Supporting Information

Material and Methods

Supporting Figure Legends

Supporting Figures

Supporting Figure 1. HFD treatment increases both hepatic and plasma triglycerides

Supporting Figure 2. Fatty acid treatment leads to an increase in lipid content and miR-24 in HepG2 Cells.

Supporting Figure 3. The crosstalk of miR-24 with *Insig1* occurs in HepG2 cells.

Supporting Figure 4. The interaction between miR-24 and *Insig1* plays an important role in lipid accumulation in HepG2 cells treated with fatty acid.

Supporting Figure 5. Insig1 mediates the inhibitory effects of miR-24 inhibitor on SREBP processing in HepG2 cells.

Supporting Figure 6. miR-24 knockdown prevents lipid accumulation in dietary obese mice.

Supporting Tables

Supporting Table 1. 411 Down-regulated Genes in Livers of Human Patients with NAFLD/NASH.

Supporting Table 2. 48 Potential Target Genes of miR-24.

Supporting Table 3. Three Down-regulated Genes in Livers of Human NAFLD/NASH that have Binding Motifs for miR-24.

Supporting Table 4. Primers for quantitative RT-PCR

Supporting Table 5. Comparison of Mice Treated with miR-24-ASO and miR-24-MM-ASO

Material and Methods

Serum Liver Function Tests. Quantitative determination of ALT, glucose, cholesterol and triglycerides was carried out with an ADVIA 1800 automated clinical chemistry system (Siemens) in the Clinical Laboratories at the University of Minnesota Medical Center and the University of California, San Francisco.

Fatty Acid Treatment of HepG2 Cells. HepG2 cells were used in this study due to their high levels of SREBP1c and SREBP2. Oleate treatment of HepG2 cells was carried out as previously described with minor revision.[35] Specifically, 1×10^5 cells were plated in 6-well plate with DMEM medium. Twenty four hours later, HepG2 cells were then treated with either the control medium (DMEM containing 1% Bovine Serum Albumin), BEC medium (DMEM containing 1% BSA and 0.30% Ethanol) or media containing the fatty acid oleate (Sodium Oleate in 1% BSA/DMEM in BEC medium). The cells were cultured for another 24 hours, and lipid accumulation was determined by Nile Red Staining.

Fatty Acid Treatment of Human Hepatocytes. Human hepatocytes were obtained from ZenBio, Inc. and cultured according to the manufacturer's protocol. Briefly, 2.5×10^5 human hepatocytes were plated in 4-well collagen I coated chamber slides. Twenty-four hours later, the hepatocytes were treated with either the control medium (DMEM containing 1% Bovine Serum Albumin), BEC medium (DMEM containing 1% BSA and 0.30% Ethanol) or 0.5 mM oleate medium (Sodium Oleate in 1% BSA/DMEM in BEC medium). The cells were cultured for another 24 hours, and lipid accumulation was determined by Nile Red Staining.

Lipid Accumulation Assay. The lipid content in both human hepatocytes and HepG2 cells was determined using Nile Red, a vital lipophilic dye (9-diethylamino-5H-benzo [alpha] phenoxazine-5-one), which has been shown to selectively stain intracellular lipid droplets. After 24 hours of treatment, cell monolayers were washed twice with PBS and incubated for 30 minutes with Nile Red solution at a final concentration of 1mg/L in PBS at 37°C. Monolayers were washed thereafter with PBS and the fluorescence was determined using a microfluorimeter.

Immunostaining. For Oil-Red-O and Nile-Red staining, 10 µm-thick sections were cut with a Leica CM3050 S cryostat from freshly frozen liver samples, air-dried, and fixed in 10% formalin. After washing, sections were stained with an ORO (Sigma)/60% isopropanol (Fisher) solution. Slides were counterstained with DAPI. Hematoxylin and eosin (H&E) as well as Oil Red O-stained liver specimens were examined by light microscopy, but Nile-Red stained liver sections were evaluated by fluorescence microscopy. For Insig1 immunostaining, paraffin-embedded liver samples were sectioned and stained with rabbit anti-Insig1 antibody at 1:100 dilutions. For fluorescence microscopy, goat anti-rabbit antibody was conjugated with Alexa Fluor 594 (Invitrogen) and used at a 1:500 dilution. Nuclear DNA was stained with 300 nM DAPI (Millipore).

Lipid and Lipoprotein Analysis. Hepatic triglyceride and cholesterol content were enzymatically measured in liver lysates using L-type TG H triglyceride kit and Cholesterol E Kits, respectively, according to the manufacturer's protocols (Wako Chemicals).

Insig1 3' UTR Luciferase Reporter Vector Construction and Luciferase Assay. To generate the luciferase reporter vectors, *Insig1* 3' UTR was amplified by PCR from human cDNA, and inserted into the pMiR-Report vector between HindIII and SacI sites (Ambion). All vector constructions were confirmed by sequencing. Twenty-four hours before transfection, 5×10^4 cells were plated per well in a 24-well plate. Then, 200 ng of *Insig1* 3' UTR reporter construct, different concentrations of miR-24 mimic and 30 ng of β-*gal* plasmid pSV-β-Galactosidase Control Vector (Promega) were transfected using Lipofectamine 2000 [25](Invitrogen). Twenty four hours after transfection, luciferase and β-galactosidase assays were performed using the Luciferase Assay System and Beta-Glo® Assay System (Promega). Luciferase activities were normalized to galactosidase activities; wells were transfected in triplicate; and each well was assayed in triplicate.

Quantitative Reverse Transcription-PCR (qRT-PCR). Total RNA was isolated with Trizol and treated with DNase I (Ambion) to eliminate genomic DNA. 1 mg RNA was used for cDNA synthesis with Superscript III reverse transcription reagent (Invitrogen). PCR amplification was performed at 50°C for 2 minutes and 95°C for 10 minutes, followed by 40 cycles at 95°C for 15 seconds and 60°C for 1 minute in a 7900 real time-PCR system with SYBR green (Applied Biosystems). For each sample, β-actin, GAPDH or 18S rRNA levels were used to normalize target gene expression. Primers for qRT-PCR were designed with Primer Express software (Applied Biosystems). For miRNA analysis, RNA was isolated with the miRNeasy kit (Qiagen). Ten ng RNA were used for miRNA-specific cDNA synthesis with the TaqMan MicroRNA Reverse Transcription Kit and Taqman MicroRNA Assays (all Applied Biosystems). PCR amplification was performed at 95°C for 10 minutes, followed by 40 cycles at 95°C for 15 seconds and 60°C for 1 minute in a 7900 real time-PCR system (Applied Biosystems). The small RNAs Sno202 and RNU6 were used to normalize target miRNA expression. Relative changes in gene and miRNA expression were determined using the $2^{-\Delta\Delta Ct}$ method.[37] Primers used for quantitative RT-PCR were listed in Supporting Table 4.

miR-24 In Situ hybridization. Liver were fixed by overnight immersion in phosphate buffered saline (PBS) containing 4% paraformaldehyde (4% PFA) at 4°C, washed in PBS, dehydrated in 15% sucrose, and embedded in OCT (Fisher). Exiqon microRNA *in situ* hybridization kit was used according to the manufacturer's protocol. Anti-miR-24 LNA and control LNA probes were used at concentrations of 25 mM and incubated at hybridizing temperature of 55°C. Anti-DIG-AP antibodies (Roche) was used at 1:100 dilution and incubated at RT for 1 hour. Positive *in situ* hybridization signals are visualized in purple, while pink depicts DAPI nuclear stain.

Western Blot Analysis. Western blot was performed following standard procedures. Insig1, SREBP1c and SREBP2 primary antibodies were purchased from Cell Signaling and Abcam; and binding was visualized using SuperSignal west femto maximum sensitivity substrate (Cat # 34095, Thermo Fisher Scientific Inc.).

Statistical Analysis. All the experiments were repeated at least three times and the error bars represent the standard error of the mean (SE). Statistical analyses were carried out using two-tailed Student's t-test; $p < 0.05$ was considered statistically significant.

Supporting Figure and Table Legends

Supporting Fig. 1. HFD treatment increases both hepatic and plasma triglycerides. (A, B) Nile Red and H&E staining showing that HFD treatment led to increased hepatic lipid accumulation in mice. (C, D) HFD treatment led to high levels of hepatic and plasma triglycerides. Lipids were extracted from the livers of mice treated with standard diet or HFD and triglycerides measured using a colorimetric assay. Data are expressed as mean ± SD. Representative histological images are shown. $^*P < 0.01$ versus controls ($n = 4$–6 per group).

Supporting Fig. 2. Fatty acid treatment leads to an increase in lipid content and miR-24 in HepG2 Cells. (A, B) Oleate treatment led to an increase in lipid content in HepG2 cells, as determined fluorimetrically using Nile Red, a selective stain for intracellular lipid droplets. (C) Oleate treatment increased miR-24 expression in HepG2 cells. ata represent mean ± SEM. $^*P < 0.05$.

Supporting Fig. 3. The crosstalk of miR-24 with *Insig1* occurs in HepG2 cells. (A) miR-24 mimic transfection into HepG2 cells inhibited expression levels of endogenous *Insig1*. (B) Knockdown of miR-24 by transfection of inhibitors into HepG2 cells caused an increase in endogenous *Insig1* mRNA levels. (C) Western blot analysis further confirmed that miR-24 repressed but miR-24 inhibitor induced protein levels of endogenous *Insig1*. *ImageJ* program was used to *quantify* western blot bands. ata represent mean ± SEM. $^*P < 0.05$.

Supporting Fig. 4. The interaction between miR-24 and *Insig1* plays an important role in lipid accumulation in HepG2 cells treated with fatty acid. (A) Q-RT-PCR revealed that oleate treatment led to up-regulated miR-24 and decreased *Insig1*. (B, C) Oleate treatment increased lipid accumulation in HepG2 cells as determined fluorimetrically using Nile Red. (D) miR-24 inhibitor transfection into oleate-treated HepG2 cells led to decreased miR-24 and increased *Insig1* as revealed by qRT-PCR. (E,

F) Higher levels of *Insig1* due to miR-24 knockdown repressed lipid accumulation in HepG2 cells, as determined fluorimetrically using Nile Red. ata represent mean ± SEM. **P* < 0.05.

Supporting Fig. 5. Insig1 mediates the inhibitory effects of miR-24 inhibitor on SREBP processing in HepG2 cells. (A) miR-24 knockdown in HepG2 cells led to increased protein levels of *Insig1*, which subsequently caused a decrease in nuclear SREBP1c and SREBP2. Additional knockdown of induced *Insig1* with siRNA restored SREBP1c and SREBP2. HepG2 cells were treated with oleate to induce miR-24, and then miR-24-ASO was transfected to knock down the upregulated miR-24. SREBP1c, SREBP2 and Insig1 protein were determined by western blot. *ImageJ* program was used to *quantify* western blot bands. (B, C) miR-24 knockdown prevented lipid accumulation in HepG2 cells, and additional knockdown of *Insig1* rescued the effect of miR-24-ASO. The lipid content in the cultured HepG2 cells was determined fluorimetrically using Nile Red. (D) Deletion of miR-24 increased expression of *Insig1*, which subsequently led to a significant decrease in mRNA levels of *SCD1*, *FASN*, *GPAT* and *HMGCR*. (E) Overexpression of miR-24 repressed expression of *Insig1*, which subsequently caused an increase in mRNA levels of lipogenic genes including *SCD1*, *FASN*, *GPAT* and *HMGCR*. MRNA levels of *SCD1*, *FASN*, *GPAT* and *HMGCR* were measured by qRT-PCR. ata represent mean ± SEM. **P* < 0.05.

Supporting Fig. 6. miR-24 knockdown prevents lipid accumulation in dietary obese mice. (A) *In situ* staining revealed that miR-24 was significantly knocked down after miR-24-ASO injection into dietary obese mice. Positive *in situ* hybridization signals are visualized in purple, while pink depicts DAPI nuclear stain. (B) MiR-24 knockdown subsequently led to an increase of Insig1, as revealed by immunostaining. (C, D) Nile red and H&E staining showed that miR-24 knockdown prevented hepatic lipid accumulation in dietary obese mice.

Supporting Table 1. 411 Down-regulated Genes in Livers of Human Patients with NAFLD/NASH.

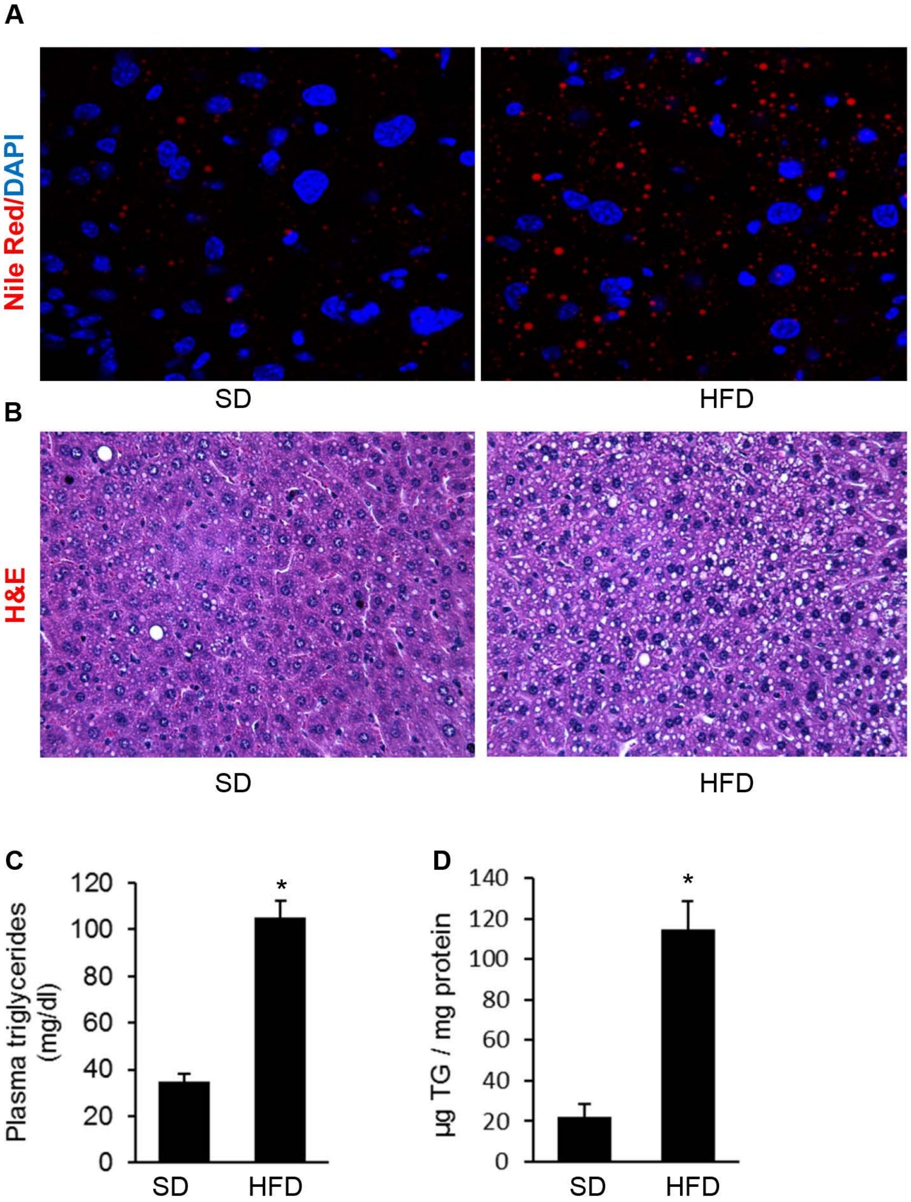
Supporting Table 2. 48 Potential Target Genes of miR-24. To determine the potential role of miR-24 in regulating lipid metabolism within hepatocytes, we predicted target genes using TargetScan and Pictar and starBase as described in Materials and Methods. To increase the prediction accuracy, we only selected overlapped hits from both Target and PicTar algorithms as well as those confirmed by Ago HITS-CLIP (high-throughput sequencing of RNAs isolated by crosslinking immunoprecipitation [HITS-CLIP] from Argonaute protein complex). Such an approach identified 48 hits that are potential target genes of miR-24.

Supporting Table 3. Three Down-regulated Genes in Livers of Human NAFLD/NASH that have Binding Motifs for miR-24. We compared 411 down-regulated genes with 48 genes that contain miR-24 binding sites, allowing us to identify three down-regulated genes in livers of human individuals with NAFLD that have binding motifs for miR-24. Furthermore, we performed Gene Oncology analysis using PathwayStudio (Elsevier) and GoMiner and observed that Insig1 is a potential regulator of lipid accumulation, leading us to focus on the role of the crosstalk between miR-24 and *Insig1* in NAFLD and hypertriglyceridemia.

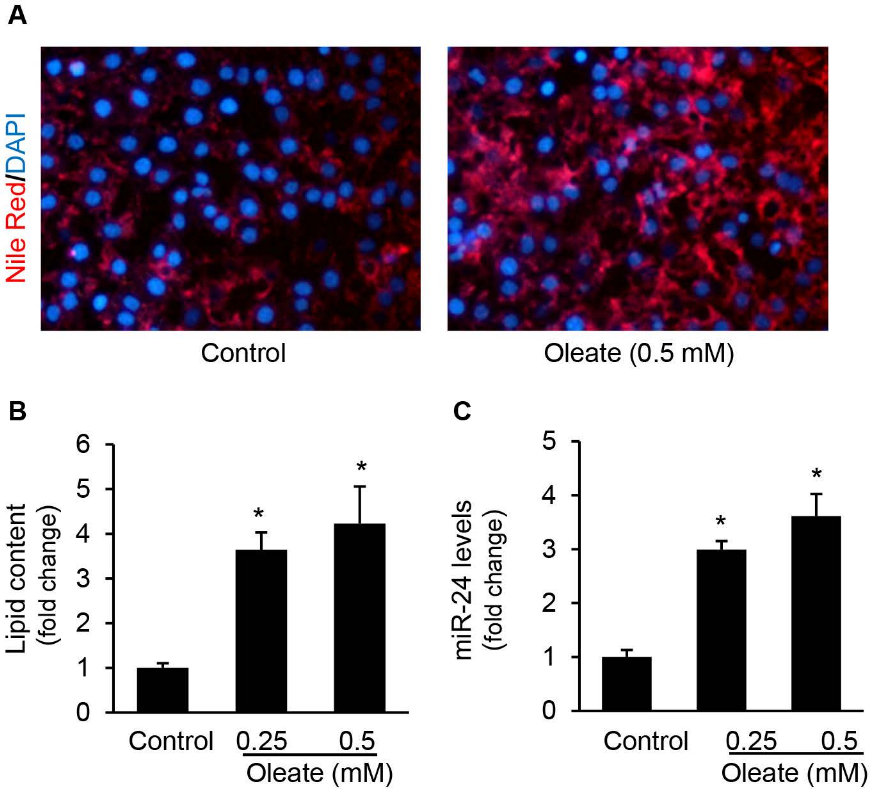
Supporting Table 4. Primers for quantitative RT-PCR.

Supporting Table 5. Comparison of Mice Treated with miR-24-ASO and miR-24-MM-ASO. In detail, C57B/l6 wild type mice were kept on normal chow until 8 weeks of age and then maintained on HFD until 16 weeks of age. At that time, the mice were given miR-24-ASO (25 mg/kg, tail-vein injection) until 20 weeks. The C57Bl/6 mice maintained on HFD and treated with miR-24-MM-ASO served as control. Mice were fasted for 8 hours before liver and blood collection. ata represent mean ± SEM. *$P < 0.05$ for level of statistical significance between miR-24-ASO and miR-24-MM-ASO treated mice.

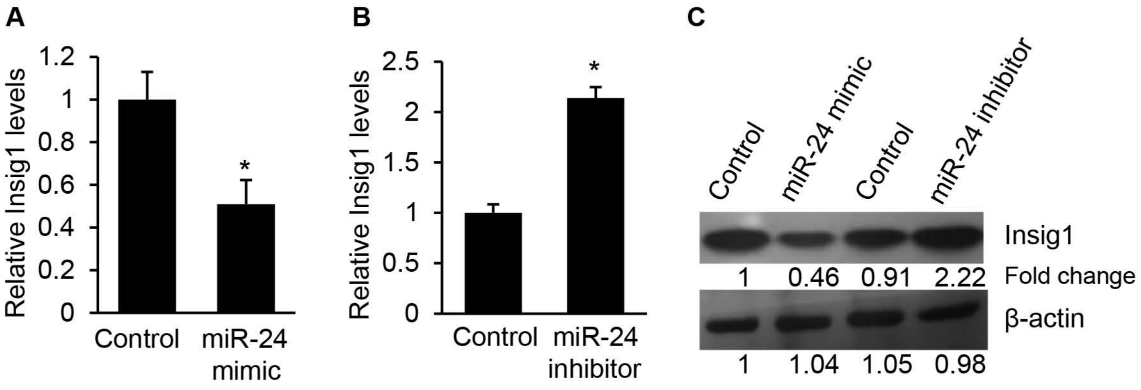
Supporting Figure 1



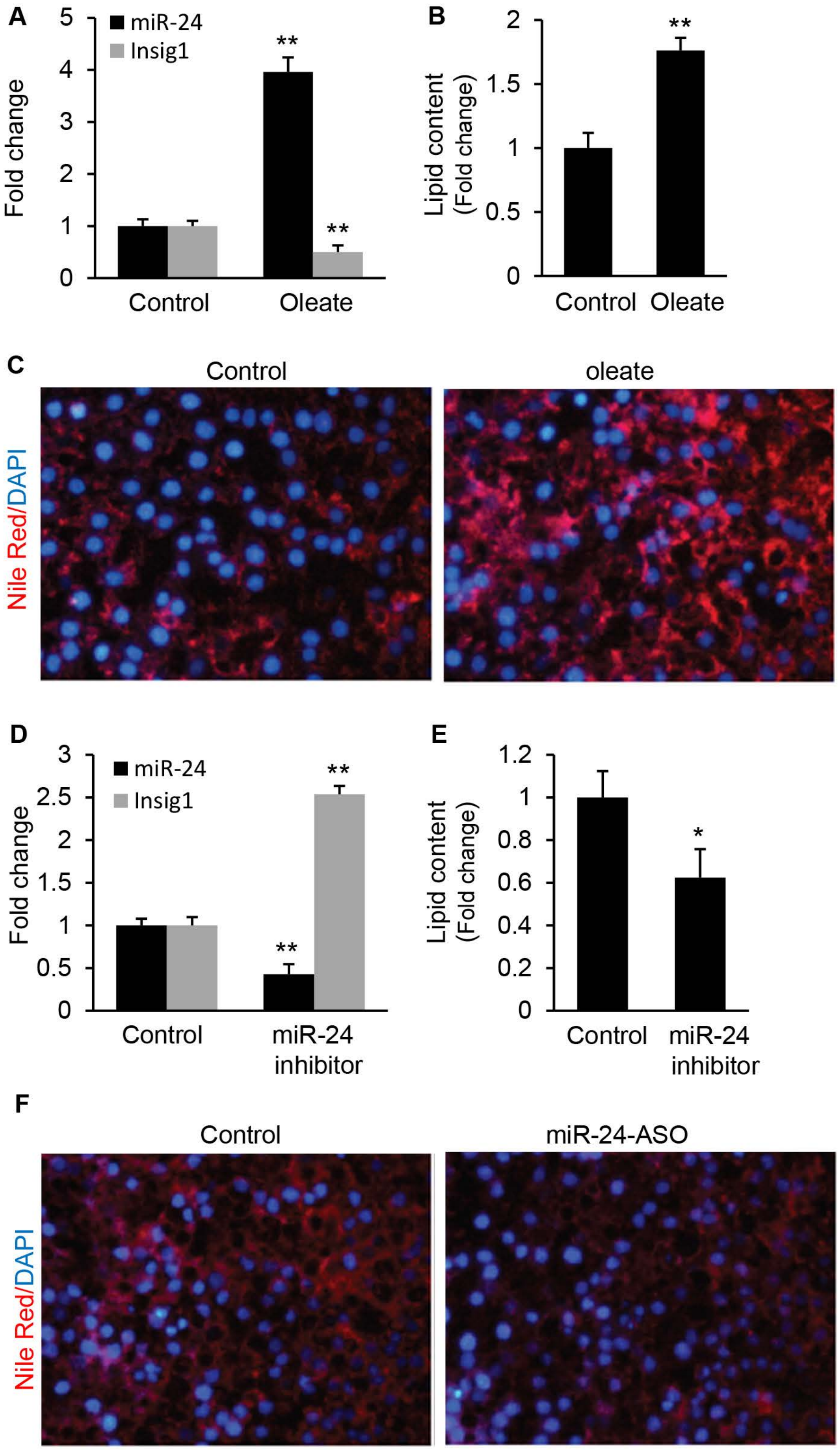
Supporting Figure 2



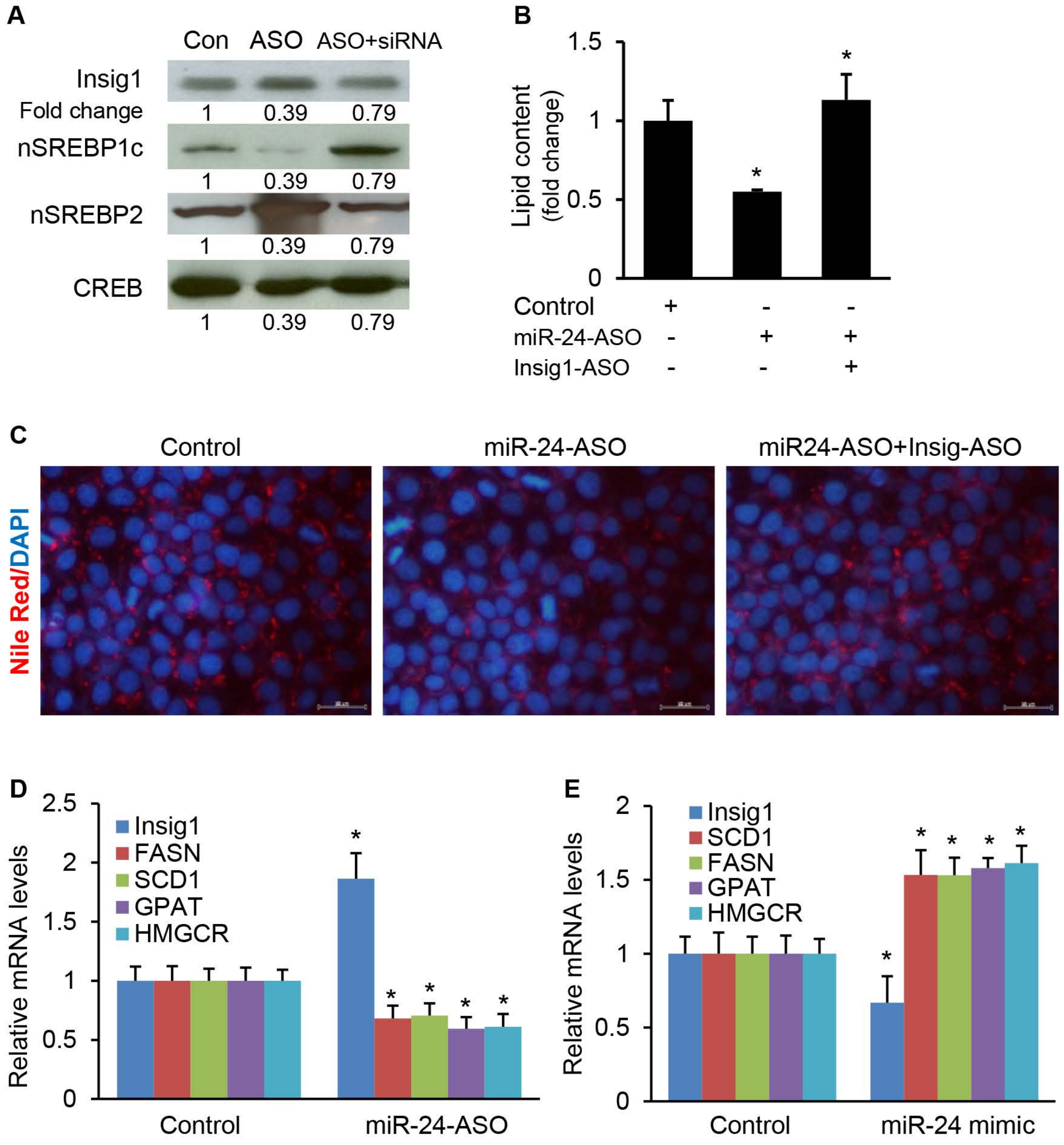
Supporting Figure 3



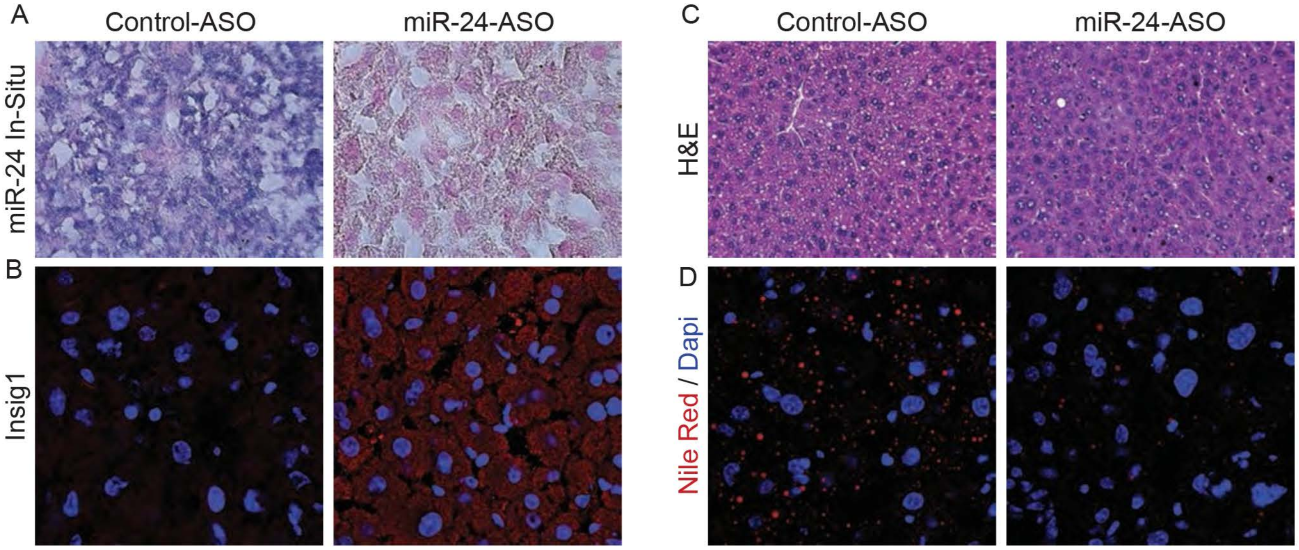
Supporting Figure 4



Supporting Figure 5



Supporting Figure 6



Supporting Table 1. 411 Down-regulated Genes in Livers of Human Patients with NAFLD/NASH.

Probe ID	LogFC (NAFLD/Normal)	*P* Value	Gene symbol	Gene Name
8123936	-0.5253034	0.04978851	NEDD9///NEDD9	neural precursor cell expressed, developmentally down-regulated 9///neural precursor cell expressed, developmentally down-regulated 9
7895081	-0.6305263	0.04943983		
7979179	-0.5030774	0.04904768	ERO1L	ERO1-like (S. cerevisiae)
7895873	-0.5563492	0.04863099		
7912706	-0.6998363	0.04848657	EPHA2	EPH receptor A2
7895267	-0.7159641	0.04827798		
7896426	-0.783815	0.04822682		
8144685	-0.5035525	0.04757799		
7894004	-0.529836	0.04729158		
7893082	-0.717114	0.04670257		
7892688	-0.5435441	0.04664537		
7892501	-0.9988008	0.04638545		
7969414	-0.7581077	0.04518542	KLF5	Kruppel-like factor 5 (intestinal)
7894599	-0.8792485	0.04515501		
8134030	-0.5011774	0.04499696	STEAP1	six transmembrane epithelial antigen of the prostate 1
7897449	-0.5138176	0.04472003	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1
8131957	-0.6298414	0.04394286	SNX10	sorting nexin 10
7981984	-0.98275	0.04328921	SNORD116-18	small nucleolar RNA, C/D box 116-18
7893003	-0.5322347	0.04322103		
8039389	-0.5859818	0.04297888	PTPRH	protein tyrosine phosphatase, receptor type, H
7964927	-1.3066047	0.04199953	TSPAN8	tetraspanin 8
8075477	-0.5514647	0.0413534	RNF185	ring finger protein 185
8049187	-0.8916716	0.04120592	EFHD1	EF-hand domain family, member D1
7894199	-0.979366	0.04083466		
7964832	-0.5737636	0.04019986		
7893173	-0.6933095	0.04011849		
7959085	-0.7702644	0.04010702		

8013112	-1.3398585	0.04006096	RASD1	RAS, dexamethasone-induced 1
8106403	-0.6635718	0.03965488	F2RL1	coagulation factor II (thrombin) receptor-like 1
7896398	-0.549868	0.03958533		
7998927	-0.7478878	0.03941006		
8084963	-0.5474177	0.03885472	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2
8040516	-0.5445119	0.03878738	MFSD2B	major facilitator superfamily domain containing 2B
7957654	-0.5326827	0.03870544	AMDHD1	amidohydrolase domain containing 1
8032834	-0.618986	0.03858141	LRG1	leucine-rich alpha-2-glycoprotein 1
7984660	-0.6727377	0.03807913		
7920256	-0.5233955	0.03786015		
8069532	-0.6052885	0.03773282	HSPA13	heat shock protein 70kDa family, member 13
7892953	-0.5827467	0.03749064		
7898693	-0.6306742	0.03689928	ALPL	alkaline phosphatase, liver/bone/kidney
8116579	-0.6189169	0.03671688	FOXQ1	forkhead box Q1
8025402	-1.0413115	0.03654429	ANGPTL4	angiopoietin-like 4
7937772	-0.5246209	0.03629419	INS-IGF2///IGF2	INS-IGF2 readthrough///insulin-like growth factor 2 (somatomedin A)
8175288	-0.518977	0.03628981	MOSPD1	motile sperm domain containing 1
7909332	-0.5284503	0.03614768	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
7896690	-0.5267387	0.03602474		
8073007	-0.5982432	0.03573051	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
7895673	-1.0051126	0.03530945		
7894788	-0.500707	0.03529408		
8104369	-0.5367299	0.03504226	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
7933872	-0.752907	0.03499603	EGR2	early growth response 2
8003560	-0.5147576	0.03472716	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1
8139889	-0.6199746	0.03469188		
7916609	-1.2876438	0.03464845	JUN	jun proto-oncogene
7981909	-0.6000776	0.03427088		
7896608	-0.5165406	0.0340204		

8052022	-0.5993708	0.03370402		
8119620	-1.1255306	0.0336937	GNMT	glycine N-methyltransferase
7893723	-0.9430944	0.033366		
7924758	-0.7582321	0.03288539		
7893850	-0.5541691	0.03244317		
7935270	-0.5386947	0.03227082	BLNK	B-cell linker
7896079	-0.870196	0.03214102		
7919600	-1.3179187	0.03211885		
7978586	-0.5280231	0.03191485	CFL2	cofilin 2 (muscle)
7925342	-0.5465499	0.0318838	ERO1LB	ERO1-like beta (S. cerevisiae)
7926484	-0.6020203	0.03174617		
8107671	-0.5548638	0.03157262		
8070489	-0.6389739	0.03133392	RIPK4	receptor-interacting serine-threonine kinase 4
8136801	-0.5173151	0.03120149	PRSS3P2///PRSS3///PRSS2	protease, serine, 3 pseudogene 2///protease, serine, 3///protease, serine, 2 (trypsin 2)
7893339	-0.5229027	0.03067851		
7978748	-0.5244771	0.03039409	FBXO33	F-box protein 33
7896378	-0.7289568	0.03036867		
8090277	-0.5502488	0.02982736	OSBPL11	oxysterol binding protein-like 11
8155508	-0.7373802	0.02957688		
7984405	-0.5312894	0.02956246	C15orf61	chromosome 15 open reading frame 61
7896533	-0.6544285	0.0294178		
8023727	-0.5714076	0.02914503	DSEL	dermatan sulfate epimerase-like
7923596	-0.5376735	0.02851715	ETNK2	ethanolamine kinase 2
7893962	-0.7120229	0.02830659		
8149720	-0.5739149	0.02764674	EGR3	early growth response 3
8068593	-0.7666417	0.02681167	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
7892724	-0.8385407	0.02679051		
7950641	-0.539566	0.02658105	KCTD14	potassium channel tetramerisation domain containing 14
8083223	-0.5763687	0.02649944	C3orf58	chromosome 3 open reading frame 58
7894834	-0.5661113	0.02601247		

7917240	-0.5111531	0.02595433	CTBS	chitobiase, di-N-acetyl-
7932794	-0.5009931	0.02587694		
8156848	-1.0400562	0.02572079	NR4A3	nuclear receptor subfamily 4, group A, member 3
8131803	-0.9824619	0.02549894	IL6	interleukin 6 (interferon, beta 2)
8129637	-0.8157712	0.02539626	VNN2	vanin 2
7962884	-1.0891501	0.02528467	RND1	Rho family GTPase 1
8160670	-0.5044479	0.02527373	AQP3	aquaporin 3 (Gill blood group)
8089013	-0.5000782	0.02501156		
7975268	-0.7553863	0.02491772	VTI1B///ARG2	vesicle transport through interaction with t-SNAREs 1B///arginase 2
7894150	-0.6609985	0.02482082		
8097801	-0.6748175	0.02480175	FAM160A1	family with sequence similarity 160, member A1
7948511	-0.5670527	0.02467195	VWCE	von Willebrand factor C and EGF domains
8097461	-1.1067402	0.02462078	CCRN4L///CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)///CCR4 carbon catabolite repression 4-like (S. cerevisiae)
7985025	-0.7841578	0.02451442	ODF3L1	outer dense fiber of sperm tails 3-like 1
8103023	-0.5407848	0.02448072		
8162276	-1.2466094	0.0243664	NFIL3	nuclear factor, interleukin 3 regulated
7895752	-0.5722766	0.02434932		
8130009	-0.5111864	0.02430985		
7967331	-0.5095312	0.02430367	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)
7896519	-0.59685	0.02421754		
7965040	-1.0712458	0.02417248	PHLDA1	pleckstrin homology-like domain, family A, member 1
8146115	-0.8207753	0.02414875	C8orf4	chromosome 8 open reading frame 4
8089112	-0.7003057	0.02398271	FILIP1L	filamin A interacting protein 1-like
8132911	-0.5201116	0.02390675		
7995342	-0.5970376	0.02375308		
8098240	-0.5631675	0.02356108		
8002760	-0.534114	0.02347278		
7982805	-0.6399177	0.02329391	GCHFR	GTP cyclohydrolase I feedback regulator
8118667	-0.5247041	0.02320314	MYL12B	myosin, light chain 12B, regulatory
7893619	-0.5612938	0.02305155		

7919751	-0.5190224	0.02302389	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)
7922646	-0.5169399	0.02288437	TOR1AIP2	torsin A interacting protein 2
7905503	-0.5236343	0.02266108	LCE2C	late cornified envelope 2C
8066513	-0.5882838	0.022509	SDC4	syndecan 4
7893549	-0.6736474	0.02244048		
8161648	-0.6689779	0.02231988	KLF9	Kruppel-like factor 9
8020724	-0.5041743	0.02231974	DSG1	desmoglein 1
8079163	-0.651555	0.02213083		
7965606	-0.8933789	0.02202228	HAL	histidine ammonia-lyase
7928308	-0.9609032	0.02197104	DDIT4	DNA-damage-inducible transcript 4
7895253	-0.6840888	0.02161753		
7980990	-0.5302789	0.02140291	C14orf142///UBR7	chromosome 14 open reading frame 142///ubiquitin protein ligase E3 component n-recognin 7 (putative)
7893624	-0.5827103	0.02134718		
7892573	-0.6941269	0.02087303		
8080958	-0.5722847	0.02083902	GPR27	G protein-coupled receptor 27
7926979	-0.9146494	0.02064692		
8083136	-0.6112498	0.02050294	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide
7905929	-0.5370957	0.0202485	EFNA1	ephrin-A1
8095680	-1.6588538	0.02005064	IL8	interleukin 8
7894251	-0.6504813	0.02002574		
8123637	-0.8065788	0.02002004	HTATSF1P2///NQO2	HIV-1 Tat specific factor 1 pseudogene 2///NAD(P)H dehydrogenase, quinone 2
7895972	-0.5449425	0.019616		
8100202	-0.7416219	0.01958113	LOC280665///CNGA1	anti-CNG alpha 1 cation channel translation product-like///cyclic nucleotide gated channel alpha 1
7975626	-0.5177171	0.01953319	ELMSAN1	ELM2 and Myb/SANT-like domain containing 1
7893539	-0.8975014	0.01925281		
7982152	-0.6358306	0.0192255		
7986661	-0.6358306	0.0192255		
7986943	-0.6358306	0.0192255		
7955719	-0.6514739	0.01913438	HIGD1A	HIG1 hypoxia inducible domain family, member 1A

7934278	-1.3558887	0.01840943	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I
7997712	-0.8324761	0.01832857	IRF8	interferon regulatory factor 8
8157264	-0.5512394	0.01795087	SLC31A2	solute carrier family 31 (copper transporters), member 2
8180318	-0.7306195	0.01787534	TGIF1	TGFB-induced factor homeobox 1
8157605	-0.7423595	0.01786786		
8110708	-0.5156707	0.01761044	TPPP	tubulin polymerization promoting protein
7895181	-0.5854569	0.01758103		
7925436	-0.6663342	0.01734027		
8169233	-0.912351	0.01725385		
7896321	-0.6130633	0.01724026		
7895153	-0.7474846	0.01710029		
7905131	-0.6031465	0.01706176	CA14	carbonic anhydrase XIV
8101699	-0.7296946	0.01705999	PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K
8020630	-0.555526	0.01698629	TTC39C	tetratricopeptide repeat domain 39C
7895971	-0.5919108	0.01687709		
8038877	-0.5011044	0.01666189	SIGLEC5	sialic acid binding Ig-like lectin 5
8088642	-0.5171738	0.01660526	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1
8135069	-1.4897627	0.01657498	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
8035445	-0.9767586	0.01640411	JUND	jun D proto-oncogene
7995324	-0.5778227	0.01636985		
8117696	-0.5012466	0.01621336	COX11	cytochrome c oxidase assembly homolog 11 (yeast)
7898655	-0.5707078	0.01617006	CDA	cytidine deaminase
8049567	-0.8612279	0.01616883	RAMP1	receptor (G protein-coupled) activity modifying protein 1
7957551	-1.1219426	0.01615871	SOCS2	suppressor of cytokine signaling 2
8132694	-2.2791786	0.01606823	IGFBP1	insulin-like growth factor binding protein 1
7924526	-0.6776029	0.01599559	TP53BP2	tumor protein p53 binding protein, 2
8099633	-0.911251	0.01598597	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
8040465	-0.6010055	0.0156272		
7895096	-0.5173221	0.01555575		
8037267	-0.5181162	0.01554196	PSG2	pregnancy specific beta-1-glycoprotein 2

7895018	-0.7159829	0.01538422		
8180319	-0.7330649	0.01515961	TGIF1	TGFB-induced factor homeobox 1
8001041	-0.5067876	0.01503265	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2
7909142	-0.5183588	0.01497523	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1
7902687	-1.557861	0.01484337	CYR61	cysteine-rich, angiogenic inducer, 61
8161610	-0.6272786	0.01462977	TMEM252	transmembrane protein 252
8041048	-0.7030326	0.01427111	FOSL2	FOS-like antigen 2
8162624	-0.8617888	0.01424785	AAED1	AhpC/TSA antioxidant enzyme domain containing 1
7896094	-0.5026811	0.01424766		
8172573	-0.5200627	0.0141162	SYP	synaptophysin
8077441	-0.5856049	0.0137106	BHLHE40	basic helix-loop-helix family, member e40
8129666	-0.6502501	0.01369339	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12
8135480	-0.5743501	0.01368888	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9
8169709	-0.6243576	0.01356165	GLRX5	glutaredoxin 5
8005233	-0.7371269	0.01355073		
7930413	-0.5734406	0.01348248	DUSP5	dual specificity phosphatase 5
7892972	-0.5202722	0.01338789		
8161238	-0.5278489	0.01333893	RAB1C	RAB1C, member RAS oncogene family pseudogene
7972745	-0.9618954	0.01330995	IRS2	insulin receptor substrate 2
7931810	-1.1777713	0.01319082	KLF6	Kruppel-like factor 6
7905329	-0.7448288	0.01315947	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11
7997245	-0.5195405	0.01315311		
7952408	-0.5181652	0.01288741	SIAE	sialic acid acetylesterase
8171837	-0.6039273	0.01282218	KLHL15	kelch-like family member 15
8026163	-0.9742234	0.0127873	IER2	immediate early response 2
8084880	-0.9120429	0.01262678	HES1	hairy and enhancer of split 1, (Drosophila)
8047217	-0.6017006	0.01259853	COQ10B	coenzyme Q10 homolog B (S. cerevisiae)
7894355	-0.5704975	0.01253764		
8030128	-0.9275809	0.01247971	PPP1R15A	protein phosphatase 1, regulatory subunit 15A
8147687	-1.0430902	0.01237213		

7912670	-0.5053147	0.01234246	UQCRHL///UQCRH	ubiquinol-cytochrome c reductase hinge protein-like///ubiquinol-cytochrome c reductase hinge protein
8098414	-0.5959358	0.01225687	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)
7940022	-0.5615178	0.01224132	RTN4RL2	reticulon 4 receptor-like 2
8036557	-0.5544486	0.01223905		
7930304	-0.559241	0.01206465	GSTO1	glutathione S-transferase omega 1
8069991	-0.9647252	0.01201486	TCP10L	t-complex 10-like
7981078	-0.5528578	0.01194369	SERPINA11	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11
8073612	-0.5782976	0.01169684	TSPO	translocator protein (18kDa)
7975779	-3.1062307	0.01163103	FOS	FBJ murine osteosarcoma viral oncogene homolog
8169210	-0.6750321	0.01133256	RIPPLY1///CLDN2	ripply1 homolog (zebrafish)///claudin 2
7922754	-0.5123124	0.01119058		
8085116	-0.5231205	0.01113563	EDEM1	ER degradation enhancer, mannosidase alpha-like 1
7894011	-0.6595602	0.01109126		
7948369	-0.6224941	0.01107388		
7936833	-0.6788443	0.01100245		
8048319	-1.1036417	0.01099844	VIL1	villin 1
7896417	-0.9393753	0.01087103		
8107100	-0.6604493	0.01068623	RGMB	RGM domain family, member B
7952249	-0.6475387	0.01065825	USP2	ubiquitin specific peptidase 2
7935679	-0.5952875	0.01061368	CPN1	carboxypeptidase N, polypeptide 1
7895902	-0.6566006	0.01059372		
7960381	-0.8570056	0.01048279	EFCAB4B	EF-hand calcium binding domain 4B
8158666	-0.5631332	0.01042546	HMCN2	hemicentin 2
7893679	-0.6974431	0.01009726		
8180317	-0.7745188	0.01001805	TGIF1	TGFB-induced factor homeobox 1
8170633	-0.5202442	0.00991461		
8175773	-0.5202442	0.00991461		
8023920	-0.5654173	0.0098425	TXNL4A	thioredoxin-like 4A
8129562	-1.0392902	0.00982472	CTGF	connective tissue growth factor

7894927	-0.6184132	0.0097476		
7944006	-0.5256585	0.0097416	RBM7	RNA binding motif protein 7
8174317	-0.5018513	0.00971218	RIPPLY1///CLDN2	ripply1 homolog (zebrafish)///claudin 2
7920971	-0.5004468	0.00968247	C1orf85	chromosome 1 open reading frame 85
7900146	-0.6054041	0.00962244	ZC3H12A	zinc finger CCCH-type containing 12A
8005473	-0.6776358	0.00949393	PAIP1	poly(A) binding protein interacting protein 1
8040949	-0.5497365	0.00947382	KRTCAP3	keratinocyte associated protein 3
8088167	-0.7504385	0.00932867	SELK	selenoprotein K
7982868	-1.6189369	0.00926747	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
7940005	-0.5172225	0.00924398	P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3
7892720	-0.6611917	0.00922895		
8079117	-0.7616835	0.0091924	CCBP2	chemokine binding protein 2
7910790	-0.5768458	0.00918347		
7893126	-0.5131467	0.00908238		
7892603	-0.7452149	0.00907764		
8125919	-0.749642	0.00872981	LOC285847///FKBP5	uncharacterized LOC285847///FK506 binding protein 5
7978644	-0.5122395	0.00866376	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
8148317	-1.7295414	0.00860086	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)
7972062	-0.509053	0.00859662	FBXL3	F-box and leucine-rich repeat protein 3
8158147	-1.1850816	0.00848416	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25
7915084	-0.5322192	0.0083308	YRDC	yrdC domain containing (E. coli)
8036031	-0.5119172	0.00818485		
8104022	-0.6554738	0.00817239	PDLIM3	PDZ and LIM domain 3
8146837	-0.6320494	0.00813753		
7914000	-1.2176968	0.00780265	NR0B2	nuclear receptor subfamily 0, group B, member 2
7903474	-0.6975002	0.00761564		
7977340	-0.6177072	0.00754527	BTBD6	BTB (POZ) domain containing 6
8112613	-0.5939775	0.00753922		

7893298	-1.0096467	0.0074884		
8180316	-0.8113979	0.00735825	TGIF1	TGFB-induced factor homeobox 1
8032051	-0.5042038	0.00735484	ODF3L2	outer dense fiber of sperm tails 3-like 2
8043682	-0.640999	0.00734006	LOC653924	glycerol-3-phosphate acyltransferase 2, mitochondrial pseudogene
8098604	-1.1952098	0.00727542	ANKRD37///UFSP2	ankyrin repeat domain 37///UFM1-specific peptidase 2
8150592	-0.9439291	0.00714897	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta
7894044	-0.7091508	0.00705606		
8172654	-0.508338	0.00697757	USP27X-AS1	USP27X antisense RNA 1 (head to head)
7909610	-0.8813908	0.00684213	ATF3	activating transcription factor 3
8161747	-0.9600115	0.0067433	ZFAND5	zinc finger, AN1-type domain 5
7894504	-0.9191786	0.00653694		
8019181	-0.5044239	0.00650815	LOC100130370	uncharacterized LOC100130370
7999171	-0.5298296	0.00648403		
8089011	-0.6140443	0.00637289	PROS1	protein S (alpha)
7966621	-1.0826975	0.00624578	SDS	serine dehydratase
8042107	-0.505525	0.00621517	EIF3F	eukaryotic translation initiation factor 3, subunit F
7896709	-0.5891329	0.00609846		
7961702	-0.5437303	0.00609408	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8
7895382	-0.5011747	0.0060812		
8063386	-0.5096244	0.00599746	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta
7972808	-0.5264641	0.0058608	CARKD	carbohydrate kinase domain containing
8097655	-0.5696299	0.00578451		
7970241	-0.5199536	0.00577709	F10	coagulation factor X
7971905	-1.0694951	0.0057561	PCDH20	protocadherin 20
8019018	-0.5099874	0.00573586	CBX4	chromobox homolog 4
8067585	-0.51639	0.00563615	BHLHE23	basic helix-loop-helix family, member e23
8037535	-0.5400099	0.0056105		
8006562	-0.5001347	0.0055153	RASL10B	RAS-like, family 10, member B
8055688	-1.0036864	0.00551162	RND3///RND3	Rho family GTPase 3///Rho family GTPase 3
7922162	-0.7869264	0.00543319	SLC19A2	solute carrier family 19 (thiamine transporter), member 2

8103411	-0.5945646	0.00534533		
8035398	-0.6693598	0.00529873	RAB3A	RAB3A, member RAS oncogene family
8156309	-1.942502	0.00512409	GADD45G	growth arrest and DNA-damage-inducible, gamma
7925950	-0.5820151	0.00509919	UCN3	urocortin 3
8012000	-0.6022922	0.00504722	RNASEK	ribonuclease, RNase K
7925128	-0.6265545	0.00501531		
7995332	-0.6412533	0.00501272		
7895999	-0.8687445	0.00499013		
8055952	-2.5584412	0.00498481	NR4A2	nuclear receptor subfamily 4, group A, member 2
8148304	-1.373629	0.0048999	TRIB1	tribbles homolog 1 (Drosophila)
7892679	-0.8871725	0.00484137		
8027390	-0.6265696	0.00483507	POP4	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)
8070665	-2.3281082	0.00474742	SIK1	salt-inducible kinase 1
8132897	-0.5130256	0.00471586	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)
8057599	-0.5230052	0.00468373	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
8022404	-0.5433508	0.0046037	FAM210A	family with sequence similarity 210, member A
7966321	-0.5279674	0.00440399	GPN3	GPN-loop GTPase 3
7902290	-0.9388264	0.0043602	CTH	cystathionase (cystathionine gamma-lyase)
8169352	-0.5938875	0.00429821	NXT2	nuclear transport factor 2-like export factor 2
7926531	-0.8595449	0.00411893	ARL5B	ADP-ribosylation factor-like 5B
7993185	-0.5111652	0.00403429	NUBP1///NUBP1	nucleotide binding protein 1///nucleotide binding protein 1
8174026	-0.5870262	0.00398512	YWHAQP8	YWHAQ pseudogene 8
8173613	-0.5310673	0.00384878	RLIM	ring finger protein, LIM domain interacting
8178435	-1.438055	0.0038228	IER3	immediate early response 3
7974870	-0.5458739	0.00368974	SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa
8154848	-0.5153887	0.0035797	PRSS3///PRSS2	protease, serine, 3///protease, serine, 2 (trypsin 2)
8030999	-0.7943339	0.00357783	ZNF331	zinc finger protein 331
8025828	-1.1722057	0.00340036	LDLR	low density lipoprotein receptor
8124848	-1.3782396	0.00331477	IER3	immediate early response 3
8179704	-1.3782396	0.00331477	IER3	immediate early response 3
7961371	-0.5740814	0.00330602	DUSP16	dual specificity phosphatase 16

7997257	-0.5769866	0.003299	ZFP1	ZFP1 zinc finger protein
8040362	-0.7043592	0.0032778		
7933723	-0.5314434	0.00324096	IPMK	inositol polyphosphate multikinase
8040103	-0.557687	0.00317976	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
8111136	-0.9999708	0.00315831	FAM134B	family with sequence similarity 134, member B
7925813	-0.5986176	0.00301798	PRR26	proline rich 26
8095341	-0.5490133	0.0029586		
7955589	-2.0511401	0.00295384	NR4A1	nuclear receptor subfamily 4, group A, member 1
8096077	-1.0598142	0.00294631		
7933084	-0.9884506	0.00294457	NAMPT	nicotinamide phosphoribosyltransferase
7903765	-3.6307022	0.00293094	GSTM1	glutathione S-transferase mu 1
7946812	-0.614843	0.00292128	RPS13	ribosomal protein S13
7939492	-0.6518034	0.0028591	C11orf96	chromosome 11 open reading frame 96
8067167	-0.7614868	0.00276895	AURKA	aurora kinase A
7928218	-0.8185629	0.00275002	CDH23	cadherin-related 23
7922523	-0.797314	0.00271326		
8172028	-0.6359934	0.00268484		
8029693	-2.9348651	0.00262087	FOSB///FOSB	FBJ murine osteosarcoma viral oncogene homolog B///FBJ murine osteosarcoma viral oncogene homolog B
8174675	-0.5367945	0.00259115	SLC25A5-AS1///SLC25A5	SLC25A5 antisense RNA 1///solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
8012349	-0.7535384	0.00254145	PER1	period circadian clock 1
7937330	-0.8171266	0.00250968	IFITM2	interferon induced transmembrane protein 2
8029489	-0.663212	0.00248663	BCAM	basal cell adhesion molecule (Lutheran blood group)
8101648	-0.6841494	0.00243953	HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11
8029507	-0.5266168	0.00240123	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)
7979725	-0.7505446	0.00239189	PLEKHH1///PIGH	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1///phosphatidylinositol glycan anchor biosynthesis, class H
7894268	-0.8288593	0.00232915		
8041561	-0.7959762	0.00223816	MORN2	MORN repeat containing 2
8028652	-1.3113392	0.00223097	ZFP36	ZFP36 ring finger protein
8142120	-0.9682252	0.00217904	NAMPT	nicotinamide phosphoribosyltransferase

8137526	-0.8492435	0.00204108	INSIG1	insulin induced gene 1
7938368	-0.6384895	0.00203324		
8152355	-0.8615485	0.00189246	SYBU	syntabulin (syntaxin-interacting)
8024485	-1.3214196	0.00188706	GADD45B	growth arrest and DNA-damage-inducible, beta
7908492	-1.0886007	0.00186775	CFHR4	complement factor H-related 4
8081036	-0.8189429	0.00186143	CADM2	cell adhesion molecule 2
8043743	-0.760129	0.00184812		
7962537	-1.0666454	0.00183031	SLC38A2	solute carrier family 38, member 2
8121794	-0.7571479	0.0016584	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A
8180275	-0.7503167	0.00162874	PCDHA1	protocadherin alpha 1
7984008	-0.6859241	0.00162347		
8044927	-0.8365517	0.0016032	INHBB	inhibin, beta B
7979886	-0.5707307	0.00155642		
8180222	-0.7096629	0.00141562	CFHR4	complement factor H-related 4
7989611	-0.6765881	0.00141216	FAM96A	family with sequence similarity 96, member A
7892628	-0.8015319	0.00137203		
8152092	-0.5892402	0.00134498		
8013804	-0.572136	0.00128594	DHRS13	dehydrogenase/reductase (SDR family) member 13
8086330	-2.0182867	0.00127648	CSRNP1	cysteine-serine-rich nuclear protein 1
7907655	-0.6926461	0.00124199		
8040473	-0.8076007	0.00121427	RHOB	ras homolog family member B
7893001	-0.6500947	0.00119276		
7895866	-1.0788601	0.0010307		
7908499	-1.0418966	0.00101041	CFHR5	complement factor H-related 5
8036902	-0.6477393	0.00100621	SERTAD1	SERTA domain containing 1
8154381	-0.8986643	0.00096913	LURAP1L	leucine rich adaptor protein 1-like
7894916	-0.754135	0.00096797		
7893573	-0.8512393	0.00095348		
8094938	-0.8446494	0.00094038	NIPAL1	NIPA-like domain containing 1
7918379	-1.4814585	0.00093872	GSTM3	glutathione S-transferase mu 3 (brain)
8001658	-0.5927376	0.00093362	C16orf80	chromosome 16 open reading frame 80

8040898	-0.6531517	0.00081725	TRIM54	tripartite motif containing 54
8067955	-0.5005392	0.00081431	CXADR	coxsackie virus and adenovirus receptor
8069574	-0.7558377	0.00077717	C21orf91	chromosome 21 open reading frame 91
7966631	-0.5445128	0.00076753	LHX5	LIM homeobox 5
8152642	-0.5413285	0.00073658	FAM83A-AS1	FAM83A antisense RNA 1
7967789	-0.7403421	0.00069574	PXMP2	peroxisomal membrane protein 2, 22kDa
7938348	-0.8505695	0.00065689	WEE1	WEE1 homolog (S. pombe)
7892578	-0.8435877	0.0006426		
8034698	-1.1453674	0.00063646	MIR23A	microRNA 23a
7899018	-0.6029719	0.00062051	TMEM57	transmembrane protein 57
8174361	-1.106472	0.00060989	TSC22D3	TSC22 domain family, member 3
8098782	-0.5700646	0.00059797	CPLX1	complexin 1
8104136	-0.5954666	0.00059212	HMX1	H6 family homeobox 1
8123800	-0.5816688	0.00058563		
8044574	-1.3848874	0.0005679	IL1RN	interleukin 1 receptor antagonist
8083569	-0.9208159	0.00052665	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase
7980096	-1.1163776	0.00039858		
8140140	-0.8820648	0.00033407	CLDN3	claudin 3
7910901	-0.6191243	0.00023535	LOC100130331	POTE ankyrin domain family, member F pseudogene
7924058	-0.665233	0.00022223	IRF6	interferon regulatory factor 6
8122732	-0.7559958	0.00018761		
8167356	-0.6303869	0.00013855	GLOD5	glyoxalase domain containing 5
8016739	-0.7544581	0.00012199	TOB1	transducer of ERBB2, 1
8115831	-1.5515257	0.00011364	DUSP1	dual specificity phosphatase 1
7916225	-0.7647516	0.00008812	RPS13	ribosomal protein S13
8095744	-0.9472907	0.00008362	AREG	amphiregulin
8121850	-1.0823673	0.00002243	HEY2	hairy/enhancer-of-split related with YRPW motif 2
7907970	-0.7411929	0.00001231		

Affymetrix Human Gene 1.1 ST Array was used for mRNA profile analysis.

Supporting Table 2. 48 potential target genes of miR-24.

miRNA Name	Gene Name	NCBI Ref.	Read Num of HITClip	TargetScanSites	PicTarSites	RNA22Sites	PITASites	miRandaSites
mmu-miR-24	Yod1	NM_178691	23229	1(47)	1(47)	0(0)	1(47)	1(47)
mmu-miR-24	Ugcg	NM_011673	23229	1(211)	1(211)	0(0)	1(211)	1(211)
mmu-miR-24	Tnks	NM_175091	23229	1(143)	2(232)	0(0)	0(0)	0(0)
mmu-miR-24	Sptlc2	NM_011479	23229	1(613)	1(613)	0(0)	1(613)	1(613)
mmu-miR-24	Sp1	NM_013672	23229	1(85)	2(124)	0(0)	1(85)	1(85)
mmu-miR-24	Snn	NM_009223	23229	1(679)	1(679)	0(0)	1(679)	1(679)
mmu-miR-24	Rnf2	NM_011277	23229	1(48)	1(48)	0(0)	1(48)	1(48)
mmu-miR-24	Rnf138	NM_207623	23229	1(21)	1(21)	0(0)	1(21)	1(22)
mmu-miR-24	Ptprd	NM_001014288	23229	1(46)	1(46)	1(46)	1(46)	1(46)
mmu-miR-24	Ogt	NM_139144	23229	1(242)	1(242)	0(0)	1(242)	1(242)
mmu-miR-24	Ndst1	NM_008306	23229	1(68)	1(68)	2(118)	0(0)	0(0)
mmu-miR-24	Matr3	NM_010771	23229	1(150)	1(150)	0(0)	1(150)	1(150)
mmu-miR-24	Klf6	NM_011803	23229	1(74)	1(74)	0(0)	1(74)	1(74)
mmu-miR-24	Igfbp5	NM_010518	23229	1(455)	5(1077)	0(0)	1(455)	0(0)
mmu-miR-24	Gria3	NM_016886	23229	1(1733)	1(1733)	0(0)	1(1733)	0(0)

mmu-miR-24	Fscn1	NM_007984	23229	1(3)	2(32)	0(0)	1(3)	1(3)
mmu-miR-24	Ell	NM_007924	23229	1(69)	1(69)	0(0)	0(0)	0(0)
mmu-miR-24	Dyrk2	NM_001014390	23229	1(84)	1(84)	0(0)	1(84)	1(84)
mmu-miR-24	Dtna	NM_207650	23229	1(52)	2(81)	0(0)	0(0)	0(0)
mmu-miR-24	D4Ertd22e	NM_001025608	23229	1(68)	1(68)	0(0)	0(0)	0(0)
mmu-miR-24	Cxadr	NM_001025192	23229	1(102)	2(308)	0(0)	0(0)	0(0)
mmu-miR-24	Cnot6	NM_212484	23229	1(48)	1(48)	0(0)	1(48)	1(48)
mmu-miR-24	Clcn3	NM_173876	23229	1(87)	1(87)	0(0)	0(0)	1(87)
mmu-miR-24	Bcl2l2	NM_007537	23229	1(424)	1(424)	1(424)	1(424)	1(424)
mmu-miR-24	Agpat3	NM_053014	23229	1(40)	1(40)	0(0)	0(0)	0(0)
mmu-miR-24	Acvr1b	NM_007395	23229	1(61)	4(285)	0(0)	2(70)	2(70)
hsa-miR-24	ZXDA	NM_007156	2490	1(3)	1(3)	0(0)	1(3)	1(3)
hsa-miR-24	ZNF217	NM_006526	2490	1(3)	1(3)	1(3)	1(3)	0(0)
hsa-miR-24	TOP1	NM_003286	2490	1(3)	1(3)	0(0)	1(3)	1(3)
hsa-miR-24	SYS1	NM_033542	2490	1(3)	1(3)	0(0)	0(0)	0(0)
hsa-miR-24	SSH2	NM_033389	2490	1(22)	1(22)	0(0)	0(0)	0(0)
hsa-miR-24	SESN1	NM_014454	2490	1(52)	1(52)	0(0)	1(52)	1(52)
hsa-miR-24	RNF2	NM_007212	2490	1(7)	1(7)	0(0)	1(7)	1(7)

hsa-miR-24	RNF138	NM_198128	2490	1(10)	1(10)	0(0)	0(0)	0(0)
hsa-miR-24	RAP2C	NM_021183	2490	1(5)	2(9)	0(0)	1(5)	0(0)
hsa-miR-24	RAB5B	NM_002868	2490	1(2)	1(2)	0(0)	1(2)	1(2)
hsa-miR-24	NET1	NM_005863	2490	1(5)	1(5)	0(0)	0(0)	0(0)
hsa-miR-24	MBD6	NM_052897	2490	1(5)	1(5)	0(0)	1(5)	1(5)
hsa-miR-24	INSIG1	NM_198337	2490	1(38)	1(38)	0(0)	1(38)	0(0)
hsa-miR-24	H2AFX	NM_002105	2490	1(226)	1(226)	0(0)	0(0)	1(226)
hsa-miR-24	FAM175B	NM_032182	2490	1(2)	1(2)	0(0)	0(0)	0(0)
hsa-miR-24	ELL	NM_006532	2490	1(2)	1(2)	0(0)	0(0)	0(0)
hsa-miR-24	DNAJB12	NM_001002762	2490	1(16)	1(16)	0(0)	1(16)	0(0)
hsa-miR-24	CNOT6	NM_015455	2490	1(8)	1(8)	0(0)	1(8)	1(8)
hsa-miR-24	CDV3	NM_017548	2490	1(1)	2(3)	0(0)	0(0)	1(1)
hsa-miR-24	CDKN1B	NM_004064	2490	1(25)	1(25)	0(0)	1(25)	0(0)
hsa-miR-24	C22orf13	NM_031444	2490	1(17)	1(17)	0(0)	0(0)	0(0)
hsa-miR-24	BCL2L11	NM_138621	2490	1(100)	1(100)	0(0)	1(100)	0(0)

Supporting Table 3. Three Down-regulated Genes in Livers of Human NAFLD/NASH that have Binding Motifs for miR-24

miRNA Name	NCBI Ref	ReadNum of HIT-Clip	TargetScan Sites	PicTar Sites	P-Value	LogFC NAFLD/NSH	Gene Symbol	Gene Name
miR-24	NM_011803	23229	1(74)	1(74)	0.01319	-1.1777713	KLF6	Kruppel-like factor 6
miR-24	NM_198337	2490	1(38)	1(38)	0.002041	-0.8492435	INSIG1	Insulin induced gene 1
miR-24	NM_001025192	23229	1(102)	2(308)	0.000814	-0.5005392	CXADR	Coxsackie virus and adenovirus receptor

Supporting Table 4. Primers for quantitative RT-PCR

Gene symbol	**Accession No.**	**Forward Primer**	**Reverse Primer**
Insig1	NM_005542	TTTTCTCAGGAGGCGTCACGGT	TCCTTGCTCTCAGAATCGGTGG
FASN	NM_004104	TTCTACGGCTCCACGCTCTTCC	GAAGAGTCTTCGTCAGCCAGGA
SCD1	NM_005063	CCTGGTTTCACTTGGAGCTGTG	TGTGGTGAAGTTGATGTGCCAGC
GPAT	NM_020918	TTGTGGCTTGCCTGCTCCTCTA	AATCACGAGCCAGGACTTCCTC
HMGCR	NM_000859	GACGTGAACCTATGCTGGTCAG	GGTATCTGTTTCAGCCACTAAGG
18S	X03205	CAGGGTTCGATTCCGTAGAG	CCTCCAGTGGATCCTCGTTA
GAPDH	NM_002046	GTCTCCTCTGACTTCAACAGCG	ACCACCCTGTTGCTGTAGCCAA

Supporting Table 5. Comparison of miR-24-ASO and miR-24-MM-ASO Treated Mice

Parameter	Scrambled treated mice	miR-24-ASO treated mice
Body weight (g)	39±2	38±1
Liver weight	2.3±0.2	2.1±0.2
Liver cholesterol concentration (mg/g)	4.5±0.3	4.4±0.2
Liver triglyceride concentration (mg/g)	138±23	79±9.7
Total plasma cholesterol(mg/dl)	153±21	134±19.7
Total plasma triglycerides (mg/dl)	134±23.4	94±4.3

Two-week-old mice (five in each group) maintained on HFD for 10 weeks were injected with miR-24-ASO or scramble for 4 weeks.