BMC Genomics **12**: 546.

Purcell-Huynh, D. A. *et al.* Transgenic mice expressing high levels of human apolipoprotein B develop severe atherosclerotic lesions in response to a high-fat diet. *The Journal of clinical investigation* **95**, 2246-2257, doi:10.1172/JCI117915 (1995).

Ramirez, C. M., et al. (2011). "MicroRNA-758 regulates cholesterol efflux through posttranscriptional repression of ATP-binding cassette transporter A1." Arterioscler Thromb Vasc Biol **31**(11): 2707-2714.

Ramirez, C. M., et al. (2013). "Control of Cholesterol Metabolism and Plasma HDL Levels by miRNA-144." Circ Res.

Rayner, K. J., et al. (2011). "Inhibition of miR-33a/b in non-human primates raises plasma HDL and lowers VLDL triglycerides." Nature **478**(7369): 404-407.

Saini, H. K., Griffiths-Jones, S. & Enright, A. J. Genomic analysis of human microRNA transcripts. *Proceedings of the National Academy of Sciences of the United States of America* **104**, 17719-17724, doi:10.1073/pnas.0703890104 (2007).

Shimano, H. *et al.* Isoform 1c of sterol regulatory element binding protein is less active than isoform 1a in livers of transgenic mice and in cultured cells. *The Journal of clinical investigation* **99**, 846-854, doi:10.1172/JCI119248 (1997).

Shirasaki, T., et al. (2013). "MicroRNA-27a Regulates Lipid Metabolism and Inhibits Hepatitis C Virus Replication in Human Hepatoma Cells." J Virol **87**(9): 5270-5286.

Sjouke, B., et al. (2011). "Familial hypercholesterolemia: present and future management." Current cardiology reports **13**(6): 527-536.

Staszel, T., et al. (2011). "Role of microRNAs in endothelial cell pathophysiology." Pol Arch Med Wewn **121**(10): 361-366.

Suarez, Y., et al. (2004). "Synergistic upregulation of low-density lipoprotein receptor activity by tamoxifen and lovastatin." Cardiovascular research **64**(2): 346-355.

Szklarczyk, D., et al. (2011). "The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored." Nucleic Acids Res **39**(Database issue): D561-568.

Thomas, P. D., et al. (2003). "PANTHER: a library of protein families and subfamilies indexed by function." Genome Res **13**(9): 2129-2141.

Vickers, K. C., et al. (2013). "MicroRNA-27b is a regulatory hub in lipid metabolism and is altered in dyslipidemia." Hepatology **57**(2): 533-542.

Voorhoeve, P. M., et al. (2006). "A genetic screen implicates miRNA-372 and miRNA-373 as oncogenes in testicular germ cell tumors." Cell **124**(6): 1169-1181.

Wang, L., et al. (2010). "Systematic evaluation of AAV vectors for liver directed gene transfer in murine models." Mol Ther **18**(1): 118-125.

Xu, Q., et al. (2013). "A regulatory circuit of miR-148a/152 and DNMT1 in modulating cell transformation and tumor angiogenesis through IGF-IR and IRS1." J Mol Cell Biol **5**(1): 3-13.

Yang, M. *et al.* Identification of miR-185 as a regulator of de novo cholesterol biosynthesis and low density lipoprotein uptake. *Journal of lipid research* **55**, 226-238, doi:10.1194/jlr.M041335 (2014).

Yu, J., et al. (2011). "MiR-148a inhibits angiogenesis by targeting ERBB3." J Biomed Res **25**(3): 170-177.

Zelcer, N., et al. (2009). "LXR regulates cholesterol uptake through Idol-dependent ubiquitination of the LDL receptor." Science **325**(5936): 100-104.

Zhang, H., et al. (2011). "MiR-148a promotes apoptosis by targeting Bcl-2 in colorectal cancer." Cell Death Differ **18**(11): 1702-1710.

Zhang, J. H., et al. (1999). "A Simple Statistical Parameter for Use in Evaluation and Validation of High Throughput Screening Assays." J Biomol Screen **4**(2): 67-73.

Zheng, B., et al. (2011). "MicroRNA-148a suppresses tumor cell invasion and metastasis by downregulating ROCK1 in gastric cancer." Clin Cancer Res **17**(24): 7574-7583.

* * *

[00157] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are intended to fall within the scope of the appended claims.

[00158] All references cited herein, including all patents, published patent applications, and published scientific articles, are incorporated by reference in their entireties for all purposes.

Table 1: Top hits from primary miRNA screen.

Number	Plate	Well	miRNA	Robust Z-score			Rank	Targets LDLR[1]	Conserved[1]	Human Liver Expression		Mouse Liver Expression	Liver Activity[5]	Response to Cholesterol[6]
				Replicate 1	Replicate 2	Replicate 3				O. Barad *et al*[2]	P. Landgraf *et al*[3]	Vickers *et al*[4]		
1	HM-01	I1	hsa-miR-140-5p	-2.31	-1.93	-2.25	I	yes	yes	/	/	low	low	↑ HFD
2	HM-02	P11	hsa-miR-876-3p	-2.09	-2.11	-2.12	I	yes	yes	/	/	/	/	/
3	HM-02	B14	hsa-miR-519a	-2.08	-2.03	-2.10	I	yes	no	/	/	/	/	/
4	HM-01	A5	hsa-miR-133b	-2.04	-2.02	-1.93	II	yes	no	/	/	/	low	/
5	HM-01	A2	hsa-miR-133a	-1.88	-2.11	-1.96	II	yes	no	/	/	/	low	/
6	HM-03	A15	hsa-miR-1244	-2.03	-1.82	-2.08	II	yes	yes	/	/	/	/	/
7	HM-02	A19	hsa-miR-128	-2.04	-1.81	-2.05	II	yes	yes	/	/	low	high	↓ HFD
8	HM-01	O3	hsa-miR-520e	-1.97	-1.78	-1.83	II	yes	no	/	/	/	high	/
9	HM-02	J13	hsa-miR-520d-3p	-1.76	-1.73	-1.75	II	yes	no	/	/	/	/	/
10	HM-01	F17	hsa-miR-520b	-1.79	-1.60	-1.78	II	yes	no	/	/	/	/	/
11	HM-02	F3	hsa-miR-520c-3p	-1.81	-1.77	-1.52	II	yes	no	/	/	/	/	/
12	HM-01	O13	hsa-miR-520a-3p	-1.67	-1.80	-1.62	II	yes	no	/	/	/	/	/
13	HM-01	K11	hsa-miR-148b	-1.63	-1.80	-1.62	II	yes	yes	medium	very low	low	medium	↑↑↑ HFD
14	HM-01	K9	hsa-miR-148a	-1.69	-1.68	-1.61	II	yes	yes	medium	very low	high	medium	↑↑↑ HFD
15	HM-01	G5	hsa-miR-372	-1.45	-1.93	-1.61	II	yes	no	/	/	/	/	
16	HM-01	C15	hsa-miR-302b	-1.60	-1.76	-1.49	II	yes	no	/	/	/	/	
17	HM-01	D17	hsa-miR-373	-1.55	-1.77	-1.44	II	yes	no	/	/	/	/	
18	HM-01	B5	hsa-miR-302a	-1.43	-1.68	-1.61	II	yes	no	/	/	/	/	
19	HM-01	E12	hsa-miR-302c	-1.38	-1.67	-1.52	II	yes	no	/	/	/	/	
20	HM-01	B3	hsa-miR-302d	-1.09	-1.77	-1.50	II	yes	no	/	/	/	/	
21	HM-02	O19	hsa-miR-17	-1.48	-1.08	-1.60	II	yes	yes	/	medium	medium	/	↓ HFD
22	HM-01	J13	hsa-miR-330-5p	-1.28	-1.24	-1.42	II	yes	no	/	/	/	/	
23	HM-02	M1	hsa-miR-454	-1.08	-1.40	-1.41	II	yes	yes	/	/	/	/	
24	HM-05	F12	hsa-miR-4644	-1.08	-1.55	-1.00	II	yes	no	/	/	/	/	
25	HM-02	F22	hsa-miR-519d	-1.33	-0.92	-1.38	II	yes	yes	/	/	/	/	
26	HM-01	A9	hsa-miR-328	-1.14	-1.32	-1.12	II	yes	yes	/	/	medium	/	↑ HFD
27	HM-01	B13	hsa-miR-93	-1.06	-1.39	-1.13	II	yes	yes	low	very low	medium	medium	↑↑↑ HFD

28	HM-01	A21	hsa-miR-20a	-0.88	-1.35	-1.14	II	yes	yes	/	/	low	high	↑ HFD
29	HM-01	C5	hsa-miR-106b	-1.27	-1.13	-0.98	II	yes	yes	/	/	low	high	↑ HFD
30	HM-02	E13	hsa-miR-758	-1.24	-1.26	-0.85	II	yes	no	/	/	/	/	/
31	HM-01	E15	hsa-miR-153	-0.83	-1.25	-1.25	II	yes	no	/	/	/	high	/
32	HM-01	C8	hsa-miR-130a	-0.96	-1.22	-1.03	II	yes	yes	/	/	high	medium	↓↓ HFD
33	HM-01	I8	hsa-miR-326	-0.95	-1.01	-1.03	III	yes	no	/	/	/	high	/
34	HM-01	F21	hsa-miR-410	-0.84	-1.13	-0.89	III	yes	no	/	/	/	/	/
35	HM-02	E18	hsa-miR-185	-1.32	-0.95	-0.48	III	yes	no	/	medium	low	medium	–
36	HM-02	E12	hsa-miR-653	-0.92	-0.87	-0.92	III	yes	no	/	/		/	
37	HM-01	P3	hsa-miR-411	-0.70	-1.08	-0.92	III	yes	no	/	/		/	
38	HM-01	K6	hsa-miR-24	-0.97	-0.98	-0.61	III	yes	no	high	high	medium	low	↑↑↑ HFD
39	HM-01	G10	hsa-miR-19b	-0.74	-0.87	-0.76	III	yes	yes	/	very low	medium	high	↑↑↑ HFD
40	HM-01	K10	hsa-miR-27b	-0.86	-1.07	-0.26	III	yes	yes	medium	medium	medium	high	↑↑ HFD

Notes: Slashes denote those miRNAs not reported in each study. Minus signs indicate no change in expression. Number of arrows indicates levels of fold change in expression, high fat diet (HFD)/chow diet (CD) (↑ low to ↑↑↑ high fold-change).
[1]TargetScan, [2]Barad *et al* , [3]Landgra *et al.,* [4]Vickers *et al* [5]Arora *et al.*

Table 2

				Robust Z-score				
Number	Plate	Well	miRNA	Replicate 1	Replicate 2	Replicate 3	Average Robust '-score	Rank
1	HM-03	E1	hsa-miR-1255a	-3.209681303	-3.382890194	-3.091428844	-3.228000114	I
2	HM-03	I3	hsa-miR-1255b	-3.016979738	-3.147914181	-2.693712192	-2.952868704	I
3	HM-05	M1	hsa-miR-4652-5p	-2.900565971	-2.823968077	-2.949064402	-2.891199483	I
4	HM-04	C2	hsa-miR-3681	-2.706948805	-2.767203709	-2.969691767	-2.81461476	I
5	HM-02	L12	hsa-miR-342-5p	-2.776879425	-2.751693566	-2.79365765	-2.77407688	I
6	HM-03	C10	hsa-miR-1293	-2.778260441	-2.773749701	-2.768698403	-2.773569515	I
7	HM-03	N19	hsa-miR-3191	-2.809752784	-2.699266072	-2.720612102	-2.74321032	I
8	HM-03	B2	hsa-miR-3190	-2.646012537	-2.580964523	-2.702258698	-2.643078586	I
9	HM-04	G17	hsa-miR-3907	-2.690364228	-2.532473724	-2.696701071	-2.639846341	I
10	HM-03	L20	hsa-miR-3165	-2.569512983	-2.614007911	-2.484835397	-2.556118764	I
11	HM-03	L17	hsa-miR-3150	-2.644726155	-2.53383707	-2.44158049	-2.540047905	I
12	HM-05	I22	hsa-miR-3689d	-2.469044112	-2.46347802	-2.588983779	-2.507168637	I
13	HM-05	D14	hsa-miR-4438	-2.280161605	-2.708215479	-2.481381479	-2.489919521	I
14	HM-04	P9	hsa-miR-4747-5p	-2.4447603	-2.468239745	-2.514147716	-2.47571592	I
15	HM-01	A13	hsa-miR-7	-2.491442455	-2.626188554	-2.225504264	-2.447711758	I
16	HM-03	O17	hsa-miR-1204	-2.461842325	-2.539909163	-2.335968606	-2.445906698	I
17	HM-03	K22	hsa-miR-205*	-2.430120398	-2.518957651	-2.382407381	-2.443828477	I
18	HM-04	O21	hsa-miR-3918	-1.833886184	-2.486387803	-2.677799507	-2.332691165	I
19	HM-05	M7	hsa-miR-4667-5p	-2.352870252	-2.204442549	-2.318373156	-2.291895319	I
20	HM-01	L11	hsa-miR-363*	-2.310495627	-2.298951756	-2.190286772	-2.266578052	I
21	HM-03	C12	hsa-miR-1294	-2.318833988	-2.24271413	-2.219364614	-2.260304244	I
22	HM-01	J7	hsa-let-7a-2*	-3.396741646	-1.605689203	-1.75972987	-2.254053573	I
23	HM-04	A10	hsa-miR-3911	-2.326859342	-2.071208589	-2.360043085	-2.252703672	I
24	HM-05	M3	hsa-miR-4655-5p	-2.260810036	-2.187609747	-2.276743625	-2.241721136	I
25	HM-04	E10	rno-miR-2964	-2.064881584	-2.814329288	-1.815472393	-2.231561089	I
26	HM-02	J20	hsa-miR-19b-1*	-2.202739842	-2.262286387	-2.210357592	-2.22512794	I
27	HM-03	C19	hsa-miR-1185	-2.135622262	-2.264734401	-2.26038982	-2.220248828	I
28	HM-03	D17	hsa-miR-548s	-2.196936301	-2.211475026	-2.194317015	-2.200909448	I
29	HM-04	H3	hsa-miR-4701-3p	-2.238925432	-1.902903164	-2.372429924	-2.171419507	I
30	HM-01	I1	hsa-miR-140-5p	-2.310196736	-1.932993019	-2.249446184	-2.164211979	I
31	HM-05	K13	hsa-miR-4425	-1.957902147	-2.299183286	-2.230984572	-2.162690002	I
32	HM-05	K15	hsa-miR-4714-5p	-2.263436869	-2.186151821	-2.017809505	-2.155799398	I
33	HM-01	E14	hsa-miR-519c-3p	-1.852520576	-2.137453557	-2.463767179	-2.151247104	I
34	HM-03	K4	hsa-miR-1973	-2.095337939	-2.09229791	-2.245051212	-2.144229021	I
35	HM-02	A10	hsa-miR-624	-2.298842291	-1.995000683	-2.101441241	-2.131761405	I
36	HM-02	O21	hsa-miR-544	-2.046430225	-2.126431866	-2.195889012	-2.122917035	I
37	HM-03	H12	hsa-miR-3144-5p	-2.287130444	-1.949671851	-2.129521344	-2.12210788	I
38	HM-04	O5	hsa-miR-3926	-2.110938555	-1.999067861	-2.244004637	-2.118003684	I
39	HM-02	P11	hsa-miR-876-3p	-2.085346784	-2.111813959	-2.118075004	-2.105078582	I
40	HM-05	I17	hsa-miR-4527	-2.082271768	-1.984442972	-2.228637564	-2.098450768	I
41	HM-01	L20	hsa-miR-609	-2.063756592	-2.165310759	-2.065013059	-2.098026803	I
42	HM-02	F10	hsa-miR-519b-3p	-2.111103943	-2.008598201	-2.152743433	-2.090815192	I
43	HM-04	P12	hsa-miR-4522	-2.146286517	-1.860064325	-2.238867521	-2.081739454	I
44	HM-02	I20	hsa-miR-367*	-2.069463937	-2.073191779	-2.079407642	-2.074021119	I
45	HM-05	A6	hsa-miR-4690-5p	-2.635407273	-1.652076411	-1.917311719	-2.068265135	I
46	HM-02	B14	hsa-miR-519a	-2.076790745	-2.025372465	-2.097936693	-2.066699968	I
47	HM-01	N10	hsa-miR-640	-2.279160971	-2.022429998	-1.893679009	-2.065089993	I
48	HM-02	C8	hsa-miR-19b-2*	-2.055090714	-2.053284112	-2.080895651	-2.063090159	I
49	HM-01	K17	hsa-miR-451	-2.07297483	-2.014390169	-2.06913086	-2.052165286	I
50	HM-04	H2	hsa-miR-4450	-2.123710733	-1.925877431	-2.081639894	-2.043742686	I
51	HM-05	G17	hsa-miR-4664-5p	-2.029955265	-2.159639046	-1.934587414	-2.041393909	I
52	HM-04	O17	hsa-miR-3674	-2.046680655	-2.072134844	-1.995818447	-2.038211315	I
53	HM-02	A6	hsa-miR-19a*	-1.896317313	-1.953284356	-2.211475131	-2.020358934	I
54	HM-03	E13	hsa-miR-1262	-1.888022138	-2.03381153	-2.132156376	-2.017996681	I
55	HM-03	H9	hsa-miR-3149	-2.140729878	-1.97116692	-1.929658457	-2.013851751	I
56	HM-05	M11	hsa-miR-4697-5p	-2.00591981	-2.130668231	-1.890093697	-2.008893913	I
57	HM-03	E12	hsa-miR-1302	-2.03984022	-1.953347745	-2.021976668	-2.005054878	I
58	HM-03	N3	hsa-miR-3140	-2.080340323	-1.919338274	-2.007529498	-2.002402698	I
59	HM-05	B7	hsa-miR-4694-5p	-1.99108583	-1.956507988	-2.057976553	-2.00185679	I
60	HM-01	A5	hsa-miR-133b	-2.043219379	-2.021202135	-1.934964473	-1.999795329	II
61	HM-01	I9	hsa-miR-147	-2.008158202	-1.931734608	-2.046243113	-1.995378641	II
62	HM-01	A2	hsa-miR-133a	-1.881434015	-2.105694419	-1.959536126	-1.98222152	II

63	HM-01	P22	hsa-miR-644	-1.968237228	-1.967786763	-1.996279546	-1.977434512	II
64	HM-03	A15	hsa-miR-1244	-2.028418781	-1.824805301	-2.078453994	-1.977226025	II
65	HM-04	D17	hsa-miR-4675	-2.012043347	-1.903229517	-2.016292849	-1.977188571	II
66	HM-04	C17	hsa-miR-3612	-1.919212946	-1.927540518	-2.078491572	-1.975081679	II
67	HM-03	B11	hsa-miR-3157	-1.784150628	-2.033020004	-2.101939532	-1.973036721	II
68	HM-05	O5	hsa-miR-3922-5p	-2.095462069	-1.904598565	-1.914455746	-1.97150546	II
69	HM-02	A19	hsa-miR-128	-2.042047562	-1.80562867	-2.049300133	-1.965658788	II
70	HM-05	P19	hsa-miR-4716-3p	-1.764110036	-2.13226995	-1.974317086	-1.956899024	II
71	HM-03	B9	hsa-miR-4259	-1.968511903	-1.89879361	-2.00280763	-1.956704381	II
72	HM-05	F14	hsa-miR-4673	-1.849093451	-2.048934802	-1.958242881	-1.952090378	II
73	HM-03	P9	hsa-miR-3127	-2.038605676	-1.778443346	-2.033736728	-1.950261917	II
74	HM-05	H13	hsa-miR-4746-3p	-1.830904468	-1.884548596	-2.128441393	-1.947964819	II
75	HM-04	J20	hsa-miR-4786-3p	-1.879998715	-1.903638726	-2.048351834	-1.943996425	II
76	HM-04	J3	hsa-miR-4790-3p	-1.981585742	-1.882251099	-1.94022232	-1.934686387	II
77	HM-05	A22	hsa-miR-4695-3p	-1.995994826	-1.620446279	-2.175966982	-1.930802695	II
78	HM-03	K2	hsa-miR-2110	-1.994566548	-1.844760916	-1.901832083	-1.913719849	II
79	HM-04	K7	hsa-miR-3913	-1.849091408	-1.839822537	-2.028597161	-1.905837035	II
80	HM-03	J22	hsa-miR-3186-3p	-1.897996663	-1.915182306	-1.864562529	-1.892580499	II
81	HM-03	C6	hsa-miR-1291	-1.951858001	-1.82444395	-1.866082482	-1.880794811	II
82	HM-03	B19	hsa-miR-3134	-1.957994288	-1.709327209	-1.97364626	-1.880322586	II
83	HM-04	I3	hsa-miR-3681*	-1.814934468	-1.733927486	-2.077209086	-1.875357013	II
84	HM-04	O22	hsa-miR-3136-3p	-1.762602706	-1.980704219	-1.879864109	-1.874390344	II
85	HM-02	I4	hsa-miR-92a-2*	-1.851925973	-1.720112495	-2.024384789	-1.865474419	II
86	HM-01	O3	hsa-miR-520e	-1.972289449	-1.776169143	-1.829223697	-1.85922743	II
87	HM-02	C2	hsa-miR-208b	-1.71616061	-1.849724452	-2.003755399	-1.85654682	II
88	HM-03	P6	hsa-miR-3170	-1.976887245	-1.828189879	-1.686301336	-1.830459487	II
89	HM-01	L8	hsa-miR-650	-2.006974206	-1.827341395	-1.656617081	-1.830310894	II
90	HM-05	C6	hsa-miR-4725-3p	-1.80597643	-1.806131223	-1.869944101	-1.827350585	II
91	HM-04	O7	hsa-miR-3915	-1.602942461	-1.774420294	-2.089030639	-1.822131131	II
92	HM-05	C19	hsa-miR-4689	-1.843930274	-1.760678224	-1.856446011	-1.820351503	II
93	HM-04	O3	hsa-miR-3605-5p	-1.815306605	-1.763135705	-1.877760803	-1.818734371	II
94	HM-05	F2	hsa-miR-4735-3p	-1.774112753	-1.830631518	-1.834387553	-1.813043941	II
95	HM-05	B22	hsa-miR-4701-5p	-1.965353758	-1.587082328	-1.855770068	-1.802735384	II
96	HM-04	E8	hsa-miR-3622a-5p	-2.074788788	-1.351614716	-1.943783223	-1.790062242	II
97	HM-05	K9	hsa-miR-4676-3p	-1.727475316	-1.795656358	-1.831967956	-1.78503321	II
98	HM-04	J15	hsa-miR-4738-5p	-2.02199457	-1.503906842	-1.805200643	-1.777034019	II
99	HM-01	I4	hsa-miR-208a	-1.811356846	-1.77181419	-1.72928977	-1.770820268	II
100	HM-05	G4	hsa-miR-4677-5p	-1.887501559	-1.802043047	-1.62164743	-1.770397346	II
101	HM-05	F9	hsa-miR-3160-5p	-2.031821522	-1.770011067	-1.484014662	-1.761949084	II
102	HM-02	K6	hsa-miR-625	-1.680428981	-1.706139035	-1.882438212	-1.75633541	II
103	HM-05	D17	hsa-miR-4513	-1.840889663	-1.836047629	-1.571310146	-1.749415813	II
104	HM-02	J13	hsa-miR-520d-3p	-1.758868367	-1.733876527	-1.745135076	-1.74595999	II
105	HM-03	K16	hsa-miR-365*	-1.721900241	-1.730581699	-1.770133605	-1.740871849	II
106	HM-01	L9	hsa-miR-499-5p	-1.772552712	-1.644090545	-1.784184935	-1.733609397	II
107	HM-05	B5	hsa-miR-3177-5p	-1.372540192	-1.918528697	-1.899761565	-1.730276818	II
108	HM-01	F17	hsa-miR-520b	-1.787801167	-1.604461934	-1.776292363	-1.722851821	II
109	HM-02	E5	hsa-miR-765	-1.664111691	-1.774585054	-1.677918855	-1.705538533	II
110	HM-02	F3	hsa-miR-520c-3p	-1.813117317	-1.772217021	-1.521032786	-1.702122375	II
111	HM-01	O13	hsa-miR-520a-3p	-1.666273873	-1.802271274	-1.619309851	-1.695951666	II
112	HM-03	N2	hsa-miR-3179	-1.797411089	-1.782821727	-1.504796967	-1.695009928	II
113	HM-03	J20	ppy-miR-1269	-1.756934039	-1.746595961	-1.577338391	-1.693622797	II
114	HM-05	C12	hsa-miR-4525	-1.751857562	-1.710858207	-1.614054974	-1.692256914	II
115	HM-04	L22	hsa-miR-4658	-1.674661447	-1.663204856	-1.733608428	-1.690491577	II
116	HM-01	K11	hsa-miR-148b	-1.62630329	-1.802069367	-1.623674524	-1.684015727	II
117	HM-02	K21	hsa-miR-224	-1.754619168	-1.687385479	-1.595675913	-1.679226853	II
118	HM-03	F2	hsa-miR-3186-5p	-1.577374055	-1.683519624	-1.756784425	-1.672559368	II
119	HM-03	B7	hsa-miR-4270	-1.834464067	-1.704996238	-1.470379962	-1.669946755	II
120	HM-05	C1	hsa-miR-4654	-1.653878546	-1.853962954	-1.483673849	-1.663838449	II
121	HM-01	G5	hsa-miR-372	-1.454040037	-1.926476882	-1.608574192	-1.66303037	II
122	HM-01	G19	hsa-miR-380*	-1.520397355	-1.777139274	-1.687490212	-1.661675613	II
123	HM-01	K9	hsa-miR-148a	-1.685567485	-1.676518937	-1.612944096	-1.658343506	II
124	HM-05	O1	hsa-miR-4712-3p	-1.777491867	-1.594477002	-1.587828142	-1.653265671	II
125	HM-04	A11	hsa-miR-3680	-1.925490304	-1.268164771	-1.76192918	-1.651861418	II
126	HM-03	E14	hsa-miR-1206	-1.696381544	-1.63978279	-1.613348859	-1.649837731	II
127	HM-04	N16	hsa-miR-4520a-3p	-1.778069104	-1.423621713	-1.743393645	-1.648361487	II
128	HM-01	B2	hsa-miR-552	-1.584268445	-1.741632939	-1.60651749	-1.644139624	II
129	HM-03	K1	hsa-miR-1272	-1.694589471	-1.567000257	-1.669335525	-1.643641751	II

130	HM-02	J10	hsa-miR-629	-1.558801392	-1.62615586	-1.703902344	-1.629619865	II
131	HM-03	B6	hsa-miR-3154	-1.647659209	-1.557705192	-1.668314568	-1.624559656	II
132	HM-01	C15	hsa-miR-302b	-1.602368744	-1.757831191	-1.492617293	-1.617605743	II
133	HM-01	B4	hsa-miR-588	-1.564350804	-1.737379799	-1.546223392	-1.615984665	II
134	HM-05	P1	hsa-miR-4772-5p	-1.840629054	-1.600305645	-1.395601918	-1.612178872	II
135	HM-01	O1	hsa-miR-520g	-1.259415042	-1.857057367	-1.69604212	-1.60417151	II
136	HM-04	F9	hsa-miR-4720-3p	-1.568311643	-1.600331328	-1.610291866	-1.592978279	II
137	HM-01	D17	hsa-miR-373	-1.55360632	-1.77477107	-1.436333697	-1.588237029	II
138	HM-05	C9	hsa-miR-4743	-1.811794488	-1.55620184	-1.395362933	-1.58778642	II
139	HM-01	M18	hsa-miR-432*	-1.768246943	-1.474648831	-1.517179906	-1.586691893	II
140	HM-01	J18	hsa-miR-659	-1.597783279	-1.504691885	-1.638210314	-1.580228493	II
141	HM-01	B5	hsa-miR-302a	-1.430569686	-1.676749531	-1.6088655	-1.572061572	II
142	HM-05	N5	hsa-miR-4712-5p	-1.567159209	-1.651888864	-1.478578621	-1.565875565	II
143	HM-01	C10	hsa-miR-507	-1.483456453	-1.534974494	-1.639617633	-1.55268286	II
144	HM-05	C14	hsa-miR-1587	-1.556551115	-1.553473358	-1.511133924	-1.540386132	II
145	HM-02	H12	hsa-let-7g*	-1.428613419	-1.505027007	-1.651477618	-1.528372681	II
146	HM-04	P3	hsa-miR-3545-5p	-0.909042123	-1.693259223	-1.972924854	-1.5250754	II
147	HM-01	E12	hsa-miR-302c	-1.383009759	-1.667194691	-1.520812736	-1.523672396	II
148	HM-02	O1	hsa-miR-193b	-1.594628508	-1.542473737	-1.433779137	-1.523627127	II
149	HM-04	I11	hsa-miR-3657	-1.514639405	-1.429552837	-1.623115155	-1.522435799	II
150	HM-03	H1	hsa-miR-3147	-1.487384969	-1.51080409	-1.508600021	-1.502263027	II
151	HM-05	E18	hsa-miR-4493	-1.558707142	-1.706289557	-1.197392644	-1.487463114	II
152	HM-01	B3	hsa-miR-302d	-1.090645045	-1.766887607	-1.504676583	-1.454069745	II
153	HM-03	K20	hsa-miR-2113	-1.532122284	-1.572570408	-1.215015698	-1.439902797	II
154	HM-01	A15	hsa-miR-378*	-1.185140507	-1.621978195	-1.509964841	-1.439027848	II
155	HM-05	E15	hsa-miR-4730	-1.643997667	-1.189844918	-1.47234641	-1.435396332	II
156	HM-05	N1	hsa-miR-4765	-1.447294738	-1.359807753	-1.480068322	-1.429056938	II
157	HM-05	E10	hsa-miR-4713-5p	-1.802122273	-1.332325831	-1.147632357	-1.427360154	II
158	HM-05	D9	hsa-miR-2467-3p	-1.401571121	-1.491315344	-1.38160198	-1.424829482	II
159	HM-03	F10	hsa-miR-3119	-1.359753318	-1.428238426	-1.478875667	-1.422289137	II
160	HM-04	K8	hsa-miR-3605-3p	-1.448146221	-1.324419002	-1.462324836	-1.41163002	II
161	HM-02	F11	hsa-miR-193b*	-1.411728093	-1.37006378	-1.44523663	-1.409009501	II
162	HM-01	G11	hsa-miR-297	-1.269425704	-1.694175156	-1.240070817	-1.401223892	II
163	HM-04	H16	hsa-miR-4487	-1.54539505	-1.164388998	-1.490416573	-1.400066874	II
164	HM-02	P4	hsa-miR-541	-1.420007095	-1.276917498	-1.502226138	-1.39971691	II
165	HM-03	P19	hsa-miR-3139	-1.497396598	-1.402817389	-1.287268411	-1.395827466	II
166	HM-02	O19	hsa-miR-17	-1.484538402	-1.079581255	-1.597718354	-1.387279337	II
167	HM-02	G3	hsa-miR-526b*	-1.399441154	-1.715143219	-1.042694215	-1.385759529	II
168	HM-05	J13	hsa-miR-4667-3p	-1.214125607	-1.583272762	-1.324311417	-1.373903262	II
169	HM-04	C10	hsa-miR-3680*	-1.347659375	-1.35197462	-1.421075503	-1.373569833	II
170	HM-03	A20	hsa-miR-1288	-1.285111741	-1.37001816	-1.430848116	-1.361992672	II
171	HM-04	C1	hsa-miR-3163	-1.136557015	-1.320101415	-1.628998457	-1.361885629	II
172	HM-02	I16	hsa-miR-422a	-1.317537724	-1.332041502	-1.426595594	-1.35872494	II
173	HM-03	I13	hsa-miR-1269	-1.660390126	-0.975129764	-1.435591988	-1.357037293	II
174	HM-04	A15	hsa-miR-544b	-1.337852723	-1.298467413	-1.42950295	-1.355274362	II
175	HM-05	C7	hsa-miR-4781-3p	-1.547573331	-1.386263803	-1.121460658	-1.351765931	II
176	HM-01	A20	hsa-miR-18b	-1.282276019	-1.44853586	-1.31083038	-1.347214086	II
177	HM-02	O12	hsa-miR-144*	-1.188867661	-1.4892187	-1.363052218	-1.347046193	II
178	HM-03	M16	hsa-miR-2116	-1.381207577	-1.354168475	-1.29608192	-1.343819324	II
179	HM-05	J21	hsa-miR-4731-5p	-1.366062116	-1.308168194	-1.345148647	-1.339792986	II
180	HM-03	O19	hsa-miR-1282	-1.511772127	-1.402798368	-1.102380305	-1.3389836	II
181	HM-05	F18	hsa-miR-378i	-1.343647297	-1.300490241	-1.353842172	-1.332659903	II
182	HM-04	B11	hsa-miR-4802-5p	-1.389402137	-1.202989177	-1.399358572	-1.330583295	II
183	HM-01	H14	hsa-miR-637	-1.150278182	-1.509963723	-1.309028449	-1.323090118	II
184	HM-03	D4	hsa-miR-3162	-1.124648686	-1.415718936	-1.426208651	-1.322192091	II
185	HM-03	N11	hsa-miR-3187	-1.22734619	-1.487364996	-1.241760302	-1.318823829	II
186	HM-04	H20	hsa-miR-4687-3p	-1.224867473	-1.233764055	-1.497187218	-1.318606249	II
187	HM-01	M12	hsa-miR-517c	-1.300833686	-1.454263758	-1.187234623	-1.314110689	II
188	HM-03	M21	hsa-miR-1208	-1.463997305	-1.448994115	-1.026416569	-1.313135996	II
189	HM-01	J13	hsa-miR-330-5p	-1.283836985	-1.240257059	-1.415200713	-1.313098252	II
190	HM-03	C5	hsa-miR-1250	-1.478946374	-1.214561084	-1.239019443	-1.3108423	II
191	HM-02	D7	hsa-miR-92a-1*	-1.385245613	-1.152628014	-1.387921674	-1.308598434	II
192	HM-02	M1	hsa-miR-454	-1.077560809	-1.398563052	-1.412476631	-1.296200164	II
193	HM-03	E10	hsa-miR-1178	-1.243383173	-1.362273832	-1.273192417	-1.292949807	II
194	HM-01	P19	hsa-miR-654-5p	-1.338823114	-1.463997866	-1.073633011	-1.29215133	II
195	HM-02	I19	hsa-miR-183*	-1.365072397	-1.186073239	-1.312082842	-1.287742826	II
196	HM-02	B5	hsa-miR-517a	-1.283377059	-1.235687593	-1.338089647	-1.2857181	II

197	HM-05	J4	hsa-miR-4781-5p	-1.45106976	-1.137406706	-1.263425207	-1.283967224	II
198	HM-03	L6	hsa-miR-3175	-1.240971006	-1.288310209	-1.31096435	-1.280081855	II
199	HM-05	C17	hsa-miR-4740-5p	-1.270966305	-1.350400061	-1.213246686	-1.278204351	II
200	HM-03	E16	hsa-miR-1180	-1.219134583	-1.246184494	-1.368010836	-1.277776638	II
201	HM-03	D3	hsa-miR-4313	-1.373577136	-1.181247757	-1.278153552	-1.277659481	II
202	HM-02	J16	hsa-miR-145*	-1.270146605	-1.229010701	-1.33213918	-1.277098829	II
203	HM-05	H18	hsa-miR-4460	-1.371188167	-1.266605574	-1.185725931	-1.274506557	II
204	HM-02	I22	hsa-miR-489	-1.238261589	-1.104696415	-1.470820799	-1.271259601	II
205	HM-03	E3	hsa-miR-1256	-1.337352325	-1.104764166	-1.355231654	-1.265782715	II
206	HM-04	B17	hsa-miR-4435	-1.311727573	-1.221795498	-1.249863953	-1.261129008	II
207	HM-03	D2	hsa-miR-378b	-1.215027549	-1.273919473	-1.289120553	-1.259355859	II
208	HM-04	B21	hsa-miR-3975	-1.35155776	-1.27809592	-1.134487665	-1.254713782	II
209	HM-05	C8	hsa-miR-3972	-1.222902861	-1.198012866	-1.338446536	-1.253120754	II
210	HM-04	P17	hsa-miR-4665-5p	-1.280320688	-1.161482174	-1.301847344	-1.247883402	II
211	HM-05	B10	hsa-miR-4779	-1.195896564	-1.435176082	-1.106535291	-1.245869312	II
212	HM-04	C13	hsa-miR-3136	-1.088771612	-1.223550662	-1.403485424	-1.238602566	II
213	HM-01	N18	hsa-miR-555	-1.364945043	-1.170447086	-1.165792816	-1.233728315	II
214	HM-04	P16	hsa-miR-378h	-1.186490874	-1.18377722	-1.330017357	-1.233428484	II
215	HM-04	E21	hsa-miR-3665	-1.353545512	-1.077956043	-1.265957419	-1.232486325	II
216	HM-05	N11	hsa-miR-4677-3p	-1.173230641	-1.423086146	-1.086812158	-1.227709648	II
217	HM-03	K13	hsa-miR-1202	-1.327439134	-1.180891862	-1.173756229	-1.227362408	II
218	HM-03	J7	hsa-miR-3118	-1.188627079	-1.269780778	-1.219380876	-1.225929578	II
219	HM-01	G7	hsa-miR-132	-0.92460311	-1.380564484	-1.350843662	-1.218670419	II
220	HM-05	F12	hsa-miR-4644	-1.084459549	-1.547512948	-1.004916106	-1.212296201	II
221	HM-02	P15	hsa-miR-148b*	-1.082018906	-1.25539874	-1.285550079	-1.207655909	II
222	HM-02	H15	hsa-miR-93*	-1.135302501	-1.243667655	-1.24384553	-1.207605229	II
223	HM-02	F22	hsa-miR-519d	-1.327189365	-0.917613947	-1.376973225	-1.207258846	II
224	HM-01	D10	hsa-miR-491-5p	-1.040460343	-1.35086467	-1.228951774	-1.206758929	II
225	HM-02	L5	hsa-miR-628-5p	-1.079242909	-1.326319432	-1.208950193	-1.204837511	II
226	HM-04	A14	hsa-miR-3691	-1.477035074	-0.849946989	-1.272486866	-1.199822976	II
227	HM-02	L3	hsa-miR-338-5p	-1.215276292	-1.222582665	-1.159123527	-1.198994162	II
228	HM-03	C13	hsa-miR-664*	-1.291522468	-1.086253149	-1.217513716	-1.198429778	II
229	HM-02	F18	hsa-miR-18a	-1.175333977	-1.25774601	-1.148691332	-1.193923773	II
230	HM-01	A9	hsa-miR-328	-1.135526479	-1.321266155	-1.123025813	-1.193272816	II
231	HM-05	E2	hsa-miR-3688-5p	-1.411953882	-1.211711296	-0.95562322	-1.193096133	II
232	HM-01	B13	hsa-miR-93	-1.058243512	-1.393525437	-1.125702357	-1.192490436	II
233	HM-01	K8	hsa-miR-34b*	-1.423108568	-1.120164311	-1.022091602	-1.188454827	II
234	HM-04	K3	hsa-miR-3689a-5p	-1.118209872	-1.31140185	-1.118796636	-1.182802786	II
235	HM-05	G2	hsa-miR-2682*	-1.360571124	-0.852189242	-1.326533565	-1.179764643	II
236	HM-03	I17	hsa-miR-1238	-1.357641402	-1.323043951	-0.844459903	-1.175048419	II
237	HM-02	E4	hsa-miR-323b-5p	-1.391627809	-0.937644984	-1.191396923	-1.173556572	II
238	HM-01	G8	hsa-miR-493*	-1.160359142	-1.233789681	-1.109892563	-1.168013796	II
239	HM-01	K15	hsa-miR-517b	-1.177343754	-1.108480924	-1.214090505	-1.166638394	II
240	HM-04	C6	hsa-miR-3679-3p	-1.387295688	-1.037371736	-1.070314968	-1.164994131	II
241	HM-03	B16	hsa-miR-3137	-1.094834636	-1.093548932	-1.304853437	-1.164412335	II
242	HM-01	J14	hsa-miR-425	-0.944496222	-1.274817794	-1.266263058	-1.161859025	II
243	HM-05	O10	hsa-miR-4474-3p	-0.993292889	-1.231903964	-1.252376553	-1.159191135	II
244	HM-04	F2	hsa-miR-4745-3p	-1.276108071	-1.034729318	-1.155587673	-1.155475021	II
245	HM-03	J1	hsa-miR-3199	-1.198666646	-1.090629941	-1.165965865	-1.15175415	II
246	HM-04	P18	hsa-miR-4445	-1.105536099	-1.203307116	-1.144197158	-1.151013458	II
247	HM-04	E17	hsa-miR-3607-5p	-1.484007296	-0.95882992	-1.008695693	-1.15051097	II
248	HM-04	D1	hsa-miR-4680-5p	-1.127749775	-1.084474638	-1.238753936	-1.150326116	II
249	HM-02	F17	hsa-miR-450b-3p	-1.193375887	-1.068563273	-1.172692119	-1.144877093	II
250	HM-03	C4	hsa-miR-1207-5p	-1.120420134	-1.30923899	-1.000937198	-1.143532107	II
251	HM-04	L12	hsa-miR-4524	-0.884573273	-1.21178866	-1.317355534	-1.137905822	II
252	HM-03	F12	hsa-miR-3160	-1.249651168	-1.097053187	-1.066743142	-1.137815832	II
253	HM-02	F1	hsa-miR-202	-1.025775063	-1.162377922	-1.209386215	-1.132513066	II
254	HM-03	A16	hsa-miR-1286	-1.147289383	-1.268508915	-0.980108888	-1.131969062	II
255	HM-01	A21	hsa-miR-20a	-0.884025363	-1.354738918	-1.144591712	-1.127785331	II
256	HM-01	C5	hsa-miR-106b	-1.268143974	-1.12797139	-0.983898786	-1.126671383	II
257	HM-01	K18	hsa-miR-433	-1.355095375	-0.986691786	-1.031373869	-1.12438701	II
258	HM-03	I15	hsa-miR-1270	-1.125546387	-1.147818233	-1.077680237	-1.117014952	II
259	HM-02	E13	hsa-miR-758	-1.238321309	-1.262286508	-0.848456898	-1.116354905	II
260	HM-05	O20	hsa-miR-4684-3p	-1.025948878	-1.188650148	-1.127461927	-1.114020318	II
261	HM-02	B22	hsa-miR-23b*	-1.220144573	-1.042264057	-1.077411586	-1.113273405	II
262	HM-03	L18	hsa-miR-3184	-1.317174415	-1.221184756	-0.799806609	-1.112721927	II
263	HM-01	E15	hsa-miR-153	-0.828489955	-1.253444548	-1.254289908	-1.112074804	II

264	HM-01	E22	hsa-miR-296-5p	-1.151447043	-1.184835321	-0.991354676	-1.109212347	II
265	HM-02	K19	hsa-miR-579	-0.970488618	-1.039251418	-1.311423239	-1.107054425	II
266	HM-02	L7	hsa-miR-132*	-0.83114844	-1.10186601	-1.387614353	-1.106876268	II
267	HM-01	B20	hsa-miR-31	-0.982560346	-1.031367972	-1.290194993	-1.101374437	II
268	HM-01	I10	hsa-miR-124	-0.710146195	-1.274597282	-1.317416065	-1.100719847	II
269	HM-02	F6	hsa-miR-129*	-1.073899428	-1.045044634	-1.183128837	-1.100690966	II
270	HM-05	K6	hsa-miR-4684-5p	-1.166629134	-1.187919726	-0.944684684	-1.099744515	II
271	HM-04	C14	hsa-miR-3934	-1.100830705	-1.142353293	-1.049194012	-1.097459337	II
272	HM-05	D10	hsa-miR-4659b-3p	-1.286303319	-1.140064745	-0.861570133	-1.095979399	II
273	HM-04	L15	hsa-miR-4502	-1.025762102	-0.970681348	-1.289606391	-1.095349947	II
274	HM-04	K9	hsa-miR-3943	-1.019378809	-1.14328679	-1.115748787	-1.092804795	II
275	HM-02	G14	hsa-miR-452	-0.881739934	-1.204455443	-1.191709594	-1.09263499	II
276	HM-03	O6	hsa-miR-2117	-1.001757239	-1.182220457	-1.092721915	-1.092233204	II
277	HM-04	L7	hsa-miR-4703-3p	-1.09738902	-1.056706726	-1.113488195	-1.089194647	II
278	HM-05	H9	hsa-miR-4430	-1.111587906	-0.893050578	-1.255501887	-1.086713457	II
279	HM-01	C2	hsa-miR-497	-0.674789253	-1.32967805	-1.229311933	-1.077926412	II
280	HM-02	F20	hsa-miR-892b	-1.148617767	-1.13385003	-0.94934178	-1.077269859	II
281	HM-04	G9	hsa-miR-3150b	-1.063555397	-0.970448917	-1.190911511	-1.074971942	II
282	HM-04	I14	hsa-miR-3922	-1.12492918	-1.021533189	-1.076494065	-1.074318811	II
283	HM-01	C8	hsa-miR-130a	-0.964601368	-1.219118048	-1.027680705	-1.070466707	II
284	HM-04	I19	hsa-miR-3682	-0.619152798	-1.322908575	-1.247079584	-1.063046986	II
285	HM-02	D5	hsa-miR-185*	-1.039055739	-1.02613659	-1.118870563	-1.061354297	II
286	HM-02	O8	hsa-miR-29b-2*	-0.972879942	-1.069015179	-1.122826207	-1.05490711	II
287	HM-05	I11	hsa-miR-4693-3p	-1.116181077	-0.888204035	-1.159619074	-1.054668062	II
288	HM-03	J2	hsa-miR-3155	-0.933797528	-1.482904342	-0.736624572	-1.051108814	II
289	HM-05	L21	hsa-miR-4664-3p	-1.052304301	-1.095809931	-0.985660336	-1.044591523	II
290	HM-01	C13	hsa-miR-129-3p	-1.055142169	-1.153338665	-0.913694161	-1.040724998	II
291	HM-05	F22	hsa-miR-4784	-1.021083282	-1.011052716	-1.077458984	-1.036531661	II
292	HM-02	N18	hsa-miR-450b-5p	-0.888674809	-1.099264674	-1.119697663	-1.035879048	II
293	HM-05	P17	hsa-miR-3064-3p	-1.139759519	-0.962084355	-1.004911829	-1.035585234	II
294	HM-04	H6	hsa-miR-4642	-1.153915062	-0.904978809	-1.047219701	-1.035371191	II
295	HM-01	D14	hsa-miR-601	-0.901755641	-1.168689721	-1.032944298	-1.03446322	II
296	HM-05	B18	hsa-miR-4669	-1.230783691	-1.07215434	-0.795668319	-1.032868783	II
297	HM-02	N3	hsa-miR-636	-0.955413675	-1.118312405	-1.020848617	-1.031524899	II
298	HM-02	E6	hsa-miR-30c-1*	-1.069665177	-0.962341465	-1.03901474	-1.023673794	II
299	HM-05	F3	hsa-miR-4708-5p	-0.988783075	-1.031756623	-1.046895238	-1.022478312	II
300	HM-01	H3	hsa-miR-193a-3p	-1.301444837	-0.657739758	-1.106828162	-1.022004253	II
301	HM-02	O10	hsa-miR-483-5p	-0.809976074	-1.092644808	-1.141888248	-1.014836377	II
302	HM-05	G1	hsa-miR-378d	-1.384496728	-0.669844089	-0.988980124	-1.014440314	II
303	HM-05	C5	hsa-miR-3545-3p	-0.97011928	-1.004222808	-1.060891713	-1.0117446	II
304	HM-02	A14	hsa-miR-29b-1*	-1.025156769	-0.916764702	-1.08057302	-1.007498164	II
305	HM-04	A16	hsa-miR-3664	-1.089211288	-0.97115098	-0.96075813	-1.007040133	II
306	HM-05	I3	hsa-miR-4505	-1.013741677	-0.847818275	-1.149163501	-1.003574484	II
307	HM-05	N17	hsa-miR-4515	-0.9003029	-1.148833999	-0.960477812	-1.003204904	II
308	HM-05	I7	hsa-miR-4788	-0.99369584	-0.841570117	-1.173729167	-1.002998375	II
309	HM-05	I5	hsa-miR-4681	-0.884680093	-1.001658271	-1.120048861	-1.002129075	II
310	HM-04	L11	hsa-miR-4459	-1.146487816	-0.715485926	-1.133351247	-0.998441663	III
311	HM-01	I8	hsa-miR-326	-0.947064699	-1.013210351	-1.032601301	-0.99762545	III
312	HM-04	D16	hsa-miR-4749-5p	-1.022527441	-0.934103755	-1.035107068	-0.997246088	III
313	HM-04	B5	hsa-miR-4718	-0.925052514	-0.931411117	-1.131021322	-0.995828318	III
314	HM-02	L2	hsa-miR-744*	-0.928262257	-1.049704579	-0.986277669	-0.988081502	III
315	HM-01	M10	hsa-miR-195	-1.103294622	-0.960512647	-0.900202808	-0.988003359	III
316	HM-01	N3	hsa-miR-646	-1.038977971	-0.977094423	-0.928127838	-0.981400077	III
317	HM-04	D9	hsa-miR-4432	-0.953899734	-0.999110652	-0.971080045	-0.97469681	III
318	HM-02	K17	hsa-miR-671-3p	-1.010065401	-1.090100705	-0.823382982	-0.974516363	III
319	HM-01	O14	hsa-miR-199a-5p	-1.105691194	-0.973409941	-0.840963165	-0.973354767	III
320	HM-04	H17	hsa-miR-4688	-1.177183421	-0.767090917	-0.9563529	-0.966875746	III
321	HM-03	C14	hsa-miR-1206	-1.033710826	-0.898936235	-0.965450253	-0.966032438	III
322	HM-02	B16	hsa-miR-510	-1.162353311	-0.858587347	-0.870831334	-0.963923998	III
323	HM-01	P13	hsa-miR-557	-0.933790849	-1.032828875	-0.924918061	-0.963845928	III
324	HM-03	P12	hsa-miR-3176	-1.099027698	-0.95036835	-0.840574737	-0.963323595	III
325	HM-03	D1	hsa-miR-3131	-0.901557092	-1.092808326	-0.894860886	-0.963075435	III
326	HM-02	P5	hsa-miR-149*	-0.762397657	-0.91890423	-1.207820626	-0.963040838	III
327	HM-02	H10	hsa-miR-486-3p	-1.109340865	-0.72392094	-1.048641769	-0.960634525	III
328	HM-05	C18	hsa-miR-3942-3p	-0.836971141	-1.140712487	-0.903241404	-0.960308344	III
329	HM-05	D4	hsa-miR-4436a	-1.047597278	-0.916150446	-0.913559024	-0.959102249	III
330	HM-05	O11	hsa-miR-4518	-0.900373586	-0.949009605	-1.013809487	-0.954397559	III

331	HM-01	F21	hsa-miR-410	-0.837858483	-1.128995226	-0.887269242	-0.951374317	III
332	HM-03	J14	hsa-miR-4321	-1.064132141	-0.887201559	-0.898763352	-0.950032351	III
333	HM-04	N13	hsa-miR-4800-5p	-1.129367947	-0.812758195	-0.907433882	-0.949853341	III
334	HM-01	D8	hsa-miR-642a	-0.885675195	-1.002613361	-0.9528775	-0.947055352	III
335	HM-04	L9	hsa-miR-4715-5p	-0.879220472	-0.975021192	-0.980618258	-0.944953307	III
336	HM-02	L18	hsa-miR-576-3p	-0.846767046	-0.802403672	-1.178640245	-0.942603654	III
337	HM-05	L9	hsa-miR-4650-5p	-1.063771164	-0.916568592	-0.839626848	-0.939988868	III
338	HM-03	E22	hsa-miR-1908	-0.929251765	-0.930531859	-0.955240692	-0.938341438	III
339	HM-04	N14	hsa-miR-4728-5p	-0.594333545	-1.17364633	-1.04663568	-0.938205185	III
340	HM-05	M8	hsa-miR-4782-3p	-0.855326107	-0.946258629	-1.004987819	-0.935524185	III
341	HM-05	E19	hsa-miR-4507	-0.913761887	-1.14195252	-0.749545447	-0.935086618	III
342	HM-05	J7	hsa-miR-4439	-1.082993264	-0.656999358	-1.048679816	-0.929557479	III
343	HM-05	D20	hsa-miR-4750	-0.956539449	-0.873692746	-0.951411549	-0.927214581	III
344	HM-04	K2	hsa-miR-3925	-0.749655355	-0.94891974	-1.081829424	-0.926801506	III
345	HM-02	O22	hsa-miR-30c-2*	-0.968719134	-0.906139703	-0.903902953	-0.92625393	III
346	HM-05	A3	hsa-miR-4427	-0.758674518	-0.806152995	-1.213920018	-0.926249177	III
347	HM-02	C15	hsa-miR-769-3p	-1.017032761	-0.840256043	-0.908061291	-0.921783365	III
348	HM-05	L7	hsa-miR-4725-5p	-0.97397926	-0.917403757	-0.861009367	-0.917464128	III
349	HM-02	E18	hsa-miR-185	-1.324894543	-0.945312244	-0.475664481	-0.915290423	III
350	HM-02	F4	hsa-miR-885-5p	-0.987142774	-0.987374582	-0.766139667	-0.913552341	III
351	HM-03	F15	hsa-miR-3138	-0.875209755	-0.963779511	-0.89826011	-0.912416459	III
352	HM-02	A12	hsa-miR-504	-0.906857148	-0.862071794	-0.957350274	-0.908759739	III
353	HM-02	E12	hsa-miR-653	-0.923649715	-0.869512415	-0.918711012	-0.903957714	III
354	HM-05	K21	hsa-miR-4672	-0.991309957	-1.028147183	-0.691771377	-0.903742839	III
355	HM-01	P3	hsa-miR-411	-0.703811073	-1.078304918	-0.923850439	-0.90198881	III
356	HM-03	G19	hsa-miR-1236	-0.646751716	-1.015216849	-1.016043162	-0.892670576	III
357	HM-01	K20	hsa-miR-130b	-0.857689519	-0.842884656	-0.975768505	-0.892114227	III
358	HM-02	A21	hsa-miR-22*	-0.969795022	-0.836465618	-0.864442191	-0.890234277	III
359	HM-03	A18	hsa-miR-1287	-0.953259671	-0.734633008	-0.980239914	-0.889377531	III
360	HM-05	H7	hsa-miR-4699-5p	-0.910566737	-0.654409301	-1.090011155	-0.884995731	III
361	HM-02	A8	hsa-miR-556-5p	-1.023995857	-0.754801886	-0.863727922	-0.880841888	III
362	HM-01	A18	hsa-miR-192	-0.67135344	-1.045721469	-0.919317648	-0.878797519	III
363	HM-04	G5	hsa-miR-3675-3p	-0.850749479	-0.799505385	-0.979403561	-0.876552808	III
364	HM-04	J16	hsa-miR-378e	-0.841202287	-0.852803271	-0.930850808	-0.874952122	III
365	HM-03	G1	hsa-miR-1183	-0.847763677	-0.566855871	-1.208651207	-0.874423585	III
366	HM-04	C22	hsa-miR-3678-5p	-0.854098506	-0.824821598	-0.930718906	-0.86987967	III
367	HM-03	N9	hsa-miR-3180-3p	-0.958960193	-0.789761374	-0.854467965	-0.867729844	III
368	HM-01	D22	hsa-miR-604	-0.822047193	-0.99560758	-0.778398986	-0.865351253	III
369	HM-04	J8	hsa-miR-3677-5p	-0.670712845	-0.89346009	-1.025877798	-0.863350244	III
370	HM-02	L9	hsa-miR-183	-0.709191245	-1.033572344	-0.846267103	-0.863010231	III
371	HM-01	J3	hsa-miR-423-5p	-0.986016605	-1.000500896	-0.600197043	-0.862238182	III
372	HM-02	K18	hsa-miR-378	-0.7934869	-0.878267812	-0.914716138	-0.86215695	III
373	HM-05	M21	hsa-miR-4520b-3p	-0.881249215	-0.874729117	-0.829890736	-0.861956356	III
374	HM-04	D7	hsa-miR-4639-3p	-0.858424964	-0.936156379	-0.789939121	-0.861506821	III
375	HM-03	D18	hsa-miR-3124	-0.965271069	-0.836663926	-0.780137346	-0.86069078	III
376	HM-03	E18	hsa-miR-1304	-0.965271069	-0.836663926	-0.780137346	-0.86069078	III
377	HM-04	L6	hsa-miR-3913-3p	-0.671182679	-0.934769788	-0.969982129	-0.858644865	III
378	HM-03	C16	hsa-miR-1295	-0.843165669	-0.962181939	-0.76499644	-0.856781349	III
379	HM-01	K6	hsa-miR-24	-0.968730443	-0.982887939	-0.614050897	-0.855223093	III
380	HM-01	H21	hsa-miR-708	-1.047094727	-0.255578585	-1.261409558	-0.85469429	III
381	HM-01	M11	hsa-miR-212	-0.894030557	-0.807633909	-0.847769601	-0.849811356	III
382	HM-04	B6	hsa-miR-4693-5p	-0.84057038	-0.703894417	-0.991756183	-0.845406993	III
383	HM-02	C19	hsa-miR-766	-0.85307092	-0.906454938	-0.770003376	-0.843176411	III
384	HM-04	L17	hsa-miR-4683	-0.826371333	-0.789306965	-0.906891262	-0.84085652	III
385	HM-04	M5	hsa-miR-3939	-1.001273823	-0.540249056	-0.957890443	-0.833137774	III
386	HM-04	J12	hsa-miR-4794	-0.850661248	-0.66319225	-0.982402839	-0.832085446	III
387	HM-04	I1	hsa-miR-3938	-0.94699259	-0.658688845	-0.874594995	-0.82675881	III
388	HM-02	L8	hsa-miR-218-1*	-0.69352024	-0.903349161	-0.859189494	-0.818686298	III
389	HM-02	O17	hsa-miR-33a	-0.896622113	-0.613545014	-0.928980757	-0.813049295	III
390	HM-02	F5	hsa-miR-523	-0.814820943	-0.663829887	-0.956897247	-0.811849359	III
391	HM-03	E5	hsa-miR-1257	-0.713237487	-0.822340669	-0.897284046	-0.810954067	III
392	HM-05	B4	hsa-miR-4717-5p	-0.740245202	-0.872539445	-0.818834207	-0.810539618	III
393	HM-02	L20	hsa-miR-920	-0.882969106	-0.647284635	-0.892928652	-0.807727464	III
394	HM-03	F20	hsa-miR-3152	-0.901923545	-0.887326887	-0.619947528	-0.803065987	III
395	HM-05	H5	hsa-miR-4536	-0.445342203	-1.004624922	-0.93243386	-0.794133662	III
396	HM-02	M2	hsa-miR-7-2*	-0.411188922	-0.939745119	-1.022205477	-0.791046506	III
397	HM-03	M4	hsa-miR-2278	-0.891774562	-0.8890239	-0.586002471	-0.788933644	III

398	HM-01	G10	hsa-miR-19b	-0.735221955	-0.874775769	-0.75565233	-0.788550018	III
399	HM-04	J18	hsa-miR-4778-3p	-0.849372479	-0.641084558	-0.871836879	-0.787431305	III
400	HM-03	I19	hsa-miR-1271	-0.81932422	-0.957936545	-0.584299763	-0.787186842	III
401	HM-03	B5	hsa-miR-3180-5p	-0.845541115	-0.843274642	-0.669397636	-0.786071131	III
402	HM-02	L19	hsa-miR-126	-0.883834375	-0.665431966	-0.808644388	-0.785970243	III
403	HM-03	G20	hsa-miR-675*	-0.971043187	-0.809630326	-0.571474401	-0.784049305	III
404	HM-04	M10	hsa-miR-4650-3p	-0.677473036	-0.832074687	-0.83723548	-0.782261068	III
405	HM-02	M15	hsa-let-7f-2*	-0.804177029	-0.67013142	-0.866435223	-0.78024789	III
406	HM-02	H6	hsa-miR-509-3p	-0.815506352	-0.825941243	-0.689130708	-0.776859435	III
407	HM-05	I2	hsa-miR-4738-3p	-0.866372248	-0.636928806	-0.82682818	-0.776709744	III
408	HM-05	M14	hsa-miR-4668-5p	-0.80085335	-0.813488205	-0.706002414	-0.77344799	III
409	HM-04	P14	hsa-miR-4468	-0.509761685	-0.836186385	-0.964878607	-0.770275559	III
410	HM-03	G6	hsa-miR-1911*	-1.283299178	-0.171406022	-0.846044673	-0.766916624	III
411	HM-01	E8	hsa-miR-199b-5p	-0.579792329	-0.864530076	-0.846791134	-0.763704513	III
412	HM-04	L14	hsa-miR-4762-3p	-0.568540987	-0.801951317	-0.910074028	-0.760188777	III
413	HM-05	F11	hsa-miR-4514	-1.019445149	-0.848900917	-0.397932635	-0.755426234	III
414	HM-01	A6	hsa-miR-96	-1.087817095	-0.125749438	-1.038025367	-0.750530633	III
415	HM-01	O18	hsa-miR-15b	-0.91870351	-0.949234954	-0.337854066	-0.735264177	III
416	HM-01	K10	hsa-miR-27b	-0.857838344	-1.072097448	-0.257445899	-0.72912723	III
417	HM-03	D21	hsa-miR-378c	-0.88517595	-0.433705161	-0.802056044	-0.706979052	III
418	HM-02	M5	hsa-miR-16-2*	-0.384936655	-0.87218882	-0.851759584	-0.702961686	III
419	HM-01	I15	hsa-miR-15a	-0.23503617	-0.84052635	-0.862107521	-0.645890013	III
420	HM-01	J2	hsa-miR-630	-2.654612783	-2.271200847	3.088938576	-0.612291685	III
421	HM-05	G20	hsa-miR-4510	-0.950936475	-1.10397215	0.347210578	-0.569232682	III
422	HM-02	H22	hsa-miR-542-5p	-1.042106852	-0.958861061	0.29377745	-0.569063488	III
423	HM-03	F5	hsa-miR-4269	-2.266711413	3.019057483	-1.983176641	-0.410276857	III

CLAIMS

What is claimed is:

1. An isolated oligonucleotide, wherein said oligonucleotide is capable of decreasing the level and/or activity of miR-27b.

2. The oligonucleotide of claim 1, wherein miR-27b comprises the sequence 5'-UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NOS: 1, 58-59).

3. The oligonucleotide of claim 1, wherein miR-27b consists of the sequence 5'-UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NOS: 1, 58-59).

4. The oligonucleotide of claim 1, wherein miR-27b consists of the sequence

5'- ACCUCUCUAACAAGGUGCAGAGCUUAGCUGAUUGGUGAACAGUGAUUGGUUUCCGCUUUGUUCACAGUGGCUAAGUUCUGCACCUGAAGAGAAGGUG-3' (SEQ ID NO: 2).

5. An isolated oligonucleotide, which oligonucleotide comprises the sequence complimentary to nucleotides 2-8 at the 5' end of the mature miRNA sequence of miR-27b.

6. The oligonucleotide of claim 5, wherein the mature miRNA sequence of miR-27b is 5'-UUCACAGUGGCUAAGUUCUGC -3' (SEQ ID NOS: 1, 58-59).

7. The oligonucleotide of claim 5, wherein said oligonucleotide comprises the sequence 5'-AC(T/U)G(T/U)GA-3' (SEQ ID NO: 114).

8. The oligonucleotide of claim 5, wherein said oligonucleotide comprises the sequence 5'-ACTGTGA-3' (SEQ ID NO: 115).

9. The oligonucleotide of claim 5, wherein said oligonucleotide comprises the sequence 5'-ACUGUGA-3' (SEQ ID NO: 116).

10. The oligonucleotide of any one of claims 1-9, wherein said oligonucleotide ranges from 7 to 40 nucleotides in length.

11. The oligonucleotide of claim 10, wherein said oligonucleotide ranges from 8 to 21 nucleotides in length.

12. The oligonucleotide of claim 5, wherein said oligonucleotide is capable of decreasing the level and/or activity of miR-27b.

13. An isolated oligonucleotide, wherein said oligonucleotide is capable of decreasing the level and/or activity of miR-148a.

14. The oligonucleotide of claim 13, wherein miR-148a comprises the sequence 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NOS: 6, 60-61).

15. The oligonucleotide of claim 13, wherein miR-148a consists of the sequence 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NOS: 6, 60-61).

16. The oligonucleotide of claim 13, wherein miR-148a consists of the sequence

5'-GAGGCAAAGUUCUGAGACACUCCGACUCUGAGUAUGAUAGAAGUCAGUGCA CUACAGAACUUUGUCUC-3' (SEQ ID NO: 7).

17. An isolated oligonucleotide, which oligonucleotide comprises the sequence complimentary to nucleotides 2-8 at the 5' end of the mature miRNA sequence of miR-148a.

18. The oligonucleotide of claim 17, wherein the mature miRNA sequence of miR-148a is 5'-UCAGUGCACUACAGAACUUUGU-3' (SEQ ID NOS: 6, 60-61).

19. The oligonucleotide of claim 17, wherein said oligonucleotide comprises the sequence 5'-(T/U)GCAC(T/U)G-3' (SEQ ID NO: 117).

20. The oligonucleotide of claim 17, wherein said oligonucleotide comprises the sequence 5'-TGCACTG-3' (SEQ ID NO: 118).

21. The oligonucleotide of claim 17, wherein said oligonucleotide comprises the sequence 5'-UGCACUG-3' (SEQ ID NO: 119).

22. The oligonucleotide of any one of claims 13-21, wherein said oligonucleotide ranges from 7 to 40 nucleotides in length.

23. The oligonucleotide of any one of claims 13-21, wherein said oligonucleotide ranges from 8 to 22 nucleotides in length.

24. The oligonucleotide of claim 17, wherein said oligonucleotide is capable of decreasing the level and/or activity of miR-148a.

25. The oligonucleotide of any one of claims 1-12 which is a modified oligonucleotide.

26. The modified oligonucleotide of claim 25 which comprises a modification selected from the group consisting of locked nucleic acids (LNA), 2'-fluoro (2'-F) modified nucleotides, 2'-O-methoxyethyl (2'-MOE) modified nucleotides, 2'-O-methyl (2'O-Me) modified oligonucleotides, and phosphorothiate (PS) nucleotides.

27. The oligonucleotide of any one of claims 13-24 which is a modified oligonucleotide.

28. The modified oligonucleotide of claim 27 which comprises a modification selected from the group consisting of locked nucleic acids (LNA), 2'-fluoro (2'-F) modified nucleotides, 2'-O-methoxyethyl (2'-MOE) modified nucleotides, 2'-O-methyl (2'O-Me) modified oligonucleotides, and phosphorothiate (PS) nucleotides.

29. A pharmaceutical composition comprising one or more oligonucleotides of any one of claims 1-28 and a pharmaceutically acceptable carrier or excipient.

30. A pharmaceutical composition comprising the oligonucleotide of claim 1 and a pharmaceutically acceptable carrier or excipient.

31. A pharmaceutical composition comprising the oligonucleotide of claim 5 and a pharmaceutically acceptable carrier or excipient.

32. A pharmaceutical composition comprising the oligonucleotide of claim 25 and a pharmaceutically acceptable carrier or excipient.

33. A pharmaceutical composition comprising the oligonucleotide of claim 13 and a pharmaceutically acceptable carrier or excipient.

34. A pharmaceutical composition comprising the oligonucleotide of claim 17 and a pharmaceutically acceptable carrier or excipient.

35. A pharmaceutical composition comprising the oligonucleotide of claim 27 and a pharmaceutically acceptable carrier or excipient.

36. A pharmaceutical composition comprising (i) the oligonucleotide of any one of claims 1-12, 25, and 26, (ii) the oligonucleotide of any one of claims 13-24, 27, and 28, and (iii) a pharmaceutically acceptable carrier or excipient.

37. A method for decreasing the level and/or activity of miR-27b in a cell, which method comprises administering to the cell one or more oligonucleotides of any one of claims 1-12, 25, and 26.

38. The method of claim 37, wherein said one or more oligonucleotides is administered in an amount effective for decreasing said level or activity of miR-27b.

39. A method for decreasing the level and/or activity of miR-27b in a cell, which method comprises administering to the cell the pharmaceutical composition of any one of claims 30-32 and 36.

40. The method of claim 39, wherein said pharmaceutical composition is administered in an amount effective for decreasing said level or activity of miR-27b.

41. A method for decreasing the level and/or activity of miR-148a in a cell, which method comprises administering to the cell one or more oligonucleotides of any one of claims 13-24, 27, and 28.

42. The method of claim 41, wherein said one or more oligonucleotides is administered in an amount effective for decreasing said level or activity of miR-148a.

43. A method for decreasing the level and/or activity of miR-148a in a cell, which method comprises administering to the cell the pharmaceutical composition of any one of claims 33-35 and 36.

44. The method of claim 43, wherein said pharmaceutical composition is administered in an amount effective for decreasing said level or activity of miR-148a.

45. The method of any one of claims 37-44, wherein the cell is a hepatic cell.

46. A method for increasing plasma high-density lipoprotein cholesterol (HDL-C) level and/or reducing plasma low-density lipoprotein cholesterol (LDL-C) level in a subject in need thereof, which method comprises administering to the subject a therapeutically effective amount of one or more oligonucleotides of any one of claims 1-28.

47. A method for increasing plasma high-density lipoprotein cholesterol (HDL-C) level and/or reducing plasma low-density lipoprotein cholesterol (LDL-C) level in a subject in need thereof, which method comprises administering to the subject a therapeutically effective amount of the pharmaceutical composition of any one of claims 29-36.

48. The method of claim 46 or 47, wherein the subject has a dyslipidemia or a cardiovascular disease.

49. A method for treating a disease in a subject in need thereof, which method comprises administering to the subject a therapeutically effective amount of one or more oligonucleotides of any one of claims 1-28.

50. A method for treating a disease in a subject in need thereof, which method comprises administering to the subject a therapeutically effective amount of the pharmaceutical composition of any one of claims 29-36.

51. The method of claim 49 of 50, wherein the disease is a dyslipidemia or a cardiovascular disease.

52. The method of claim 48 or 51, wherein the dyslipidemia is selected from the group consisting of hyperlipidemia, hypercholesterolemia, and low HDL/LDL ratio.

53. The method of claim 48 or 51, wherein the cardionvascular disease is selected from the group consisting of atherosclerosis, coronary artery disease, coronary heart disease, conditions associated with coronary artery disease or coronary heart disease, transient ischemic attack, and stroke.

54. The method of claim 53, wherein the condition associated with coronary artery disease or coronary heart disease is angina or myocardial infarction.

55. The method of any one of claims 46-54, wherein the one or more oligonucleotides are modified or unmodified oligonucleotides selected from the group consisting of 5'-TTCTGTAGTGCACTG-3' (SEQ ID NO: 52), 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33), 5'-AACTTAGCCACTGTGA-3' (SEQ ID NO: 54), and 5'-AGAACTTAGCCACTGTGA-3' (SEQ ID NO: 34).

56. The method of any one of claims 46-54, wherein the one or more oligonucleotides are selected from the group consisting of LNA oligonucleotide 5'-TTCTGTAGTGCACTG-3' (SEQ ID NO: 52), LNA oligonucleotide 5'-AACTTAGCCACTGTGA-3' (SEQ ID NO: 54), miRCURY LNA microRNA inhibitor 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33), miRCURY LNA microRNA inhibitor 5'- AGAACTTAGCCACTGTGA- 3' (SEQ ID NO: 34), miRCURY LNA microRNA Power inhibitor 5'-ACAAAGTTCTGTAGTGCAC-3' (SEQ ID NO: 33), and miRCURY LNA microRNA Power inhibitor 5'- AGAACTTAGCCACTGTGA-3' (SEQ ID NO: 34).

57. The method of any one of claims 46-54, wherein the subject is human.

Figure 1

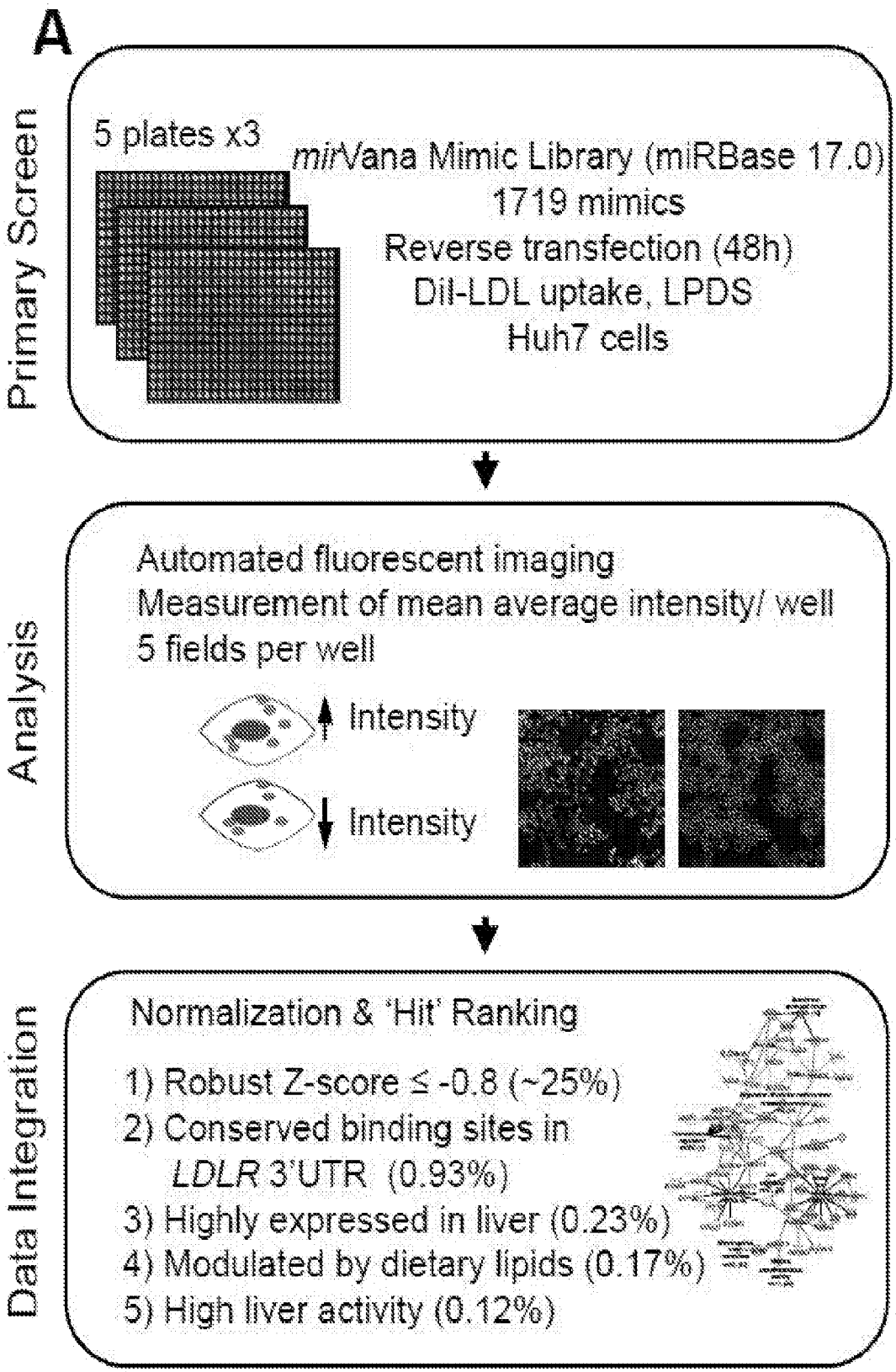

A
Primary Screen
5 plates x3
miRVana Mimic Library (miRBase 17.0)
1719 mimics
Reverse transfection (48h)
DiI-LDL uptake, LPDS
Huh7 cells
Analysis
Automated fluorescent imaging
Measurement of mean average intensity/ well
5 fields per well
Intensity
Intensity
Data Integration
Normalization & 'Hit' Ranking
1) Robust Z-score ≤ -0.8 (~25%)
2) Conserved binding sites in
LDLR 3'UTR (0.93%)
3) Highly expressed in liver (0.23%)
4) Modulated by dietary lipids (0.17%)
5) High liver activity (0.12%)

Figure 1

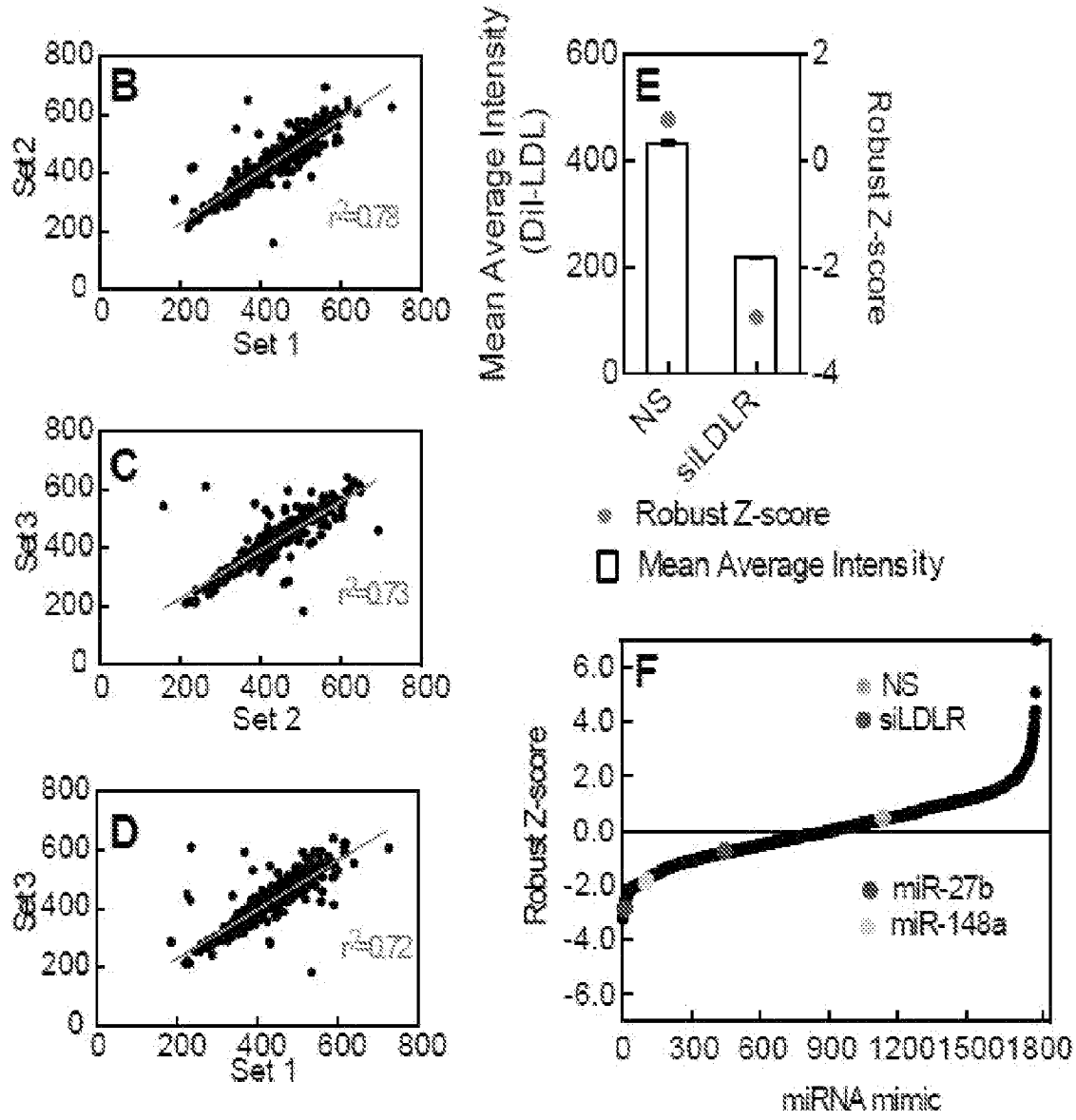

B
Set2
Set 1
r=0.78
C
Set3
Set 2
r=0.73
D
Set3
Set 1
r=0.72
E
Mean Average Intensity (DiI-LDL)
Robust Z-score
NS
siLDLR
Robust Z-score
Mean Average Intensity
F
Robust Z-score
NS
siLDLR
miR-27b
miR-148a
miRNA mimic

FIGURE 2

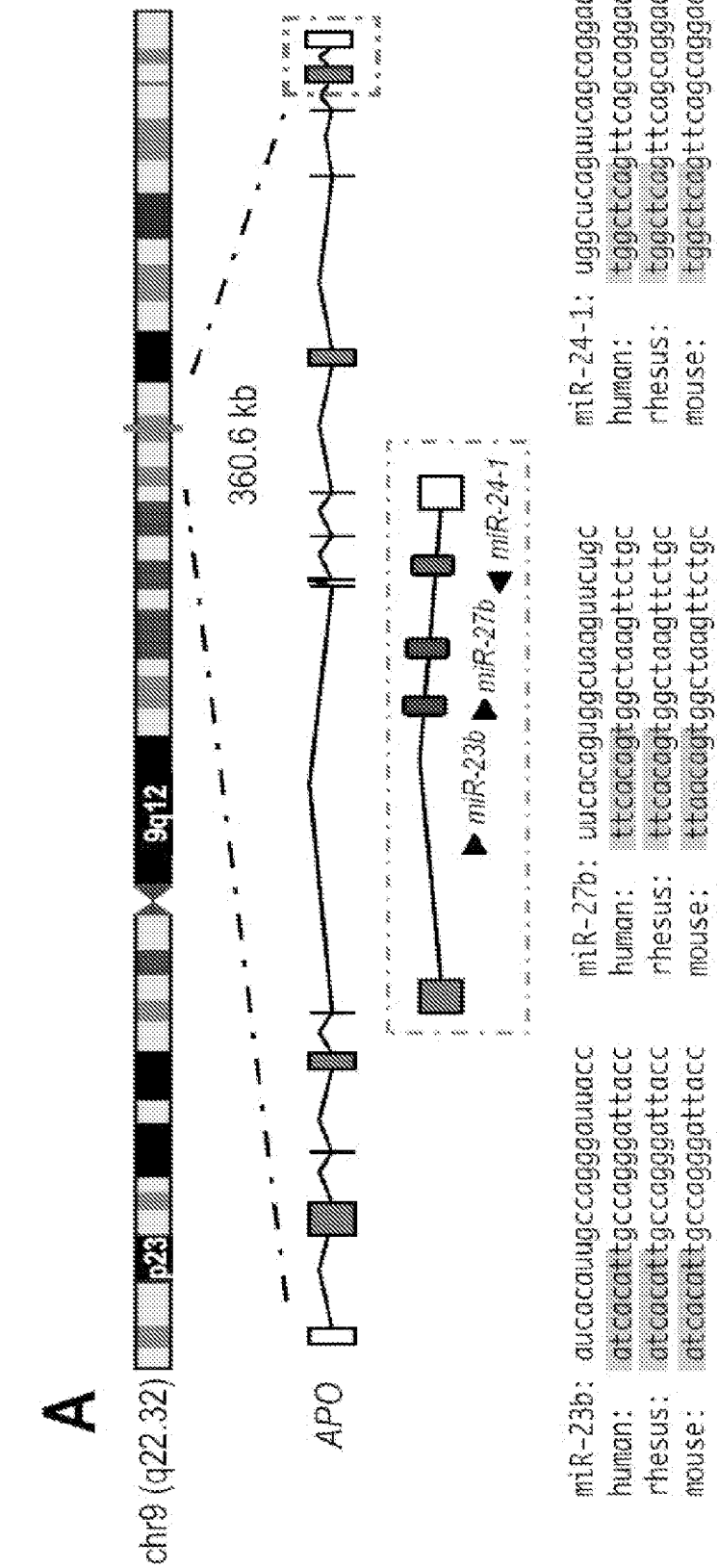

A
chr9 (q22.32)
p23
9q12
360.6 kb
APO
miR-23b
miR-27b
miR-24-1
miR-23b: aucacauugccagggauuacc
human: atcacattgccagggattacc
rhesus: atcacattgccagggattacc
mouse: atcacattgccagggattacc
miR-27b: uucacaguggcuaaguucugc
human: ttcacagtggctaagttctgc
rhesus: ttcacagtggctaagttctgc
mouse: ttcacagtggctaagttctgc
miR-24-1: uggcucaguucagcaggaacag
human: tggctcagttcagcaggaacag
rhesus: tggctcagttcagcaggaacag
mouse: tggctcagttcagcaggaacag

FIGURE 2

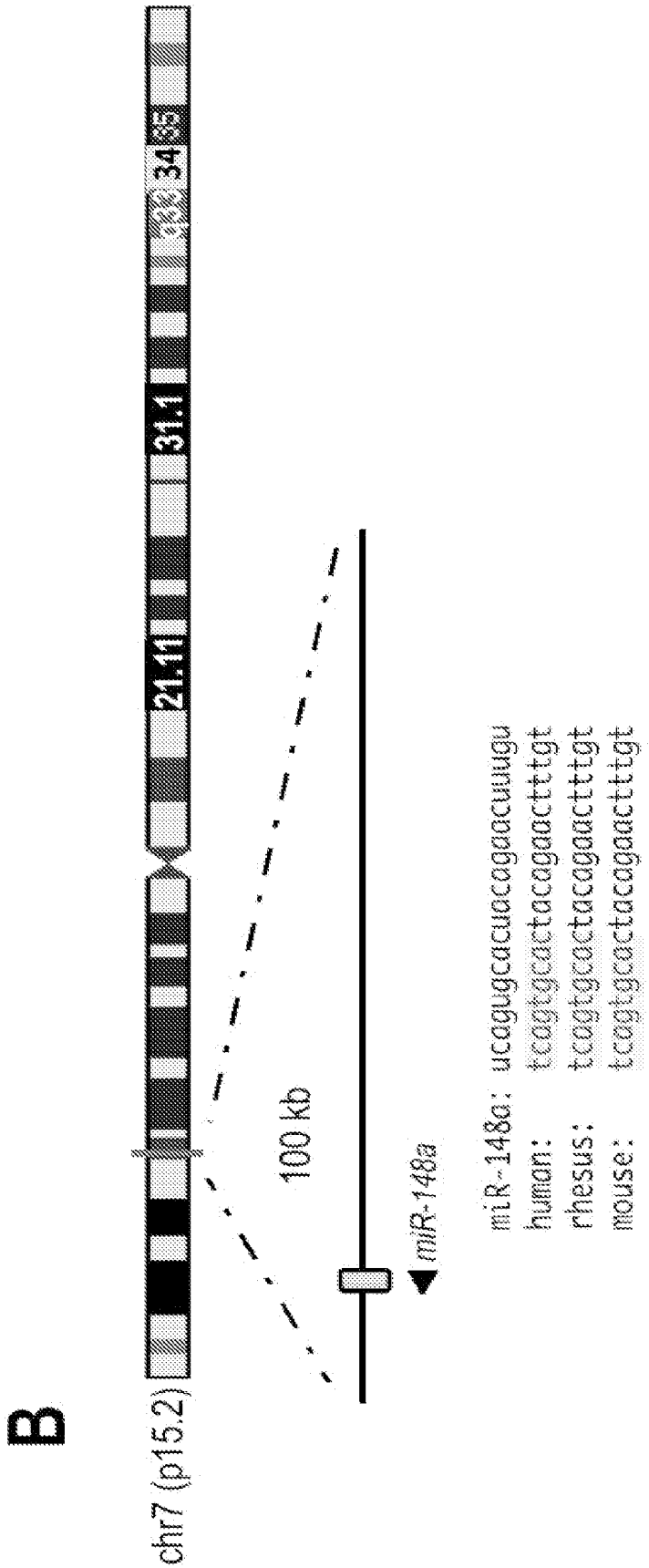

B
chr7 (p15.2)
21.11
31.1
34
100 kb
miR-148a
miR-148a: ucagugcacuacagaacuuugu
human: tcagtgcactacagaactttgt
rhesus: tcagtgcactacagaactttgt
mouse: tcagtgcactacagaactttgt

Figure 2

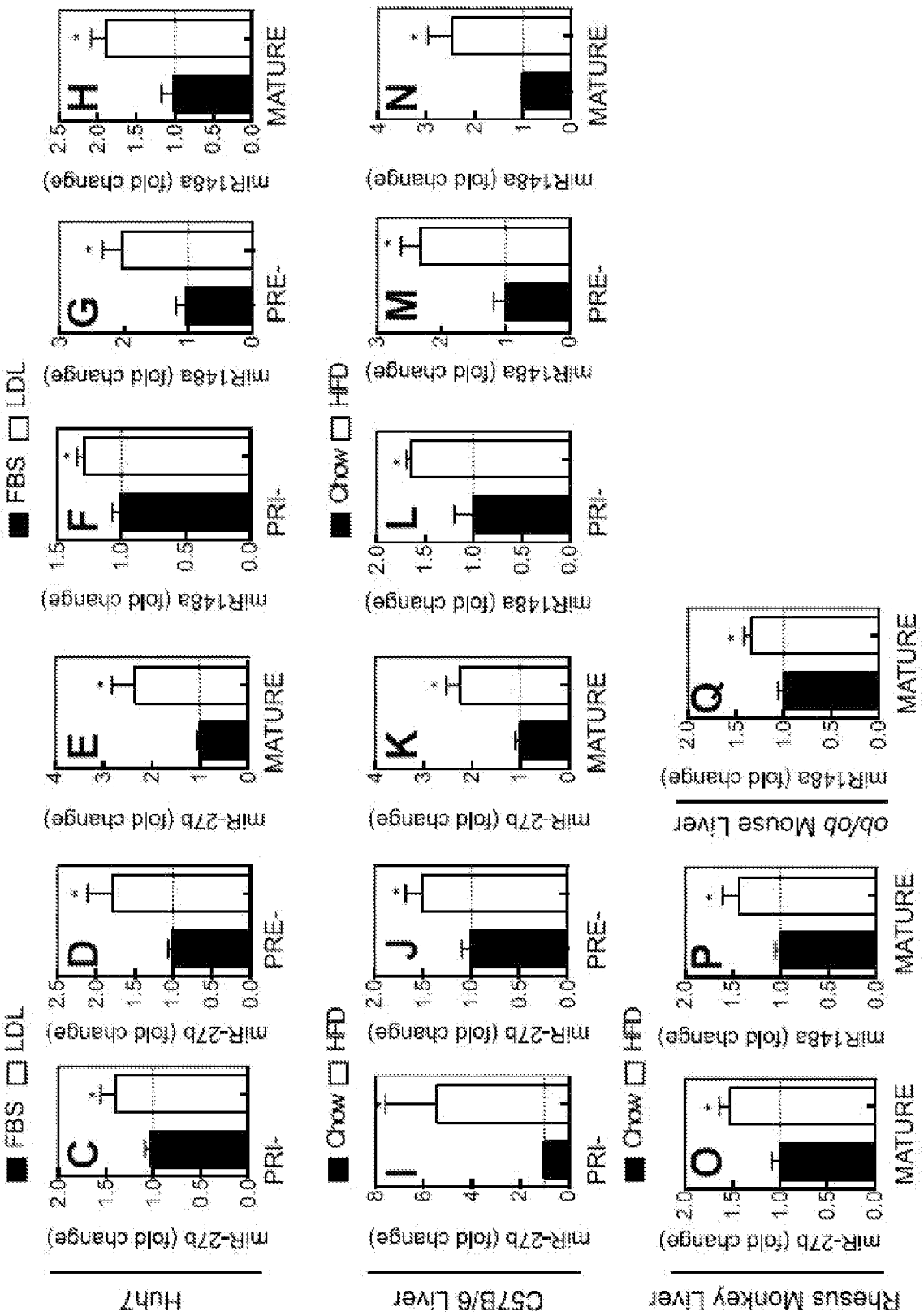

Huh7
C57B/6 Liver
Rhesus Monkey Liver
ob/ob Mouse Liver
FBS
LDL
Chow
HFD
PRI-
PRE-
MATURE
miR-27b (fold change)
miR148a (fold change)
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q

Figure 3

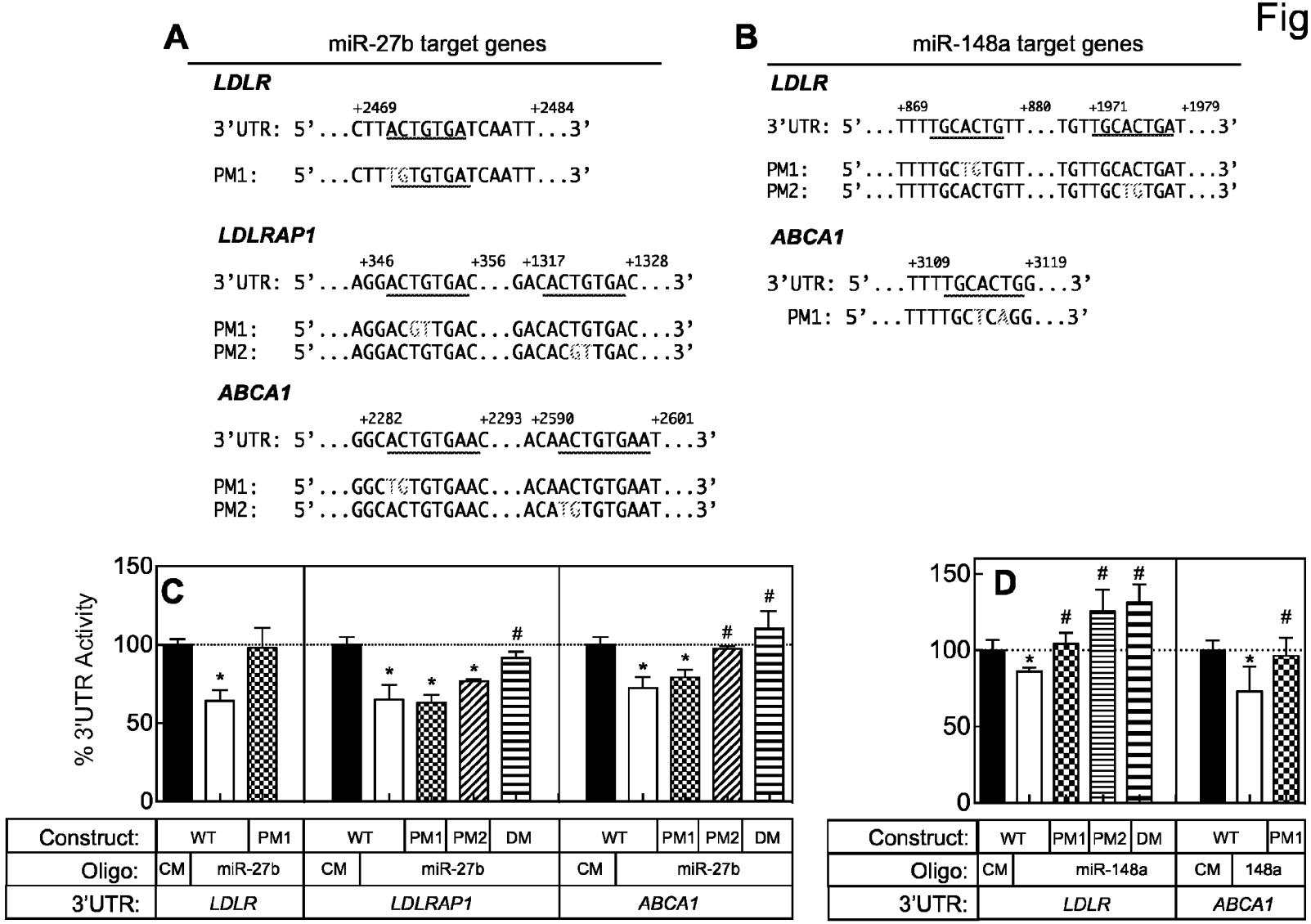


Figure 4

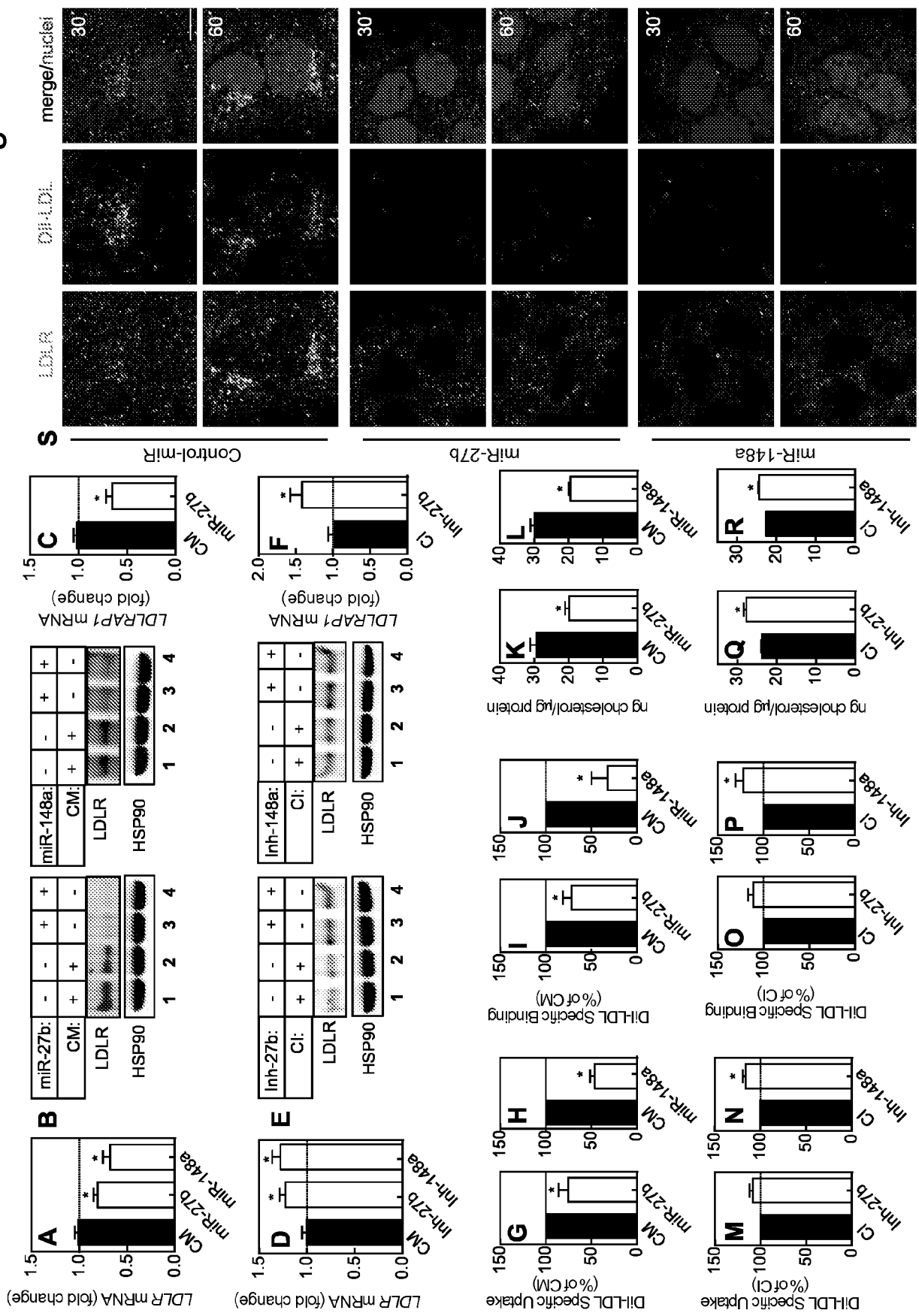

S
LDLR
DiI-LDL
merge/nuclei
30´
60´
Control-miR
miR-27b
miR-148a
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
LDLR mRNA (fold change)
LDLRAP1 mRNA (fold change)
miR-27b:
miR-148a:
Inh-27b:
Inh-148a:
CM:
CI:
LDLR
HSP90
1 2 3 4
CM
CI
miR-27b
miR-148a
Inh-27b
Inh-148a
DiI-LDL Specific Uptake (% of CM)
DiI-LDL Specific Uptake (% of CI)
DiI-LDL Specific Binding (% of CM)
DiI-LDL Specific Binding (% of CI)
ng cholesterol/µg protein

Figure 5

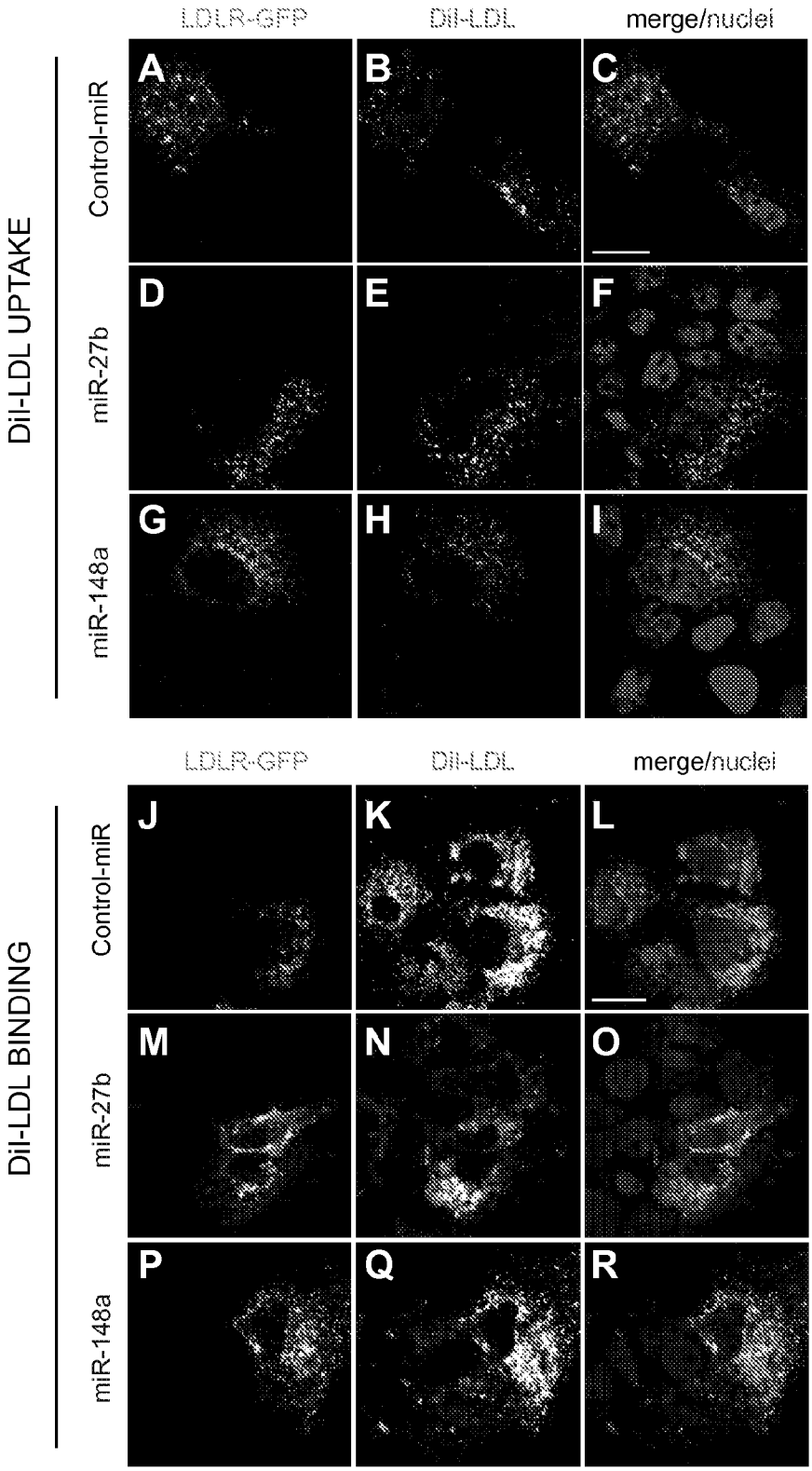

LDLR-GFP
DiI-LDL
merge/nuclei
DiI-LDL UPTAKE
Control-miR
miR-27b
miR-148a
A
B
C
D
E
F
G
H
I
LDLR-GFP
DiI-LDL
merge/nuclei
DiI-LDL BINDING
Control-miR
miR-27b
miR-148a
J
K
L
M
N
O
P
Q
R

Figure 6

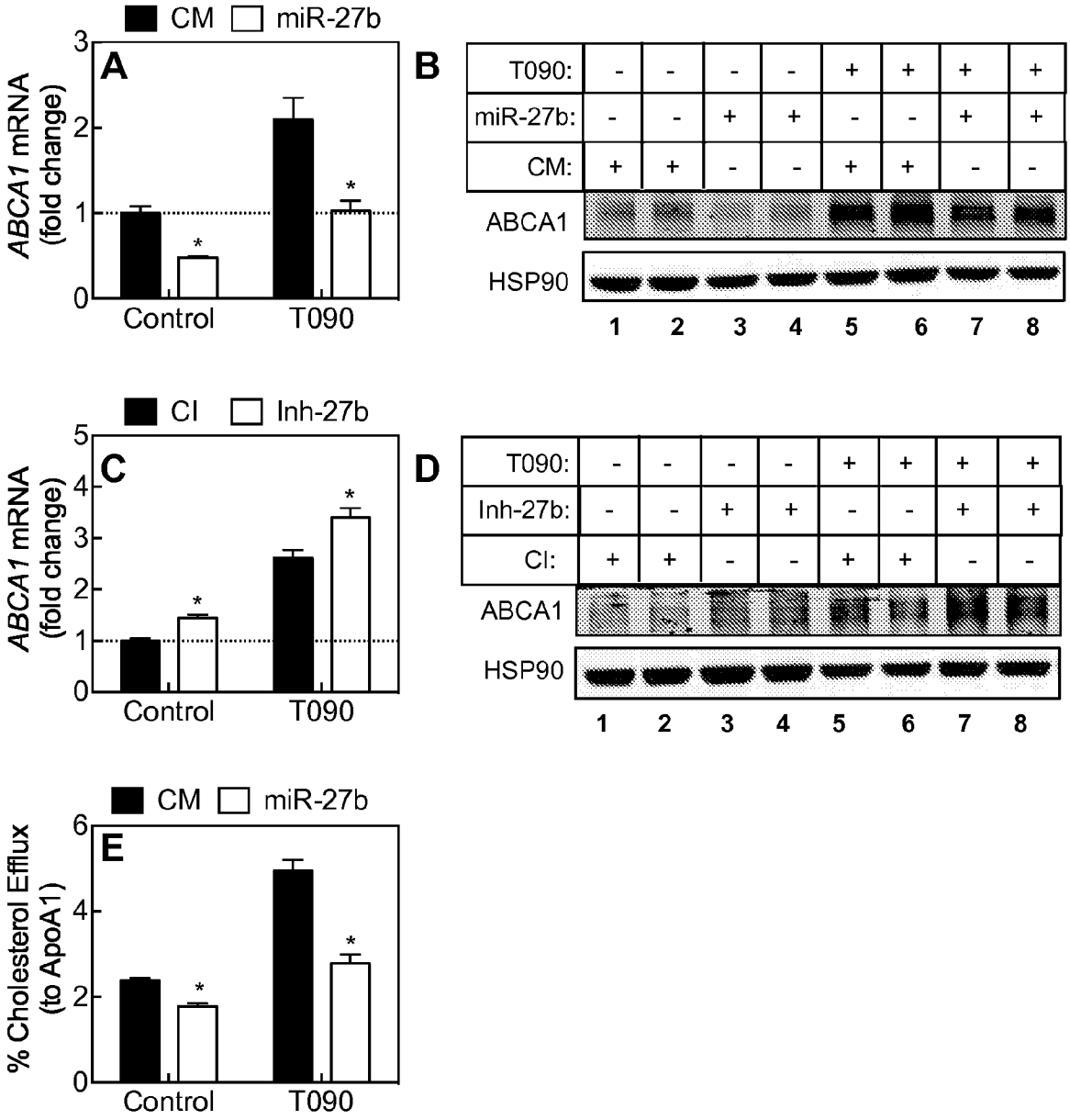

CM
miR-27b
A
ABCA1 mRNA (fold change)
Control
T090
B
T090:
miR-27b:
CM:
ABCA1
HSP90
1 2 3 4 5 6 7 8
CI
Inh-27b
C
D
Inh-27b:
CI:
% Cholesterol Efflux (to ApoA1)
E

Figure 7

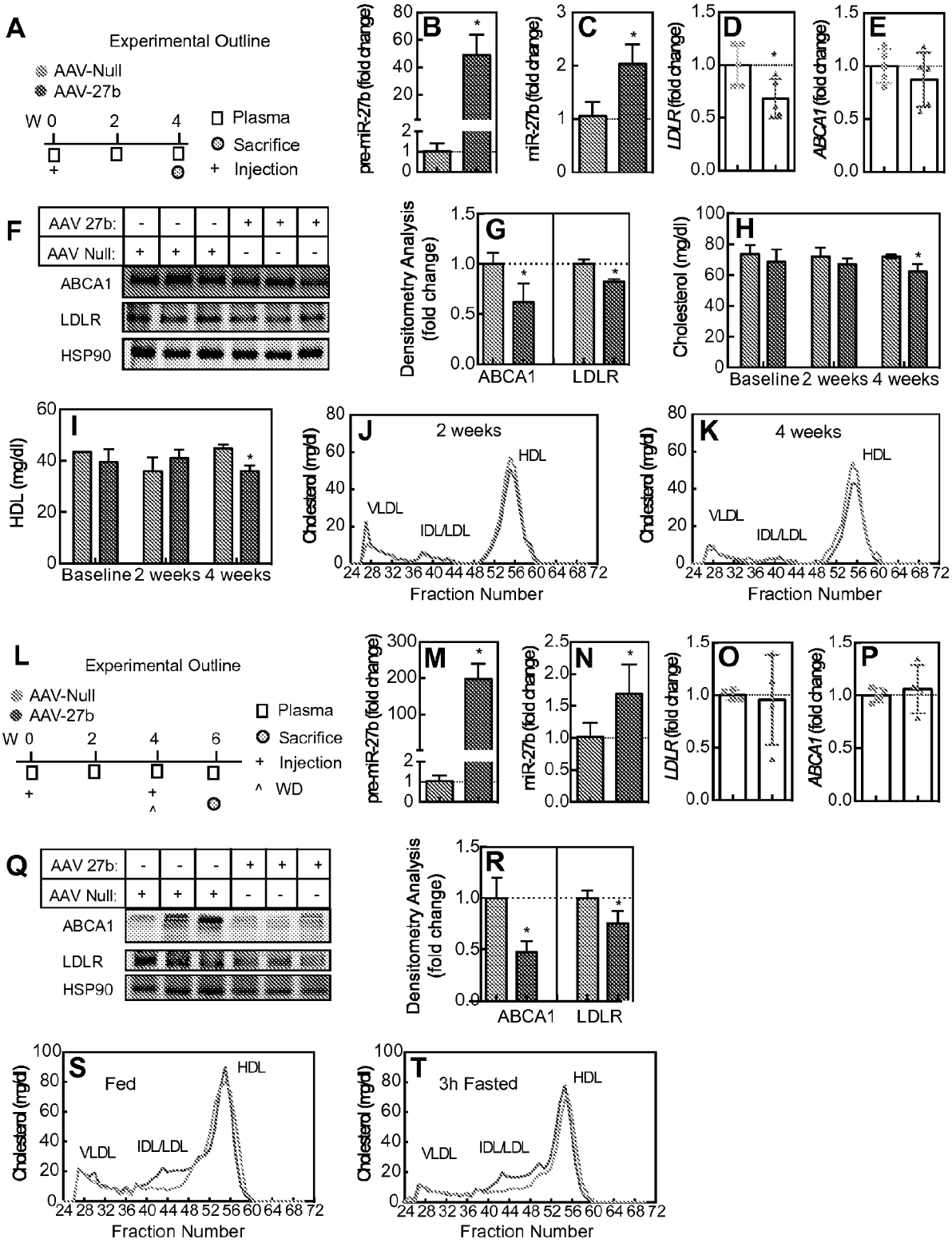

A
Experimental Outline
AAV-Null
AAV-27b
W 0 2 4
Plasma
Sacrifice
+ Injection
pre-miR-27b (fold change)
B
miR-27b (fold change)
C
LDLR (fold change)
D
ABCA1 (fold change)
E
F
AAV 27b:
AAV Null:
ABCA1
LDLR
HSP90
Densitometry Analysis (fold change)
G
ABCA1 LDLR
Cholesterol (mg/dl)
H
Baseline 2 weeks 4 weeks
HDL (mg/dl)
I
Baseline 2 weeks 4 weeks
Cholesterol (mg/dl)
J
2 weeks
HDL
VLDL
IDL/LDL
Fraction Number
K
4 weeks
L
Experimental Outline
AAV-Null
AAV-27b
W 0 2 4 6
Plasma
Sacrifice
+ Injection
^ WD
pre-miR-27b (fold change)
M
miR-27b (fold change)
N
LDLR (fold change)
O
ABCA1 (fold change)
P
Q
AAV 27b:
AAV Null:
ABCA1
LDLR
HSP90
Densitometry Analysis (fold change)
R
ABCA1 LDLR
Cholesterol (mg/dl)
S
Fed
HDL
VLDL
IDL/LDL
Fraction Number
T
3h Fasted
HDL
VLDL
IDL/LDL
Fraction Number

Figure 8

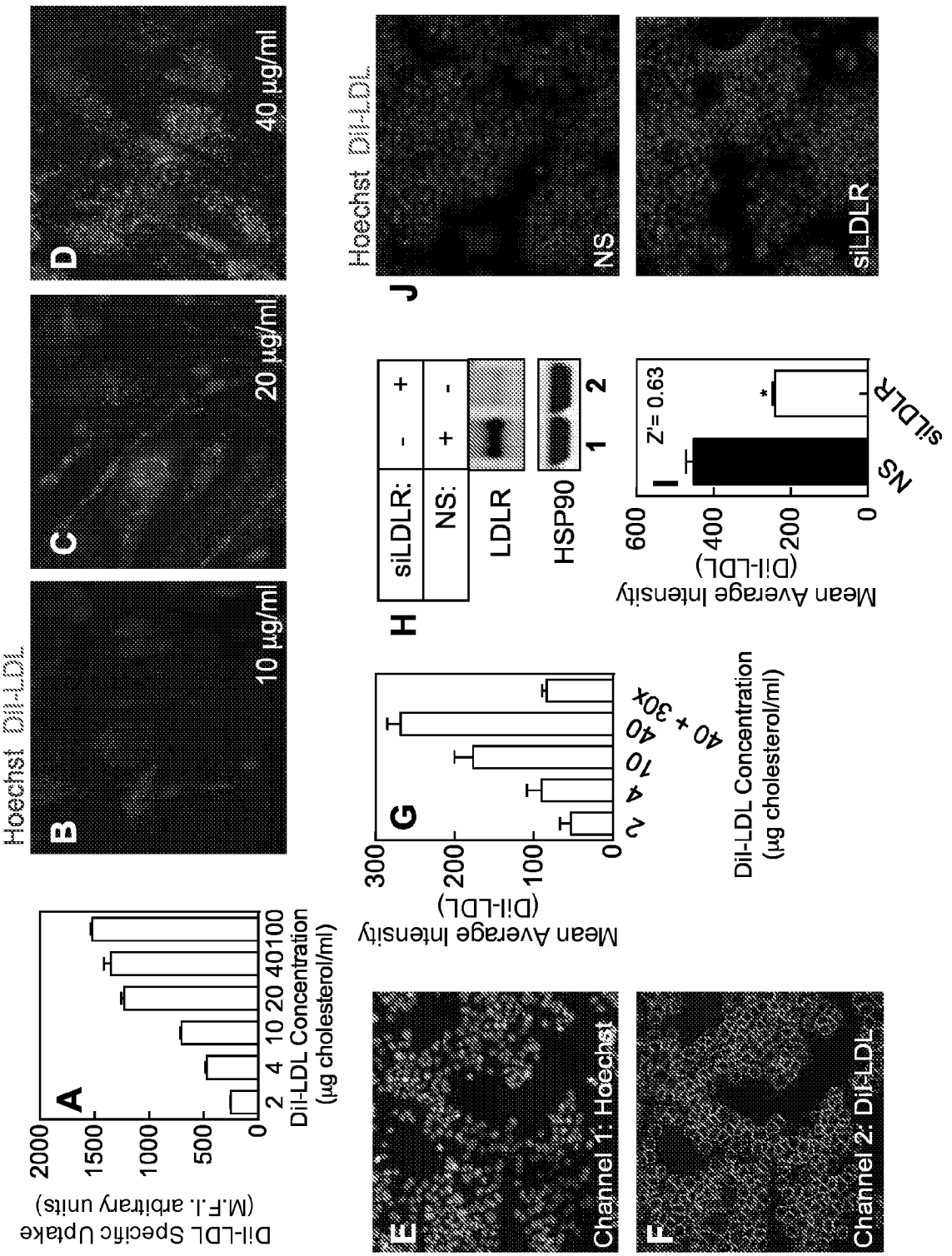

A
Dil-LDL Specific Uptake (M.F.I. arbitrary units)
2000
1500
1000
500
0
2 4 10 20 40100
Dil-LDL Concentration (µg cholesterol/ml)
Hoechst Dil-LDL
B
10 µg/ml
C
20 µg/ml
D
40 µg/ml
E
Channel 1: Hoechst
F
Channel 2: Dil-LDL
G
Mean Average Intensity (Dil-LDL)
300
200
100
0
2
4
10
40
40 + 30x
Dil-LDL Concentration (µg cholesterol/ml)
H
siLDLR:
NS:
LDLR
HSP90
1 2
Hoechst Dil-LDL
J
NS
siLDLR
Mean Average Intensity (Dil-LDL)
600
400
200
0
Z'= 0.63
NS
siLDLR

Figure 9

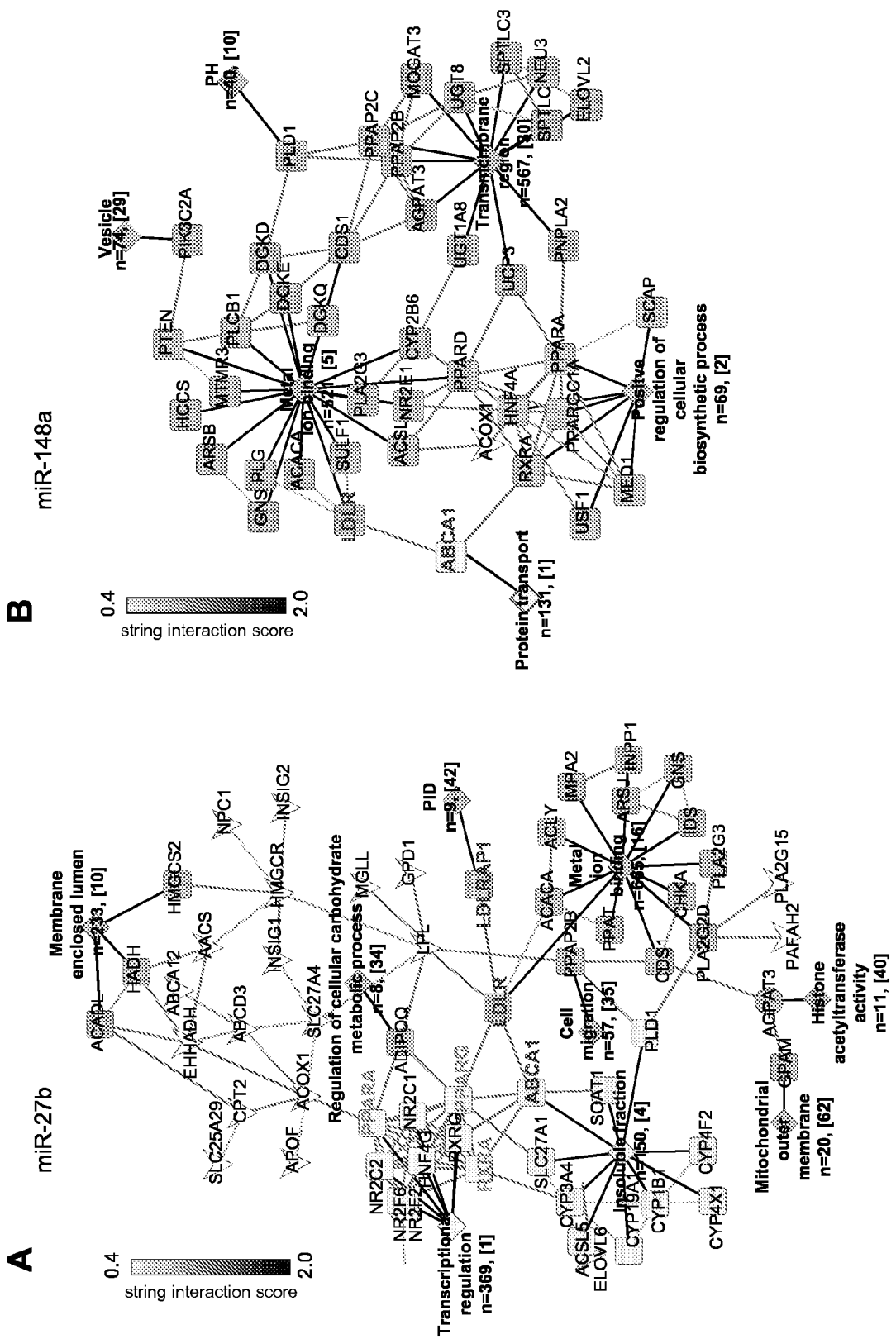

A
miR-27b
Membrane enclosed lumen n=233, [10]
Regulation of cellular carbohydrate metabolic process n=8, [34]
PID n=9, [42]
Cell migration n=57, [35]
Metal ion binding n=645, [6]
Transcription regulation n=369, [1]
Insoluble fraction n=150, [4]
Mitochondrial outer membrane n=20, [62]
Histone acetyltransferase activity n=11, [40]
0.4
2.0
string interaction score
B
miR-148a
PH n=40, [10]
Vesicle n=74, [29]
Metal ion binding n=521, [5]
Transmembrane region n=567, [30]
Positive regulation of cellular biosynthetic process n=69, [2]
Protein transport n=131, [1]
0.4
2.0
string interaction score

Figure 10

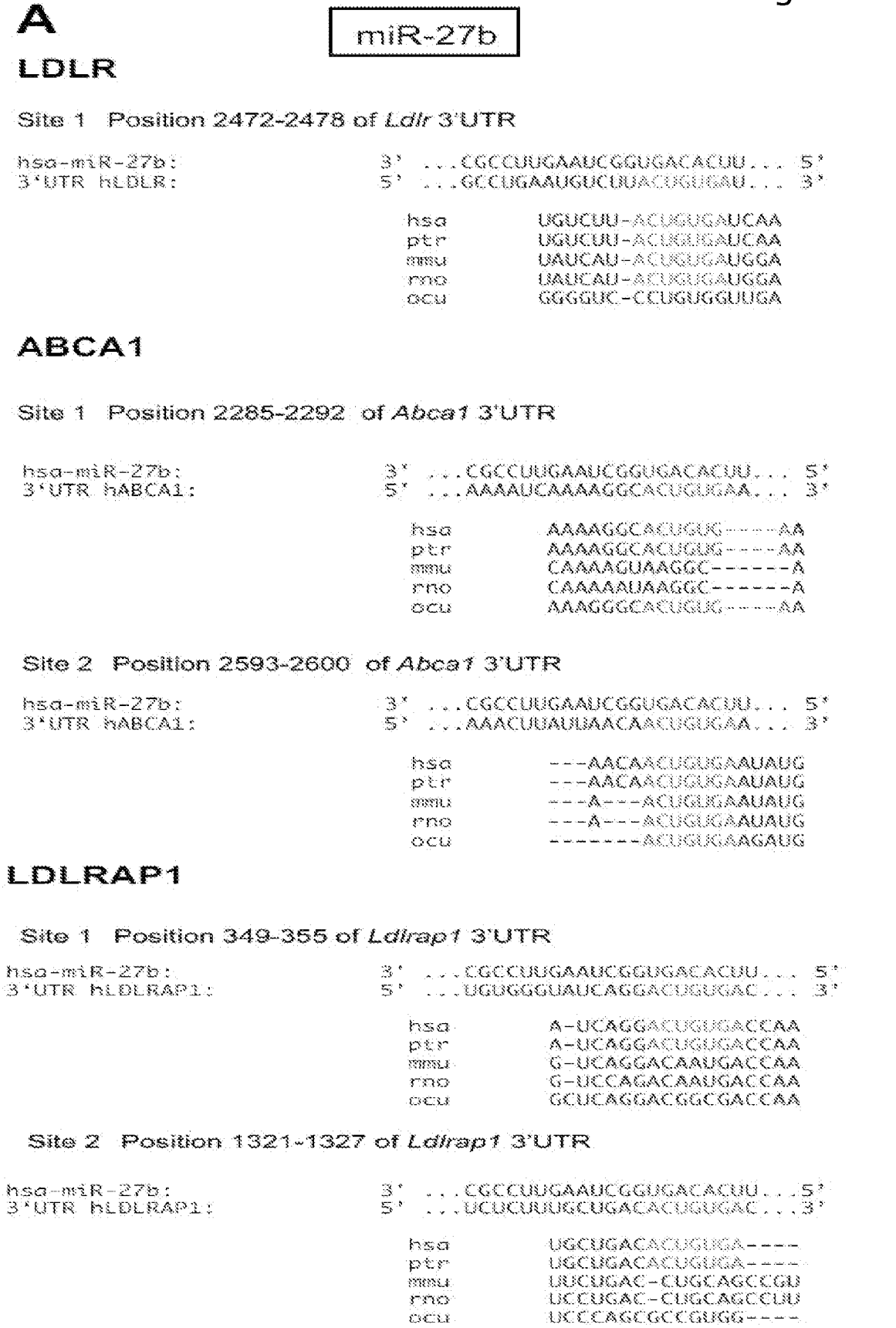

A
miR-27b
LDLR
Site 1 Position 2472-2478 of Ldlr 3'UTR
hsa-miR-27b: 3' ...CGCCUUGAAUCGGUGACACUU... 5'
3'UTR hLDLR: 5' ...GCCUGAAUGUCUUACUGUGAU... 3'
hsa UGUCUU-ACUGUGAUCAA
ptr UGUCUU-ACUGUGAUCAA
mmu UAUCAU-ACUGUGAUGGA
rno UAUCAU-ACUGUGAUGGA
ocu GGGGUC-CCUGUGGUUGA
ABCA1
Site 1 Position 2285-2292 of Abca1 3'UTR
hsa-miR-27b: 3' ...CGCCUUGAAUCGGUGACACUU... 5'
3'UTR hABCA1: 5' ...AAAAUCAAAAGGCACUGUGAA... 3'
hsa AAAAGGCACUGUG----AA
ptr AAAAGGCACUGUG----AA
mmu CAAAAGUAAGGC------A
rno CAAAAAUAAGGC------A
ocu AAAGGGCACUGUG----AA
Site 2 Position 2593-2600 of Abca1 3'UTR
hsa-miR-27b: 3' ...CGCCUUGAAUCGGUGACACUU... 5'
3'UTR hABCA1: 5' ...AAACUUAUUAACAACUGUGAA... 3'
hsa ---AACAACUGUGAAUAUG
ptr ---AACAACUGUGAAUAUG
mmu ---A---ACUGUGAAUAUG
rno ---A---ACUGUGAAUAUG
ocu -------ACUGUGAAGAUG
LDLRAP1
Site 1 Position 349-355 of Ldlrap1 3'UTR
hsa-miR-27b: 3' ...CGCCUUGAAUCGGUGACACUU... 5'
3'UTR hLDLRAP1: 5' ...UGUGGGUAUCAGGACUGUGAC... 3'
hsa A-UCAGGACUGUGACCAA
ptr A-UCAGGACUGUGACCAA
mmu G-UCAGGACAAUGACCAA
rno G-UCCAGACAAUGACCAA
ocu GCUCAGGACGGCGACCAA
Site 2 Position 1321-1327 of Ldlrap1 3'UTR
hsa-miR-27b: 3' ...CGCCUUGAAUCGGUGACACUU...5'
3'UTR hLDLRAP1: 5' ...UCUCUUUGCUGACACUGUGAC...3'
hsa UGCUGACACUGUGA----
ptr UGCUGACACUGUGA----
mmu UUCUGAC-CUGCAGCCGU
rno UCCUGAC-CUGCAGCCUU
ocu UCCCAGCGCCGUGG----

Figure 10

B

miR-148a

LDLR

Site 1 Position 872-878 of *Ldlr* 3'UTR

```
hsa-miR-148a:          3' ...UGUUUCAAGACAUCACGUGACU... 5'
3'UTR hLDLR:           5' ...UUGUGUUAUUAUUUUGCACUGU... 3'

                         hsa        AUUAUUUUGCACUGUUUU
                         ptr        AUUAUUUUGCACUGUUUU
                         mmu        CCUAGGUUGCACUGACC-
                         rno        CCUAGGUUGCACUGUUUG
                         ocu        ------------------
```

Site 2 Position 1971-1978 of *Ldlr* 3'UTR

```
hsa-miR-148a:          3' ...UGUUUCAAGACAUCACGUGACU... 5'
3'UTR hLDLR:           5' ...CCGUGUUACUGU--UGCACUGA... 3'

                         hsa        UUACUGUUGCACUGAUGUC
                         ptr        UUACUGUUGCACUGAUGUC
                         mmu        U----GUCACAUGGGUAAC
                         rno        U----GUCACACGGGUGAC
                         ocu        -------------------
```

ABCA1

Site 1 Position 3112-3118 of *Abca1* 3'UTR

```
hsa-miR-148a:          3' ...UGUUUCAAGACAUCACGUGACU... 5'
3'UTR hABCA1:          5' ...AUGGGAUCUAUUUUUGCACUGG... 3'

                           hsa      CUAUUUUUGCACUGGAAU
                           ptr      CUAUUUUUGCACUGGAAU
                           mmu      CUAUUUUUGCACUGGAAU
                           rno      CUAUUUUUGCACUGGAAU
                           ocu      CUAUUUUUGCACUGGAAU
```

Figure 11

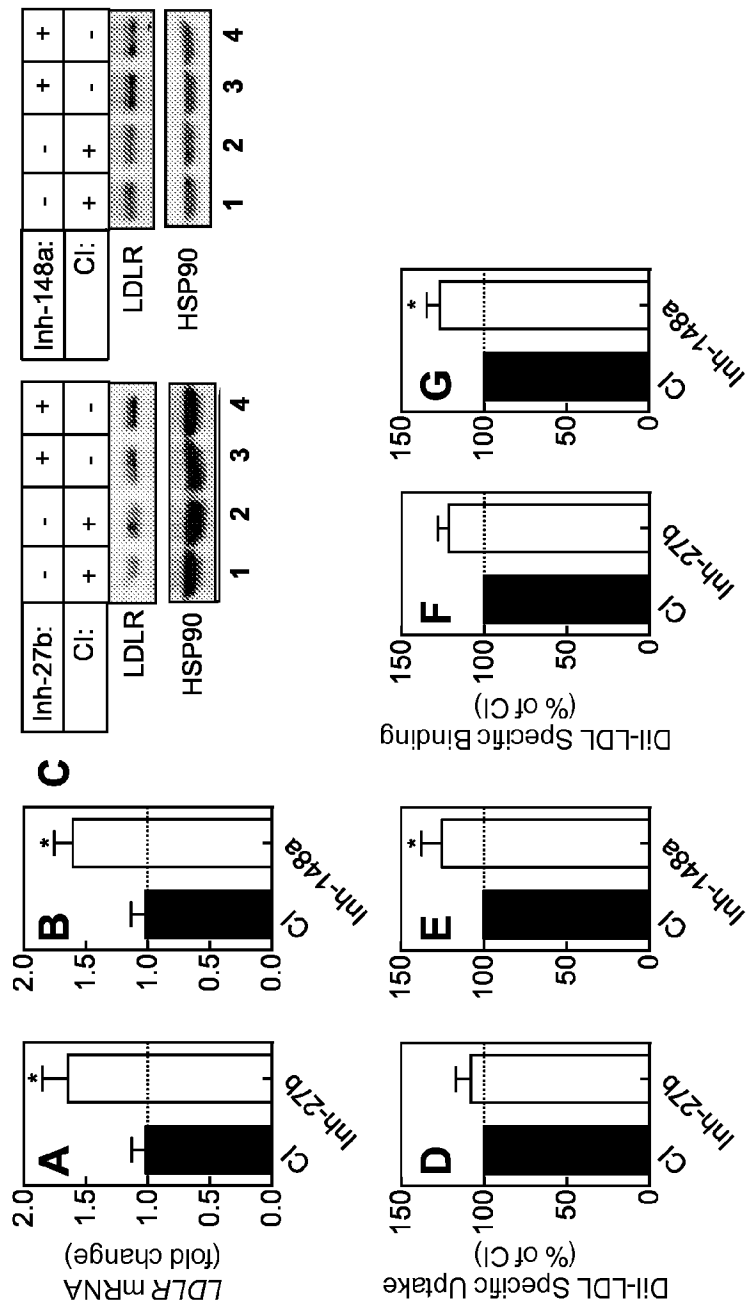
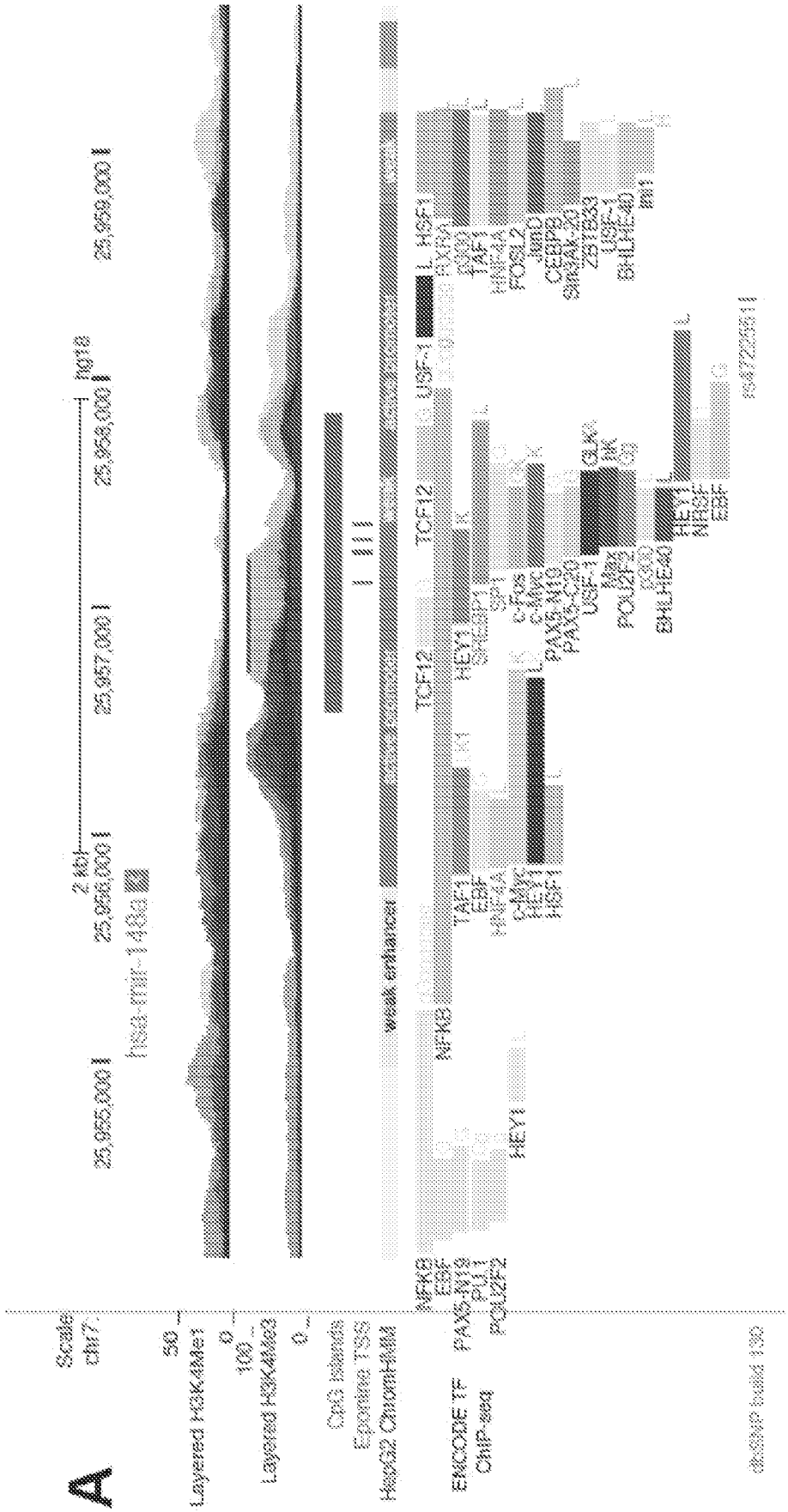

A
B
C
D
E
F
G
LDLR mRNA (fold change)
Dil-LDL Specific Uptake (% of Cl)
Dil-LDL Specific Binding (% of Cl)
Cl
Inh-27b
Inh-148a
Inh-27b:
Inh-148a:
LDLR
HSP90
1 2 3 4

Figure 12


A
Scale
chr7:
2 kb
25,955,000
25,956,000
25,957,000
25,958,000
25,959,000
hsa-mir-148a
weak enhancer
Layered H3K4Me1
Layered H3K4Me3
CpG Islands
Exonic TSS
HepG2 ChromHMM
ENCODE TF ChIP-seq
NFKB
EBF
PAX5-N19
PU1
POU2F2
HEY1
TAF1
EBF
HNF4A
cMyc
HEY1
HSF1
NFKB
HEY1
SREBP1
SP1
c-Fos
c-Myc
PAX5-N19
PAX5-C20
USF-1
Max
POU2F2
BHLHE40
TCF12
USF-1
HSF1
RXRA
AP-2alpha
TAF1
HNF4A
FOSL2
JunD
CEBPB
SMAD4
ZBTB33
USF-1
BHLHE40
Rad21
HEY1
NR3C1
EBF
rs4722811

17/22

Figure 12

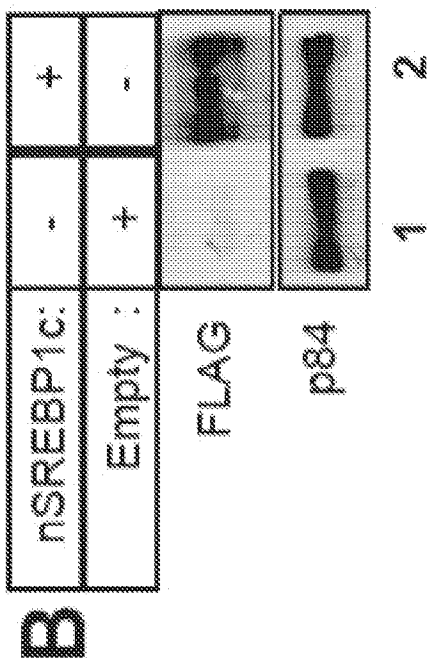
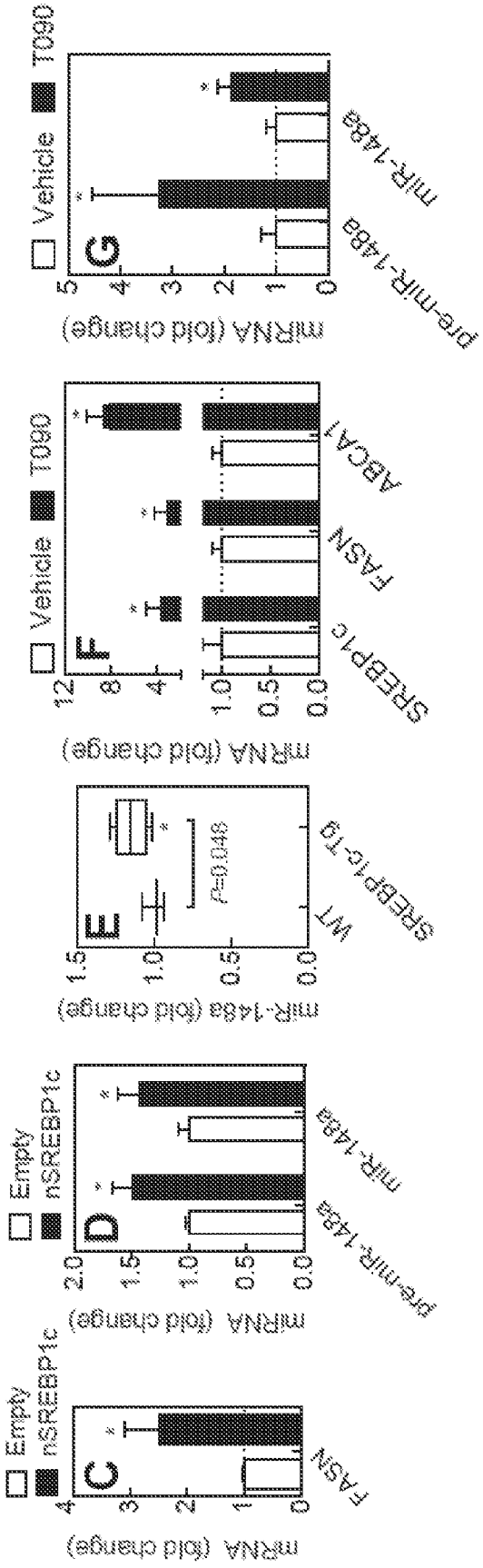


Figure 12


mRNA (fold change)
Empty
nSREBP1c
FASN
C
pre-miR-148a
miR-148a
D
miR-148a (fold change)
WT
SREBP1c-Tg
E
p=0.048
mRNA (fold change)
Vehicle
T090
SREBP1c
FASN
ABCA1
F
mRNA (fold change)
Vehicle
T090
pre-miR-148a
miR-148a
G

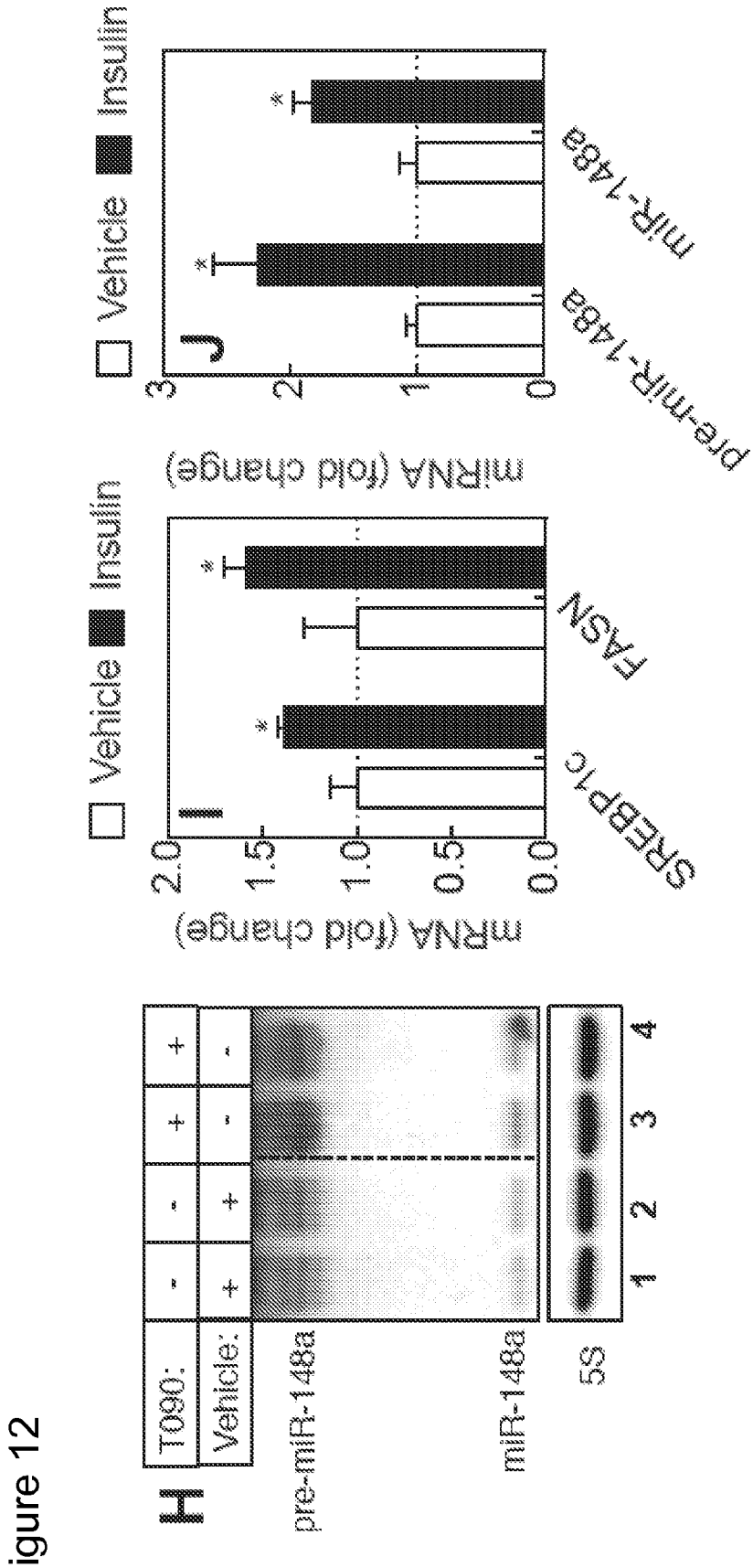

H
T090:
Vehicle:
pre-miR-148a
miR-148a
5S
1
2
3
4
I
mRNA (fold change)
SREBP1c
FASN
Vehicle
Insulin
J
miRNA (fold change)
pre-mir-148a
mir-148a
Vehicle
Insulin

Figure 12

Figure 12

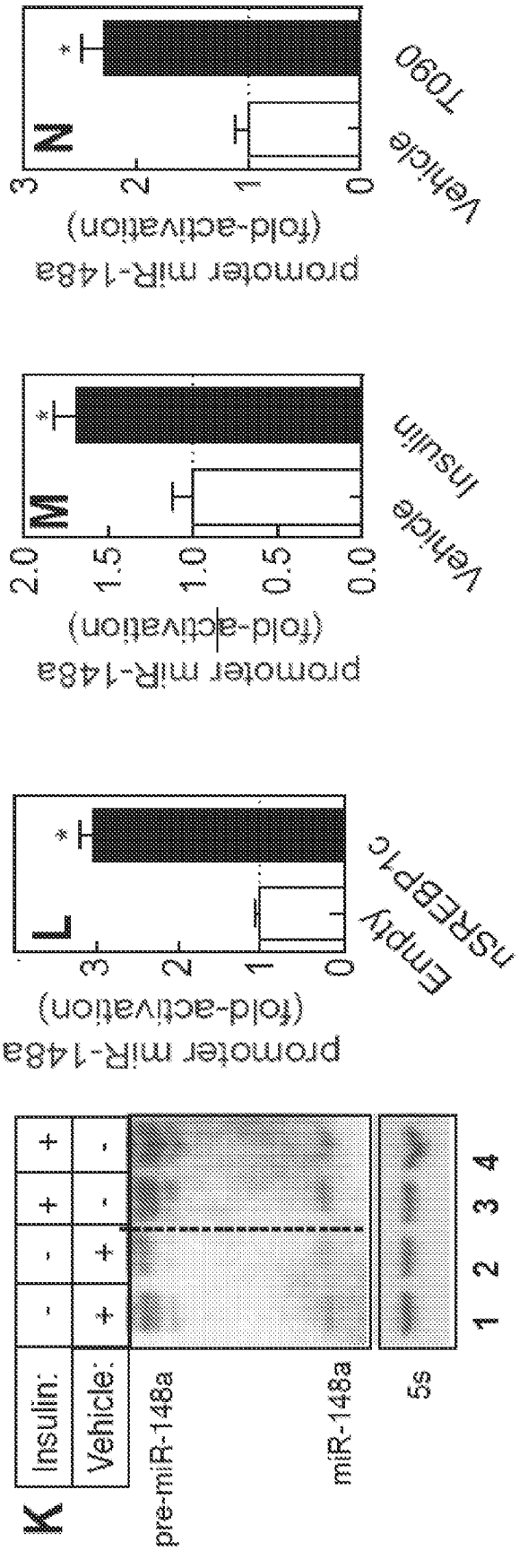

K
Insulin:
Vehicle:
pre-miR-148a
miR-148a
5s
1 2 3 4
promoter miR-148a (fold-activation)
Empty
hSREBP1c
L
M
N
Vehicle
Insulin
T090

Figure 13

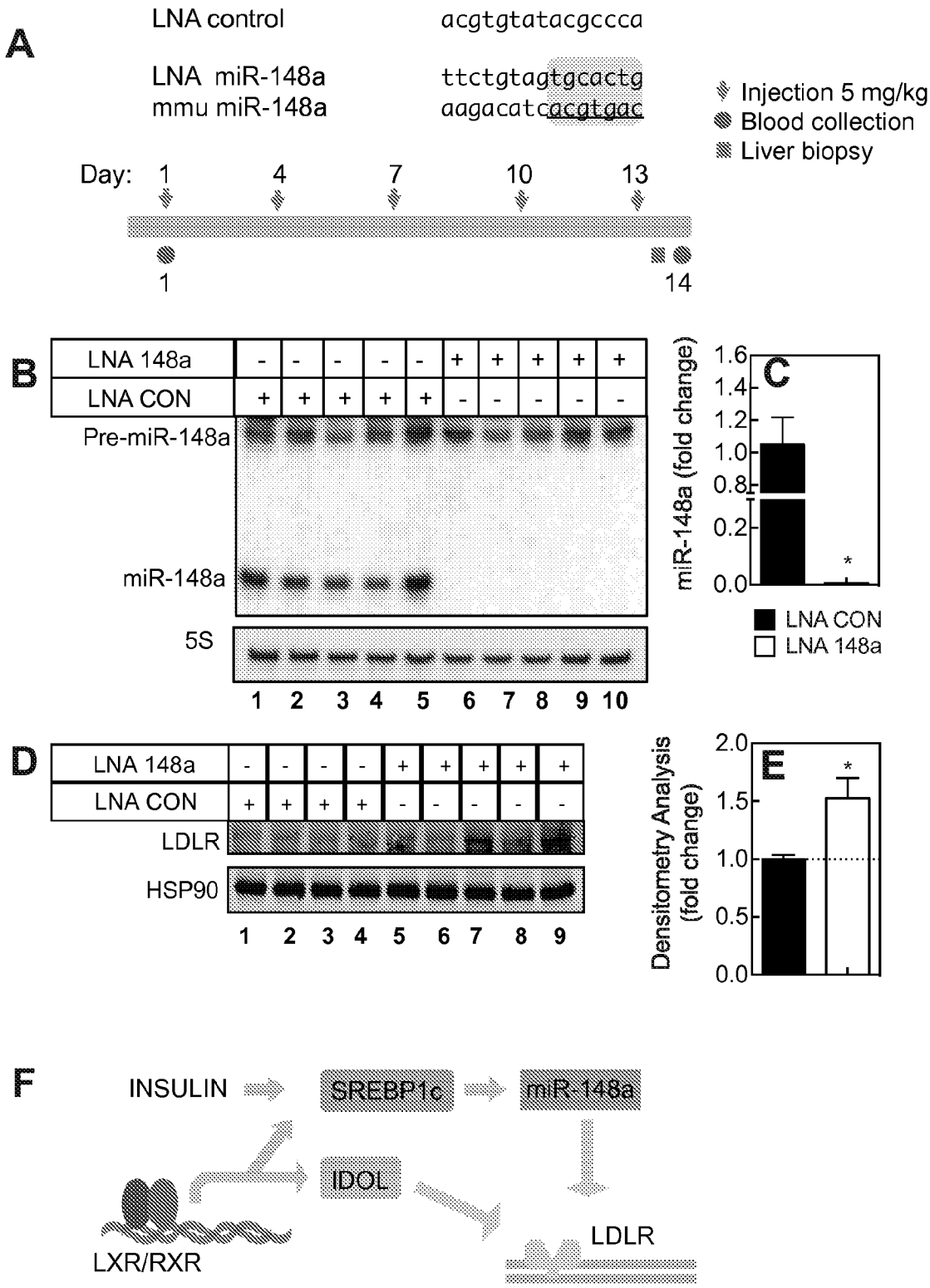
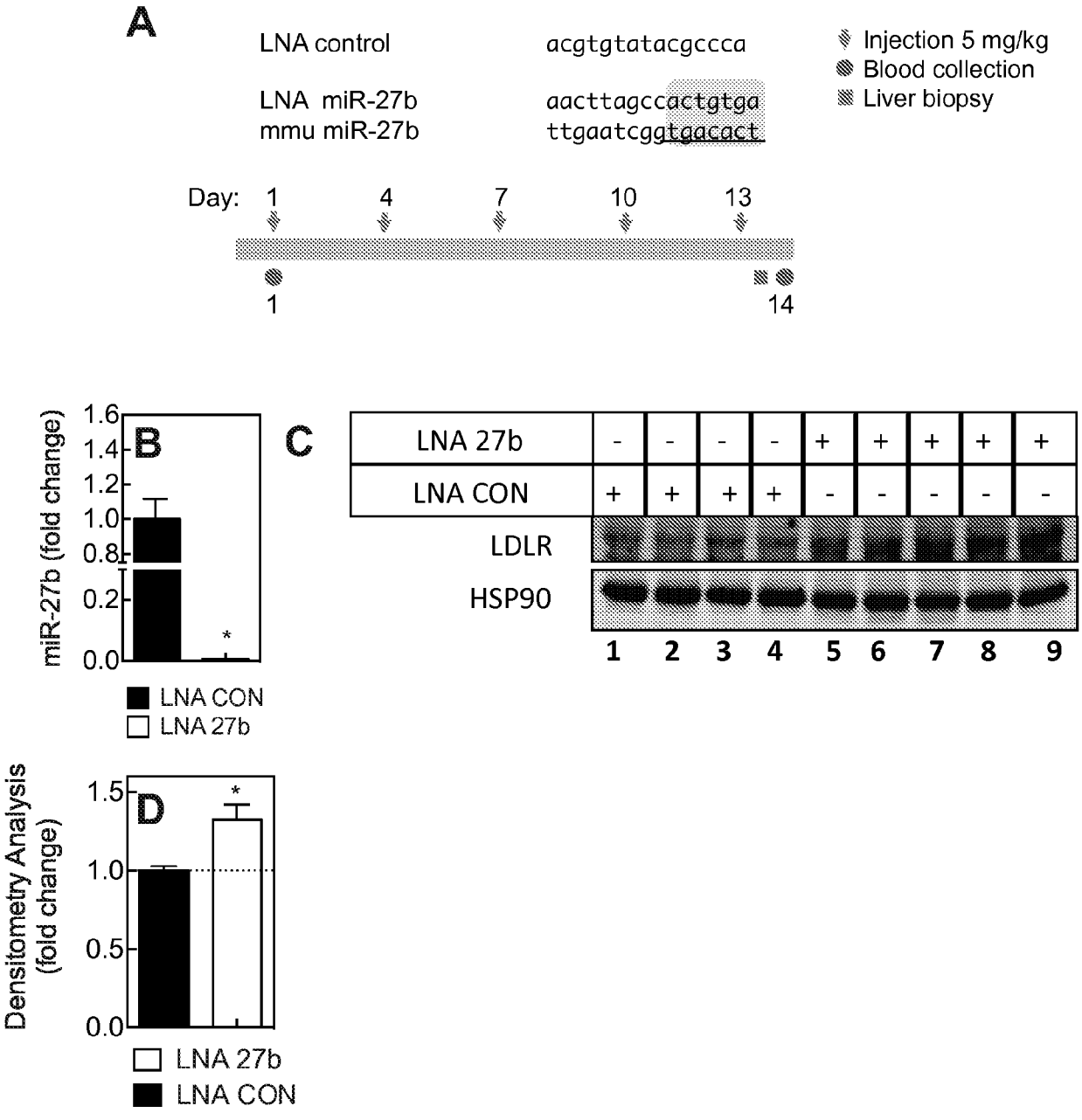

A
LNA control
acgtgtatacgccca
LNA miR-148a
ttctgtagtgcactg
mmu miR-148a
aagacatcacgtgac
Injection 5 mg/kg
Blood collection
Liver biopsy
Day: 1 4 7 10 13
1
14
B
LNA 148a
LNA CON
Pre-miR-148a
miR-148a
5S
1 2 3 4 5 6 7 8 9 10
C
miR-148a (fold change)
1.6
1.4
1.2
1.0
0.8
0.2
0.0
*
LNA CON
LNA 148a
D
LNA 148a
LNA CON
LDLR
HSP90
1 2 3 4 5 6 7 8 9
E
Densitometry Analysis (fold change)
2.0
1.5
1.0
0.5
0.0
*
F
INSULIN
SREBP1c
miR-148a
IDOL
LDLR
LXR/RXR

Figure 14


A
LNA control
acgtgtatacgccca
LNA miR-27b
aacttagccactgtga
mmu miR-27b
ttgaatcggtgacact
Injection 5 mg/kg
Blood collection
Liver biopsy
Day: 1 4 7 10 13
1
14
B
miR-27b (fold change)
1.6
1.4
1.2
1.0
0.8
0.2
0.0
*
LNA CON
LNA 27b
C
LNA 27b - - - - + + + + +
LNA CON + + + + - - - - -
LDLR
HSP90
1 2 3 4 5 6 7 8 9
D
Densitometry Analysis (fold change)
1.5
1.0
0.5
0.0
*
LNA 27b
LNA CON

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2014/042196

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - A61K 31/7105 (2014.01)
CPC - C12N 2310/141 (2014.09)
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)
IPC(8) - A61K 31/7105; C07H 21/02, 21/04; C12N 15/11, 15/113 (2014.01)
USPC - 536/22.1, 23.1, 24.1, 24.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
CPC - C12N 15/, 15/113, 2310/14, 2310/113, 2310/141; C12Q 2600/178 (2014.09)

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

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/0161004 A1 (BROWN et al) 12 July 2007 (12.07.2007) entire document	1, 4, 13, 16
X	US 2005/0261218 A1 (ESAU et al) 24 November 2005 (24.11.2005) entire document	1-3, 13-15, 30, 33
X	US 2009/0143326 A1 (OBAD et al) 04 June 2009 (04.06.2009) entire document	5-12, 17-24, 31, 34
A	US 2012/0283319 A1 (ESAU et al) 08 November 2012 (08.11.2012) entire document	1-24, 30-32, 33, 34

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

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 October 2014	19 NOV 2014
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Authorized officer: Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2014/042196

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

   a. (means)

   ☐ on paper

   ☒ in electronic form

   b. (time)

   ☐ in the international application as filed

   ☐ together with the international application in electronic form

   ☒ subsequently to this Authority for the purposes of search

2. ☒ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

SEQ ID NOs: 1, 2, 6, 7, 58, 59, 60, 61, and 114-119 were searched.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2014/042196

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

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

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

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

3. ☒ Claims Nos.: 25-29, 32, 35-57
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

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

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.