SUPPLEMENTARY DATA

Supplementary Figures

Supplementary Figure S1-The map of pHBAAV-U6-MCS-CMV-EGFP vector
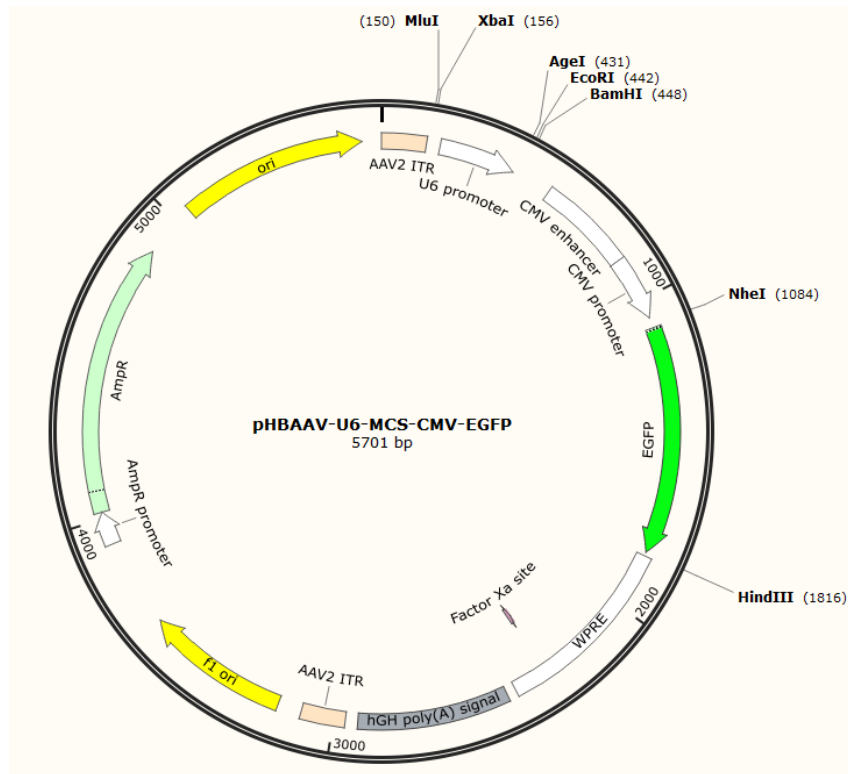
Supplementary Figure S2 Sequence alignment of qPCR products in metabolic tissues with full length of lnc866 after Sanger sequencing. A-C: Upper panel, the sequence of lnc866 in islets, skeletal muscle and perirenal adipose tissue; lower panel, sequence alignment. D-F: Sanger sequence results with no matching sequences of lnc866 in liver, peritesticular adipose tissue, and brown adipose tissue.
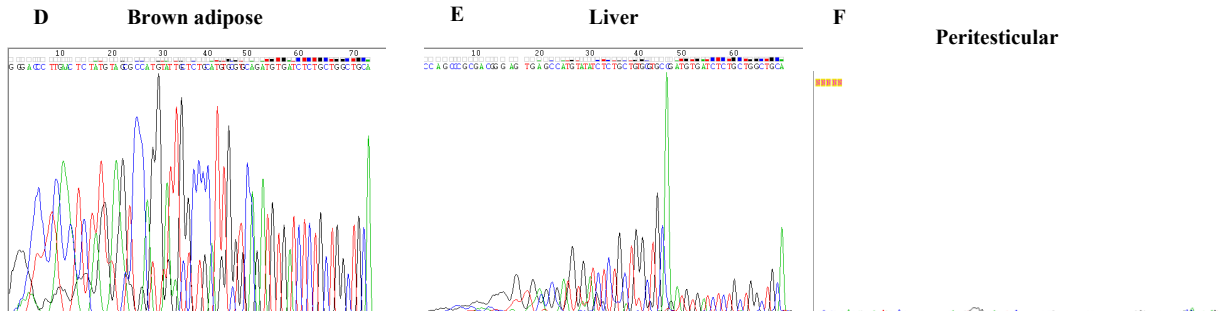
Supplementary Figure S3-Identification of human homologous sequences of lnc866. (A) Searching for human homologous sequences using NCBI-BLAST. (B) Upper panel, Sanger sequencing results of qPCR product of human islets; lower panel, sequence alignment of qPCR products with full length of AL137118.20.

A

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Human DNA sequence from clone RP11-108P5 on chromosome 13q14.12-21.1, com...	Homo sapiens	141	263	39%	7e-28	65.32%	162446	AL137118.20

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

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              |     |||||||||||||||| |  || ||||| | || ||| ||| ||||| ||||
Sbjct  144390  CCCCCTAACCATGATCAAATCACCATTCATTTCTCCCA-TGTCTTATTTAGATAAGATTT   144332

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Sbjct  144331  GCTTC-AGAAATGAATTGCCAAGACATTCACAATGTTCATTTGGGAAGTGGCATTTCTTC   144273

Query  2328   ACAATAACCTTTGAAAGGGTTGAGAAT----ATACTCAC-AGaaaaaaaCCAGGATATGC   2382
              ||| | ||    |||  |||||||    |||   | |   || |   ||||||||| |
Sbjct  144272  ACAGTGACTTCCCCAAGACTTGAGAAAGCCCATATGGAGTAGGAAAGACTCTGGATACAC   144213

Query  2383   CTGCCCCCAGTTTACTCCTCCTCCTCCAAACATCATTCAGAGTCTTTCTCGGCTGCTTTA   2442
              | |  ||||| | | ||||  | | || |   |  || || |    |  |||| | |
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Sbjct  144095  GTTCTGAATTCTCTCGAGTAGGCTCAAGTAATAGGTATAGTAAATTTATTTTCAATAACT   144036

Query  2558   CCCTTTTGAAATGGATAGTTTGTGTTCATGGAAGGCAATGTTCTGCTT-GTCTTAGTTTA   2616
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Sbjct  143699  ACTTGTCTTATTCTTCATGGATATTACATTTTCATCTTTGTTTTTCTGAATTCTGACATA   143640

Query  2971   GT   2972
              ||
Sbjct  143639  GT   143638
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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

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Query  433     TCATTTAACTGACAAGGGACAGGACTGGAATTCTAACCAAG--CTACCTGACATCGGCA-  489
               ||  ||  ||    ||| | |||  ||| ||||| || || ||  |||||||| | |
Sbjct  146602  ACACTTAGCTACTAAGTGGCAGAACTAGAATTGTAGCCCAGGCCTGTCTGACATCAGTAA  146543

Query  490     -TGTTCTTGA  498
                |||||||||
Sbjct  146542  CTGTTCTTGA  146533
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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

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Query  1590    GAGGG-CACTTTAAACTTCTTTGTTAGCCTTGCCAGCATTTCCCCTTTGATTCAGGTTGA  1648
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Query  1649    AATAGTTAACCTAGA----ATTGGATCTCAGCCTGGTGAGAACTTCCTCTGAAGTTCATG  1704
               ||| ||  |  ||| ||   || |||||||||||| || |    |||| | | ||| |
Sbjct  145255  AATGATTGTTCCAGAGCTTCCTGAATCTCAGCCTGTTG----TTTCTTCAGTA-TTC-TG  145202

Query  1705    TTATGTCTTTTAACCAAATC-CCCCT---------TGTATCTCCTCAAAGAGAAATTCTC  1754
               || || |  ||||| ||| || || ||        | | |||||||| ||| ||||||||
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Query  1755    CTTCAATGGTCGTGGCATTCCTTCCTTTA  1783
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Sbjct  145143  CCTCA---GTGATTGCATGCCTTTCTTTA  145118
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B
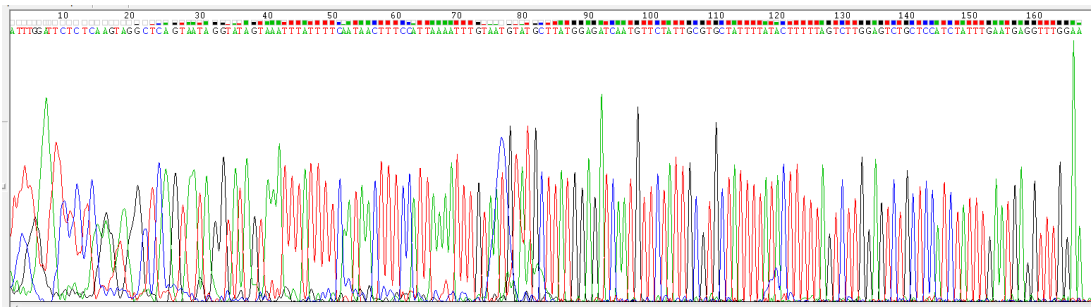
⬇ Download ∨   GenBank Graphics

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
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Sbjct  144083  GAGAATTCAGAACTAATATTAGAGGAAGAAATGGGCACA  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 μm. **shNC-V**, the negative control shRNA engineered into the AAV9 vector; **sh866-V**, AAV9 vector carrying shRNA-lnc866. Representative image of 3 independent experiments.


shNC-V   sh866-V
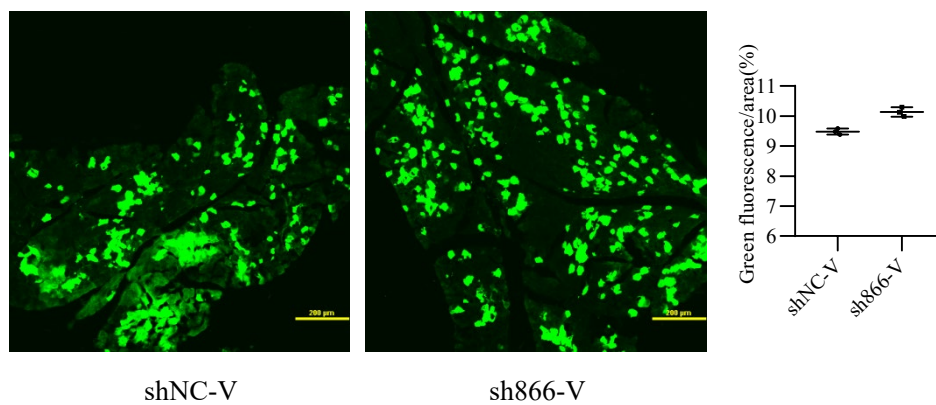
Supplementary Figure S5-Effect of AL137118.20 Smart Silencer on stearic acid-impaired GSIS. $^{*}P\text{<}0.05$, $^{**}P\text{<}0.01$ *versus* the ss-NC group; $^{\wedge}P\text{<}0.05$, $^{\wedge\wedge}P\text{<}0.01$ *versus* the SA+ss-AL group. **SA**, stearic acid; **ss-AL**, Smart Silencer for AL137118.20; **ss-NC**, negative control of ss-AL. $n = 5$ samples from normolipidemic individuals.
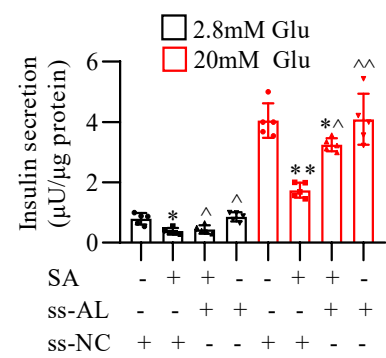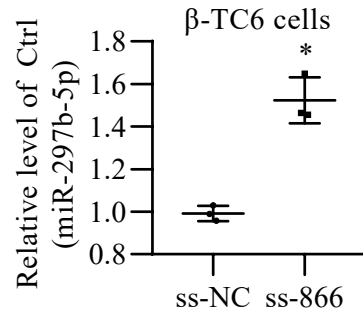
Supplementary Figure S6-Inhibitoty efficiency of Smart Silencer for AL137118.20 in the absence and presence of stearic acid. $^{*}P<0.05$, $^{**}P<0.01$ *versus* the ss-NC group; $^{\wedge}P<0.05$, $^{\wedge\wedge}P<0.01$ *versus* the SA+ss-AL group. **SA**, stearic acid; **ss-AL**, Smart Silencer for AL137118.20; **ss-NC**, negative control of ss-AL. $n = 5$ samples from normolipidemic individuals.
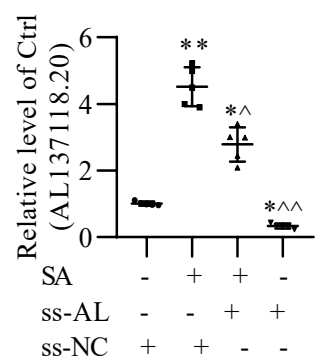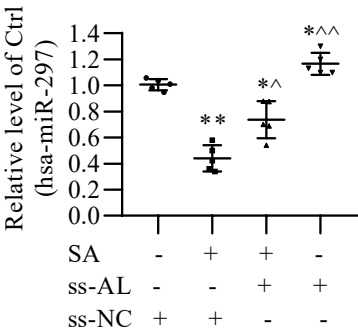
Supplementary Figure S7-The co-expression network of lnc866, miR-297b-5p, and relevant mRNAs. Yellow circle: lnc866; pink circle: miR-297b-5p; green circle: mRNAs; black line: negative relationship.
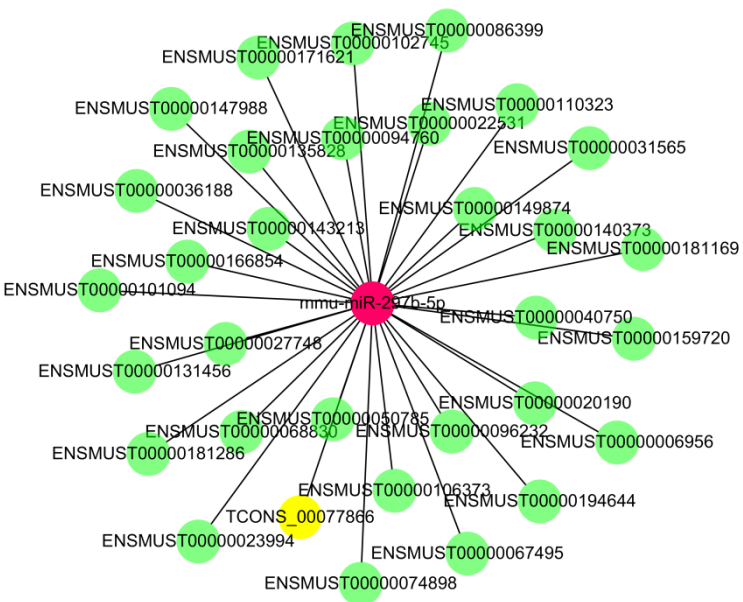
Supplementary Figure S8-Inhibitory effect of Smart Silencer for lnc866 on miR-297b-5p expression in β-TC6 cell. $^{*}P$＜0.05 *versus* the ss-NC group. **ss-866**, Smart Silencer for lnc866; **ss-NC**, the negative control of Smart Silencer. n = 3 independent cell cultures per group.
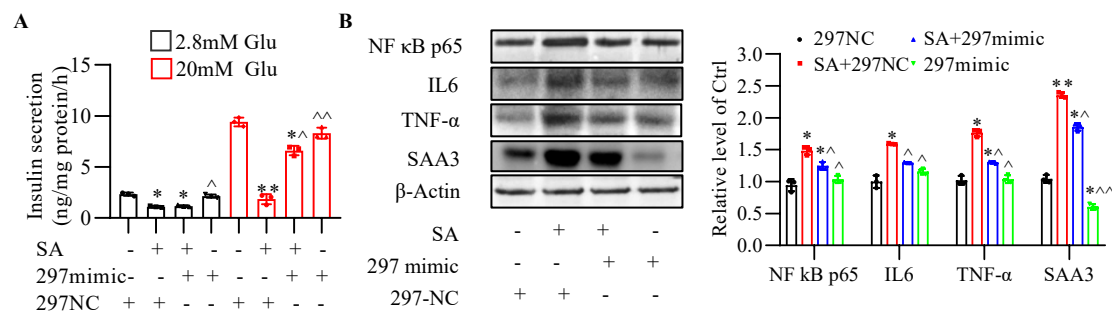
Supplementary Figure S9-Change in the expression of hsa-miR-297 after knockdown of AL137118.20 in the presence of stearic acid. [*]$P<0.05$, [**]$P<0.01$ *versus* the ss-NC group; [^]$P<0.05$, [^^]$P<0.01$ *versus* the SA+ss-AL group. **SA**, stearic acid; **ss-AL**, Smart Silencer for AL137118.20; **ss-NC**, 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 β-TC6 cells without stearic acid treatment. (*A*) miR-297b-5p expression after the transfection of miR-297b-5p mimic or AMO-297b-5p in β-TC6 cells. (*B*) Insulin concentration after the transfection of a miR-297b-5p mimic or AMO-297b-5p in β-TC6 cells. (*C*) Western blots showing the protein expression of NF κB p65, IL6, and TNF-α following the transfection of a miR-297b-5p mimic or AMO-297b-5p in β-TC6 cells. $^*P<0.05$, $^{**}P<0.01$ *versus* the AMO-NC group; $^\wedge P<0.05$, $^{\wedge\wedge}P<0.01$ *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.
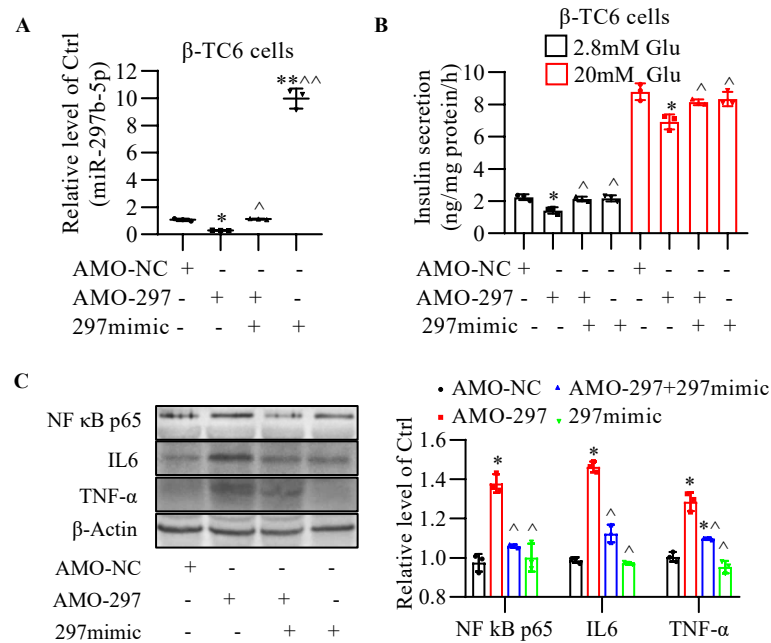
Supplementary Figure S11-Role of miR-297b-5p in stearic acid treated mouse islets. (*A*) Protection of the stearic acid–impaired glucose-stimulated insulin secretion (GSIS) after the transfection of a miR-297b-5p mimic. (*B*) Western blot showing the effects of miR-297b-5p on the expressions of NF κB p65, IL6, TNF-α and SAA3 following stearic acid treatment. $^*P<0.05$, $^{**}P<0.01$ *versus* the 297NC group; $^\wedge P<0.05$, $^{\wedge\wedge}P<0.01$ *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.
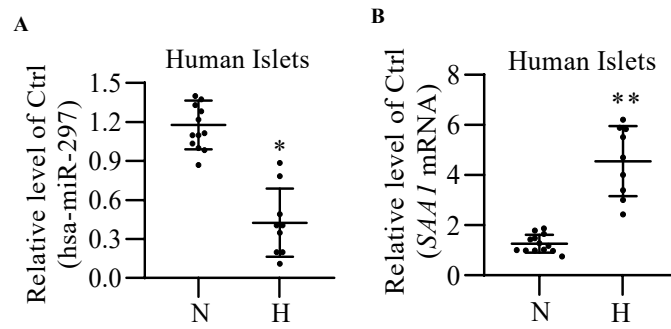
Supplementary Figure S13-Involevement of SAA3 in stearic acid treated mouse islets. (*A*) Restoration of the stearic acid–impaired glucose-stimulated insulin secretion (GSIS) after the knocking down of *Saa3*. (*B*) Effects of si-*Saa3* on NF κB p65, IL6, TNF-α and SAA3 protein expression in the presence 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.
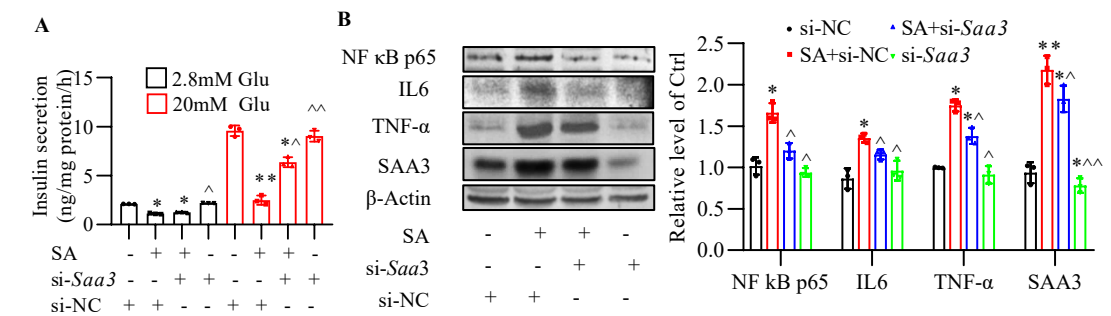
Supplementary Figure S14-Sequence alignment of human *SAA1* in islets with mouse *Saa3*. (A) Sanger sequencing results of *SAA1* in human islets. (B) Upper panel, searching for the mouse homologous sequence of qPCR product of human *SAA1* in islets; lower panel, sequence alignment of qPCR product of human *SAA1* in islets with mouse *Saa3*.

A

B

Supplementary Tables

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

name	sequence
Promoter of U6	GAGGGCCTATTTCCCATGATTCCTTCATATTTGCA TATACGATACAAGGCTGTTAGAGAGATAATTGGA ATTAATTTGACTGTAAACACAAAGATATTAGTAC AAAATACGTGACGTAGAAAGTAATAATTTCTTGG GTAGTTTGCAGTTTTAAAATTATGTTTTAAAATG GACTATCATATGCTTACCGTAACTTGAAAGTATTT CGATTTCTTGGCTTTATATATCTTGTGGAAAGGA C
EGFP	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGG GGTGGTGCCCATCCTGGTCGAGCTGGACGGCGA CGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGA CCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCCACCCTCGTGACCACCCTGA CCTACGGCGTGCAGTGCTTCAGCCGCTACCCCG ACCACATGAAGCAGCACGACTTCTTCAAGTCCG CCATGCCCGAAGGCTACGTCCAGGAGCGCACCA TCTTCTTCAAGGACGACGGCAACTACAAGACCC GCGCCGAGGTGAAGTTCGAGGGCGACACCCTG GTGAACCGCATCGAGCTGAAGGGCATCGACTTC AAGGAGGACGGCAACATCCTGGGGCACAAGCT GGAGTACAACTACAACAGCCACAACGTCTATAT CATGGCCGACAAGCAGAAGAACGGCATCAAGG TGAACTTCAAGATCCGCCACAACATCGAGGACG GCAGCGTGCAGCTCGCCGACCACTACCAGCAGA ACACCCCCATCGGCGACGGCCCCGTGCTGCTGC

	CCGACAACCACTACCTGAGCACCCAGTCCGCCC
	TGAGCAAAGACCCCAACGAGAAGCGCGATCAC
	ATGGTCCTTAAGGAGTTCGTGACCGCCGCCGGG
	ATCACTCTCGGCATGGACGAGCTGTACAAGTAA
siRNA for shNC-V	TTCTCCGAACGTGTCACGTAA
shRNA for shNC-V	Top strand:
	GATCCGTTCTCCGAACGTGTCACGTAATTCAAG
	AGATTACGTGACACGTTCGGAGAATTTTTTC
	Bottom strand:
	AATTGAAAAAATTCTCCGAACGTGTCACGTAAT
	CTCTTGAATTACGTGACACGTTCGGAGAACG
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*10^12 µg/mL
viral titer for shNC-V	3.5*10^12 µg/mL

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 lnc866

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-*Saa3*	GGAGTTGACAGCCAAAGAT
siRNA-*Rela*	GAAGCACAGATACCACCAA
siRNA-*Il6*	GGACTGATGCTGGTGACAA
siRNA-*Tnfα*	GACAACCAACTAGTGGTGC

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

Gene		sequences (5' to 3')
TCONS_00077866-1	Forward	TGTTCCTTCGTGATTCCAGCATCG
(mouse)	Reverse	GCAGCCAGCAGAGATCACATCG
TCONS_00077866-2	Forward	TCAGCAACGGCTTCCAGATC
(mouse)	Reverse	AACGATAGCAGCCACTAGGTGG
AL137118.20	Forward	TCCAAACCTCATTCAAATAG
(human)	Reverse	TGTGCCCATTTCTTCCTC
TCONS_00089573	Forward	ATCAACTCAGCACACTGGAGCATG
(mouse)	Reverse	CAGAAGCGACAGGCATCAGCAG
TCONS_00230830	Forward	GCTGTCTCATTCACCGCCAGTC
(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
Saa3 (mouse)	Forward	GAAGTTCACGGGACATGGAG
	Reverse	TTCAGCACATTGGGATGTTT

SAA1 (human)	Forward	TCGGGACATGTGGAGAGCCTAC
	Reverse	CGCACCATGGCCAAAGAATC
Il6 (mouse)	Forward	TGTGACTCCAGCTTATCTCTTGG
	Reverse	TGATGGATGCTACCAAACTGGA
Tnf-α (mouse)	Forward	ACAAGGTACAACCCATCGGC
	Reverse	CCCTCACACTCACAAACCAC
Rela (mouse)	Forward	GAGGGGAAACAGATCGTCCA
	Reverse	ATTTCCGCCTCTGGCGAATG
Actb (mouse)	Forward	GGTCAGAAGGACTCCTATGTGG
	Reverse	TGTCGTCCCAGTTGGTAACA
ACTB (human)	Forward	ATGGATGATGATATCGCC
	Reverse	GATGCCTCTCTTGCTCTG

hsa: human

Supplementary Table S7 The $\log_2$ fold change of differentially expressed lncRNAs that were exclusively expressed in the stearic acid compared with control group.

name	Regulation	$\log_2$ fold change	*P* 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

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

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

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

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

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

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

Supplementary Table S8 The $\log_2$ fold change of differentially expressed lncRNAs that were exclusively expressed in the palmitic acid compared with control group.

name	Regulation	$\log_2$ fold change	*P* 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

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

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

Supplementary Table S9 The $\log_2$ fold change of differentially expressed lncRNAs in the stearic acid group compared with palmitic acid group.

name	Regulation	$\log_2$ fold change	P 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[***]
C16:0, PA (Palmitic acid)	138.903±22.389	261.133±25.807[***]
C16: 1, PLA (Palmitoleic acid)	9.266±1.207	4.922±1.622[**]
C18: 0, SA (Stearic acid)	63.812±7.864	178.928±27.844[***]
C18: 1, OA (Oleic acid)	58.269±14.821	110.339±20.038[***]
C18: 2, LA (Linoleic acid)	115.355±11.066	138.366±13.582[*]
γ-C18:3, γ-LNA (γ-Linolenic acid)	4.707±0.236	8.267±1.585[**]
C18: 3, LNA (Linolenic acid)	82.182±13.182	40.567±15.673[**]
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[***]
C20: 5, EPA (Eicosapentaenoic acid)	6.172±1.111	2.681±0.669[***]
C22: 5, DPA (Docosapentaenoic acid)	1.673±0.623	1.675±0.828
C22: 6, DHA (Docosahexaenoic acid)	151.763±15.323	150.278±13.046

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

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

Supplementary Table S11 Full sequence of lnc866

TGCAATGGTACCTGTGTGTGTGGTAGTGGTGGTCTGTGTGGGAGGGAGTCCTCTCTTCATGTCACCTTTA
TATACACAGGGACTTCCAGGTGAGCAGCCACAGGCCCCTGAGCAAGCTGAGAAGGTAATATCCCACACTG
TTCTTTGAACAGCTTCAGCAACGGCTTCCAGATCTGTCTTTCTGCTCTGGCCCCAGGGATGTTATATTTC
ACTGGCCGTTGAAATCAGTGCCTGTCATTTTCCAGGCTGACGCTGCTCACTGGGTGAGTCAGTTGTTTGG
GTATGAACAGCAAAGCCTCGGATGCAGCTGCCAAAAGGGTGTGTTTGCCTTCACTTCCGGGGACTCTCTC
TCAGCTGCCACCTAGTGGCTGCTATCGTTGCTGTGGTTGTTATTCTGCAAGTGAGATAATTAAGGTTTAG
AAGAGTCTAAAGTCATTTAACTGACAAGGGACAGGACTGGAATTCTAACCAAGCTACCTGACATCGGCAT
GTTCTTGACTCTTCCCATCATAATGGATGCTCTTTGCGTCTGTGTTCCTTCGTGATTCCAGCATCGGCTC
ATCTTCCAAACATCTATGAAGTCCCAGGATTGGCCCCATTGGTCCGATGTGATCTCTGCTGGCTGCCTTC
CTTTTATGAAGGACTTATATACTCGAGGAGAGGACAAAGAAAAGCAAAACAAGAAGTTTTTGTGTGCGTT
GATGCTACACTGAGATGAGCTCCTAGAGCTAAGAGTCATGTGGAGCAAACAGGTTTGATCCCCTGGAGAG
GGGACCAATTATTCCTATGAGATAAATGGAAATTAGGAAGGCCCAAGAAAGAAAGGGGCTCTGTCAAGAC
CCTCCATGAAGAATAAGCAGCCCATAAGACATCCCAGGACCCAGAAGGTCATTCTGGGACACAAGTCACA
TGACTAACTAGCTTCAAGCCAAGACCAAGATGATGGTCTGTTTGGACACTGACTTTGTCTCAATTCCTAG
AAGGATGATGGCTATCAACCCATTTTAAAGAGCACTGTTTTACAGGGGAGACTCCTGTAGAAGAGGTGAG
GAAAAAATAAATTAATTAATTAATTAATTTAATTAATTAATTAAAAAAGAAAAGGTGAAGAGCCTT
TCTTCCCTTGGAGACCTAGAATATGCATGGAATGCTGTCCTGGACTATGGTGGGAAGTCTGGTTGGCTGT
GTGTCATAGCTCTAGGCTCACCCATCCCTCAGAACCTCATAGTATCATGTGCATAACTTAAAACTGTAGA
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TTCGTCTTCATTTTTCCAAGGTCTGATACAGTGATATCATGGGGAGATGAGAATCTAATATGAAATATTT
CAGTTCATCTCTACTTT
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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^2)	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***	47.279±2.523***	30.620±2.219^^^
Glucose (mmol/l)	4.840±1.056	10.239±2.24**	7.385±0.63*^	4.900±0.533^^
TC (mmol/l)	2.963±0.143	6.014±0.679***	6.000±0.657***	2.657±0.506^^^
TG (mmol/l)	0.786±0.122	1.755±0.090**	1.704±0.120**	0.742±0.099^^
HDL-C (mmol/l)	2.403±0.125	4.281±0.380**	4.560±0.489**	2.195±0.457^^
LDL-C (mmol/l)	0.218±0.033	1.180±0.305**	1.210±0.233**	0.154±0.017^^
Insulin (pmol/l)	106.683±0.316	298.09±0.151*	208.569±0.039*^	98.476±0.012^^
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	*P* value
mmu-miR-297b-5p	ENSMUST00000022531	-0.995	3.69E-05
mmu-miR-297b-5p	ENSMUST00000050785	-0.995	4.47E-05
mmu-miR-297b-5p	ENSMUST00000074898	-0.992	1.01E-04
mmu-miR-297b-5p	ENSMUST00000020190	-0.992	1.02E-04
mmu-miR-297b-5p	ENSMUST00000159720	-0.991	1.08E-04
mmu-miR-297b-5p	ENSMUST00000006956	-0.986	3.00E-04
mmu-miR-297b-5p	ENSMUST00000181286	-0.985	3.34E-04
mmu-miR-297b-5p	ENSMUST00000036188	-0.984	3.79E-04
mmu-miR-297b-5p	ENSMUST00000181169	-0.983	4.48E-04
mmu-miR-297b-5p	ENSMUST00000068830	-0.982	4.60E-04
mmu-miR-297b-5p	ENSMUST00000166854	-0.979	6.58E-04
mmu-miR-297b-5p	ENSMUST00000086399	-0.978	7.04E-04
mmu-miR-297b-5p	ENSMUST00000023994	-0.977	8.13E-04
mmu-miR-297b-5p	ENSMUST00000027748	-0.975	9.10E-04
mmu-miR-297b-5p	ENSMUST00000131456	-0.968	1.50E-03
mmu-miR-297b-5p	ENSMUST00000067495	-0.966	1.69E-03
mmu-miR-297b-5p	ENSMUST00000140373	-0.965	1.78E-03
mmu-miR-297b-5p	ENSMUST00000102745	-0.954	3.16E-03
mmu-miR-297b-5p	ENSMUST00000040750	-0.949	3.91E-03
mmu-miR-297b-5p	ENSMUST00000171621	-0.947	4.10E-03
mmu-miR-297b-5p	ENSMUST00000031565	-0.944	4.66E-03
mmu-miR-297b-5p	ENSMUST00000101094	-0.937	5.86E-03
mmu-miR-297b-5p	ENSMUST00000096232	-0.937	5.87E-03
mmu-miR-297b-5p	ENSMUST00000147988	-0.929	7.46E-03
mmu-miR-297b-5p	ENSMUST00000094760	-0.929	7.46E-03
mmu-miR-297b-5p	ENSMUST00000106373	-0.926	7.98E-03

mmu-miR-297b-5p	ENSMUST00000110323	-0.924	8.47E-03
mmu-miR-297b-5p	ENSMUST00000149874	-0.908	1.21E-02
mmu-miR-297b-5p	ENSMUST00000194644	-0.902	1.38E-02
mmu-miR-297b-5p	ENSMUST00000135828	-0.896	1.57E-02
mmu-miR-297b-5p	ENSMUST00000143213	-0.887	1.84E-02

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	*P* 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	*P* 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

lnc866: TCONS_00077866; PCC, Pearson correlation coefficients.

Supplementary Table S17 RNA-seq showing the log$_2$ fold change of differential expression of 31 mRNAs in co-expression network in stearic acid-treated β-TC6 cells

Ensemble ID	Gene name	Regulation	log$_2$ fold change	*P* 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 (Sclt1)	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