

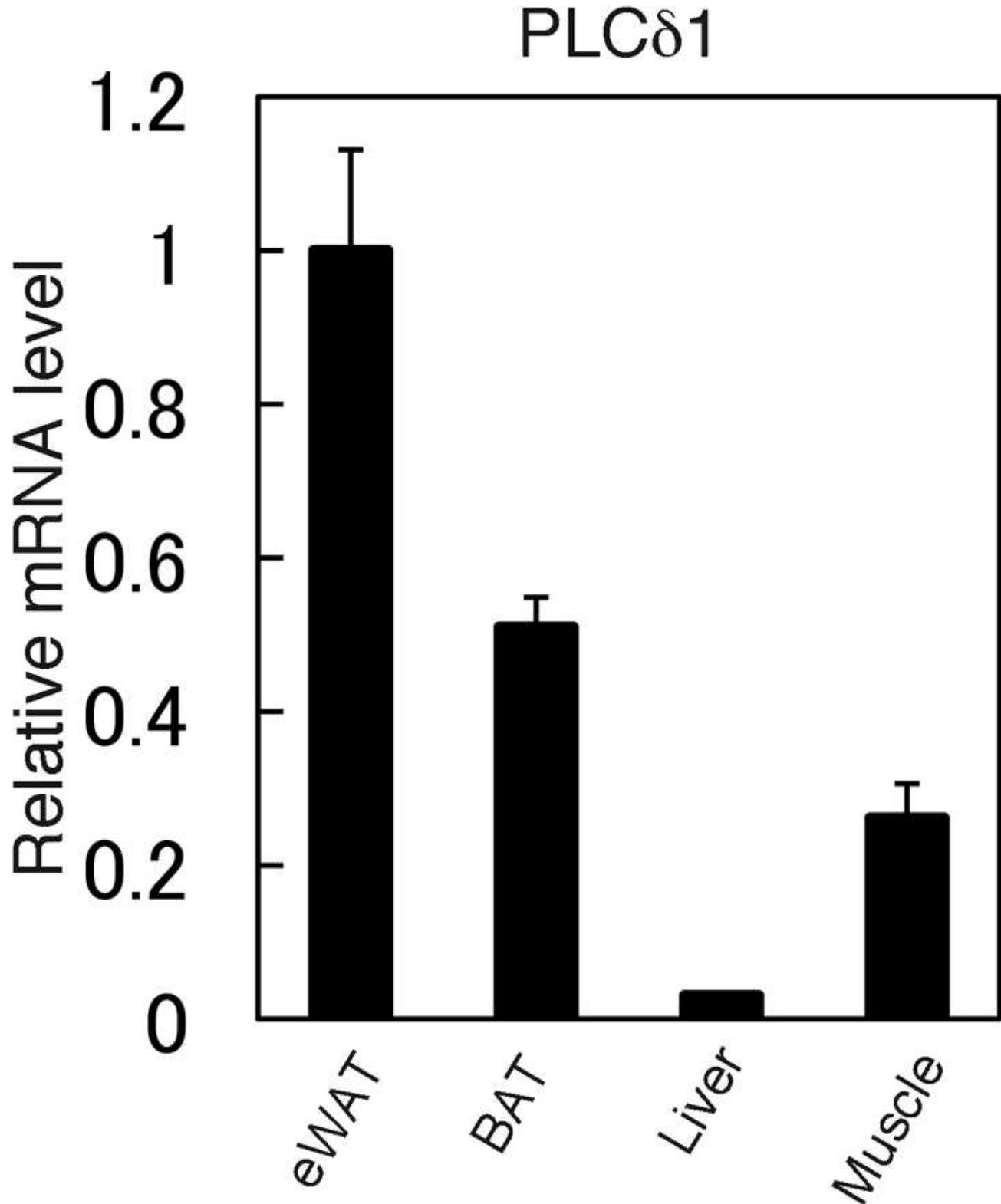
SUPPLEMENTARY DATA

Supplementary Table 1. Primers for qRT-PCR.

Name	NCBI Gene ID	Gene Symbol	Primer Sequence
Acadl	11363	Acadl	F: 5' - GGA CTCCGGTTC TCTCTCCA -3' R: 5' - TGCAATCGGGTACTCCACA -3'
acyl-Coenzyme A dehydrogenase, long-chain			
Acadm	11364	Acadm	F: 5' - AGGTTTCAAGATCGCAATGG -3' R: 5' - CTCCTTGGTGCTCCACTAGC -3'
acyl-Coenzyme A dehydrogenase, medium chain			
Acox1	11430	Acox1	F: 5' - CAGGAAGAGCAAGGAAGTGG -3' R: 5' - CCTTCTGGCTGATCCATA -3'
acyl-Coenzyme A oxidase 1, palmitoyl			
Adiponectin	11450	Adipoq	F: 5' - GCACTGGCAAGTCTACTGCAA -3' R: 5' - GTAGGTGAAGAGAACGGCCTTGT -3'
adiponectin, C1Q and collagen domain containing			
Adipsin	11537	Cfd	F: 5' - GCCTGATTCCTGCATCAACT -3' R: 5' - GCGCAGATTGCAGGTGTGCT -3'
complement factor D (adipsin)			
Adrb3	11556	Adrb3	F: 5' - GGGCGAACTGGTTGCGAACT -3' R: 5' - CAAAGGACACGGCAGCGGACA -3'
adrenergic receptor, beta 3			
aP2	11770	Fabp4	F: 5' - GATGCCTTTGTGGAACT -3' R: 5' - CTGCTGTTGCGGTGATT -3'
fatty acid binding protein 4, adipocyte			
CD36	12491	Cd36	F: 5' - AAGCTATTGCGACATGATT -3' R: 5' - GATCCGAAACACAGCGTAGAT -3'
CD36 antigen			
C/EBP α	12606	Cebpa	F: 5' - CAAGAACAGCAACGAGTACCG -3' R: 5' - GTCACCTGATCACTCCAGCAC -3'
CCAAT/enhancer binding protein (C/EBP), alpha			
C/EBP β	12608	Cebpb	F: 5' - CCAAGAAGACGGTGGACAA -3' R: 5' - CAAGTCCCGAGGGTGTCT -3'
CCAAT/enhancer binding protein (C/EBP), beta			
C/EBP δ	12609	Cebpd	F: 5' - ATCGACTTCAGCGCTACA -3' R: 5' - GCTTTGTGGTTGTGTTGAA -3'
CCAAT/enhancer binding protein (C/EBP), delta			
Cidea	12683	Cidea	F: 5' - ATCACAACCTGGCTGGTTACG -3' R: 5' - TACTACCCGGTGTCCATTCT -3'
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A			
Cpt1a	12894	Cpt1a	F: 5' - GCTGCTTCCCCTCACAAGTCC -3' R: 5' - GCTTTGGCTGCTGTGTCAGTATGC -3'
carmitine palmitoyltransferase 1a, liver			
Cpt1b	12895	Cpt1b	F: 5' - CCCATGTGCTCCTACCAGAT -3' R: 5' - CCTTGAAGAAGCGACCTTTG -3'
carmitine palmitoyltransferase 1b, muscle			
DIO2	13371	Dio2	F: 5' - CAGTGTGGTGCACGTCTCCAATC -3' R: 5' - TGAACCAAGTGTACCACAG -3'
deiodinase, iodothyronine, type II			
Fasn	14104	Fasn	F: 5' - GCTGGCATTCGTGATGGAGTCGT -3' R: 5' - AGGCCACCAGTGATGTAAGTCT -3'
Fatty acid synthase			
Glucokinase	103988	Gck	F: 5' - GAAGTGCCTCCTGCTAAC -3' R: 5' - CTTCCAGGCCACAACATT -3'
GLUT4	20528	Slc2a4	F: 5' - TGCTCTCCTGCAGTGTGATT -3' R: 5' - TTCAGCTCAGCTAGTGCCTGTC -3'
solute carrier family 2 (facilitated glucose transporter), member 4			
G6Pase	14377	G6pc	F: 5' - CCTCCTCAGCCTATGCTGTC -3' R: 5' - AACATCGGAGTGCCTTTGG -3'
glucose-6-phosphatase, catalytic			
IL-6	16193	Il6	F: 5' - GCTACCAAACTGGATATAATCAGGA -3' R: 5' - CCAGGTAGCTATGGTACTCCAGAA -3'
interleukin 6			
HB-EGF	15200	Hbegf	F: 5' - TTCTTCGGGTGCTACTTCTGT -3' R: 5' - AAAGTCCCTGCTCTTCTCT -3'
heparin-binding EGF-like growth factor			
KLF15	66277	Klf15	F: 5' - TACACCAAGAGCAGCCACT -3' R: 5' - AACTCATCTGAGCGGAAAA -3'
Kruppel-like factor 15			
Leptin	16846	Lep	F: 5' - CCTCATCAAGACCATTGTCACT -3' R: 5' - TCTCCAGTCTATTGGCTATCTG -3'
leptin			
LPL	16956	Lpl	F: 5' - AGGACCCTGAAGACAC -3' R: 5' - GGCACCAACTCTCATA -3'
lipoprotein lipase			
PEPCK	18534	Pck1	F: 5' - CTGGACCTCAGTGAAGACA -3' R: 5' - TCGATGCCTCCAGTAAAC -3'
phosphoenolpyruvate carboxykinase 1, cytosolic			
PGC1 α	19017	Ppargc1a	F: 5' - CCCTGCCATTGTAAAGACC -3' R: 5' - TGCTGCTGTTCTGTTTTC -3'
peroxisome proliferative activated receptor, gamma, coactivator 1 alpha			
PLC δ 1	18799	PLCd1	F: 5' - TTGTGGTAGCAGTGCCTGAC -3' R: 5' - AGGCTGTTCCAGGGGATAGT -3'
phospholipase C, delta 1			
PPAR α	19013	Ppara	F: 5' - CCGAGGCTCTGTATCA -3' R: 5' - GGGCAGCTGACTGAGGAA -3'
peroxisome proliferator activated receptor alpha			
PPAR γ	19016	Pparg	F: 5' - CTTGCTGTGGGATGTCTCACA -3' R: 5' - GATCCCGCAACAGCTTCTCT -3'
peroxisome proliferator activated receptor gamma			
PRDM16	70673	Prdm16	F: 5' - GACATTCCAATCCCACCAGA -3' R: 5' - CACCTCTGTATCCCGCAGCA -3'
PR domain containing 16			
p21	12575	Cdkn1a	F: 5' - GCAGACCAGCCTGACAGATTT -3' R: 5' - GAGAGGGCAGGACGCGTAT -3'
cyclin-dependent kinase inhibitor 1A (p21)			
Resistin	57264	Retn	F: 5' - GCTGCTGCCAAGGCTGAT -3' R: 5' - TCTCCTTCCACCATGTAGTTT -3'
resistin			
SCD1	20249	Scd1	F: 5' - GCGATACTCTGGTGCTCA -3' R: 5' - CCCAGGGAACAGGATATT -3'
stearoyl-Coenzyme A desaturase 1			
TNF α	21926	Tnf	F: 5' - GACCCTCACATCAGATCATCTTCT -3' R: 5' - CCTCCACTGGTGGTTTGCT -3'
tumor necrosis factor			
UCP1	22227	Ucp1	F: 5' - ACTGCCACACCTCCAGTCACT -3' R: 5' - CTTTGCTCACTCAGGATTTGG -3'
uncoupling protein 1 (mitochondrial, proton carrier)			
UCP3	22229	Ucp3	F: 5' - TACCAACCTTGGCTAGACG -3' R: 5' - GTCCAGGAGAGGACTTGC -3'
uncoupling protein 3 (mitochondrial, proton carrier)			

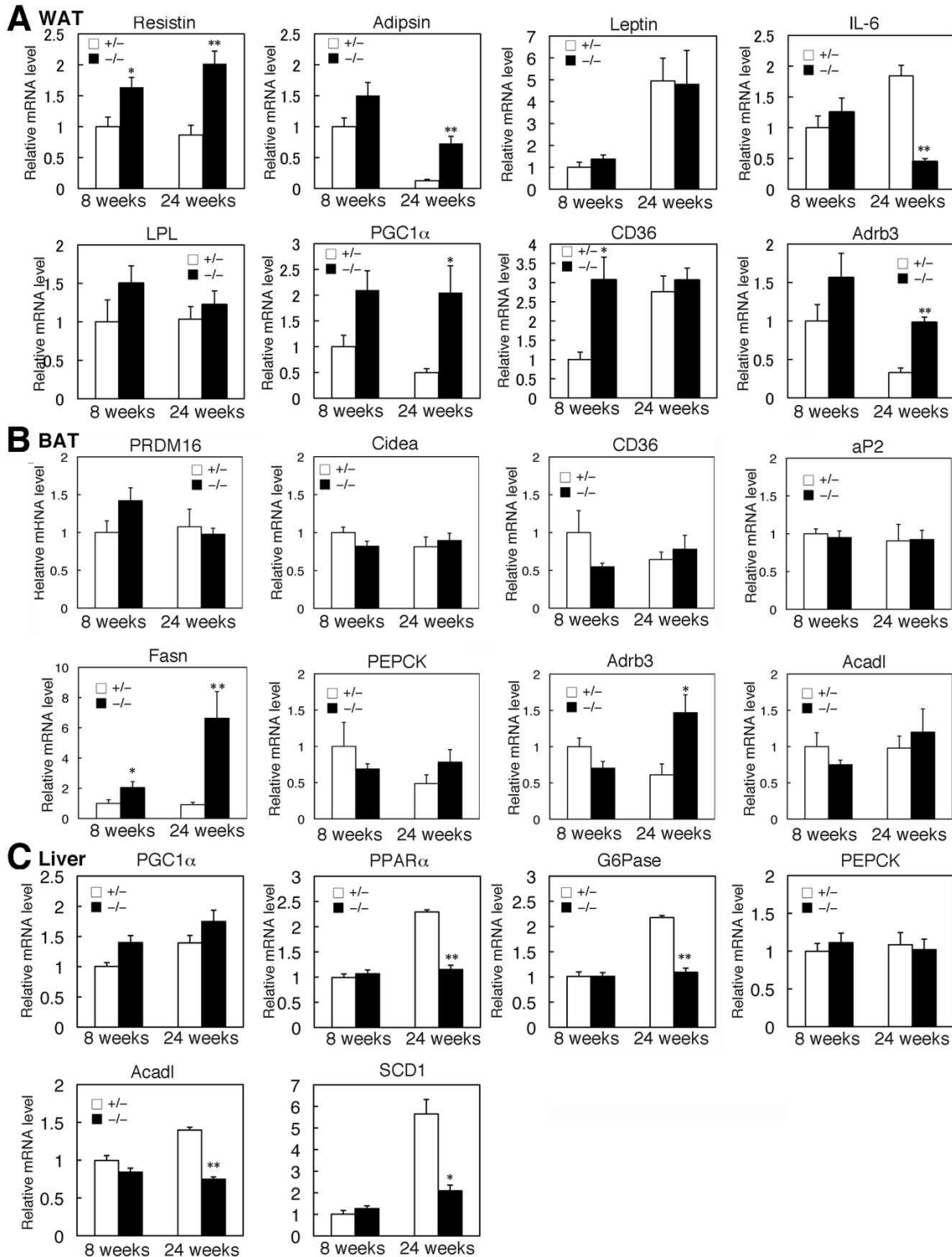
SUPPLEMENTARY DATA

Supplementary Figure 1. Expression of PLC δ 1 in metabolic tissues. *PLC δ 1* mRNA expression level in eWAT, BAT, liver and muscle from 8-week-old *PLC δ 1*^{+/+} mice (n = 4) fed with RD was analyzed by qRT-PCR. The mRNA levels are normalized to 36B4 as an internal control. Values are expressed as the mean \pm SEM.



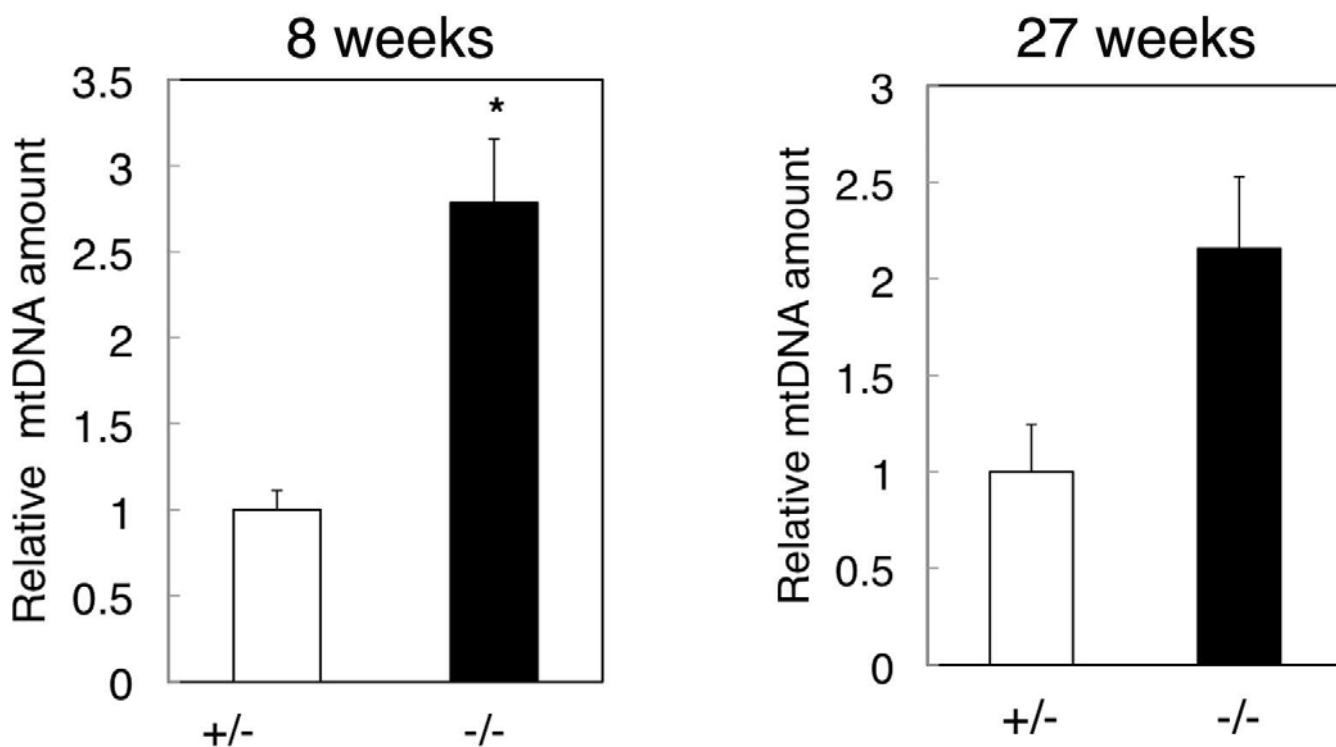
SUPPLEMENTARY DATA

Supplementary Figure 2. Gene expression patterns in metabolic tissues from mice fed with HFD. **A:** mRNA levels in eWAT of 8-week-old *PLCδ1^{+/-}* mice (n = 7) or *PLCδ1^{-/-}* mice (n = 11), or 24-week-old *PLCδ1^{+/-}* mice (n = 9) or *PLCδ1^{-/-}* mice (n = 8) were detected by qRT-PCR. **B:** mRNA levels in BAT of 8-week-old *PLCδ1^{+/-}* mice (n = 9) or *PLCδ1^{-/-}* mice (n = 11), or 24-week-old *PLCδ1^{+/-}* mice (n = 9) or *PLCδ1^{-/-}* mice (n = 8) were examined. **C:** mRNA levels in liver in 8-week-old *PLCδ1^{+/-}* mice (n = 10) or *PLCδ1^{-/-}* mice (n = 6), or 24-week-old *PLCδ1^{+/-}* mice (n = 6) or *PLCδ1^{-/-}* mice (n = 5) were detected by qRT-PCR.



SUPPLEMENTARY DATA

Supplementary Figure 3. Amount of mitochondrial DNA (mtDNA) was increased in BAT of *PLCδ1*^{-/-} mice. Mitochondria were isolated from BAT of 8-week-old (n = 3) or 27-week-old mice (n = 3). mtDNA was extracted and normalized to the tissue protein amount. The relative mtDNA amount of *PLCδ1*^{-/-} is shown by defining that of *PLCδ1*^{+/-} as 1.0. Relative values are expressed as the mean ± SEM. *P < 0.05.



SUPPLEMENTARY DATA

Supplementary Figure 4. Enhanced metabolic rate in hairless mice. *A, B:* Oxygen consumption (VO_2) and carbon dioxide production (VCO_2) was measured by using an indirect calorimeter system in 12-week-old C57BL/6 mice (control) or hair removal in C57BL/6 mice (shaved) (*A*) ($n = 4$) and in BALB/c mice (control) or BALB/c nude mice (nude) (*B*) ($n = 4$). Values are expressed as the mean \pm SEM.

