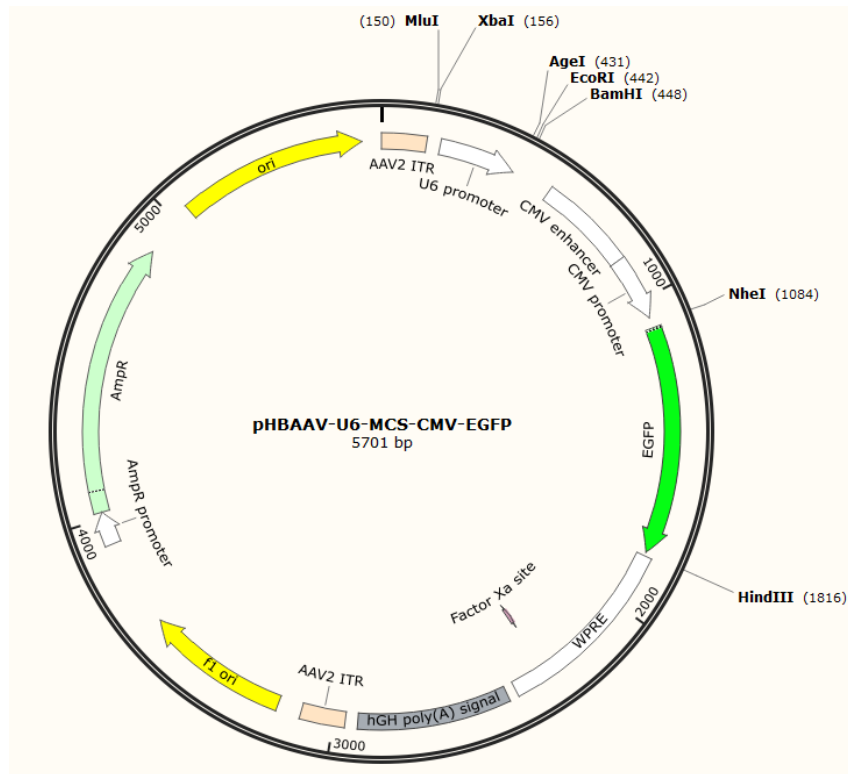


## SUPPLEMENTARY DATA

### Supplementary Figures

#### Supplementary Figure S1-The map of pHBAAV-U6-MCS-CMV-EGFP vector



**A**

Islets

Query\_29965 Length: 3027 Number of Matches: 1  
to 379 [Graphics](#)

Expect	Identities	Gaps	Strand
8e-90	178/179(99%)	1/179(0%)	Plus/Plus
GTATATTACTGCGGGTGA-TGAGTGCTCATTTTCAGGCTGACGCTGCAC	76		
TTATATTACTGCGGGTGA-MATTAATCTGCTATTTTCAGGCTGACGCTGCAC	260		
TGGTGATGCTATTTTGGTATGACGCAAGGCTGACGCTGACGCTGACGCTG	136		
CTTTTCTGCTGATTTTGGTATGACGCAAGGCTGACGCTGACGCTGACGCTG	320		
CTTTTCTGCTGATTTTGGTATGACGCAAGGCTGACGCTGACGCTGACGCTG	195		
CTTTTCTGCTGATTTTGGTATGACGCAAGGCTGACGCTGACGCTGACGCTG	379		

**B**

Skeletal muscle

Sequence ID: Query\_81869 Length: 3027 Number of Matches: 1  
Range 1: 573 to 626 [Graphics](#)

Score	Expect	Identities	Gaps	Strand
87.9 bits(47)	6e-22	52/54(96%)	1/54(1%)	Plus/Plus
Query 14 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	66			
Sbjct 873 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	626			

**C**

Perineral adipose

Sequence ID: Query\_109171 Length: 3027 Number of Matches: 1  
Range 1: 573 to 626 [Graphics](#)

Score	Expect	Identities	Gaps	Strand
93.5 bits(50)	1e-22	53/54(98%)	1/54(1%)	Plus/Plus
Query 13 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	66			
Sbjct 873 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	626			

**D**

Brown adipose

Sequence ID: Query\_109171 Length: 3027 Number of Matches: 1  
Range 1: 573 to 626 [Graphics](#)

Score	Expect	Identities	Gaps	Strand
93.5 bits(50)	1e-22	53/54(98%)	1/54(1%)	Plus/Plus
Query 13 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	66			
Sbjct 873 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	626			

**E**

Liver

Sequence ID: Query\_109171 Length: 3027 Number of Matches: 1  
Range 1: 573 to 626 [Graphics](#)

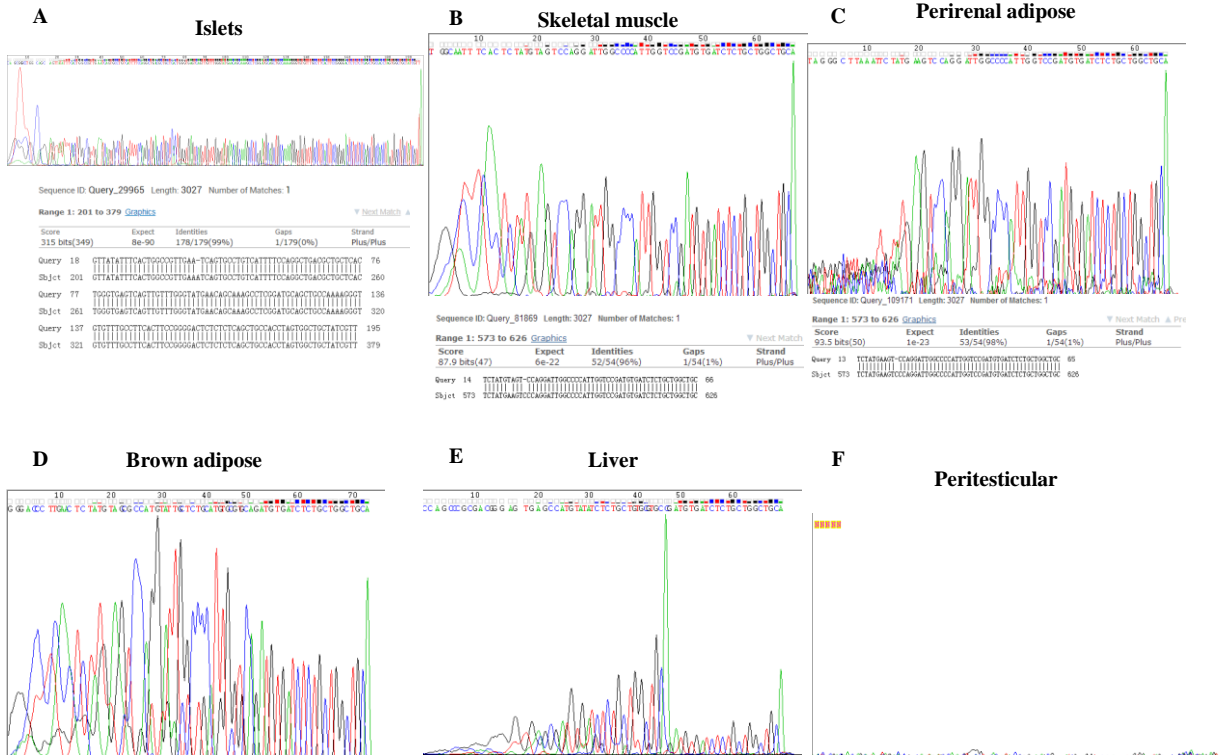
Score	Expect	Identities	Gaps	Strand
93.5 bits(50)	1e-22	53/54(98%)	1/54(1%)	Plus/Plus
Query 13 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	66			
Sbjct 873 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	626			

**F**

Peritesticular

Sequence ID: Query\_109171 Length: 3027 Number of Matches: 1  
Range 1: 573 to 626 [Graphics](#)

Score	Expect	Identities	Gaps	Strand
93.5 bits(50)	1e-22	53/54(98%)	1/54(1%)	Plus/Plus
Query 13 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	66			
Sbjct 873 TTTATGATTC-CAGGATTCGCCCATATTGGCCGATGATCTCTCTGACTGC	626			



**Supplementary Figure S3-Identification of human homologous sequences of Inc866.** (A) Searching for human homologous sequences using NCBI-BLAST. (B) Upper panel, Sanger sequencing results of qPCR product of human islets; lower panel, sequence alignment of qPCR products with full length of AL137118.20.

**A**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Human DNA sequence from clone RP11-108P5 on chromosome 13q14.12-21.1 com... <a href="#">Homo sapiens</a>		141	263	39%	7e-28	65.32%	162446	<a href="#">AL137118.20</a>

### Human DNA sequence from clone RP11-108P5 on chromosome 13q14.12-21.1, complete sequence

Sequence ID: [AL137118.20](#) Length: 162446 Number of Matches: 3

Range 1: 143638 to 144449 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
141 bits(155)	7e-28	550/842(65%)	51/842(6%)	Plus/Minus
Query 2152	ATCAAGTCTTTGCTTTCTTTGGACAGCAACTATCCCTATTTTAA-CTACTTTTGAAGT	2210		
Sbjct 144449	ATCGAGCATTGCTTTCTTTGGTCAGCAGCTGTTC-TCTTGCAGACCCTCCTGTGGT	144391		
Query 2211	TTCTTGAACCATGATCAAATAA---TTTATTTCCCTCAGTGTCTATGTTGGATAATATTT	2267		
Sbjct 144390	CCCCCTAACCATGATCAAATCACCATTCAATTTCTCCCA-TGTCTTATTTAGATAAGATT	144332		
Query 2268	TCCTGTAGAAATCGTCTGTAAAGACATTAATAGCACTAGTTTGAAGAAGTAGCATTCTAC	2327		
Sbjct 144331	GCTTC-AGAAATGAATTGCCAAGACATTCACAATGTTTCATTTGGGAAGTGGCATTCTTC	144273		
Query 2328	ACAATAACCTTTGAAAGGGTTGAGAAT---ATACTCAC-AGAAAAAACAGGATATGC	2382		
Sbjct 144272	ACAGTGACTTCCCCAAGACTTGAGAAAGCCCATATGGAGTAGGAAAGACTCTGGATACAC	144213		
Query 2383	CTGCCCCAGTTTACTCCTCCTCCTCCAAACATCATTGAGTCTTTCTCGGCTGCTTTA	2442		
Sbjct 144212	CAGATCCAGCTCATTCCTTTTACTC--AACAAAAT-CACAGCTTTTCTTACTGCCTCA	144156		
Query 2443	TTCCAATCACCAGCTGAAGACAGTTCTAGCTCTGGTGCCCTTT---CCTCCAATATGA	2498		
Sbjct 144155	TTCCAAAAGCCAGCTGTGGAATGTTCTGGCTGCTGTGCCCATTTCTTCTCTAATATTA	144096		
Query 2499	GTCATGAATCTTCTCCAGTAATTTTCAGCCGTAGGTGTATCTGATA-ACATGAGGTATCT	2557		
Sbjct 144095	GTTCTGAATTTCTCTCGAGTAGGCTCAAGTAATAGGTATAGTAAATTTATTTCAATAACT	144036		
Query 2558	CCCTTTTGAATGAGTATGTTGTTGTTTCATGGAAGGCAATGTTCTGCTT-GTCTTAGTTTA	2616		
Sbjct 144035	TTCCATTAAAAATTTGTAATGTATGCTTATGGAGATCAATGTTCTATTGCGTGCTATTTTA	143976		
Query 2617	TGATGATTTTGGTCTTGGACTTTGCTTGTGAGTTTCTGAATGGGCTCGAGTAATGTCT	2676		
Sbjct 143975	TACT--TTTGTGCTTGGAGTCTGCTCCATCTATT-TGAATGAGGTTGGATAGATGTTT	143919		
Query 2677	GCCTTTGTGCTTTTAATACATGCCACAACTCGGGGGAAAAAAGAAAACCACTGACAC	2736		
Sbjct 143918	GCCTTGGTGTCTTCTTAATATATTCCTTAAGCCTGA---ACAAAAG-----CCTGACA-	143870		
Query 2737	AGTAATCATGGGC--TCATCATTTCTTCTCATCAGGAACAGCTTTGCACAGTAATAAAG	2794		
Sbjct 143869	--TGACCAATGCCCACTCATCATTTTCTTCTCTTCAGGAATTGTTTGTGCAATAATAAAA	143812		
Query 2795	TTCTGTTGCTT--TAGTCATTTGCTTGTGTGTCAGAGCCAAAAACGTATTGGACTGGA	2852		
Sbjct 143811	TGCTATTGCTTCTTAGTGATTTGTATGTGGCAAAAGAGCCAAAAATTATATCTG-CTGGA	143753		
Query 2853	GGAAGAGCTTGTGCTTAGAAAACAAAAGT-CACTCCTTCCAAACCTAATAAACTCTG	2911		
Sbjct 143752	T-----CTTGTGCTTAAAAACAAAATCCGTTTCTTTTTCAGGTATGATATAA-TTTG	143700		
Query 2912	GC-TGTTGTAGTCTTCATGGGTGTTACACTTTTCGTCTTCATTTTCCAAGGTCTGATACA	2970		
Sbjct 143699	ACTTGTCTTATTCTTCATGGATATTACATTTTCATCTTGTGTTTCTGAATTCTGACATA	143640		
Query 2971	GT 2972			
Sbjct 143639	GT 143638			

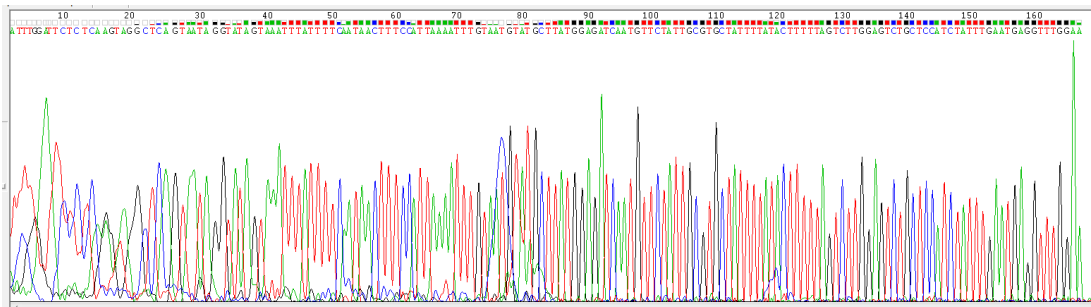
Range 2: 146533 to 146662 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Identities	Gaps	Strand
63.5 bits(69)	2e-04	93/130(72%)	4/130(3%)	Plus/Minus
Query 373	TATCGTTGCTGTGGTTGTTATTCTGCAAGTGAGATAATTAAGGTTTAGAAGAGTCTAAAG	432		
Sbjct 146662	TATCATTTGTTGTGGTTGTTATTTTACGAATGAGAGAATTCAGCTTTGGGCTGGTCTAACA	146603		
Query 433	TCATTTAACTGACAAGGGACAGGACTGGAATTCTAACCAAG--CTACCTGACATCGGCA-	489		
Sbjct 146602	ACACTTAGCTACTAAGTGGCAGAACTAGAATTGTAGCCCAGGCCTGTCTGACATCAGTAA	146543		
Query 490	-TGTTCTTGA 498			
Sbjct 146542	CTGTTCTTGA 146533			

Range 3: 145118 to 145375 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Identities	Gaps	Strand
59.0 bits(64)	0.002	178/269(66%)	26/269(9%)	Plus/Minus
Query 1530	TGATCATTTCTGTACTCTCTGCAAAGTACCAGCCTAACTGTCCAACCTCCTCCGGAACCT	1589		
Sbjct 145375	TGATCATTTTTGTTCTTCTGTTCATTACCAGCCTAACAGGGTCACTTCACCTGGGCCCT	145316		
Query 1590	GAGGG-CACCTTTAACTTCTTTTGTTAGCCTTGCCAGCATTTCCTTTGATTTCAGGTTGA	1648		
Sbjct 145315	TGGAGACACTTTGGACATTTCTTGTTAGACTTTTCAGACCTAACCTTTGGTTTCAGGTTGA	145256		
Query 1649	AATAGTTAACCTAGA-----ATTGGATCTCAGCCTGGTGAGAACTTCCTCTGAAGTTCATG	1704		
Sbjct 145255	AATGATTGTTCCAGAGCTTCCTGAATCTCAGCCTGTTG----TTTCTTCAGTA-TTC-TG	145202		
Query 1705	TTATGTCTTTTAACCAAATC-CCCCT-----TGTATCTCCTCAAAGAGAAATTCCTC	1754		
Sbjct 145201	TTGTGCCTCTTAATCAAGTCTCCACTCCCAGGCTCTTCTCTCCTC--AGAAAAATTCCTC	145144		
Query 1755	CTTCAATGGTCGTGGCATTCCCTTCCTTTA 1783			
Sbjct 145143	CCTCA---GTGATTGCATGCCTTTCTTTA 145118			

B



[Download](#) [GenBank](#) [Graphics](#)

Human DNA sequence from clone RP11-108P5 on chromosome 13q14.12-21.1, complete sequence  
Sequence ID: [AL137118.20](#) Length: 162446 Number of Matches: 1

Range 1: 143963 to 144121 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

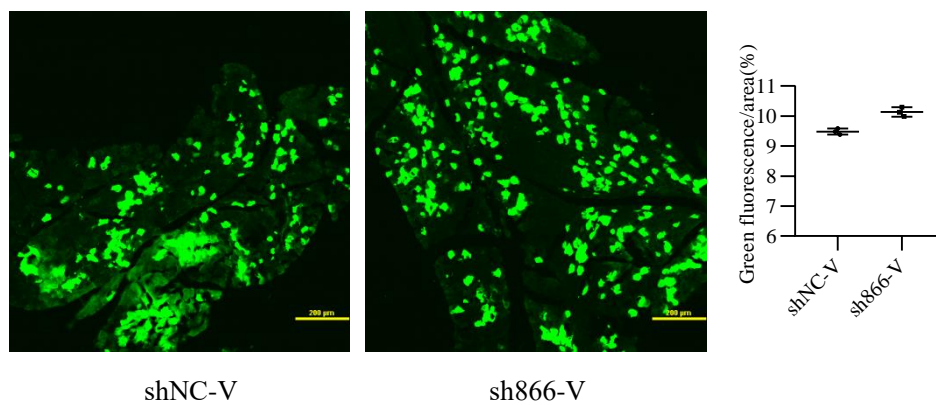
Score	Expect	Identities	Gaps	Strand
279 bits(309)	5e-71	158/159(99%)	1/159(0%)	Plus/Plus
Query 10	AGACTAAAA-CTATAAAATAGCAAGCAATAGAACATTGATCTCCATAAGCATACATTACA	68		
Sbjct 143963	AGACTAAAAAGTATAAAATAGCAAGCAATAGAACATTGATCTCCATAAGCATACATTACA	144022		
Query 69	AATTTTAATGCAAGTTATTGAAAAATAATTTACTATACTATTACTTGAGCCTACTCGA	128		
Sbjct 144023	AATTTTAATGCAAGTTATTGAAAAATAATTTACTATACTATTACTTGAGCCTACTCGA	144082		
Query 129	GAGAAATTCAGAACTAATATTAGAGGAACAAATGGGCACA 167			
Sbjct 144083	GAGAAATTCAGAACTAATATTAGAGGAACAAATGGGCACA 144121			

**Supplementary Figure S4-Confocal image of GFP investigation in pancreas sections after injection of sh866-V or shNC-V into mice via an intraductal route.**

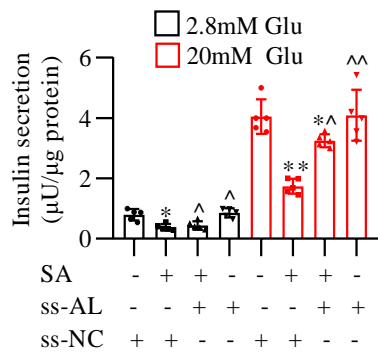
Quantification of the GFP signals was performed using NIH Image J 1.52 software.

Graph representing the number of pancreas with GFP expression in whole area.

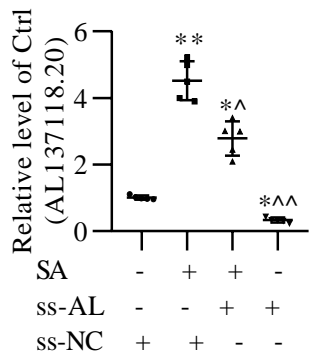
Scale bar: 200  $\mu$ m. **shNC-V**, the negative control shRNA engineered into the AAV9 vector; **sh866-V**, AAV9 vector carrying shRNA-lnc866. Representative image of 3 independent experiments.



**Supplementary Figure S5-Effect of AL137118.20 Smart Silencer on stearic acid-impaired GSIS.** \* $P<0.05$ , \*\* $P<0.01$  versus the ss-NC group; ^ $P<0.05$ , ^^ $P<0.01$  versus the SA+ss-AL group. SA, stearic acid; ss-AL, Smart Silencer for AL137118.20; ss-NC, negative control of ss-AL.  $n = 5$  samples from normolipidemic individuals.



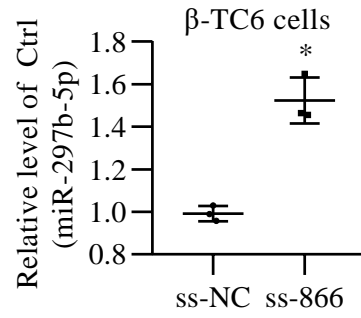
**Supplementary Figure S6-Inhibitory efficiency of Smart Silencer for AL137118.20 in the absence and presence of stearic acid.** \* $P<0.05$ , \*\* $P<0.01$  *versus* the ss-NC group; ^ $P<0.05$ , ^^ $P<0.01$  *versus* the SA+ss-AL group. **SA**, stearic acid; **ss-AL**, Smart Silencer for AL137118.20; **ss-NC**, negative control of ss-AL.  $n = 5$  samples from normolipidemic individuals.



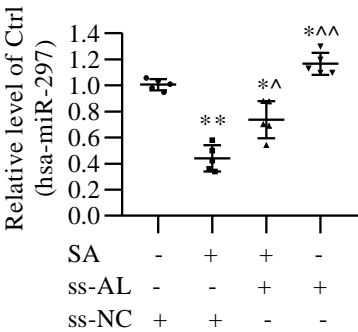
**Supplementary Figure S7-The co-expression network of lnc866, miR-297b-5p, and relevant mRNAs.** Yellow circle: lnc866; pink circle: miR-297b-5p; green circle: mRNAs; black line: negative relationship.



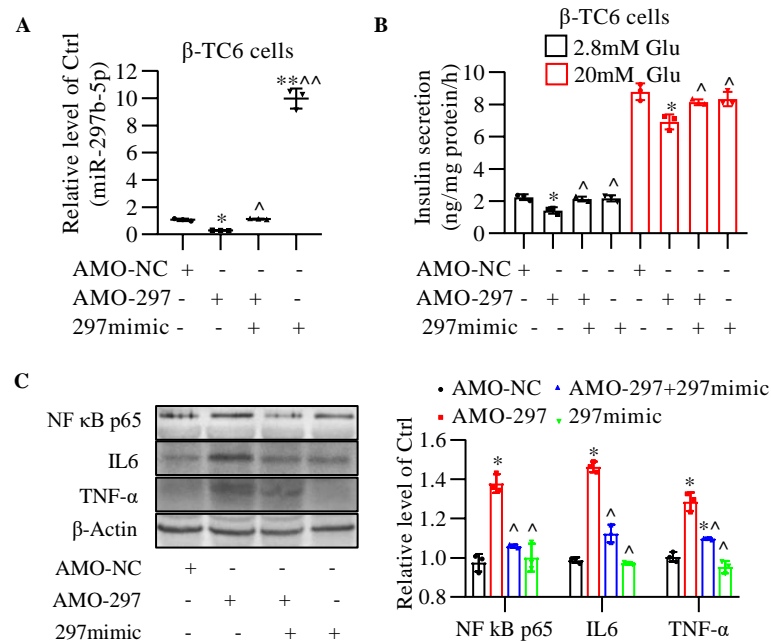
**Supplementary Figure S8-Inhibitory effect of Smart Silencer for lnc866 on miR-297b-5p expression in  $\beta$ -TC6 cell.** \* $P < 0.05$  versus the ss-NC group. **ss-866**, Smart Silencer for lnc866; **ss-NC**, the negative control of Smart Silencer.  $n = 3$  independent cell cultures per group.



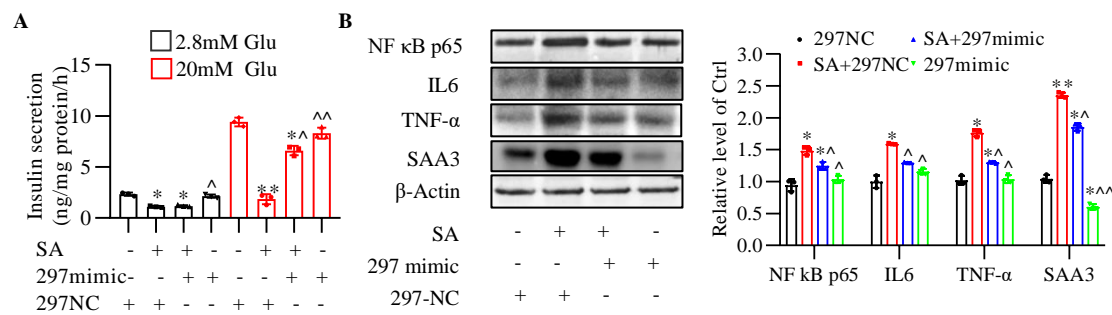
**Supplementary Figure S9-Change in the expression of hsa-miR-297 after knockdown of AL137118.20 in the presence of stearic acid.** \* $P<0.05$ , \*\* $P<0.01$  versus the ss-NC group; ^ $P<0.05$ , ^^ $P<0.01$  versus the SA+ss-AL group. **SA**, stearic acid; **ss-AL**, Smart Silencer for AL137118.20; **ss-NC**, negative control of ss-AL.  $n = 5$  samples from normolipidemic individuals.



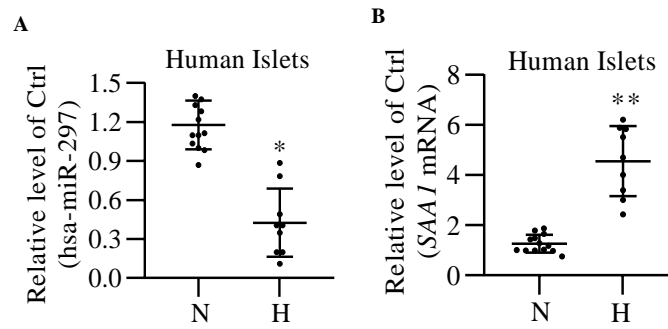
**Supplementary Figure S10-Effect of AMO-297 on GSIS and inflammatory factors level in  $\beta$ -TC6 cells without stearic acid treatment.** (A) miR-297b-5p expression after the transfection of miR-297b-5p mimic or AMO-297b-5p in  $\beta$ -TC6 cells. (B) Insulin concentration after the transfection of a miR-297b-5p mimic or AMO-297b-5p in  $\beta$ -TC6 cells. (C) Western blots showing the protein expression of NF  $\kappa$ B p65, IL6, and TNF- $\alpha$  following the transfection of a miR-297b-5p mimic or AMO-297b-5p in  $\beta$ -TC6 cells. \* $P$ <0.05, \*\* $P$ <0.01 *versus* the AMO-NC group; ^ $P$ <0.05, ^^ $P$ <0.01 *versus* the stearic acid AMO-297 group. **AMO-297**, anti-miR-297b-5p oligonucleotides; **AMO-NC**, negative control of AMO-297; **297mimic**, miR-297b-5p mimics.  $n$  = 3 independent cell cultures per group.



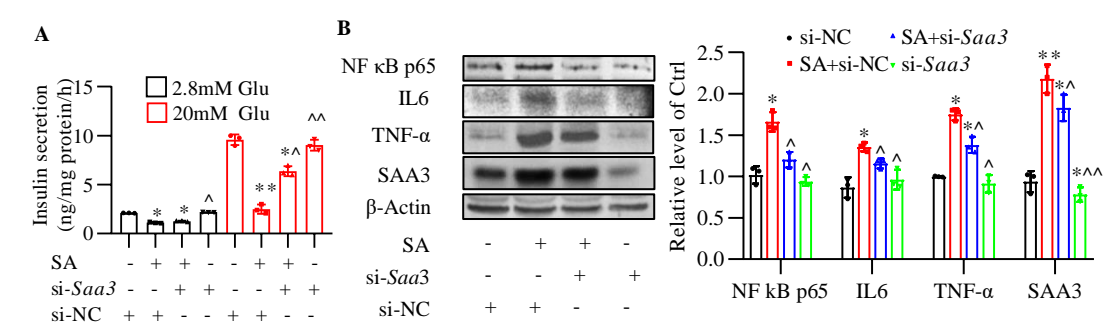
**Supplementary Figure S11-Role of miR-297b-5p in stearic acid treated mouse islets.** (A) Protection of the stearic acid–impaired glucose-stimulated insulin secretion (GSIS) after the transfection of a miR-297b-5p mimic. (B) Western blot showing the effects of miR-297b-5p on the expressions of NF  $\kappa$ B p65, IL6, TNF- $\alpha$  and SAA3 following stearic acid treatment. \* $P$ <0.05, \*\* $P$ <0.01 *versus* the 297NC group; ^ $P$ <0.05, ^^ $P$ <0.01 *versus* the SA+297NC group. SA, stearic acid; **297NC**, negative control of miR-297b-5p; **297mimic**, miR-297b-5p mimics.  $n$  = 3 independent cell cultures per group.



**Supplementary Figure S12-Changes in expressions of hsa-miR-297 and *SAA1* in islets from patients with hyperlipidemia.** \* $P < 0.05$ , \*\* $P < 0.01$  versus the N groups. N, normal lipidemic participants; H, hyperlipidemic patients. n=13 and 9 samples in N and H group, respectively.

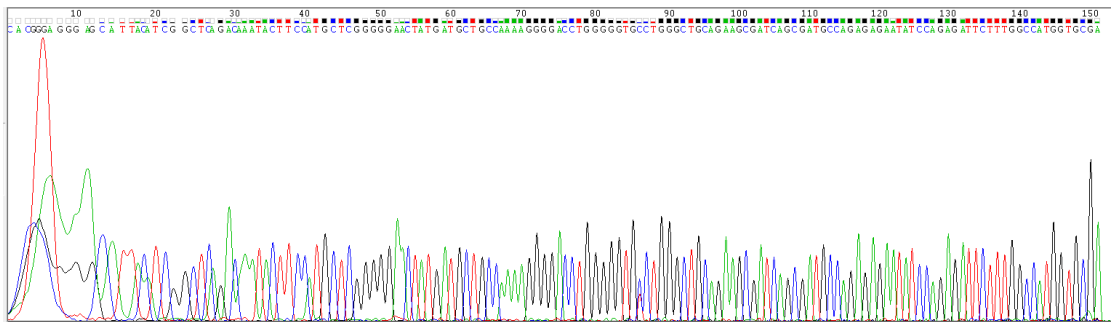


**Supplementary Figure S13-Involvement of SAA3 in stearic acid treated mouse islets.** (A) Restoration of the stearic acid–impaired glucose-stimulated insulin secretion (GSIS) after the knocking down of *Saa3*. (B) Effects of si-*Saa3* on NF κB p65, IL6, TNF-α and SAA3 protein expression in the presence of stearic acid. SA, stearic acid; **si-*Saa3***, siRNA for *Saa3*; **si-NC**, negative control of si-*Saa3*. \**P*<0.05, \*\**P*<0.01 versus the si-NC group; ^*P*<0.05, ^^*P*<0.01 versus the SA+si-*Saa3* group. *n* = 3 independent cell cultures per group.



**Supplementary Figure S14-Sequence alignment of human *SAA1* in islets with mouse *Saa3*.** (A) Sanger sequencing results of *SAA1* in human islets. (B) Upper panel, searching for the mouse homologous sequence of qPCR product of human *SAA1* in islets; lower panel, sequence alignment of qPCR product of human *SAA1* in islets with mouse *Saa3*.

**A**



**B**

Sequences producing significant alignments										Download	New	Select columns	Show	100	
<input checked="" type="checkbox"/> select all	10 sequences selected									GenBank	Graphics	Distance tree of results	New	MSA Viewer	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession						
Transcripts															
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.3.(Saa3).mRNA	Mus.musculus	133	133	83%	4e-29	83.33%	531	NM_011315.3						
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.2.(Saa2).transcript.variant.4.mRNA	Mus.musculus	123	123	76%	7e-26	83.48%	822	NM_001379269.1						
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.2.(Saa2).transcript.variant.1.mRNA	Mus.musculus	123	123	76%	7e-26	83.48%	609	NM_011314.3						
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.2.(Saa2).transcript.variant.2.mRNA	Mus.musculus	123	123	76%	7e-26	83.48%	606	NM_001357491.2						
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.2.(Saa2).transcript.variant.3.mRNA	Mus.musculus	123	123	76%	7e-26	83.48%	825	NM_001379268.1						
<input checked="" type="checkbox"/>	PREDICTED: Mus.musculus.serum.amyloid.A.1.(Saa1).transcript.variant.X2.mRNA	Mus.musculus	114	114	78%	1e-23	81.36%	1026	XM_006540725.2						
<input checked="" type="checkbox"/>	PREDICTED: Mus.musculus.serum.amyloid.A.1.(Saa1).transcript.variant.X1.mRNA	Mus.musculus	114	114	78%	1e-23	81.36%	1029	XM_006540724.2						
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.1.(Saa1).transcript.variant.1.mRNA	Mus.musculus	114	114	78%	1e-23	81.36%	609	NM_009117.4						
<input checked="" type="checkbox"/>	Mus.musculus.serum.amyloid.A.1.(Saa1).transcript.variant.2.mRNA	Mus.musculus	114	114	78%	1e-23	81.36%	612	NM_001357493.1						
<input checked="" type="checkbox"/>	Mus.musculus.strain.C57BL/6J.chromosome.7.GRCm39	Mus.musculus	107	410	55%	1e-21	88.10%	144995196	NC_000073.7						

[Download](#) ▼ [GenBank](#) [Graphics](#)

Mus musculus serum amyloid A 3 (Saa3) mRNA.

Sequence ID: [NM\\_011315.3](#) Length: 531 Number of Matches: 1

Range 1: 181 to 306 [GenBank](#) [Graphics](#) ▼ [Next Match](#)

Score	Expect	Identities	Gaps	Strand
133 bits(147)	4e-29	105/126(83%)	0/126(0%)	Plus/Plus
Query 24	CTCAGACAAATACTTCCATGCTCGGGGGA	ACTATGATGCTGCCAAAAGGGGACCTGGGGG	83	
Sbjct 181	CTCAGACAAATACTTCCATGCTCGGGGGA	ACTATGATGCTGCCCGGAGGGGTCCCGGGGG	240	
Query 84	TGCCTGGGCTGCAGAAGCGATCAGCGATGCCAGAGAGAATATCCAGAGATTCTTTGGCCA	143		
Sbjct 241	AGCCTGGGCTGCTAAAGTCATCAGCGATGCCAGAGAGGCTGTTCAGAAATTACGGGACA	300		
Query 144	TGGTGC	149		
Sbjct 301	TGGAGC	306		

## Supplementary Tables

**Supplementary Table S1** The details of sh866-V and shNC-V

name	sequence
Promoter of U6	GAGGGCCTATTTCCCATGATTCCTTCATATTTGCA TATACGATACAAGGCTGTTAGAGAGATAATTGGA ATTAATTTGACTGTAAACACAAAGATATTAGTAC AAAATACGTGACGTAGAAAGTAATAATTTCTTGG GTAGTTTGCAGTTTTTAAAATTATGTTTTTAAAATG GACTATCATATGCTTACCGTAACTTGAAAGTATTT CGATTTCTTGGCTTTATATATCTTGTGGAAAGGA C
EGFP	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGG GGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGA CGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGA CCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCCACCCTCGTGACCACCCTGA CCTACGGCGTGCAGTGCTTCAGCCGCTACCCCG ACCACATGAAGCAGCACGACTTCTTCAAGTCCG CCATGCCCCGAAGGCTACGTCCAGGAGCGCACCA TCTTCTTCAAGGACGACGGCAACTACAAGACCC GCGCCGAGGTGAAGTTCGAGGGCGACACCCTG GTGAACCGCATCGAGCTGAAGGGCATCGACTTC AAGGAGGACGGCAACATCCTGGGGCACAAGCT GGAGTACAACACTACAACAGCCACAACGTCTATAT CATGGCCGACAAGCAGAAGAACGGCATCAAGG TGAACCTTCAAGATCCGCCACAACATCGAGGACG GCAGCGTGCAGCTCGCCGACCACTACCAGCAGA ACACCCCCATCGGCGACGGCCCCGTGCTGCTGC

	CCGACAACCACTACCTGAGCACCCAGTCCGCCC
	TGAGCAAAGACCCCAACGAGAAGCGCGATCAC
	ATGGTCCTTAAGGAGTTCGTGACCGCCGCCGGG
	ATCACTCTCGGCATGGACGAGCTGTACAAGTAA
siRNA for shNC-V	TTCTCCGAACGTGTCACGTAA
shRNA for shNC-V	Top strand:
	GATCCGTTCTCCGAACGTGTCACGTAATTCAAG
	AGATTACGTGACACGTTTCGGAGAATTTTTTC
	Bottom strand:
	AATTGAAAAAATTCTCCGAACGTGTCACGTAAT
	CTCTTGAATTACGTGACACGTTTCGGAGAACG
siRNA for sh866-V	CAGCCTGGTGAGAACTTCCTCTGAA
shRNA for sh866-V	Top strand:
	AATTCGCAGCCTGGTGAGAACTTCCTCTGAATT
	CAAGAGATTCAGAGGAAGTTCTCACCAGGCTGT
	TTTTTG
	Bottom strand:
	GATCCAAAAAACAGCCTGGTGAGAACTTCCTCT
	GAATCTCTTGAATTCAGAGGAAGTTCTCACCAG
	GCTGCG
viral titer for sh866-V	1.2*10 <sup>12</sup> µg/mL
viral titer for shNC-V	3.5*10 <sup>12</sup> µg/mL

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**shNC-V**, the negative control shRNA engineered into the AAV9 vector; **sh866-V**, AAV9 vector carrying shRNA-lnc866; **EGFP**, enhanced green fluorescent protein; **AAV9**, Adeno-Associated Virus serotype 9.

**Supplementary Table S2** The composition of the diet for mice

Ingredients	Low fat diet	High SA diet
Cornstarch (g/kg)	367.5	40
Casein (g/kg)	213.465	258.45
Dextrinized cornstarch (g/kg)	121.53	121.53
Sucrose (g/kg)	88.91	88.91
Lard (g/kg)	0	316.6
Soybean oil (g/kg)	51	32.31
Fiber (g/kg)	40	64.61
Mineral mix (AIN-93G-MX) (g/kg)	12.92	12.92
Vitamin mix (AIN-93G-VX) (g/kg)	12.92	12.92
L-cystine (g/kg)	3.88	3.88
Choline bitartrate (g/kg)	2.58	2.58
Calcium carbonate (g/kg)	16.8	16.8
Calcium hydrogen phosphate (g/kg)	7.11	7.11
Potassium citrate(g/kg)	21.32	21.32
Edible blue dye (g/kg)	0.065	0.065
Energy (kcal/kg)	3851.82	5242.95

**SA:** stearic acid

**Supplementary Table S3** Target sequences of Smart Silencer for mouse Inc866

Gene	sequences
siRNA-1 target sequence	CTGCAAGTGAGATAATTAA
siRNA-2 target sequence	GCATTCCTTCCTTTAAACA
siRNA-3 target sequence	GAGAATATACTCACAGAAA
antisense oligonucleotides target sequence-1	ACGGCTTCCAGATCTGTCTT
antisense oligonucleotides target sequence-2	CGCAGCACATACCTCACATT
antisense oligonucleotides target sequence-3	CCTCCTCCTCCAAACATCAT

**Supplementary Table S4** Target sequences of Smart Silencer for human  
AL137118.20

Gene	sequences
siRNA-1 target sequence	GCAATTCATTTCTGAAGCA
siRNA-2 target sequence	GGAGCAGACTCCAAGACTA
siRNA-3 target sequence	CACTAAGAAGCAATAGCAT
antisense oligonucleotides target sequence-1	ATCATACCTGAAAGAAACGG
antisense oligonucleotides target sequence-2	GGCATTGTCATGTCAGGCTT
antisense oligonucleotides target sequence-3	TAGATGGAGCAGACTCCAAG

**Supplementary Table S5** Target sequences of siRNAs used in this study

name	sequences
siRNA- <i>Saa3</i>	GGAGTTGACAGCCAAAGAT
siRNA- <i>Rela</i>	GAAGCACAGATACCACCAA
siRNA- <i>Il6</i>	GGACTGATGCTGGTGACAA
siRNA- <i>Tnfa</i>	GACAACCAACTAGTGGTGC

**Supplementary Table S6** Primer sequences used for qRT-PCR in this study

Gene		sequences (5' to 3')
TCONS_00077866-1	Forward	TGTTTCCTTCGTGATTCCAGCATCG
(mouse)	Reverse	GCAGCCAGCAGAGATCACATCG
TCONS_00077866-2	Forward	TCAGCAACGGCTTCCAGATC
(mouse)	Reverse	AACGATAGCAGCCACTAGGTGG
AL137118.20	Forward	TCCAAACCTCATTCAAATAG
(human)	Reverse	TGTGCCCATTCTTCCTC
TCONS_00089573	Forward	ATCAACTCAGCACACTGGAGCATG
(mouse)	Reverse	CAGAAGCGACAGGCATCAGCAG
TCONS_00230830	Forward	GCTGTCTCATTACCGCCAGTC
(mouse)	Reverse	CGGGAAGTCAAAGGAGAGGCAG
TCONS_00230836	Forward	AACCACAGGCTTCGGGATAGTC
(mouse)	Reverse	CAAGCATAACAGGCGGGAAGTC
TCONS_00252600	Forward	CCGGAGCATTGTCCAGTATACC
(mouse)	Reverse	GCGTCCGTGATAATTGGATGTG
miR-297b-5p	Reverse transcription	GTCGTATCCAGTGCGTGTCGTGGAGTC
		GGCAATTGCACTGGATACGACACATGT
	Forward	GGGGATGTATGTGTGCATGA
	Reverse	GTATCCAGTGCGTGTCGTG
hsa-miR-297	Reverse transcription	GTCGTATCCAGTGCGTGTCGTGGAGTC
		GGCAATTGCACTGGATACGACCATGCA
	Forward	AUGUAUGUGUGCAUGUGCAUG
	Reverse	GTATCCAGTGCGTGTCGTG
U6	Reverse transcription	CGCTTCACGAATTTGCGTGTCAT
	Forward	GCTTCGGCAGCACATATACTA
	Reverse	CGCTTCACGAATTTGCGTGTC
<i>Saa3</i> (mouse)	Forward	GAAGTTCACGGGACATGGAG
	Reverse	TTCAGCACATTGGGATGTTT

<i>SAAI</i> (human)	Forward	TCGGGACATGTGGAGAGCCTAC
	Reverse	CGCACCATGGCCAAAGAATC
<i>Il6</i> (mouse)	Forward	TGTGACTCCAGCTTATCTCTTGG
	Reverse	TGATGGATGCTACCAAACCTGGA
<i>Tnf-<math>\alpha</math></i> (mouse)	Forward	ACAAGGTACAACCCATCGGC
	Reverse	CCCTCACACTCACAAACCAC
<i>Rela</i> (mouse)	Forward	GAGGGGAAACAGATCGTCCA
	Reverse	ATTTCCGCCTCTGGCGAATG
<i>Actb</i> (mouse)	Forward	GGTCAGAAGGACTCCTATGTGG
	Reverse	TGTCGTCCCAGTTGGTAACA
<i>ACTB</i> (human)	Forward	ATGGATGATGATATCGCC
	Reverse	GATGCCTCTCTTGCTCTG

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**hsa:** human

**Supplementary Table S7** The log<sub>2</sub> fold change of differentially expressed lncRNAs that were exclusively expressed in the stearic acid compared with control group.

name	Regulation	log <sub>2</sub> fold change	<i>P</i> value
TCONS_00088788	Down	-2.093	3.10E-66
TCONS_00038546	Ups	2.027	1.38E-45
TCONS_00184470	Down	-2.262	2.48E-33
TCONS_00233737	Down	-1.935	3.26E-28
TCONS_00100616	Down	-5.992	4.43E-28
TCONS_00233734	Down	-1.596	4.06E-24
TCONS_00128285	Ups	1.645	1.53E-17
TCONS_00098808	Ups	4.455	1.47E-15
TCONS_00139241	Ups	2.896	7.29E-14
TCONS_00164947	Down	-4.105	1.10E-12
TCONS_00077866	Ups	4.055	1.21E-12
TCONS_00250720	Down	-3.783	3.50E-12
TCONS_00146205	Ups	1.012	9.31E-12
TCONS_00184468	Down	-2.351	1.99E-11
TCONS_00068951	Ups	1.519	3.83E-11
TCONS_00239172	Down	-3.593	4.32E-11
TCONS_00004655	Ups	3.733	4.55E-11
TCONS_00078259	Down	-3.770	7.39E-11
TCONS_00057572	Down	-2.086	1.33E-10
TCONS_00102704	Ups	2.883	1.77E-10
TCONS_00009134	Ups	1.060	2.22E-10
TCONS_00088298	Ups	1.537	4.73E-10
TCONS_00088299	Ups	1.679	7.43E-10
TCONS_00195490	Ups	1.567	8.60E-10
TCONS_00239170	Down	-2.512	1.45E-09
TCONS_00088303	Ups	1.598	1.50E-09

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TCONS_00119905	Ups	3.432	7.65E-09
TCONS_00088508	Ups	1.307	9.09E-09
TCONS_00252600	Down	-2.123	9.87E-09
TCONS_00185019	Down	-1.554	1.63E-08
TCONS_00214621	Down	-1.027	5.73E-08
TCONS_00230409	Down	-1.190	1.51E-07
TCONS_00148776	Down	-1.313	1.72E-07
TCONS_00216021	Down	-3.085	2.69E-07
TCONS_00233223	Ups	1.471	3.98E-07
TCONS_00230836	Ups	1.328	5.06E-07
TCONS_00266371	Down	-3.003	6.33E-07
TCONS_00277357	Down	-1.996	7.77E-07
TCONS_00281906	Ups	1.972	9.00E-07
TCONS_00081253	Ups	2.272	9.17E-07
TCONS_00139248	Ups	2.864	9.90E-07
TCONS_00140517	Ups	2.042	1.08E-06
TCONS_00180861	Ups	2.938	1.19E-06
TCONS_00075608	Down	-2.929	1.24E-06
TCONS_00039986	Ups	2.724	1.81E-06
TCONS_00002604	Ups	1.124	3.00E-06
TCONS_00150272	Ups	1.401	3.34E-06
TCONS_00206490	Down	-1.346	4.48E-06
TCONS_00277850	Down	-2.785	4.65E-06
TCONS_00102063	Ups	2.781	4.93E-06
TCONS_00167285	Down	-1.892	4.94E-06
TCONS_00195486	Ups	1.810	6.28E-06
TCONS_00055673	Down	-1.121	6.39E-06
TCONS_00129289	Ups	2.737	6.83E-06
TCONS_00078368	Ups	1.220	7.33E-06

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TCONS_00057680	Ups	2.550	7.71E-06
TCONS_00080826	Down	-2.643	8.01E-06
TCONS_00249717	Down	-1.194	8.76E-06
TCONS_00178715	Ups	1.903	9.69E-06
TCONS_00139249	Ups	2.677	1.09E-05
TCONS_00009803	Ups	2.530	1.19E-05
TCONS_00147061	Down	-2.392	1.38E-05
TCONS_00112651	Ups	1.420	1.86E-05
TCONS_00230832	Down	-2.552	1.96E-05
TCONS_00128361	Ups	1.675	2.02E-05
TCONS_00130143	Ups	2.403	2.02E-05
TCONS_00132360	Ups	2.084	2.20E-05
TCONS_00006080	Down	-2.089	2.47E-05
TCONS_00001016	Ups	1.209	2.60E-05
TCONS_00252056	Down	-2.549	2.91E-05
TCONS_00102705	Ups	2.367	3.07E-05
TCONS_00045226	Ups	1.695	3.08E-05
TCONS_00233739	Down	-1.961	3.09E-05
TCONS_00150270	Ups	2.395	3.62E-05
TCONS_00079147	Down	-1.064	3.69E-05
TCONS_00069352	Ups	2.515	3.76E-05
TCONS_00148782	Down	-1.258	3.78E-05
TCONS_00252654	Ups	1.088	4.03E-05
TCONS_00111794	Down	-2.504	4.05E-05
TCONS_00055672	Down	-1.016	5.07E-05
TCONS_00214972	Down	-1.347	5.22E-05
TCONS_00006084	Down	-1.362	5.23E-05
TCONS_00144520	Ups	1.982	5.54E-05
TCONS_00230831	Ups	2.460	5.75E-05

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TCONS_00099264	Ups	2.457	5.77E-05
TCONS_00008230	Ups	1.518	6.26E-05
TCONS_00150267	Ups	2.437	6.65E-05
TCONS_00056121	Ups	2.382	6.67E-05
TCONS_00249350	Down	-1.122	7.18E-05
TCONS_00099186	Down	-1.258	7.76E-05
TCONS_00196774	Down	-1.515	8.59E-05
TCONS_00099319	Down	-1.694	9.01E-05
TCONS_00260686	Down	-1.056	9.60E-05
TCONS_00203893	Down	-1.488	1.04E-04
TCONS_00230830	Down	-1.491	1.05E-04
TCONS_00008865	Down	-1.238	1.13E-04
TCONS_00068952	Ups	1.280	1.14E-04
TCONS_00036859	Ups	2.358	1.14E-04
TCONS_00120345	Down	-1.381	1.27E-04
TCONS_00177728	Ups	1.819	1.29E-04
TCONS_00003674	Ups	2.087	1.35E-04
TCONS_00088499	Ups	2.115	1.51E-04
TCONS_00180688	Ups	1.904	1.64E-04
TCONS_00043156	Down	-1.683	1.76E-04
TCONS_00077760	Ups	1.852	1.99 E-04
TCONS_00080805	Down	-1.004	2.09E-04
TCONS_00247074	Down	-2.243	2.14E-04
TCONS_00131805	Down	-2.195	2.24E-04
TCONS_00002586	Ups	1.032	2.32E-04
TCONS_00088531	Ups	1.649	2.41E-04
TCONS_00233736	Down	-1.577	2.53E-04
TCONS_00040100	Ups	1.475	2.69E-04
TCONS_00157692	Ups	1.773	2.71E-04

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TCONS_00236795	Ups	1.303	2.96E-04
TCONS_00145605	Down	-2.209	3.00E-04
TCONS_00027006	Ups	1.276	3.02E-04
TCONS_00163485	Ups	1.973	3.02E-04
TCONS_00184225	Down	-1.336	3.30E-04
TCONS_00184460	Down	-2.135	3.34E-04
TCONS_00178829	Down	-2.188	3.41E-04
TCONS_00252057	Ups	2.183	3.49E-04
TCONS_00129531	Down	-2.024	3.49E-04
TCONS_00217905	Ups	1.042	3.53E-04
TCONS_00088238	Ups	2.083	3.60E-04
TCONS_00056019	Down	-1.220	3.64E-04
TCONS_00248344	Down	-1.730	3.81E-04
TCONS_00263683	Down	-2.162	4.00E-04
TCONS_00203344	Down	-1.467	4.06E-04
TCONS_00266071	Down	-1.156	4.14E-04
TCONS_00281912	Ups	1.232	4.28E-04
TCONS_00123053	Down	-1.189	4.34E-04
TCONS_00278906	Ups	2.1430	4.44E-04
TCONS_00121253	Down	-1.672	4.45E-04
TCONS_00161581	Down	-1.077	4.54E-04
TCONS_00129760	Down	-1.096	4.61E-04
TCONS_00002601	Ups	1.053	4.92E-04
TCONS_00047022	Down	-2.109	4.95E-04
TCONS_00196773	Down	-1.474	5.32E-04
TCONS_00221124	Ups	1.403	5.74E-04
TCONS_00111420	Down	-1.016	6.20E-04
TCONS_00006072	Ups	2.078	6.44E-04
TCONS_00195489	Ups	1.218	6.53E-04

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TCONS_00123093	Ups	1.197	6.54E-04
TCONS_00108495	Down	-1.327	6.58E-04
TCONS_00235952	Down	-1.130	6.92E-04
TCONS_00114840	Ups	2.036	7.07E-04
TCONS_00180689	Ups	1.160	8.48E-04
TCONS_00128357	Ups	1.885	9.01E-04
TCONS_00080780	Down	-1.600	9.45E-04
TCONS_00278334	Ups	1.024	9.49E-04
TCONS_00182959	Down	-1.124	9.90E-04
TCONS_00252601	Down	-1.588	1.04E-03
TCONS_00202594	Ups	1.993	1.06E-03
TCONS_00249723	Down	-1.327	1.10E-03
TCONS_00026862	Ups	1.985	1.10E-03
TCONS_00089573	Down	-1.976	1.10E-03
TCONS_00217223	Down	-1.980	1.14E-03
TCONS_00002528	Ups	1.987	1.14E-03
TCONS_00077762	Ups	1.398	1.17E-03
TCONS_00236022	Down	-1.770	1.24E-03
TCONS_00148773	Down	-1.079	1.29E-03
TCONS_00053707	Down	-1.355	1.30E-03
TCONS_00103585	Ups	1.734	1.30E-03
TCONS_00078111	Down	-1.919	1.31E-03
TCONS_00129930	Ups	1.349	1.32E-03
TCONS_00176551	Ups	1.032	1.33E-03
TCONS_00158955	Ups	1.949	1.34E-03
TCONS_00249349	Down	-1.754	1.42E-03
TCONS_00197656	Ups	1.480	1.44E-03
TCONS_00077761	Ups	1.082	1.52E-03
TCONS_00114790	Ups	1.909	1.65E-03

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TCONS_00110262	Down	-1.907	1.67E-03
TCONS_00088377	Down	-1.082	1.73E-03
TCONS_00213910	Ups	1.880	1.80E-03
TCONS_00035996	Ups	1.877	1.84E-03
TCONS_00237351	Ups	1.324	1.87E-03
TCONS_00026810	Down	-1.875	1.87E-03
TCONS_00078108	Down	-1.900	1.88E-03
TCONS_00001993	Ups	1.502	1.94E-03
TCONS_00247953	Ups	1.749	2.01E-03
TCONS_00274730	Ups	1.884	2.03E-03
TCONS_00103408	Ups	1.885	2.04E-03
TCONS_00163455	Ups	1.455	2.09E-03
TCONS_00260769	Down	-1.851	2.10E-03
TCONS_00057573	Ups	1.846	2.13E-03
TCONS_00205706	Ups	1.214	2.14E-03
TCONS_00023590	Ups	1.443	2.24E-03
TCONS_00038441	Down	-1.850	2.29E-03
TCONS_00009804	Ups	1.778	2.33E-03

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**Supplementary Table S8** The log<sub>2</sub> fold change of differentially expressed lncRNAs that were exclusively expressed in the palmitic acid compared with control group.

name	Regulation	log <sub>2</sub> fold change	<i>P</i> value
TCONS_00088788	Down	-1.332	1.03E-86
TCONS_00233737	Down	-1.448	1.59E-46
TCONS_00088299	Ups	1.540	1.48E-20
TCONS_00184470	Down	-1.512	2.64E-19
TCONS_00038546	Ups	1.172	1.70E-18
TCONS_00009134	Ups	1.080	9.36E-15
TCONS_00184468	Down	-1.755	2.23E-12
TCONS_00088303	Ups	1.641	1.66E-11
TCONS_00195490	Ups	1.395	3.95E-11
TCONS_00139241	Ups	2.208	4.84E-10
TCONS_00119905	Ups	2.697	7.69E-10
TCONS_00068951	Ups	1.274	3.08E-09
TCONS_00233736	Down	-1.391	3.22E-09
TCONS_00184465	Down	-2.134	1.52E-08
TCONS_00088298	Ups	1.152	1.85E-08
TCONS_00147061	Down	-2.362	5.54E-08
TCONS_00239170	Down	-1.748	1.21E-07
TCONS_00216021	Down	-2.326	1.31E-07
TCONS_00167285	Down	-1.996	1.65E-07
TCONS_00089983	Ups	1.093	1.96E-07
TCONS_00279975	Ups	2.262	2.85E-07
TCONS_00102704	Ups	2.031	4.12E-07
TCONS_00139249	Ups	2.194	6.35E-07
TCONS_00132357	Ups	1.913	8.57E-07
TCONS_00077761	Ups	1.229	8.97E-07
TCONS_00251038	Down	-2.123	1.36E-06

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TCONS_00233223	Ups	1.230	1.60E-06
TCONS_00161572	Down	-1.988	5.68E-06
TCONS_00195486	Ups	1.422	6.51E-06
TCONS_00185019	Down	-1.072	7.83E-06
TCONS_00078368	Ups	1.114	1.08E-05
TCONS_00034820	Ups	1.866	1.88E-05
TCONS_00260772	Ups	1.862	2.03E-05
TCONS_00251541	Ups	1.846	2.78E-05
TCONS_00248344	Down	-1.620	3.17E-05
TCONS_00004655	Ups	1.799	4.15E-05
TCONS_00006080	Down	-1.186	4.52E-05
TCONS_00009803	Ups	1.776	5.55E-05
TCONS_00140517	Ups	1.530	5.98E-05
TCONS_00176551	Ups	1.137	8.62E-05
TCONS_00281906	Ups	1.400	1.32E-04
TCONS_00260686	Down	-1.035	1.45E-04
TCONS_00003674	Ups	1.644	1.52E-04
TCONS_00002586	Ups	1.005	1.59E-04
TCONS_00132360	Ups	1.493	1.60E-04
TCONS_00045226	Ups	1.384	1.69E-04
TCONS_00150272	Ups	1.138	1.96E-04
TCONS_00201964	Ups	1.523	2.12 E-04
TCONS_00034821	Down	-1.043	2.44 E-04
TCONS_00026344	Ups	1.599	2.71 E-04
TCONS_00027006	Ups	1.071	3.27E-04
TCONS_00203893	Down	-1.186	3.59E-04
TCONS_00177728	Ups	1.469	3.91E-04
TCONS_00102705	Ups	1.550	4.36E-04
TCONS_00068931	Down	-1.019	4.44E-04

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TCONS_00057680	Ups	1.533	5.03E-04
TCONS_00200419	Ups	1.442	5.37E-04
TCONS_00216016	Ups	1.515	5.70E-04
TCONS_00099319	Down	-1.252	6.11E-04
TCONS_00006281	Ups	1.115	7.06E-04
TCONS_00121322	Ups	1.404	7.10E-04
TCONS_00184054	Down	-1.047	7.67E-04
TCONS_00088531	Ups	1.288	8.41E-04
TCONS_00132387	Ups	1.463	8.78E-04
TCONS_00065563	Ups	1.387	1.12E-03
TCONS_00233739	Down	-1.167	1.29E-03
TCONS_00277357	Down	-1.094	1.45E-03
TCONS_00043156	Down	-1.218	1.51E-03
TCONS_00088300	Ups	1.349	1.53E-03
TCONS_00144481	Down	-1.085	1.54E-03
TCONS_00281912	Ups	1.034	1.63E-03
TCONS_00098803	Ups	1.376	1.67E-03
TCONS_00078337	Ups	1.354	1.99E-03
TCONS_00045330	Ups	1.332	2.04E-03
TCONS_00200446	Down	-1.265	2.09E-03
TCONS_00142000	Down	-1.268	2.19E-03
TCONS_00008230	Ups	1.072	2.25E-03
TCONS_00149049	Ups	1.344	2.29E-03
TCONS_00266371	Down	-1.338	2.37E-03
TCONS_00149141	Ups	1.198	2.49E-03
TCONS_00129208	Ups	1.331	2.54E-03

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**Supplementary Table S9** The log<sub>2</sub> fold change of differentially expressed lncRNAs  
in the stearic acid group compared with palmitic acid group.

name	Regulation	log <sub>2</sub> fold change	<i>P</i> value
TCONS_00088523	Down	-2.749	1.72E-11
TCONS_00142000	Ups	2.128	2.08E-07
TCONS_00230836	Ups	1.015	5.45E-07
TCONS_00145596	Down	-1.995	1.13E-06
TCONS_00039055	Down	-1.807	2.96E-06
TCONS_00089573	Down	-1.733	1.68E-05
TCONS_00039236	Ups	1.708	2.06E-05
TCONS_00252600	Down	-1.375	3.14E-05
TCONS_00247138	Ups	1.634	4.35E-05
TCONS_00139202	Ups	1.592	5.99E-05
TCONS_00034820	Down	-1.599	6.24E-05
TCONS_00167853	Ups	1.622	6.65E-05
TCONS_00230830	Down	-1.179	8.27E-05
TCONS_00201321	Down	-1.549	1.04E-04
TCONS_00077866	Ups	1.586	1.07E-04
TCONS_00281901	Down	-1.521	2.05E-04
TCONS_00002278	Down	-1.471	2.07E-04

**Supplementary Table S10** The composition of fasting serum NEFAs profile in  
normal and HSD mice at 22 weeks

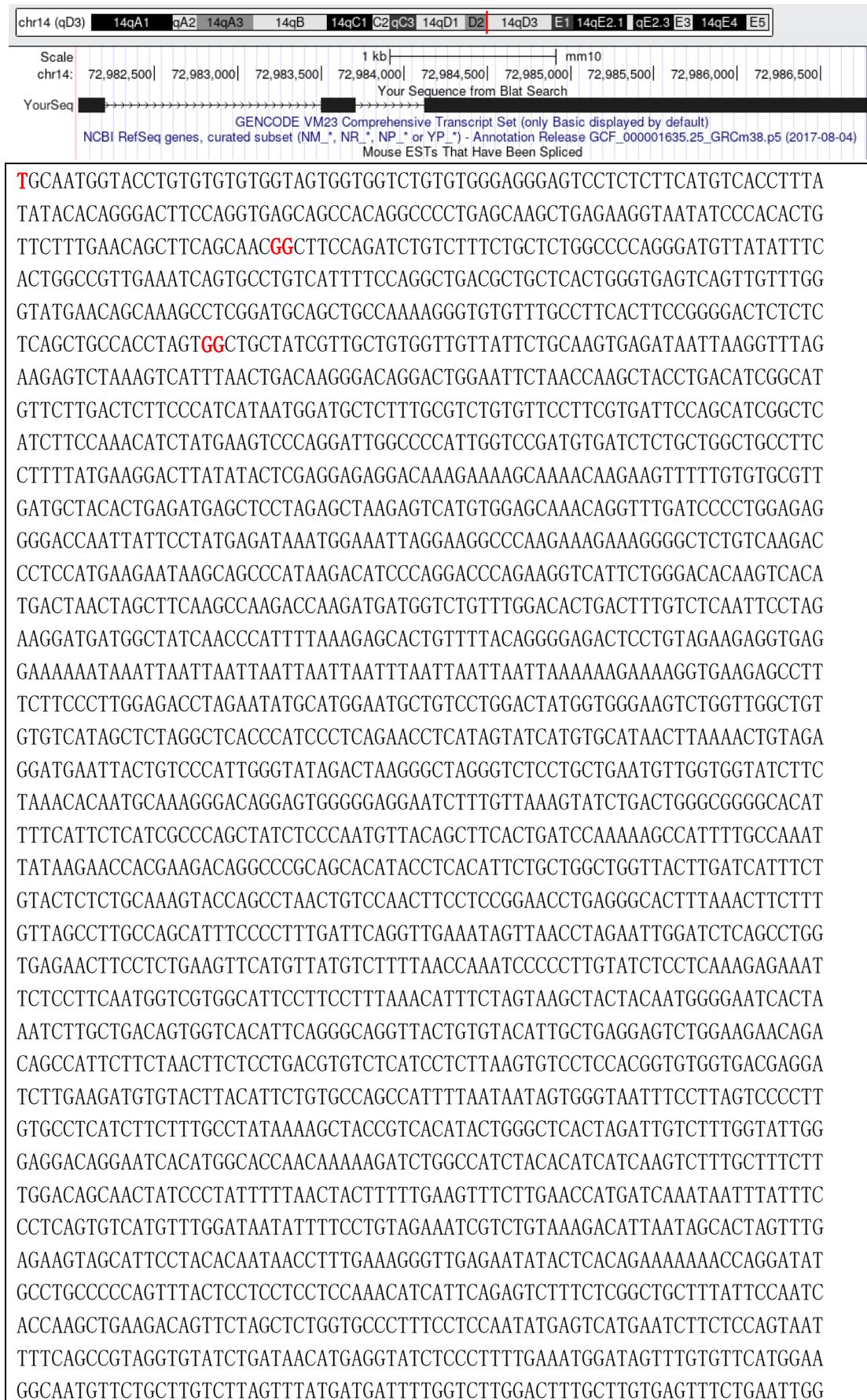
FFAs (μg/ml)	Normal mice	HSD mice
C14:0, MA (Myristic acid)	4.151±0.508	7.237±0.654 <sup>***</sup>
C16:0, PA (Palmitic acid)	138.903±22.389	261.133±25.807 <sup>***</sup>
C16: 1, PLA (Palmitoleic acid)	9.266±1.207	4.922±1.622 <sup>**</sup>
C18: 0, SA (Stearic acid)	63.812±7.864	178.928±27.844 <sup>***</sup>
C18: 1, OA (Oleic acid)	58.269±14.821	110.339±20.038 <sup>***</sup>
C18: 2, LA (Linoleic acid)	115.355±11.066	138.366±13.582 <sup>*</sup>
γ-C18:3, γ-LNA (γ-Linolenic acid)	4.707±0.236	8.267±1.585 <sup>**</sup>
C18: 3, LNA (Linolenic acid)	82.182±13.182	40.567±15.673 <sup>**</sup>
C20: 2, EDA (Eicosadienoic acid)	6.601±0.774	7.178±0.781
C20: 4, AA (Arachidonic acid)	80.679±10.041	110.817±28.302 <sup>***</sup>
C20: 5, EPA (Eicosapentaenoic acid)	6.172±1.111	2.681±0.669 <sup>***</sup>
C22: 5, DPA (Docosapentaenoic acid)	1.673±0.623	1.675±0.828
C22: 6, DHA (Docosaheptaenoic acid)	151.763±15.323	150.278±13.046

Saturated fatty acids	206.867±26.340	447.298±38.126 <sup>***</sup>
Total fatty acids	608.180±47.674	897.074±56.754 <sup>***</sup>
Percentage of SA (%)	10.484±0.873	19.998±3.231 <sup>***</sup>
Percentage of PA (%)	22.796±2.821	29.113±2.228 <sup>***</sup>
PA/SA ratio	2.193:1	1.489:1 <sup>*</sup>

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Values are means ± SD. *n* = 35 mice in each group. <sup>\*</sup>*P*<0.05, <sup>\*\*</sup>*P*<0.01, <sup>\*\*\*</sup>*P*<0.001, compared with the value of normal mice group. **HSD**, high stearic acid diet.

**Supplementary Table S11** Full sequence of lnc866



GTCTGAGTAATTGTCTGCCTTTGTGTCTTTTAATACATGCCACAACTCGGGGAAAAAGAAAACCACC  
TGACACAGTAATCATGGGCTCATCTTCTCTCATCAGGAACAGCTTGCACAGTAATAAAGTTCTGT  
TGCTTTAGTCATTTGCTTGTGTCAGAAGAGCCAAAAACGTATTGGACTGGAGGAAGAGCTTGTTGCCT  
TAGAAACAAAAGTCACTCCTTCCAAACCTAATAAACTCTGGCTGTTGTAGTCTTCATGGGTGTTACACT  
TTCGTCTTCATTTTCCAAGGTCTGATACAGTGATATCATGGGGAGATGAGAATCTAATATGAAATATTT  
CAGTTCATCTCTACTT**T**

Red font represents the start and end base of each exon of lnc866.

**Supplementary Table S12** Characteristic and serum analysis of normolipidemic and hyperlipidemic participants

Characteristics	Normolipidemic (n=13)	Hyperlipidemic (n=9)
Age (years)	53.08±9.71	56.44±6.06
Sex (female/male)	8/5	4/5
BMI (kg/m <sup>2</sup> )	22.10±2.10	25.17±2.06
Glucose (mmol/L)	5.07±0.82	6.09±0.97
TC (mmol/L)	4.46±1.44	6.77±1.07**
TG (mmol/L)	1.29±0.22	2.94±0.60**
HDL-C (mmol/L)	1.34±0.46	0.78±0.24*
LDL-C (mmol/L)	2.36±0.83	4.07±0.66**

\* $P<0.05$ ; \*\* $P<0.01$ , compared with the value of normolipidemic participants.

**Supplementary Table S13** Body weight and serum analysis in normal and HSD mice  
at 22 weeks.

Characteristics	shNC-V+C	shNC-V+HSD	sh866-V+HSD	sh866-V+C
Body weight (g)	30.646±4.567	47.415±1.386 <sup>***</sup>	47.279±2.523 <sup>***</sup>	30.620±2.219 <sup>^^</sup>
Glucose (mmol/l)	4.840±1.056	10.239±2.24 <sup>**</sup>	7.385±0.63 <sup>*^</sup>	4.900±0.533 <sup>^^</sup>
TC (mmol/l)	2.963±0.143	6.014±0.679 <sup>***</sup>	6.000±0.657 <sup>***</sup>	2.657±0.506 <sup>^^</sup>
TG (mmol/l)	0.786±0.122	1.755±0.090 <sup>**</sup>	1.704±0.120 <sup>**</sup>	0.742±0.099 <sup>^^</sup>
HDL-C (mmol/l)	2.403±0.125	4.281±0.380 <sup>**</sup>	4.560±0.489 <sup>**</sup>	2.195±0.457 <sup>^^</sup>
LDL-C (mmol/l)	0.218±0.033	1.180±0.305 <sup>**</sup>	1.210±0.233 <sup>**</sup>	0.154±0.017 <sup>^^</sup>
Insulin (pmol/l)	106.683±0.316	298.09±0.151 <sup>*</sup>	208.569±0.039 <sup>*^</sup>	98.476±0.012 <sup>^^</sup>
Food intake (g/d)	3.928±0.459	3.651±0.923	3.669±0.824	3.861±0.522

After feeding for 22 weeks, the food intake, body weight, fasting blood glucose, plasma insulin levels, TC, TG, LDL-C and HDL-C levels were measured in C57BL/6J mice. All the parameters were detected and calculated in the fasting state. Displayed mode was mean ± SD, n=35 mice per group. \* $P<0.05$ ; \*\* $P<0.01$ , \*\*\* $P<0.001$ , compared with the value of shNC-V+C mice. ^ $P<0.05$ ; ^^ $P<0.01$ , ^^ $P<0.001$ , compared with the value of shNC-V+HSD mice. **TC**, total cholesterol; **TG**, triacylglycerol; **HDL-C**, high-density lipoprotein cholesterol; **LDL-C**, low-density lipoprotein cholesterol; **sh866-V+C**, 6 weeks after sh866-V injection, mice were fed with chow diet. **shNC-V**, the negative control shRNA engineered into the AAV9 vector; **sh866-V**, AAV9 vector carrying shRNA-lnc866; C, chow diet; **HSD**, high stearic acid diet; **shNC-V+C**, 6 weeks after shNC-V injection, mice were fed

with chow diet; **shNC-V+HSD**, 6 weeks after shNC-V injection, mice were fed with HSD; **sh866-V+HSD**, 6 weeks after sh866-V injection, mice were fed with HSD.

**Supplementary Table S14** The negative relationship between miR-297b-5p and 31

mRNAs in co-expression network			
miRNA	mRNA	PCC	<i>P</i> value
mmu-miR-297b-5p	ENSMUST000000022531	-0.995	3.69E-05
mmu-miR-297b-5p	ENSMUST000000050785	-0.995	4.47E-05
mmu-miR-297b-5p	ENSMUST000000074898	-0.992	1.01E-04
mmu-miR-297b-5p	ENSMUST000000020190	-0.992	1.02E-04
mmu-miR-297b-5p	ENSMUST000000159720	-0.991	1.08E-04
mmu-miR-297b-5p	ENSMUST000000006956	-0.986	3.00E-04
mmu-miR-297b-5p	ENSMUST000000181286	-0.985	3.34E-04
mmu-miR-297b-5p	ENSMUST000000036188	-0.984	3.79E-04
mmu-miR-297b-5p	ENSMUST000000181169	-0.983	4.48E-04
mmu-miR-297b-5p	ENSMUST000000068830	-0.982	4.60E-04
mmu-miR-297b-5p	ENSMUST000000166854	-0.979	6.58E-04
mmu-miR-297b-5p	ENSMUST000000086399	-0.978	7.04E-04
mmu-miR-297b-5p	ENSMUST000000023994	-0.977	8.13E-04
mmu-miR-297b-5p	ENSMUST000000027748	-0.975	9.10E-04
mmu-miR-297b-5p	ENSMUST000000131456	-0.968	1.50E-03
mmu-miR-297b-5p	ENSMUST000000067495	-0.966	1.69E-03
mmu-miR-297b-5p	ENSMUST000000140373	-0.965	1.78E-03
mmu-miR-297b-5p	ENSMUST000000102745	-0.954	3.16E-03
mmu-miR-297b-5p	ENSMUST000000040750	-0.949	3.91E-03
mmu-miR-297b-5p	ENSMUST000000171621	-0.947	4.10E-03
mmu-miR-297b-5p	ENSMUST000000031565	-0.944	4.66E-03
mmu-miR-297b-5p	ENSMUST000000101094	-0.937	5.86E-03
mmu-miR-297b-5p	ENSMUST000000096232	-0.937	5.87E-03
mmu-miR-297b-5p	ENSMUST000000147988	-0.929	7.46E-03
mmu-miR-297b-5p	ENSMUST000000094760	-0.929	7.46E-03
mmu-miR-297b-5p	ENSMUST000000106373	-0.926	7.98E-03

mmu-miR-297b-5p	ENSMUST000000110323	-0.924	8.47E-03
mmu-miR-297b-5p	ENSMUST000000149874	-0.908	1.21E-02
mmu-miR-297b-5p	ENSMUST000000194644	-0.902	1.38E-02
mmu-miR-297b-5p	ENSMUST000000135828	-0.896	1.57E-02
mmu-miR-297b-5p	ENSMUST000000143213	-0.887	1.84E-02

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PCC, Pearson correlation coefficients

**Supplementary Table S15** The negative relationship between TCONS\_00077866  
and mmu-miR-297b-5p in co-expression network

miRNA	mRNA	PCC	<i>P</i> value
mmu-miR-297b-5p	TCONS_00077866	-0.964	1.93E-03

**PCC**, Pearson correlation coefficients

**Supplementary Table S16** The positive relationship between lnc866 and 31 mRNAs  
in co-expression network

lncRNA	mRNA	PCC	<i>P</i> value
TCONS_00077866	ENSMUST00000022531	0.967	1.46E-03
TCONS_00077866	ENSMUST00000050785	0.967	1.67E-03
TCONS_00077866	ENSMUST00000074898	0.977	8.04E-04
TCONS_00077866	ENSMUST00000020190	0.965	1.82E-03
TCONS_00077866	ENSMUST00000159720	0.985	3.48E-04
TCONS_00077866	ENSMUST00000006956	0.943	4.85E-03
TCONS_00077866	ENSMUST00000181286	0.924	8.47E-03
TCONS_00077866	ENSMUST00000036188	0.983	4.14E-04
TCONS_00077866	ENSMUST00000181169	0.929	7.31E-03
TCONS_00077866	ENSMUST00000068830	0.971	1.23E-03
TCONS_00077866	ENSMUST00000166854	0.974	1.01E-03
TCONS_00077866	ENSMUST00000086399	0.969	1.47E-03
TCONS_00077866	ENSMUST00000023994	0.998	4.19E-06
TCONS_00077866	ENSMUST00000027748	0.998	4.32E-06
TCONS_00077866	ENSMUST00000131456	0.993	7.50E-05
TCONS_00077866	ENSMUST00000067495	0.865	2.61E-02
TCONS_00077866	ENSMUST00000140373	0.880	2.09E-02
TCONS_00077866	ENSMUST00000102745	0.943	4.77E-03
TCONS_00077866	ENSMUST00000040750	0.992	9.84E-05
TCONS_00077866	ENSMUST00000171621	0.848	3.30E-02
TCONS_00077866	ENSMUST00000101094	0.894	1.63E-02
TCONS_00077866	ENSMUST00000096232	0.994	5.14E-05
TCONS_00077866	ENSMUST00000147988	0.901	1.42E-02
TCONS_00077866	ENSMUST00000094760	0.983	4.41E-04
TCONS_00077866	ENSMUST00000106373	0.992	8.79E-05
TCONS_00077866	ENSMUST00000110323	0.948	3.94E-03

TCONS_00077866	ENSMUST00000149874	0.864	2.63E-02
TCONS_00077866	ENSMUST00000194644	0.935	6.29E-03
TCONS_00077866	ENSMUST00000031565	0.988	2.12E-04
TCONS_00077866	ENSMUST00000135828	0.913	1.11E-02
TCONS_00077866	ENSMUST00000143213	0.959	2.49E-03

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Inc866: TCONS\_00077866; PCC, Pearson correlation coefficients.

**Supplementary Table S17** RNA-seq showing the log<sub>2</sub> fold change of differential expression of 31 mRNAs in co-expression network in stearic acid-treated  $\beta$ -TC6 cells

Ensemble ID	Gene name	Regulation	log <sub>2</sub> fold change	<i>P</i> value
ENSMUST00000022531	large tumor suppressor 2 (Lats2)	Up	2.445	1.57E-07
ENSMUST00000050785	lipocalin 2 (Lcn2)	Up	5.881	4.66E-53
ENSMUST00000074898	Haptoglobin (Hp)	Up	6.940	7.85E-126
ENSMUST00000020190	vanin 3 (Vnn3)	Up	3.151	9.46E-15
ENSMUST00000159720	alpha-kinase 1(Alpk1)	Up	4.294	8.75E-25
ENSMUST00000006956	serum amyloid A 3 (Saa3)	Up	6.127	5.32E-112
ENSMUST00000181286	Gm16685	Up	2.886	8.01E-26
ENSMUST00000036188	zinc finger CCCH type containing 12A (Zc3h12a)	Up	2.420	1.55E-22
ENSMUST00000181169	Not in the database	Up	3.502	3.23E-26
ENSMUST00000068830	cannabinoid receptor 2 (macrophage) (Cnr2)	Up	2.178	1.95E-06
ENSMUST00000166854	transmembrane protein 39a (Tmem39a)	Up	2.584	2.69E-08
ENSMUST00000086399	intercellular adhesion molecule 1 (Icam1)	Up	6.190	3.98E-73
ENSMUST00000023994	serine (or cysteine) peptidase inhibitor, clade G, member 1(Serping1)	Up	4.044	1.64E-23
ENSMUST00000027748	regulator of G-protein signaling 16 (Rgs16)	Up	3.062	4.60E-21
ENSMUST00000131456	serine (or cysteine) peptidase inhibitor, clade	Up	4.205	1.09E-24

	G, member 1 (Serping1)				
ENSMUST00000067495	wingless-type MMTV integration site family, member 11 (Wnt11)	Up	1.460	8.79E-06	
ENSMUST00000140373	sodium channel and clathrin linker 1 (Sc1t1)	Up	3.528	3.95E-15	
ENSMUST00000102745	tumor necrosis factor, alpha-induced protein 2 (Tnfaip2)	Up	3.703	1.44E-16	
ENSMUST00000040750	leukemia inhibitory factor (Lif)	Up	4.082	6.94E-24	
ENSMUST00000171621	TRAF-interacting protein with forkhead-associated domain (Tifa)	Up	6.642	2.47E-67	
ENSMUST00000031565	fascin actin-bundling protein 1 (Fscn1)	Up	2.876	1.59E-13	
ENSMUST00000101094	OTU domain, ubiquitin aldehyde binding 2 (Otub2)	Up	3.835	7.10E-20	
ENSMUST00000096232	CCAAT/enhancer binding protein (C/EBP), delta (Cebpd)	Up	3.551	9.28E-36	
ENSMUST00000147988	cilia and flagella associated protein 44 (Cfap44)	Up	1.888	4.65E-05	
ENSMUST00000094760	SH3 domain containing 21 (Sh3d21)	Up	2.589	2.68E-08	
ENSMUST00000106373	sulfotransferase family 1A, phenol-preferring,	Up	2.478	1.05E-07	

	member 1 (Sult1a1)			
ENSMUST00000110323	CDK5 regulatory subunit associated protein 1-like 1 (Cdkal1)	Up	2.288	8.94E-07
ENSMUST00000149874	CASP8 and FADD-like apoptosis regulator (Cflar)	Up	1.943	2.81E-05
ENSMUST00000194644	Gm37628	Up	1.050	4.63E-03
ENSMUST00000135828	zinc finger protein 783 (Zfp783)	Up	1.491	1.20E-03
ENSMUST00000143213	BTB (POZ) domain containing 19 (Btbd19)	Up	2.747	3.56E-09

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