Supplementary Table1. Product Data-D12451

Formula

Product #D12451		gm%	kcal%
Protein		24	20
Carbohydrate		41	35
Fat		24	45
	Total		100
	kcal/gm	4.73	

Ingredient	gm	kcal
Casein, 30 Mesh	200	800
L-Cystine	3	12
Corn Starch	72.8	291
Maltodextrin 10	100	400
Sucrose	172.8	691
Cellulose, BW200	50	0
Soybean Oil	25	225
Lard*	177.5	1598
Mineral Mix S10026	10	0
DiCalcium Phosphate	13	0
Calcium Carbonate	5.5	0
Potassium Citrate, 1 H2O	16.5	0
Vitamin Mix V10001	10	40
Choline Bitartrate	2	0
FD&C Red Dye #40	0.05	0
Total	**858.15**	**4057**

Formulated by E. A. Ulman, Ph.D., Research Diets, Inc., 8/26/98 and 3/11/99.

*Typical analysis of cholesterol in lard = 0.72 mg/gram.
Cholesterol (mg)/4057 kcal = 167.8
Cholesterol (mg)/kg = 195.5

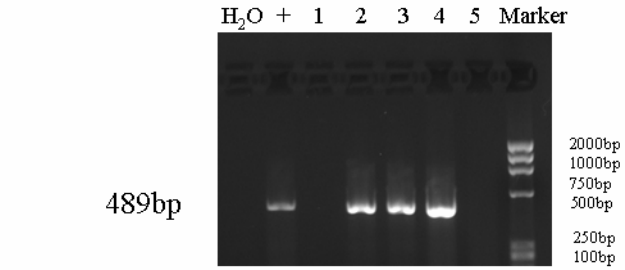
Supplementary Table 2. S100A16 Reverse Complementary Oligonucleotides

oligo DNA	5’-3’
13MR0109-01-F	TGCTGAACAACTGCCTTCTCCAGCTCGTTTTGGCCACTGACTGACGAGCTGGAAGGCAGTTGT
13MR0109-01-R	CCTGAACAACTGCCTTCCAGCTCGTCAGTCAGTGGCCAAAACGAGCTGGAGAAGGCAGTTGT
13MR0109-02-F	TGCTGTTCTGGATGAGCTTGTCAGCTGTTTTGGCCACTGACTGACAGCTGACACTCATCCAGA
13MR0109-02-R	CCTGTTCTGGATGAGTGTCAGCTGTCAGTCAGTGGCCAAAACAGCTGACAAGCTCATCCAGA
13MR0109-03-F	TGCTGTTCGGAAGCTGGACTTGCTGAGTTTTGGCCACTGACTGACTCAGCAAGCAGCTTCCGA
13MR0109-03-R	CCTGTTCGGAAGCTGCTTGCTGAGTCAGTCAGTGGCCAAAACTCAGCAAGTCCAGCTTCCGA
13MR0109-04-F	TGCTGTGGTGATTCCACCAATCATGGGTTTTGGCCACTGACTGACCCATGATTTGGAATCACC
13MR0109-04-R	CCTGTGGTGATTCCAAATCATGGGTCAGTCAGTGGCCAAAACCCATGATTGGTGGAATCACC
Negative-F	TGCTGAAATGTACTGCGCGTGGAGACGTTTTGGCCACTGACTGACGTCTCCACGCAGTACAT
Negative-R	CCTGAAATGTACTGCGTGGAGACGTCAGTCAGTGGCCAAAACGTCTCCACGCGCAGTACATT

Supplementary Table 3. 11β-HSD1 Reverse Complementary Oligonucleotides

Oligo DNA	5’-3’
14MR0018-1-F	TGCTGTTTCCTTCATAGCTGTTTCTGGTTTTGGCCACTGACTGACCAGAAACATATGAAGGAAA
14MR0018-1-R	CCTGTTTCCTTCATATGTTTCTGGTCAGTCAGTGGCCAAAACCAGAAACAGCTATGAAGGAAAC
14MR0018-2-F	TGCTGTAAATTGCTCCGCAAATGTCAGTTTTGGCCACTGACTGACTGACATTTGGAGCAATTTA
14MR0018-2-R	CCTGTAAATTGCTCCAAATGTCAGTCAGTCAGTGGCCAAAACTGACATTTGCGGAGCAATTTAC
14MR0018-3-F	TGCTGAGGCCAAGGACACAGAGAGTGGTTTTGGCCACTGACTGACCACTCTCTGTCCTTGGCCT
14MR0018-3-R	CCTGAGGCCAAGGACAGAGAGTGGTCAGTCAGTGGCCAAAACCACTCTCTGTGTCCTTGGCCTC
14MR0018-4-F	TGCTGATGATATGCCATTTCTCTTCCGTTTTGGCCACTGACTGACGGAAGAGATGGCATATCAT
14MR0018-4-R	CCTGATGATATGCCATCTCTTCCGTCAGTCAGTGGCCAAAACGGAAGAGAAATGGCATATCATC
Negative-F	TGCTGAAATGTACTGCGCGTGGAGACGTTTTGGCCACTGACTGACGTCTCCACGCAGTACATTT
Negative-R	CCTGAAATGTACTGCGTGGAGACGTCAGTCAGTGGCCAAAACGTCTCCACGCGCAGTACATTTC

Supplementary Fig. 1



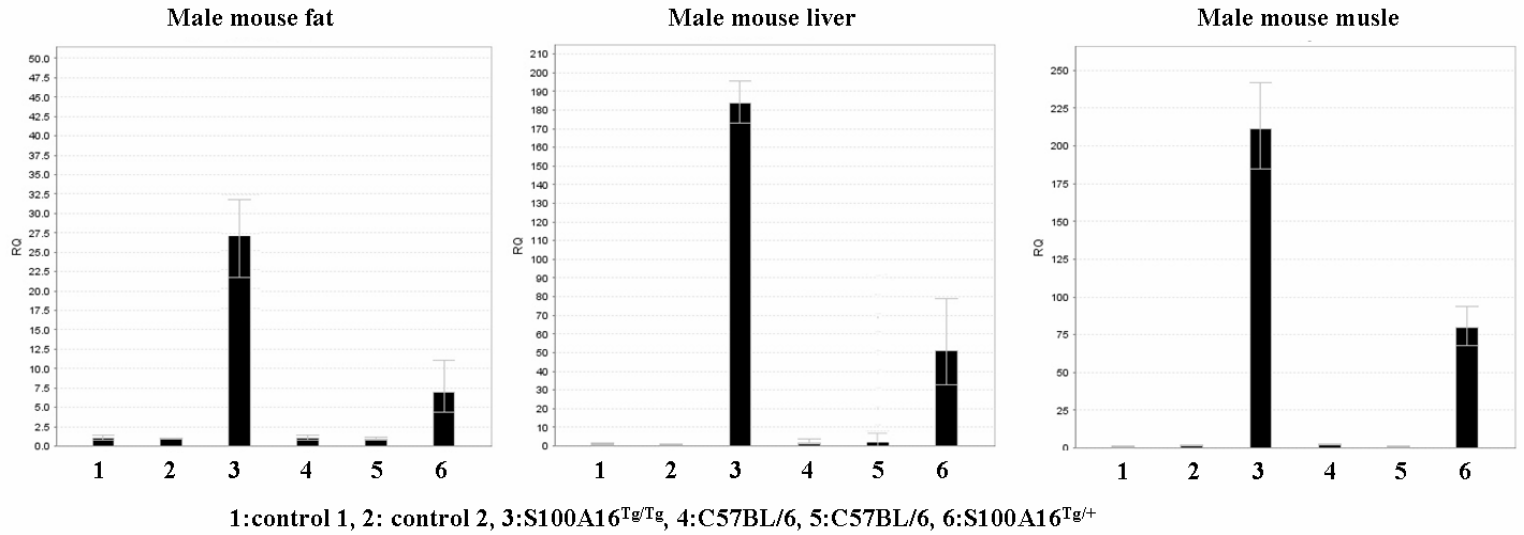
H_2O: negtive control, +: postive control, 1:C57BL/6, 2:S100A16$^{Tg/+}$, 3:S100A16$^{Tg/+}$, 4:S100A16$^{Tg/+}$, 5:S100A16$^{Tg/+}$,

Pimer : S100A16$^{Tg/+}$-F 5'-TTGTGCTGTCTCATCATTTTGG-3'
S100A16$^{Tg/+}$-R 5'-ACCAGCCACCACCTTCTGATA-3'

Supplementary Fig.1. Genotyping of S100A16 transgenic (S100A16$^{Tg/+}$) mouse using PCR.

Total RNA from tails of C57BL/6 and S100A16$^{Tg/+}$ mouse was purified using Trizol Reagent (Invitrogen). The allele S100A16 was identified using PCR, and S100A16 region as shown in 489bp line in this figure. H_2O: negtive control, +: postive control, 1:C57BL/6, 2:S100A16$^{Tg/+}$, 3:S100A16$^{Tg/+}$, 4:S100A16$^{Tg/+}$, 5:S100A16$^{Tg/+}$, Marker: 100bp, 250bp, 500bp, 750bp, 1000bp,2000bp.

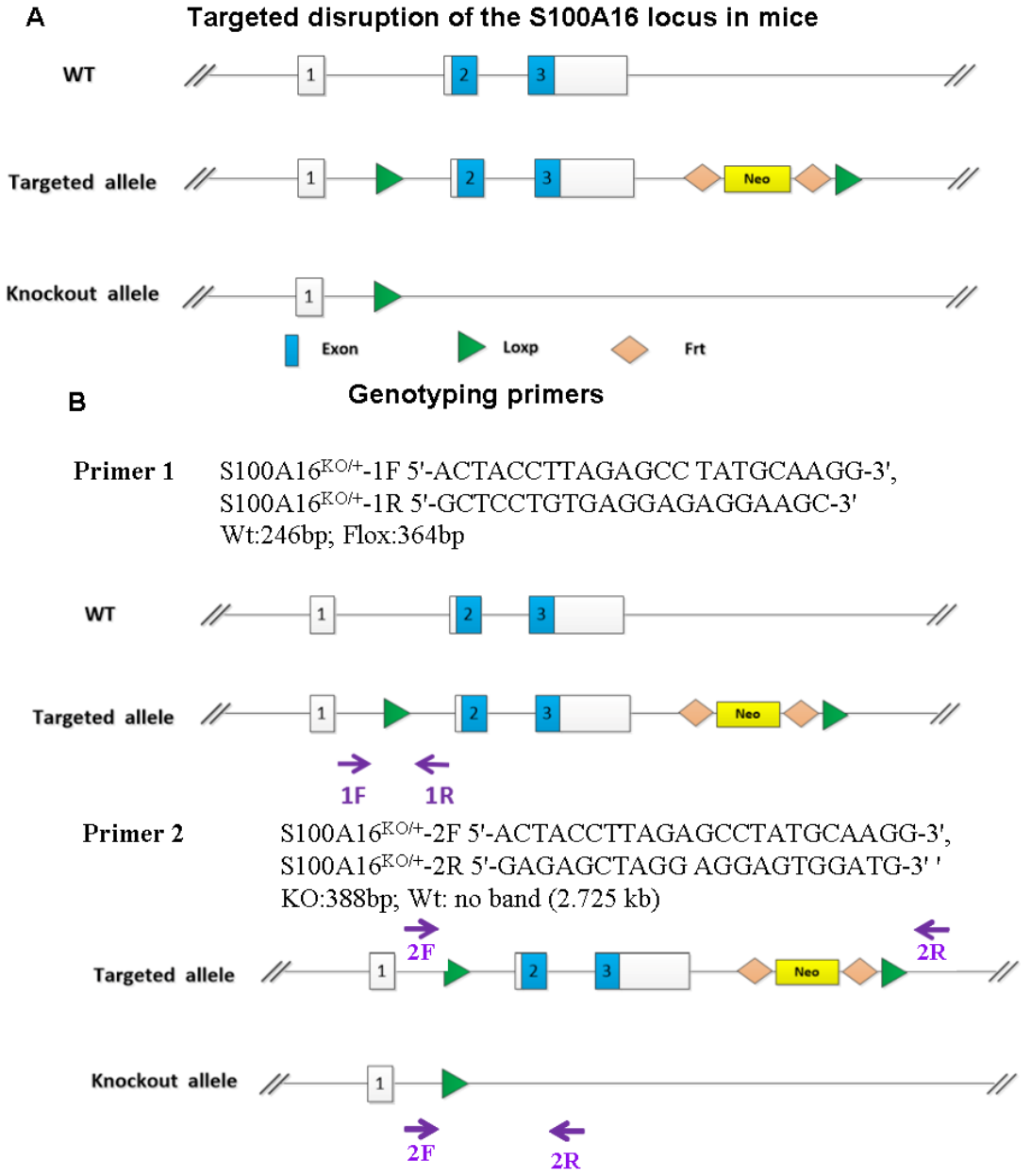
Supplementary Fig. 2



Supplementary Fig.2. The levels of S100A16 isoforms in wild-type C57BL/6 and S100A16 transgenic heterzygous ($S100A16^{Tg/+}$) mice were determined by Q-PCR.

Total RNAs from fat, liver, and musle of the male mice were purified using Trizol Reagent. The primers are β-actin-F 5'-TGACGTGGACATCCGCAAAG-3', β-actin-R 5'-CTGGAAGGTGGACAGCGAGG-3';S100A16-F5'-AGTACAGCCTGGTCAAGAACA-3', S100A16-R 5'-TCCCTGTGTCCGACAGCAT-3'. For the Q-PCR reaction, the total RNA was mixed with the primers according to the manufacturer's instructions of the SYBR Premix Ex Taq (TAKARA RR420A).

Supplementary Fig. 3



Supplementary Fig.3. Targeted Disruption of the s100a16 Locus.

S100A16 Knockout heterozygous mouse ($S100A16^{KO/+}$) were generated at the Model Animal Research Center Of Nanjing University. Loxp points were added before the second exon and behind the third exons in the N-terminal sequence of s100a16 gene (A). Embryonic stem cells with one of the s100a16 alleles deleted were used to create chimeras and further develop a stable heterozygous mouse strain. The mice were then back-crossed with C57BL/6 mice.The genotype of fetuses was determined by genomic PCR with specific primers (B). $S100A16^{KO/+}$-1F 5'-ACTACCTTAGAGCC TATGCAAGG-3', $S100A16^{KO/+}$-1R 5'-GCTCCTGTGAGGAGAGGAAGC-3'; $S100A16^{KO/+}$-2F 5'-ACTACCTTAGAGCCTATGCAAGG-3', $S100A16^{KO/+}$-2R 5'-GAGAGCTAGG AGGAGTGGATG-3'. (C), tails were cutted from the mice and total RNAs from tails were purified using Trizol Reagent. PCR was used to determine the genotypes of mice with specific primers.