Supplementary Figure Legend

Figure S1. Identification of lncRNAs differentially expressed in the liver of hyperlipidemia mice. Serum**(A)** and hepatic **(B)** lipid levels of mice after ND and HFD treatment for 23 weeks (n=4/group). **(C)** RT-qPCR analysis of lncRNA expression levels of mice after ND and HFD treatment for 23 weeks (n=3/group). All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure S2. Characterization of the non-coding property, expression profile and sub-cellular location of lncRHL. (A) Nucleotide sequences of full-length Gm26584 analyzed by RACE. **(B)** Gene structure of lncRHL (Gm26584) and Rapid amplification of cDNA ends (RACE) in the mouse genome. **(C)** Coding potency of lncRHL sequence was analyzed using the Coding Potential Calculator (website) lncBATE1, lncLSTR served as control non-coding gene. CCAAT/enhancer-binding protein alpha (Cebpα) and Eukaryotic translation initiation factor 4F α3 (Eif4α3) served as control coding genes. Scores above 0 suggest coding potential, whereas scores below 0 represent no coding potential. **(D)** FISH analysis in Hepa1-6 cells. lncRHL sub-cellular localization in mouse Hepa1-6 was assessed by a laser confocal microscopy. *Red*, lncRHL or snRNA U6 or 18S. snRNA U6 and 18S were selected as a positive control for nucleus or cytosol, respectively, blue,4',6-diamidino-2-phenylindole staining. Magnification: x400. **(E)** RT-qPCR analysis of lncRHL expression in primary hepatocytes in the presence or absence of 400 μM oleic acid (OA) for 6 h (n=3/group). All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure S3. Blood chemistry analysis of liver-specific knockdown of lncRHL in

mice. The samples analyzed here were from the same samples used in Fig 2. **(A-C)** Knockdown of lncRHL increases serum NEFA **(A)**, LDL-C **(B)** but decreases HDL-C **(C)** levels in mice. Levels of NEFA, LDL-C and HDL-C in serum of control (Ad-Scrambel) or lncRHL knockdown (Ad-shlncRHL) mice were measured using enzymatic kits (n=8/group). All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure S4. Knockdown of lncRHL has no effect on mRNA levels of genes involved in hepatic lipogenesis and fatty acid oxidation. The samples analyzed here were from the same samples used in Fig 2. **(A)** Relative mRNA levels of genes involved in lipogenesis and fatty acid oxidation in the livers of control (Ad-Scrambel) or lncRHL knockdown (Ad-shlncRHL) mice under ND or HFD conditions. Total RNA was subjected to RT-qPCR quantification and mRNA levels were expressed relative to Ad-Scramle under ND conditions, respectively (n=4/group). **(B)** Western blot analysis of protein levels of PCSK9 and LPL in serum of control (Ad-Scrambel) or lncRHL knockdown (Ad-shlncRHL) mice under ND or HFD conditions. Albumin (ALB) as loading control of serum (n=3/group). All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure S5 Knockdown of lncRHL has no effect on cell mortality of primary hepatocytes. (A) Relative mRNA levels of genes involved in lipogenesis and fatty acid oxidation in primary hepatocytes transfected with ssNC or sslncRHL (100 nM) for 6 h. Total RNA was subjected to RT-qPCR quantification and mRNA levels were expressed relative to ssNC control cells (n=3/group). **(B)** Apoptotic rates of mice primary

hepatocytes were measured by flow cytometry after transfected with ssNC or sslncRHL (100 nM) for 48 h. Representative flow cytometry of cells stained with Annexin V-FITC and PI (left) and quantitative analysis (right) of apoptotic cells of primary hepatocytes (n=3/group). **(C)** Apoptotic rates of mice primary hepatocytes were measured by TUNEL analysis after transfected with ssNC or sslncRHL (100 mM). Representative image of TUNEL staining (left) and quantitative analysis (right) of TUNEL positive cells (n=10/group). Scale bar, 40 μm. These experiments were repeated three times with similar results. All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure S6. Depletion of MTTP blocks VLDL secretion in primary hepatocytes with knockdown of lnRHL. 6-8 weeks old *C57BL/6J* male mice were infected with 2.5×10^{11} recombinant adenovirus particles of Ad-shNC or Ad-shMTTP through tail vein injection for 7 days. After that, primary hepatocytes were isolated and transfected with ssNC or sslncRHL (100 nM) for knockdown of lncRHL. **(A)** Knockdown lncRHL-induced increases in the mRNA level of Mttp were abolished by depletion of MTTP in primary hepatocytes. The mRNA levels of *lncRHL*, *Mttp* and *ApoB* were assessed by RT-qPCR (n=3/group). **(B)** Depletion of MTTP increases intracellular TAG level in primary hepatocytes with knockdown of lncRHL. The intracellular TAG level was measured using TAG assay kit and normalized to total protein (n=3/group). **(C)** Depletion of MTTP inhibits VLDL secretion in primary hepatocytes with knockdown of lncRHL. The secreted VLDL in the medium was measured using ELISA kit and normalized to total protein (n=3/group). **(D)** Depletion of MTTP reduces protein levels

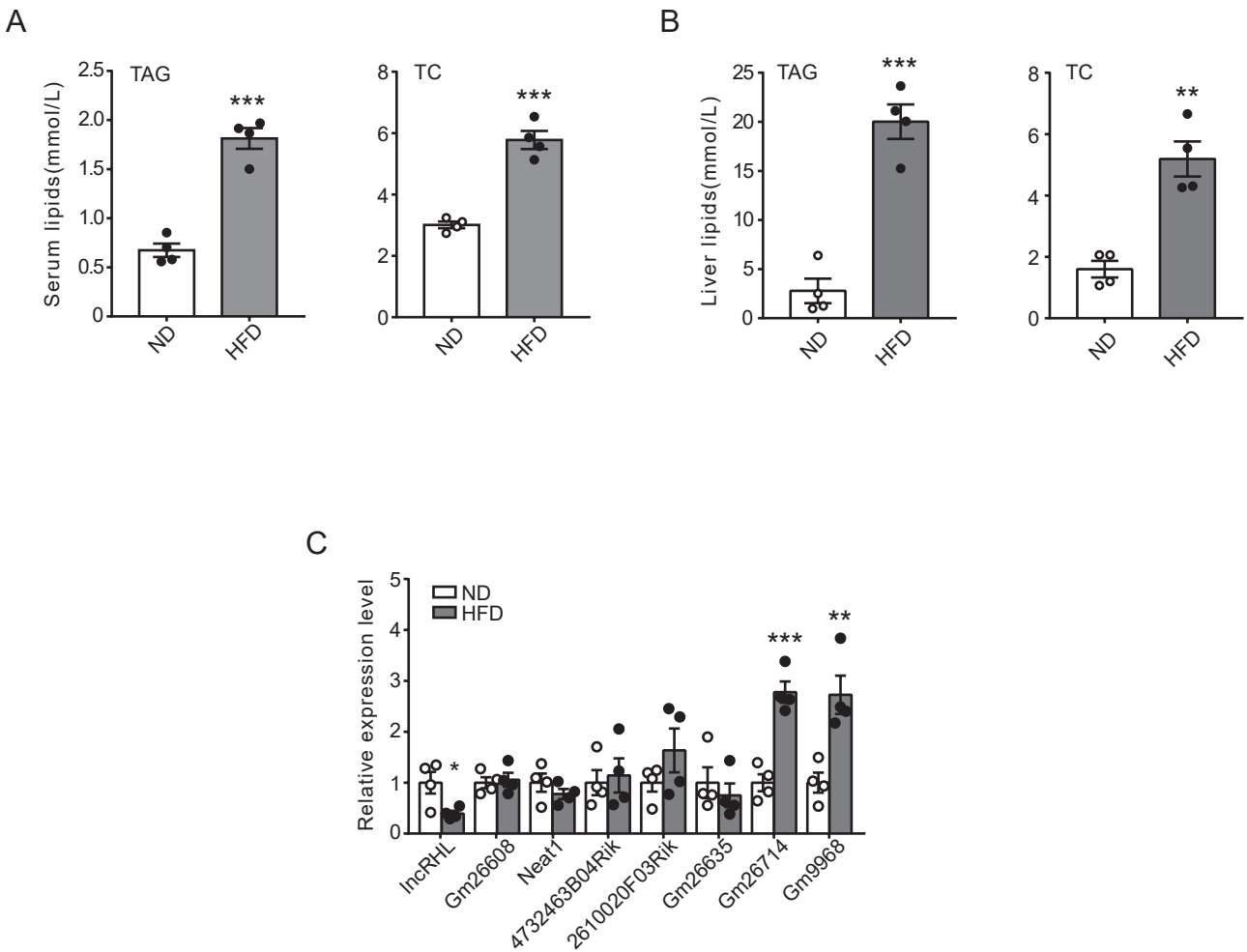
of ApoB in culture medium of primary hepatocytes with knockdown of lncRHL (n=3/group). Representative western blot of ApoB protein levels in culture medium of primary hepatocytes with knockdown of lncRHL (upper). Ponceaus S staining as loading control (lower). **(E)** Depletion of MTTP restores protein levels of MTTP in Primary hepatocytes with knockdown of lncRHL. Western blot (left) and quantitative analysis (right) of MTTP and ApoB protein levels. All values are as Mean ± SEM. *p < 0.05, **p < 0.01, ***p < 0.001. These experiments were repeated three times with similar results.

Figure S7. Identification of interact protein of lncRHL. (A) Proteins associated with lncRHL were visualized by silver staining following RNA pull-down. **(B)** KEGG pathway analysis showed that the global gene expression profiles interacting with lncRHL were highly correlated with Metabolic pathways and NAFLD programs identified from RNA pull-down. **(C)** Mass spectrometry experiment revealed that lncRHL interacted with hnRNPs family proteins in primary hepatocytes. **(D)** hnRNPU binding sites within lncRHL by used online bioinformatics analysis tools (RBPmap, StarBase v2.0).

Figure S8. Knockdown of hnRNPU decreases BMAL1 expression *in vitro*. (A) Relative mRNA level of hnRNPU in liver of mice injected with Ad-Scramble or Ad-shlncRHL (n=4/group). The samples analyzed here were from the same samples used in Fig 2. **(B)** Knockdown of hnRNPU reduces mRNA level of *Bmal1* in primary hepatocytes. Primary hepatocytes were transfected with control siRNA or siRNAs targeting hnRNPU (#1 and #2) for 24 h. Total RNA was subjected to RT-PCR

quantification and mRNA levels of hnRNPU and Bmal1 were expressed relative to control siRNA treated cells. **(C)** Knockdown of hnRNPU reduces protein level of BMAL1 in primary hepatocytes. Representative Western blot (left) and quantitative (right) analysis of protein levels of hnRNPU and BAML1 in primary hepatocytes with or without knockdown of hnRNPU. Primary hepatocytes were transfected with control siRNA or siRNAs targeting hnRNPU (#1 and #2) for 24 h followed by treatments with 400 μM oleic acid (OA) for 6 h. These experiments were repeated three times with similar results. All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure S9. Overexpression of lncRHL rescues expression level of hnRNPU and BMAL1 in lncRHL knockdown primary hepatocytes. (A) Overexpression of lncRHL restores mRNA levels of *Bmal1, Gata4, Shp and Mttp* in lncRHL knockdown primary hepatocytes. After transfected with ssNC or sslncRHL for 12 h, the primary hepatocytes were infected with Ad-lncRHL or Ad-β-gal for 6 h. Total RNA was subjected to RT-PCR quantification and mRNA levels were expressed relative to ssNC treated cells. (n=3/group). **(B)** Overexpression of lncRHL restores protein levels of hnRNPU and BAML1 in lncRHL knockdown primary hepatocytes. After transfected with ssNC or sslncRHL for 12 h, the primary hepatocytes were infected with Ad-lncRHL or Ad-β-gal for 6 h. Representative Western blot (left) and quantitative analysis (right) of protein levels of hnRNPU and BMAL1 in primary hepatocytes. (n=3/group). These experiments were repeated three times with similar results. All values are as Mean ± SEM. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.


A
TAG
Serum lipids(mmol/L)
2.5
2.0
1.5
1.0
0.5
0
***
ND
HFD
TC
8
6
4
2
0
***
ND
HFD
B
TAG
Liver lipids(mmol/L)
25
20
15
10
5
0
***
ND
HFD
TC
8
6
4
2
0
**
ND
HFD
C
ND
HFD
Relative expression level
5
4
3
2
1
0
*
***
**
IncRHL
Gm26608
Neat1
4732463B04Rik
2610020F03Rik
Gm26635
Gm26714
Gm9968

A

5’
GAAGAGAAAAGATTTCTAAAAGGATTCCATGTGTATTTAGGCCTTCTCCAACCATCTGCC
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AAGAATGTACAACCAGCAGGTCCCCTTTTGCAGTAAAGGGCATTATACTTGAAGGGGCA
TACTCATTTTTTCCTCAGGTCAGAGGCAGAGGGAAGAGTTAACAGTGATCAAATAGAGAC
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ACACATTTCTGTTGTATGATTTGCTATGATTTTGGTTTCCTGAGACATTTGTTCCCTACAG
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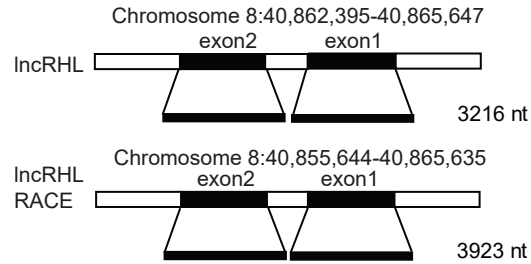
B



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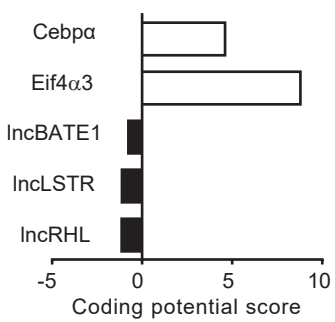

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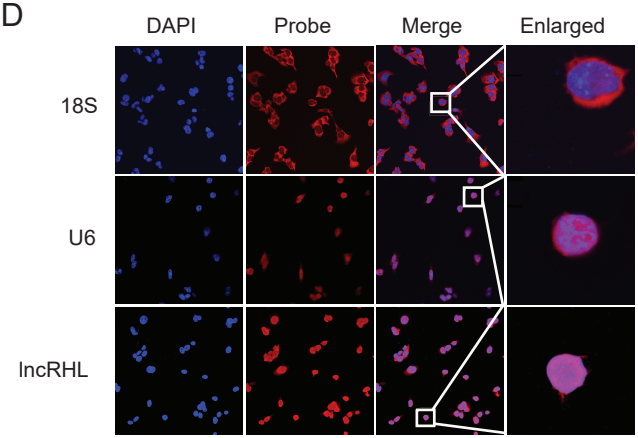

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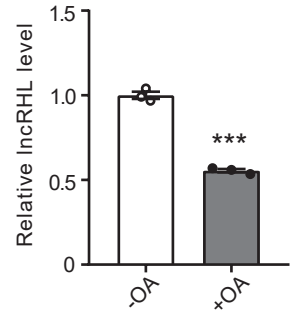

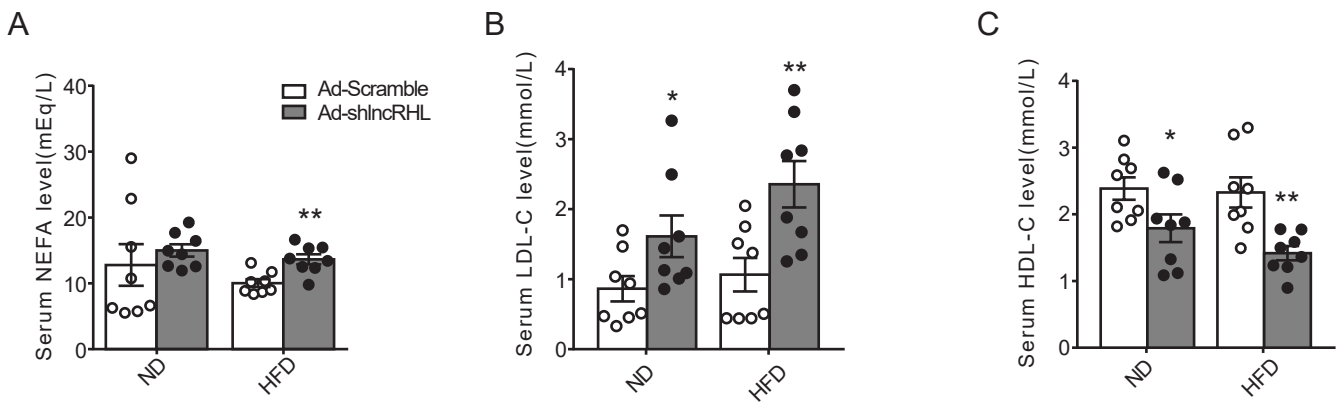
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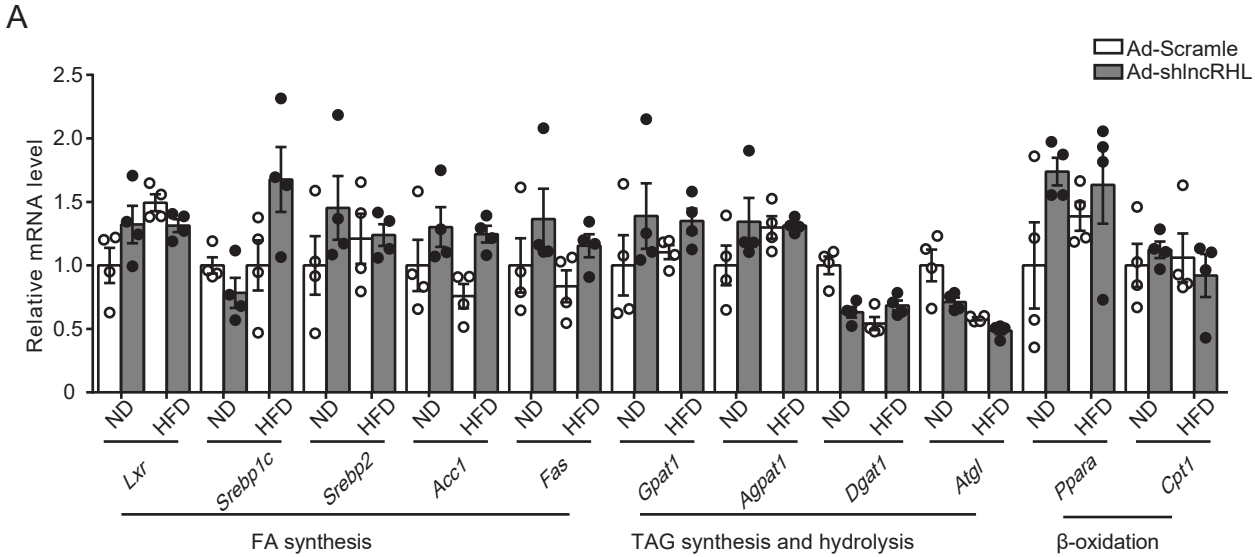
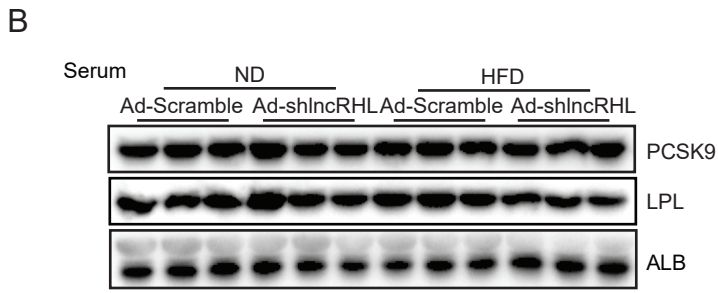
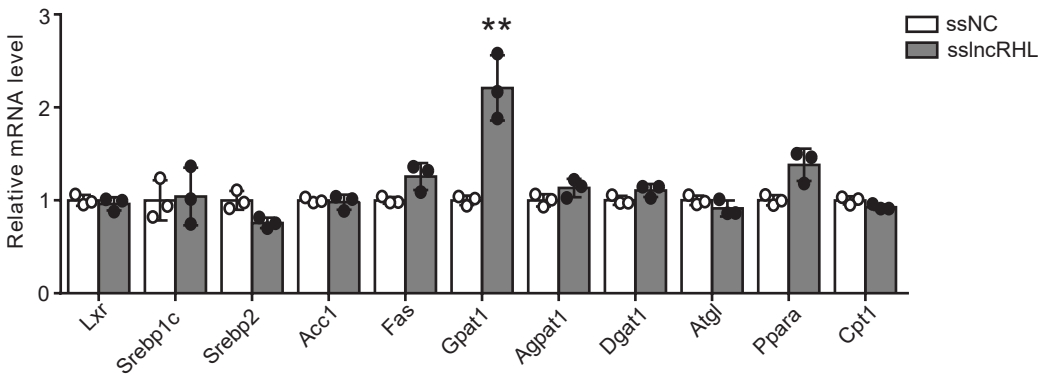
Serum NEFA level(mEq/L)
40
30
20
10
0
Ad-Scramble
Ad-shlncRHL
**
ND
HFD
B
Serum LDL-C level(mmol/L)
4
3
2
1
0
*
**
ND
HFD
C
Serum HDL-C level(mmol/L)
4
3
2
1
0
*
**
ND
HFD

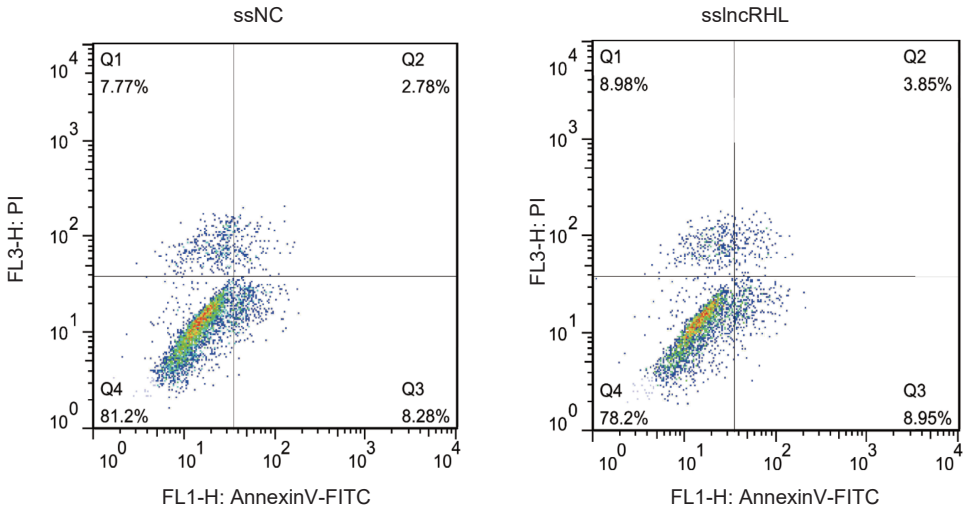

A
Ad-Scramle
Ad-shlncRHL
Relative mRNA level
2.5
2.0
1.5
1.0
0.5
0
ND
HFD
Lxr
Srebp1c
Srebp2
Acc1
Fas
Gpat1
Agpat1
Dgat1
Atgl
Ppara
Cpt1
FA synthesis
TAG synthesis and hydrolysis
β-oxidation

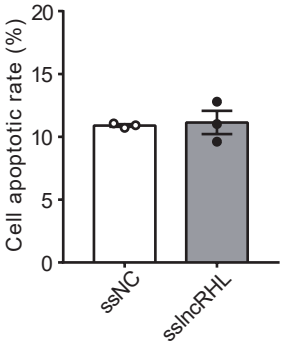

B
Serum
ND
HFD
Ad-Scramble
Ad-shlncRHL
Ad-Scramble
Ad-shlncRHL
PCSK9
LPL
ALB

A

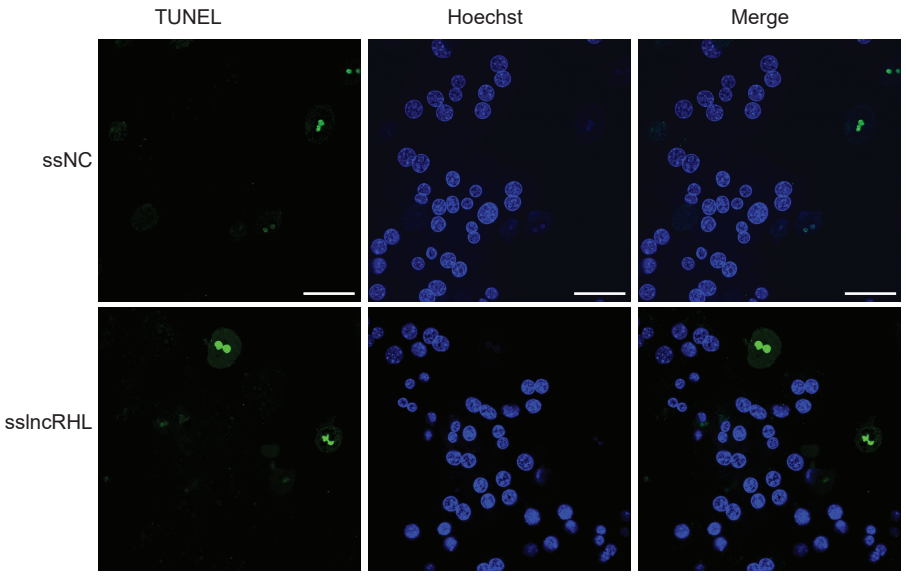

Relative mRNA level
3
2
1
0
**
ssNC
sslncRHL
Lxr
Srebp1c
Srebp2
Acc1
Fas
Gpat1
Agpat1
Dgat1
Atgl
Ppara
Cpt1

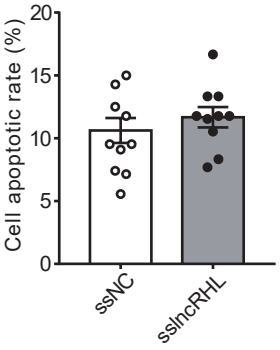
B

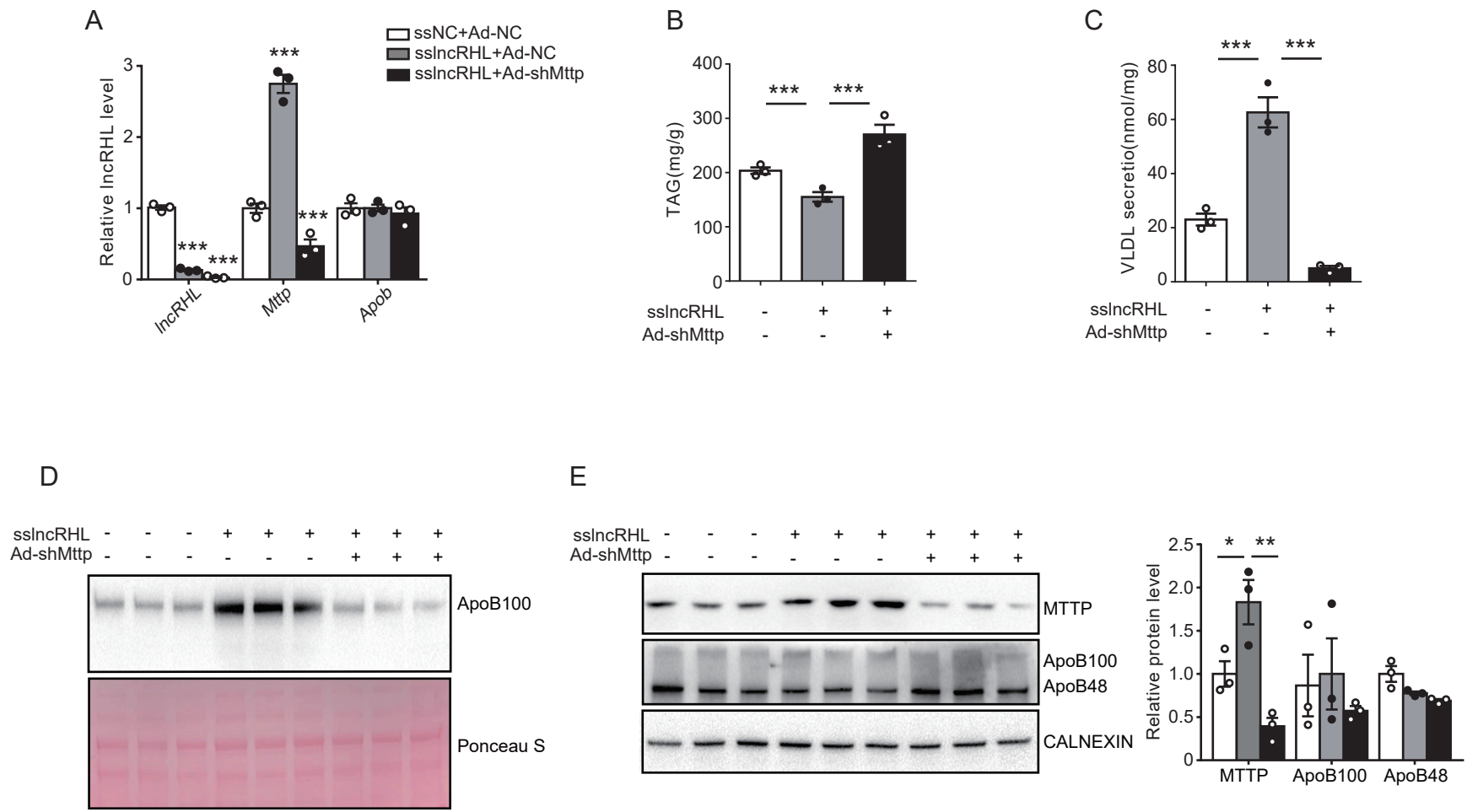

ssNC
sslncRHL
Q1
7.77%
Q2
2.78%
Q4
81.2%
Q3
8.28%
Q1
8.98%
Q2
3.85%
Q4
78.2%
Q3
8.95%
FL3-H: PI
FL1-H: AnnexinV-FITC


Cell apoptotic rate (%)
20
15
10
5
0
ssNC
sslncRHL

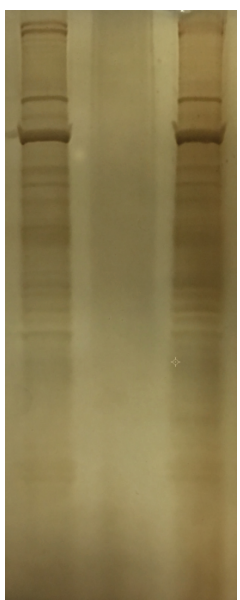
C


TUNEL
Hoechst
Merge
ssNC
sslncRHL


Cell apoptotic rate (%)
20
15
10
5
0
ssNC
sslncRHL


A
ssNC+Ad-NC
ssIncRHL+Ad-NC
ssIncRHL+Ad-shMttp
Relative IncRHL level
IncRHL
Mttp
Apob
B
TAG(mg/g)
ssIncRHL
Ad-shMttp
C
VLDL secretio(nmol/mg)
ssIncRHL
Ad-shMttp
D
ssIncRHL
Ad-shMttp
ApoB100
Ponceau S
E
ssIncRHL
Ad-shMttp
MTTP
ApoB100
ApoB48
CALNEXIN
Relative protein level
MTTP
ApoB100
ApoB48

A



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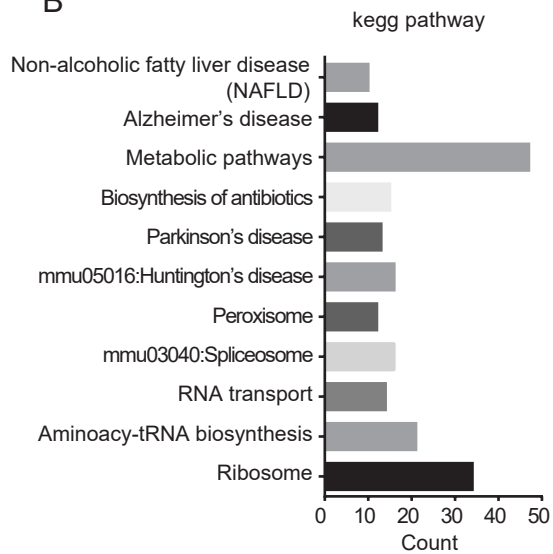


C

Gene name	Description		Pept	Uniqu	Seque	Unique	sMol.	iBAQ gm2	iBAQ only
Hnrnpa0	Heterogeneous nuclear ribonucleoprotein A0	1	1	2.6	2.6	30.53	28775	0	
Hnrnpa1	Heterogeneous nuclear ribonucleoprotein A1	2	2	7.8	7.8	38.833	27533	0	
Hnrnpa2b1	Isoform 3 of Heterogeneous nuclear ribonucleoproteins A2/B1	6	6	19.6	19.6	32.46	1172100	0	
Hnrnpab	Heterogeneous nuclear ribonucleoprotein A/B	2	2	8.7	8.7	33.816	227890	0	
Hnrnpd	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	4	4	40.2	40.2	12.139	810440	0	
Hnrnpf	Heterogeneous nuclear ribonucleoprotein F	4	3	12.3	9.9	45.729	111610	0	
Hnrnph1	Heterogeneous nuclear ribonucleoprotein H	2	1	5.5	3.4	51.217	2332.9	0	
Hnrnpk	Heterogeneous nuclear ribonucleoprotein K	6	6	15.5	15.5	48.562	70577	0	
Hnrnpl	Heterogeneous nuclear ribonucleoprotein L (Fragment)	3	3	5	5	66.821	26796	0	
Hnrnpll	Heterogeneous nuclear ribonucleoprotein L-like	1	1	3	3	35.346	8682.9	0	
Hnrnpm	Heterogeneous nuclear ribonucleoprotein M	1	1	2.5	2.5	68.161	1741.1	0	
Hnrnpu	Heterogeneous nuclear ribonucleoprotein U	2	2	2.3	2.3	86.805	16572	0	

D

General calculation parameters

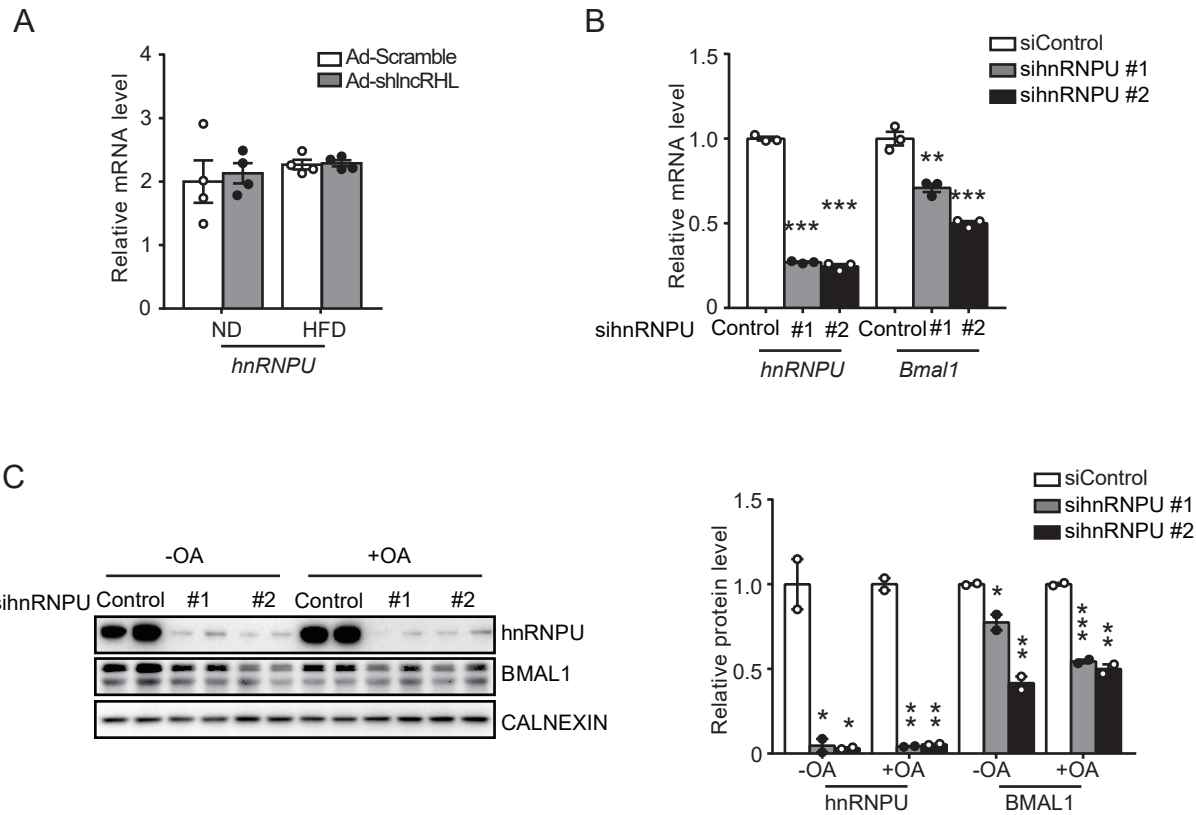
Genome: Mouse (mm10)
Selected motifs: HNRNPU(Hs/Mm):uguauug
Stringency level: High
Conservation filter: Off

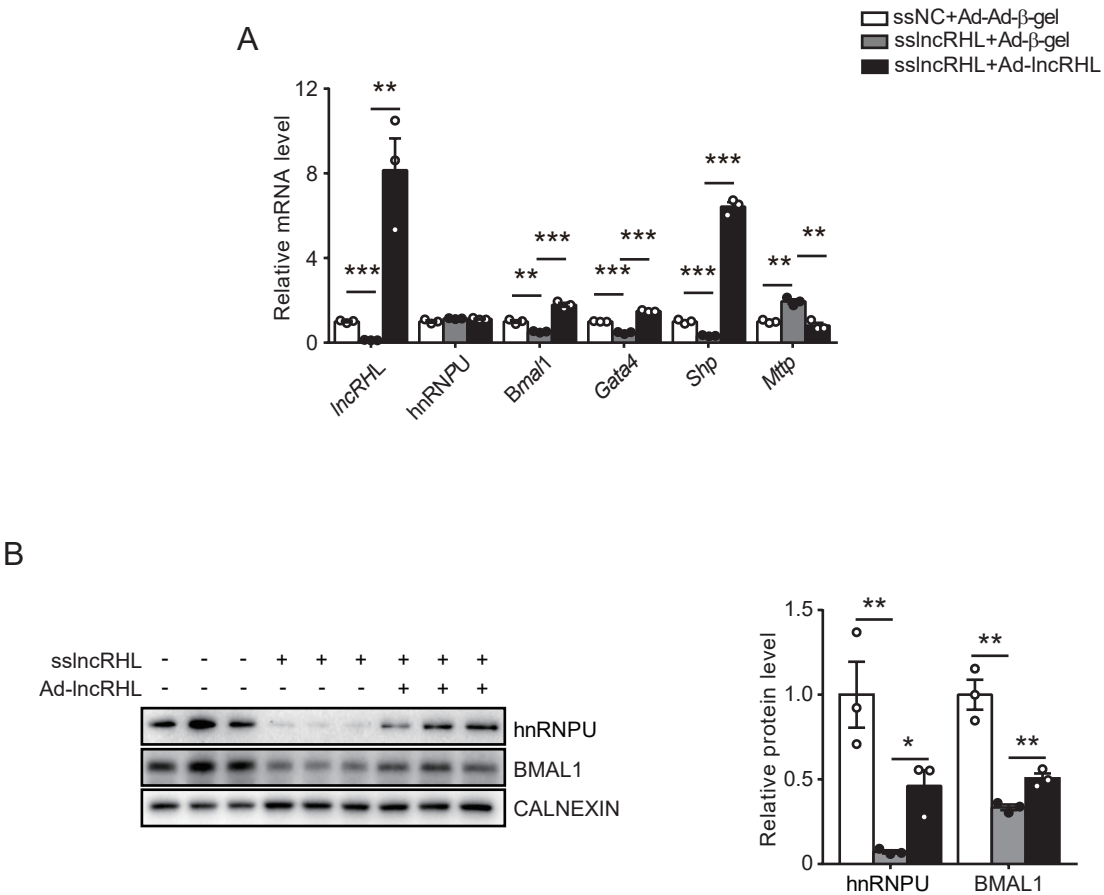
Results for sequence: lncRHL
Genomic position: N/A (BLAT could not find at least 95% identity match for the sequence).
View binding sites predictions summary

Protein: HNRNPU(Hs/Mm)

Position	Motif	Occurrence	Z-score	P-value
173	uguauug	aagaauaaacagaugaaguugggacugucgugacuagcuauugccugcuggaaauga	2.672	3.77e-03
571	uguauug	caguaauuaguuuggggucacccagugucugguguacuguagggacccaguaaguuu	2.672	3.77e-03
578	uguauug	uaguuuggggucacccagugucugguguacuguagggacccaguaaguuuucaggga	3.250	5.77e-04
583	uguauug	uggggucacccagugucugguguacuguagggacccaguaaguuuucagggaaagca	2.891	1.92e-03
2274	uguauug	agacaguuuuuucauaguuuaaaguuuguauuggauuaacucuacuucuggcaucuag	2.125	1.68e-02

Predictions summary: Download predictions summary as text file


A
Relative mRNA level
Ad-Scramble
Ad-shlncRHL
ND
HFD
hnRNPU
B
Relative mRNA level
siControl
sihnRNPU #1
sihnRNPU #2
sihnRNPU
Control
#1
#2
hnRNPU
Bmal1
C
-OA
+OA
sihnRNPU
hnRNPU
BMAL1
CALNEXIN
Relative protein level
hnRNPU
BMAL1


A
ssNC+Ad-Ad-β-gel
sslncRHL+Ad-β-gel
sslncRHL+Ad-lncRHL
Relative mRNA level
12
8
4
0
lncRHL
hnRNPU
Bmal1
Gata4
Shp
Mttp
B
sslncRHL
Ad-lncRHL
hnRNPU
BMAL1
CALNEXIN
Relative protein level
1.5
1.0
0.5
0
hnRNPU
BMAL1

Supplementary Table S1. Summarized reads information of RNA sequencing.

Samples	**ND**	**HFD**
Raw Reads Number	97,697,212	81,641,384
Raw Bases Number	12,212,151,500	10,205,173,000
Clean Reads Number	93,697,058	74,533,490
Clean Reads Rate (%)	95.91	91.29
Clean Bases Number	11,712,132,250	9,316,686,250
Low-quality Reads Number	401,960	324,800
Low-quality Reads Rate (%)	0.41	0.4
Ns Reads Number	53,394	43,116
Ns Reads Rate(%)	0.05	0.05
Adapter Polluted Reads Number	3,544,800	6,739,978
Adapter Polluted Reads Rate (%)	3.63	8.26
Raw Q30 Bases Rate (%)	95.9	95.74
Clean Q30 Bases Rate (%)	96.24	96.22
rRNA Mapping Reads Number	387,186	851,682
rRNA Mapping Rate (%)	0.4	1.04
Total Clean Reads Number	93,309,872	73,681,808
Total Clean Bases Number	11,663,734,000	9,210,226,000
Total Q30(%)	96.24	96.23

Supplementary Table S2. lncRNAs response to induction of high fat diet.

Gene	ND	HFD	FoldChange
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ENSMUSG00000097474	46276.95153	8577.126972	0.185343388
ENSMUSG00000085499	2031.42935	6634.356044	3.265856154
ENSMUSG00000108546	2403.03228	6438.012173	2.679120138
ENSMUSG00000097762	9661.676177	3988.880737	0.412855975
ENSMUSG00000097654	511.9862589	1240.06655	2.422069984
ENSMUSG00000092274	3113.206768	1033.388792	0.331937089
ENSMUSG00000085840	355.0872441	826.7110335	2.328191303
ENSMUSG00000097673	1973.62445	640.701051	0.324631695
ENSMUSG00000097838	206.4460722	578.6977234	2.803142329
ENSMUSG00000097082	115.6098004	568.3638355	4.916225385
ENSMUSG00000089719	1907.561707	527.0282839	0.276283741
ENSMUSG00000097213	1304.739176	516.6943959	0.396013552
ENSMUSG00000108575	181.6725435	506.360508	2.787215384
ENSMUSG00000101596	16.51568577	444.3571805	26.90516074
ENSMUSG00000107736	165.1568577	372.0199651	2.252525086
ENSMUSG00000097764	834.0421315	361.6860772	0.433654444
ENSMUSG00000097168	132.1254862	341.0183013	2.581018327
ENSMUSG00000106659	858.8156602	341.0183013	0.397079743
ENSMUSG00000096938	867.0735031	341.0183013	0.393298031
ENSMUSG00000097332	767.9793884	330.6844134	0.430590219
ENSMUSG00000100546	33.03137155	289.3488617	8.759819777
ENSMUSG00000096958	90.83627175	268.6810859	2.957861223
ENSMUSG00000029092	644.1117451	248.01331	0.385047023
ENSMUSG00000085298	16.51568577	186.0099825	11.26262543
ENSMUSG00000099937	57.8049002	186.0099825	3.217892979
ENSMUSG00000105076	66.06274309	186.0099825	2.815656357
ENSMUSG00000097431	49.54705732	165.3422067	3.337074201
ENSMUSG00000097039	8.257842886	93.00499127	11.26262543
ENSMUSG00000089652	8.257842886	82.67110335	10.0112226
ENSMUSG00000086212	173.4147006	41.33555167	0.238362443
ENSMUSG00000097160	107.3519575	20.66777584	0.192523512
ENSMUSG00000021874	107.3519575	20.66777584	0.192523512
ENSMUSG00000090263	132.1254862	20.66777584	0.156425353
ENSMUSG00000097698	148.641172	20.66777584	0.139044758
ENSMUSG00000038917	181.6725435	20.66777584	0.113763893
ENSMUSG00000105440	82.57842886	10.33388792	0.125140283
ENSMUSG00000101588	132.1254862	10.33388792	0.078212677
ENSMUSG00000086707	66.06274309	5.166943959	0.078212677
ENSMUSG00000097085	66.06274309	5.166943959	0.078212677
ENSMUSG00000108603	74.32058598	5.166943959	0.069522379

lnc_716	17306.32746	3244.954491	0.187501045
lnc_443	709.7232079	7202.216066	10.14792244
lnc_438	1091.881858	7439.651761	6.813605065
lnc_717	15886.88104	6015.037594	0.378616645
lnc_565	4312.933341	39.57261575	0.009175337
lnc_65	163.7822788	3957.261575	24.16172009
lnc_219	27.29704646	3878.116343	142.0709141
lnc_337	13047.98821	4907.004353	0.376073635
lnc_79	3494.021947	39.57261575	0.011325806
lnc_332	2675.110553	79.1452315	0.02958578
lnc_403	2620.51646	39.57261575	0.015101075
lnc_589	764.3173009	4352.987732	5.695262593
lnc_532	218.3763717	2770.083102	12.68490305
lnc_412	27.29704646	2136.92125	78.28397309
lnc_530	327.5645575	2532.647408	7.731750429
lnc_176	218.3763717	2216.066482	10.14792244
lnc_217	1419.446416	39.57261575	0.027878908
lnc_650	27.29704646	1345.468935	49.28990898
lnc_459	1201.070044	39.57261575	0.0329478
lnc_264	1201.070044	39.57261575	0.0329478
lnc_222	982.6936725	39.57261575	0.040269533
lnc_83	1419.446416	237.4356945	0.167273447
lnc_344	4367.527434	1978.630787	0.453032252
lnc_765	27.29704646	870.5975465	31.89347052
lnc_115	3275.645575	1266.323704	0.386587521
lnc_751	2019.981438	4194.697269	2.076601889
lnc_559	27.29704646	712.3070835	26.0946577
lnc_697	54.59409292	712.3070835	13.04732885
lnc_709	1528.634602	3244.954491	2.122779694
lnc_560	709.7232079	79.1452315	0.111515631
lnc_26	600.5350221	39.57261575	0.0658956
lnc_236	545.9409292	39.57261575	0.07248516
lnc_298	27.29704646	474.871389	17.39643846
lnc_723	27.29704646	474.871389	17.39643846
lnc_169	163.7822788	791.452315	4.832344018

Supplementary Table S3. Detailed gene mapping for KEGG pathway analysis.

Gene Name	Location	Gene Name	Location
U2AF2	nucleus	SNRPE	nucleus&cytosol
RBMX	nucleus	SMNDC1	nucleus&cytosol
HNRNPU	nucleus	SRSF3	nucleus&cytosol
SNRPA	nucleus	PRPF19	nucleus&cytosol
DHRS4	nucleus	HNRNPM	nucleus&cytosol
UQCRC2	nucleus	SRSF5	nucleus&cytosol
SLC25A5	nucleus	HNRNPK	nucleus&cytosol
CYCS	nucleus	PCBP1	nucleus&cytosol
ATP5F1	nucleus	SNRPD2	nucleus&cytosol
NDUFA13	nucleus	DDX5	nucleus&cytosol
VDAC1	nucleus	HNRNPA1	nucleus&cytosol
DLST	nucleus	MARS	nucleus&cytosol
ACADM	nucleus	LARS	nucleus&cytosol
BDH1	nucleus	RARS	nucleus&cytosol
ALDH6A1	nucleus	KARS	nucleus&cytosol
CMAS	nucleus	EIF2B5	nucleus&cytosol
RPL31	cytosol	EIF3E	nucleus&cytosol
RPL8	cytosol	EIF2S1	nucleus&cytosol
EIF2S3X	cytosol	EIF3A	nucleus&cytosol
EIF2S3Y	cytosol	STRAP	nucleus&cytosol
EIF3C	cytosol	FXR1	nucleus&cytosol
EIF3D	cytosol	EIF4G1	nucleus&cytosol
EIF4G3	cytosol	RPL10A	nucleus&cytosol
EIF3B	cytosol	RPS20	nucleus&cytosol
EIF4E	cytosol	RPL12	nucleus&cytosol
EIF3G	cytosol	RPS24	nucleus&cytosol
EIF4A2	cytosol	RPSA	nucleus&cytosol
EIF2S2	cytosol	RPL26	nucleus&cytosol
EIF3I	cytosol	RPL27	nucleus&cytosol
PABPC1	cytosol	RPS9	nucleus&cytosol
EIF2B3	cytosol	RPS6	nucleus&cytosol
EIF2B4	cytosol	RPS4X	nucleus&cytosol
YARS	cytosol	RPS5	nucleus&cytosol
NARS	cytosol	RPS8	nucleus&cytosol
DARS	cytosol	RPS19	nucleus&cytosol
SARS	cytosol	RPS17	nucleus&cytosol
EPRS	cytosol	RPL22	nucleus&cytosol
VARS	cytosol	RPS14	nucleus&cytosol
IARS	cytosol	RPS12	nucleus&cytosol
TRAS	cytosol	RPS13	nucleus&cytosol
FARSB	cytosol	RPS10	nucleus&cytosol
FARSA	cytosol	RPS11	nucleus&cytosol

ACOX1	cytosol	RPLP0	nucleus&cytosol
EHHADH	cytosol	RPL9	nucleus&cytosol
EPHX2	cytosol	RPL17	nucleus&cytosol
IDH2	cytosol	RPL19	nucleus&cytosol
ABCD3	cytosol	RPL15	nucleus&cytosol
HSD17B4	cytosol	RPL35	nucleus&cytosol
HSD17B10	cytosol	RPS15A	nucleus&cytosol
DBT	cytosol	RPS3	nucleus&cytosol
SDS	cytosol	RPS25	nucleus&cytosol
ACOX1	cytosol	RPS26	nucleus&cytosol
HSD17B10	cytosol	RPS28	nucleus&cytosol
SORD	cytosol	RPL7	nucleus&cytosol
DHCR7	cytosol	CYC1	nucleus&cytosol
IDH2	cytosol	ATP5C1	mitochondrion
HSD17B4	cytosol	NDUFA4	mitochondrion
SARDH	cytosol	ATP5D	mitochondrion
HPD	cytosol	COX7A2	mitochondrion
EPHX2	cytosol	NDUFB7	mitochondrion
DBT	cytosol	BCKDHA	mitochondrion
AKR1D1	cytosol	GCDH	mitochondrion
CDC42	cytosol	BCKDHA	mitochondrion
DHRS4	nucleus&cytosol	GCDH	mitochondrion
SHMT2	nucleus&cytosol	HOGA1	mitochondrion
HADH	nucleus&cytosol	TST	mitochondrion
UGDH	nucleus&cytosol	ATP5D	membrane
HADH	nucleus&cytosol	GT1A7C	membrane
ACLY	nucleus&cytosol	DAD1	membrane
SHMT2	nucleus&cytosol	DDOST	membrane
TFAM	nucleus&cytosol	ATP5C1	membrane
CoX4I1	nucleus&cytosol	SLC27A2	peroxisome
SCP2	nucleus&cytosol	AP2A2	plasma membrane
PRDX5	nucleus&cytosol	AP2M1	lysosomal membrane
HACL1	nucleus&cytosol	P4HA3	endoplasmic reticulum
SNRPF	nucleus&cytosol		

Supplementary Table S4. Sequences of primers and siRNAs used in this study.

Gene	Primer sequence (5'→3')	Size (bp)	Application
lncRHL	F:CTTCGCTTTCTTCAGTCTTG	20	qPCR
	R:AAACAGTCTCATGCTGCTCT	20	
TfIIb	F:CTCTGTGGCGGCAGCAGCTATTT	23	qPCR
	R:CGAGGGTAGATCAGTCTGTAGGA	23	
45s	F:GTGCCCTCACGTGTTTCACTTT	22	qPCR
	R:TAGGAGACAAACCTGGAACGCT	22	
Lxr	F:TCTGGAGACGTCACGGAGGTA	21	qPCR
	R:CCCGGTTGTAACTGAAGTCCTT	22	
Srebp1c	F:GGAGCCATGGATTGCACATT	20	qPCR
	R:GGCCCGGGAAGTCACTGT	18	
Srebp2	F:GCAGCAACGGGACCATTCT	19	qPCR
	R:CCCCATGACTAAGTCCTTCAACT	23	
Acc1	F:TGGACAGACTGATCGCAGAGAAAG	24	qPCR
	R:TGGAGAGCCCCACACACA	18	
Fas	F:GCTGCGGAAACTTCAGGAAAT	21	qPCR
	R:AGAGACGTGTCACTCCTGGACTT	23	
Gpat	F:CAACACCATCCCCGACATC	19	qPCR
	R:GTGACCTTCGATTATGCGATCA	22	
Agpat1	F:GCTGGCTGGCAGGAATCAT	19	qPCR
	R:GTCTGAGCCACCTCGGACAT	20	
Dgat1	F:GAGGCCTCTCTGCCCCTATG	20	qPCR
	R:GCCCCTGGACAACACAGACT	20	
Atgl	F:GAGAGAACGTCATCATATCCCACTT	25	qPCR
	R:CCACAGTACACCGGGATAAATGT	23	
Pparaα	F:ACAAGGCCTCAGGGTACCA	19	qPCR
	R:GCCGAAAGAAGCCCTTACAG	20	
Cpt1	F:TTGCCCTACAGCTGGCTCATTTCC	24	qPCR
	R:GCACCCAGATGATTGGGATACTGT	24	
Mttp	F:CCTACCAGGCCCAACAAGAC	20	qPCR
	R:CGCTCAATTTTGCATGTATCC	21	
ApoB	F:CGTGGGCTCCAGCATTCTA	19	qPCR
	R:TCACCAGTCATTTCTGCCTTTG	22	
36B4	F:TGCATCAGTACCCCATTCTATCA	23	qPCR
	R:AAGGTGTAATCCGTCTCCACAGA	23	
hnRNPU	F:ATGAGTTCTTCGCCTGTTAATGT	23	qPCR
	R:CCTGGAGTCGATCCATGAGA	20	
Bmal1	F:TCAAGACGACATAGGACACCT	21	qPCR
	R:GGACATTGGCTAAAACAACAGTG	23	
Shp	F:TGGGTCCCAAGGAGTATGC	19	qPCR
	R:GCTCCAAGACTTCACACAGTG	21	
Gata4	F:CACGCTGTGGCGTCGTAAT	19	qPCR
	R:CTGGTTTGAATCCCCTCCTTC	21	

Abcg5	F:TGGATCCAACACCTCTATGCTAAA	24	qPCR
	R:GGCAGGTTTTCTCGATGAACTG	22	
Gm26608	F:TCCCTCCAAGAAGCGGACTT	20	qPCR
	R:AACTGCTGGGCTGTCTTAGC	20	
Neat1	F:AGGAGAAGCGGGGCTAAGTA	20	qPCR
	R:TAGGACACTGCCCCCATGTA	20	
4732463B04Rik	F:GTTGTCTTAGCTCCGTCTC	19	qPCR
	R:ACTTAGCCCATACCGACT	18	
2610020F03Rik	F:CTGACGGCAAGGGAGTATGG	20	qPCR
	R:AGCGGACGTGAAGATGACTC	20	
Gm26635	F:GTGATTCTTCCTCTCCCAGGC	21	qPCR
	R:ATGCACCCTCAGGAAGTCTG	20	
Gm26714	F:GGACGGGCTTACTCGAAGAG	20	qPCR
	R:CCCGAGCTTTGTTCACCCTT	20	
Gm9968	F:GTGCAGATGTGCCACTGAAA	20	qPCR
	R:TGCCTCCATGCACAGTTACATA	22	
siRNA1-lncRHL	F:ACAGAGUACCAAACAUGAA	19	Smart Silencer
	R:UUCAUGUUUGGUACUCUGU	19	
siRNA2-lncRHL	F:CCGAACAUAAACUCAUUAA	19	Smart Silencer
	R:UUAAUGAGUUUAUGUUCGG	19	
siRNA3-lncRHL	F:CCACAAGUCCUCAGAGUUU	19	Smart Silencer
	R:AAACUCUGAGGACUUGUGG	19	
ASO1-lncRHL	F:GCCAUCCGUUAAGAUUCUGC	20	Smart Silencer
	R:GCAGAAUCUUAACGGAUGGC	20	
ASO2-lncRHL	F:CACUGAACAUGUGUUAGGUC	20	Smart Silencer
	R:GACCUAACACAUGUUCAGUG	20	
ASO3-lncRHL	F:UGGUUGCCAAGCUGCAACAU	20	Smart Silencer
	R:AUGUUGCAGCUUGGCAACCA	20	
5'-RACE lncRHL1	F:CGGGTCGCAGAACTTGGACATA	22	RACE
	R:TATGTCCAAGTTCTGCGACCCG	22	
5'-RACE lncRHL2	F:GTCACTAGAGTTCTGGGAGAC	21	RACE
	R:GTCTCCCAGAACTCTAGTGAC	21	
3'-RACE lncRHL1	F:CCGCGCTCTACCCGCAACTTACTGG	25	RACE
	R:CCAGTAAGTTGCGGGTAGAGCGCGG	25	
3'-RACE lncRHL2	F:GCAGCGCTCTGCGGATTCCAAGCT	24	RACE
	R:AGCTTGGAATCCGCAGAGCGCTGC	24	
siRNA1-hnRNPU	F:GCTTTGAGATGAAGGTAACAGAGAA	25	siRNA
	R:TTCTCTGTTACCTTCATCACAAAGC	25	
siRNA2-hnRNPU	F:ACATGAAGTTCGGATTGGCTGGTCA	25	siRNA
	R:TGACCAGCCAATCCGAACTTCATGT	25	
Ad-shlncRHL	F:TGCTTAGTACTGCACTTATT	20	Adenovirus
	R:AATAAGTGCAGTACTAAGCA	20	
Ad-shMttp	F:CCTGAACATCTTCCAGTACAT	21	Adenovirus
	R:ATGTACTGGAAGATGTTCAGG	21	

Supplementary Table S5. Antibody list for western-blot analysis.

Name	Detail	Dilution
Rabbit Polyclonal anti-ABCG5	Proteintech(27722-1-AP)	1:1000
Mouse monoclonal anti-Albumin	Santa Cruz Biotechnology(sc-271605)	1:500
Mouse monoclonal anti-APOA1	Santa Cruz Biotechnology(sc-376818)	1:500
Goat polyclonal anti-APOB	Milipore(AB742)	1:1000
Mouse monoclonal anti-BMAL1	Santa Cruz Biotechnology(sc-365645)	1:500
Rabbit polyclonal anti-CALNEXIN	ENZO life sciences(ADI-SPA-860)	1:3000
Mouse monoclonal anti-GATA4	Santa Cruz Biotechnology(sc-25310)	1:500
Rabbit monoclonal anti-HA	Cell Signaling Technology(#3724)	1:1000
Mouse monoclonal anti-hnRNPA2B1	Santa Cruz Biotechnology(sc-374053)	1:500
Mouse monoclonal anti-hnRNPL	Santa Cruz Biotechnology(sc-32317)	1:500
Mouse monoclonal anti-hnRNPU	Santa Cruz Biotechnology(sc-32315)	1:500
Rabbit polyclonal anti-LAMIN B	Bioworld(AP6001)	1:5000
Mouse monoclonal anti-LPL	Santa Cruz Biotechnology(sc-373759)	1:500
Mouse monoclonal anti-MTTP	BD Transduction Laboratories (612022)	1:5000
Mouse monoclonal anti-PCSK9	Santa Cruz Biotechnology(sc-515082)	1:500
Rabbit monoclonal anti-PDI	Cell Signaling Technology(#3501)	1:1000
Mouse monoclonal anti-SHP	Santa Cruz Biotechnology(sc-271511)	1:500
Rabbit monoclonal anti-TUBULIN	Santa Cruz Biotechnology(sc-9104)	1:500