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Supplemental Information

Lsd1 Ablation Triggers Metabolic Reprogramming of Brown Adipose Tissue

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Supplemental Informations

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Supplemental Figures and Legends

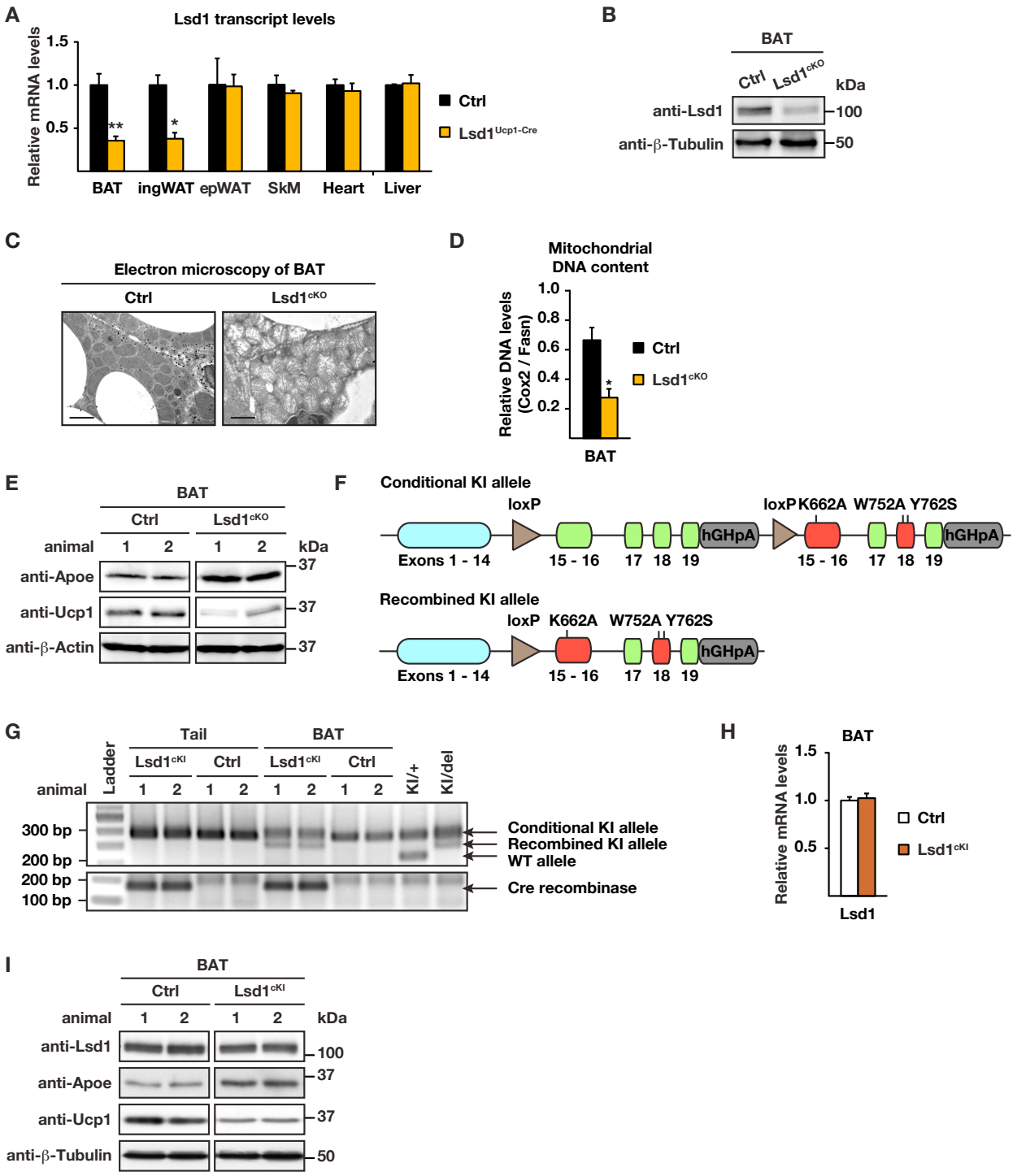


Figure S1 (related to Figure 1). Lsd1 represses the expression of WAT-selective genes in BAT.
(A) Relative Lsd1 mRNA levels in interscapular brown adipose tissue (BAT), inguinal white adipose tissue (ingWAT), epididymal white adipose tissue (epWAT), skeletal muscle (SkM), heart, and liver of control (Ctrl) and Lsd1^{cKO} mice (mean + SEM, *p<0.05, **p<0.01, Ctrl n = 9, Lsd1^{cKO} n = 7).
(B) Western blot analysis of Lsd1 in BAT of Ctrl and Lsd1^{cKO} mice. β-Tubulin was used as a loading control.
(C) Ultrastructure analysis of representative BAT sections of Ctrl and Lsd1^{cKO} mice. Scale bar: 2 µm.
(D) Ratio of mitochondria to nuclear DNA content assessed by quantitative PCR of the mitochondria-encoded Cox2 and the nuclear-encoded Fasn gene in BAT of Ctrl and Lsd1^{cKO} mice (mean + SEM, *p<0.05, n = 5).
(E) Western blot analysis of Apoe and Ucp1 in BAT of Ctrl and Lsd1^{cKO} mice. β-Actin was used as a loading control.
(F) Scheme depicting the *Lsd1* knock-in (KI) allele.
(G) Genotyping of mouse tail and BAT biopsies of Ctrl and Lsd1^{cKO} mice for the presence of Lsd1 conditional or recombined KI alleles (upper panel), or Ucp1-Cre recombinase (lower panel) by semi-quantitative PCR.
(H) Relative Lsd1 mRNA levels in BAT of Ctrl and Lsd1^{cKI} mice (mean + SEM, Ctrl n = 7, Lsd1^{cKI} n = 6).
(I) Western blot analysis of Lsd1, Apoe, and Ucp1 in BAT of Ctrl and Lsd1^{cKI} mice. β-Tubulin was used as a loading control.

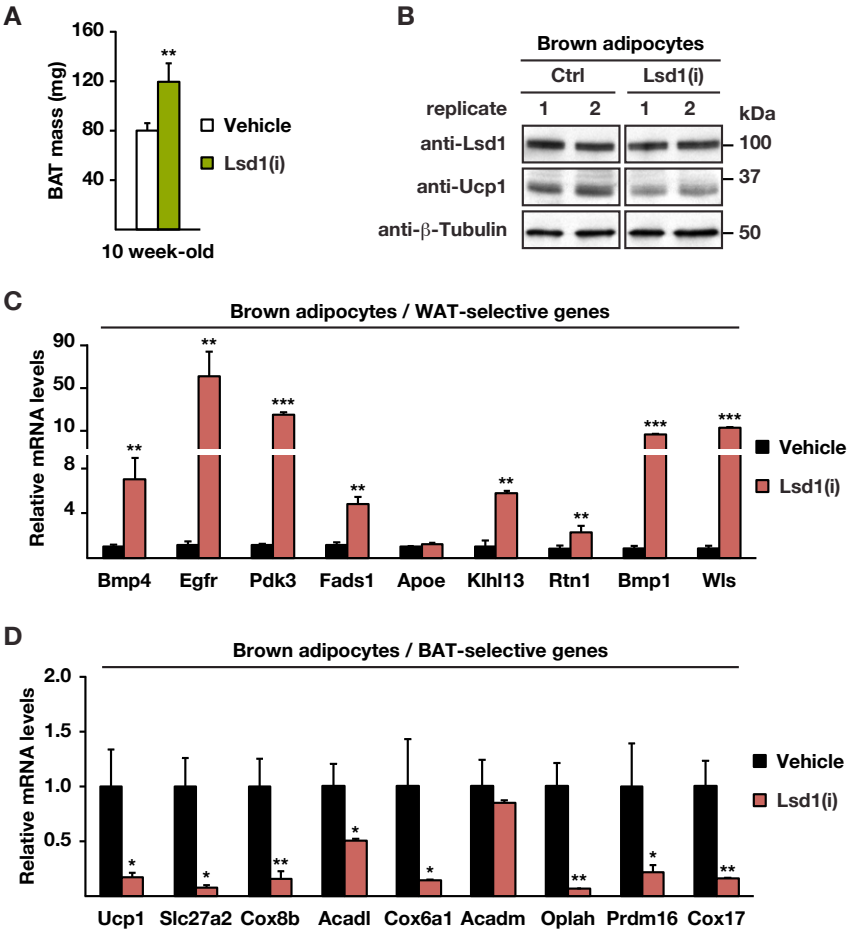
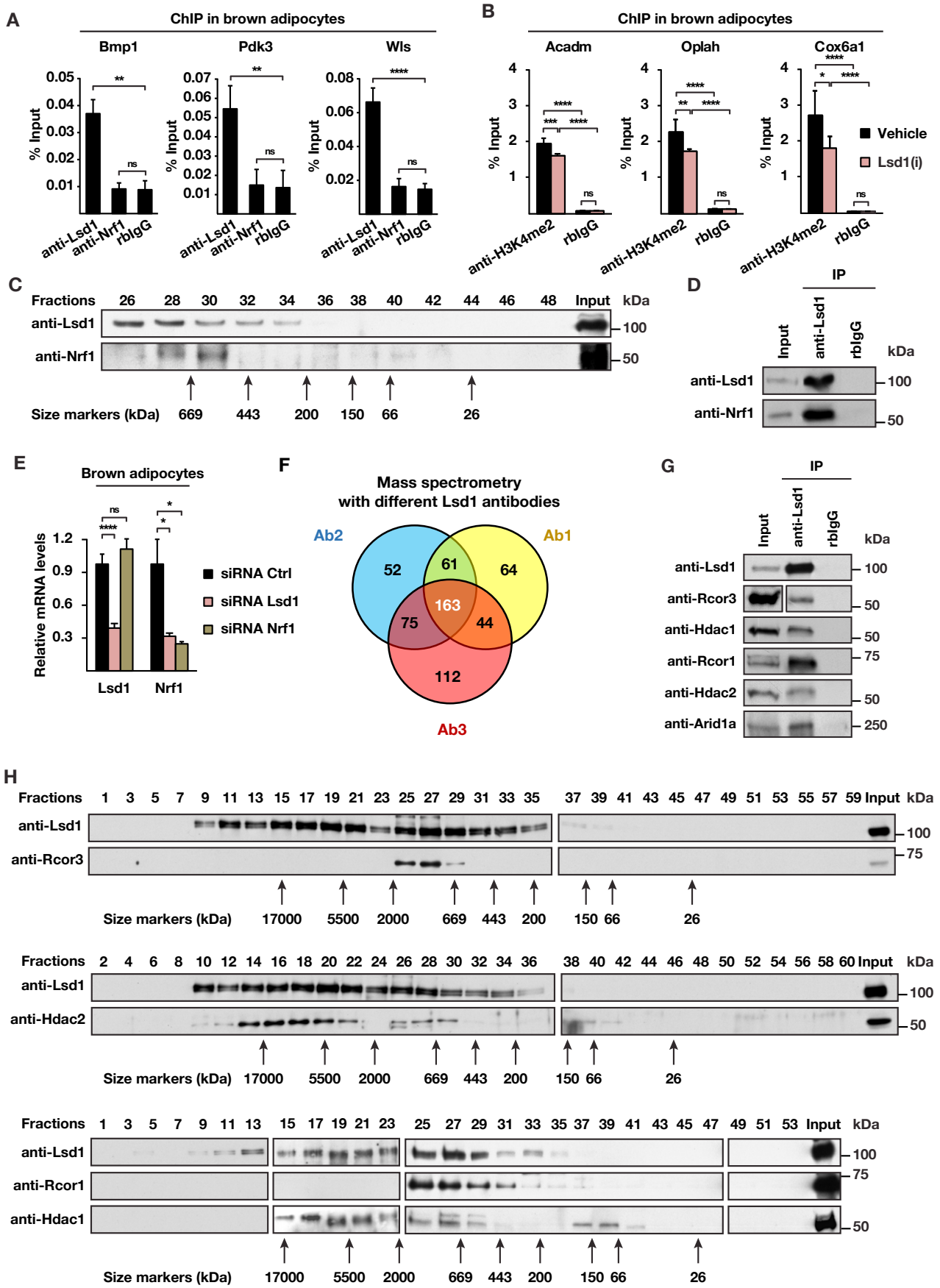


Figure S2 (related to Figure 2). The demethylase activity of Lsd1 is required to maintain BAT properties.
(A) Mass of BAT of 10 week-old mice treated with vehicle or Lsd1-specific inhibitor [Lsd1(i)] (mean + SEM, **p<0.01, vehicle n = 6, Lsd1(i) n = 7).
(B) Western blot analysis of Lsd1 and Ucp1 in brown adipocytes treated with vehicle or Lsd1(i). β-Tubulin was used as a loading control.
(C-D) Relative mRNA levels of (C) WAT- and (D) BAT-selective genes in brown adipocytes treated with vehicle or Lsd1(i) (mean + SEM, *p<0.05, **p<0.01, ***p<0.001, n = 6).


A
ChIP in brown adipocytes
Bmp1
Pdk3
Wls
% Input
anti-Lsd1
anti-Nrf1
rbIgG
B
ChIP in brown adipocytes
Acadm
Oplah
Cox6a1
anti-H3K4me2
Vehicle
Lsd1(i)
C
Fractions
Input
kDa
anti-Lsd1
anti-Nrf1
Size markers (kDa)
D
IP
E
Brown adipocytes
Relative mRNA levels
siRNA Ctrl
siRNA Lsd1
siRNA Nrf1
Lsd1
Nrf1
F
Mass spectrometry
with different Lsd1 antibodies
Ab1
Ab2
Ab3
G
anti-Rcor3
anti-Hdac1
anti-Rcor1
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H
anti-Hdac2

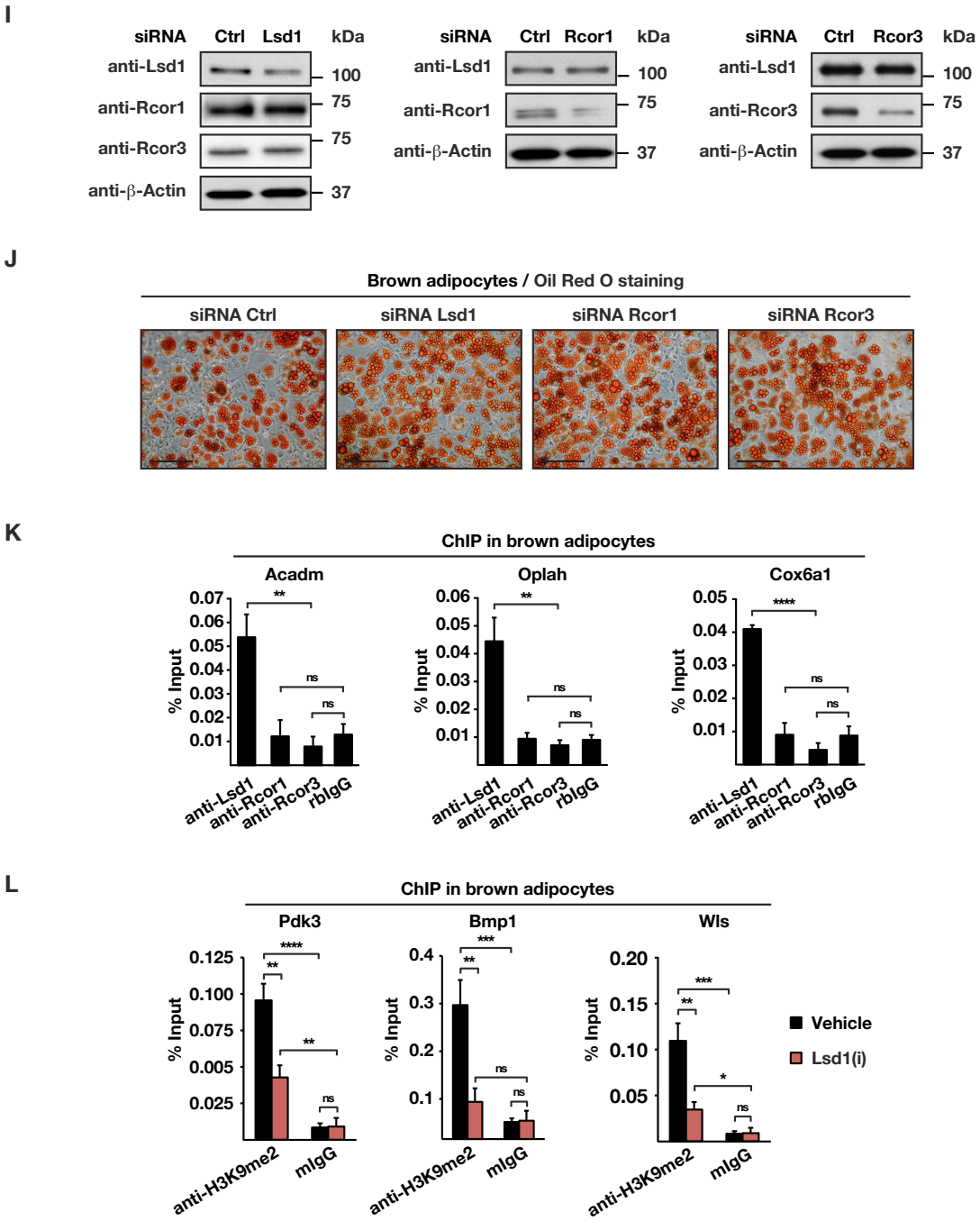


Figure S3 (related to Figure 3). Lsd1 regulates the brown fat program through a dual mechanism

(A) ChIP analysis to detect promoter occupancy performed with anti-Lsd1 and anti-Nrf1 antibodies or rabbit IgG (rbIgG) in brown adipocytes for indicated genes. The precipitated chromatin was quantified by qPCR analysis with primers flanking Lsd1-binding sites in the indicated genes (mean + SEM, n = 3).

(B) ChIP analysis to detect promoter occupancy performed with anti-H3K4me2 antibody or rbIgG in brown adipocytes treated with Lsd1(i) or vehicle. The precipitated chromatin was quantified by qPCR analysis with primers flanking Lsd1-binding sites in the indicated genes (mean + SEM, n = 3).

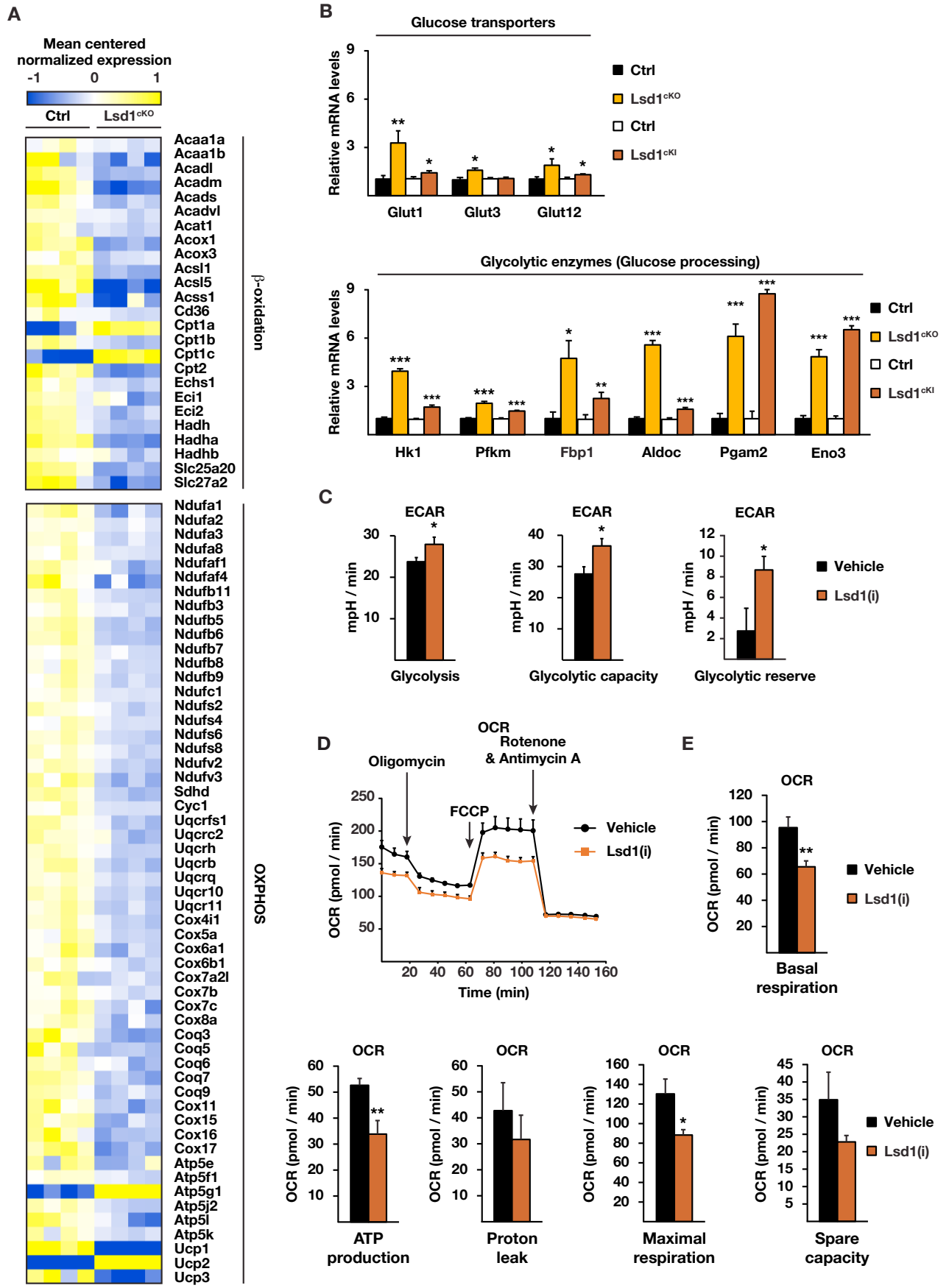
(C) Western blot analysis of individual fractions of brown adipocyte nuclear extracts obtained after gel filtration. Membranes were decorated with Lsd1 or Nrf1 antibody.

(D) Immunoprecipitation of Nrf1 with Lsd1 antibody from BAT nuclear extracts. Membranes were decorated with Lsd1 or Nrf1 antibody. Rabbit IgG (rbIgG) served as a control.

(E) Relative mRNA levels of Lsd1 and Nrf1 in brown adipocytes transfected with siRNA Ctrl, siRNA Lsd1, or siRNA Nrf1 (mean + SEM, n = 3). In agreement with previous data (Duteil et al., 2014), knock-down of Lsd1 results in reduced mRNA levels of Nrf1.

(F) Venn diagram depicting the overlap between Lsd1 interacting proteins identified by immunoprecipitation using three different Lsd1 antibodies followed by mass spectrometry. Ab1 and Ab2 correspond to 2 homemade anti-Lsd1 antibodies (see Experimental procedures for details) and Ab3 corresponds to the L-4481 (Sigma) anti-Lsd1 antibody.

(G) Immunoprecipitation of components of the CoREST complex with Lsd1 antibody from BAT nuclear extracts. Membranes were decorated with the indicated antibodies. Rabbit IgG (rbIgG) served used as a control.
(H) Western blot analysis of individual fractions of brown adipocyte nuclear extracts obtained after gel filtration. Membranes were decorated with the indicated antibodies.
(I) Western blot analysis of Lsd1, Rcor1, and Rcor3 in brown adipocytes transfected with siRNA Ctrl, siRNA Lsd1, siRNA Rcor1, or siRNA Rcor3. β-Tubulin was used as a loading control.
(J) Oil red O staining of brown adipocytes transfected with siRNA Ctrl, siRNA Lsd1, siRNA Rcor1, or siRNA Rcor3. Scale bar: 50 μm.
(K-L) ChIP analysis to detect promoter occupancy performed with (K) anti-Lsd1, anti-Rcor1, and anti-Rcor3 antibody or rbIgG, and (L) anti-H3K9me2 antibody or mIgG in brown adipocytes treated with Lsd1(i) or vehicle. The precipitated chromatin was quantified by qPCR analysis with primers flanking Lsd1-binding sites in the indicated genes (mean + SEM, n = 3).
(A), (E), (K): one-way ANOVA; (B), (L): two-way ANOVA; *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$.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Mean centered normalized expression
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0
1
Ctrl
Lsd1cKO
Acaa1a
Acaa1b
Acadl
Acadm
Acads
Acadvl
Acat1
Acox1
Acox3
Acsl1
Acsl5
Acss1
Cd36
Cpt1a
Cpt1b
Cpt1c
Cpt2
Echs1
Eci1
Eci2
Hadh
Hadha
Hadhb
Slc25a20
Slc27a2
β-oxidation
Ndufa1
Ndufa2
Ndufa3
Ndufa8
Ndufaf1
Ndufaf4
Ndufb11
Ndufb3
Ndufb5
Ndufb6
Ndufb7
Ndufb8
Ndufb9
Ndufc1
Ndufs2
Ndufs4
Ndufs6
Ndufs8
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Ndufv3
Sdhd
Cyc1
Uqcrfs1
Uqcrc2
Uqcrh
Uqcrb
Uqcrq
Uqcr10
Uqcr11
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Cox6a1
Cox6b1
Cox7a2l
Cox7b
Cox7c
Cox8a
Coq3
Coq5
Coq6
Coq7
Coq9
Cox11
Cox15
Cox16
Cox17
Atp5e
Atp5f1
Atp5g1
Atp5j2
Atp5l
Atp5k
Ucp1
Ucp2
Ucp3
OXPHOS
B
Glucose transporters
Relative mRNA levels
Ctrl
Lsd1cKO
Ctrl
Lsd1cKI
Glut1
Glut3
Glut12
Glycolytic enzymes (Glucose processing)
Hk1
Pfkm
Fbp1
Aldoc
Pgam2
Eno3
C
ECAR
mpH / min
Glycolysis
Glycolytic capacity
Glycolytic reserve
Vehicle
Lsd1(i)
D
OCR
Oligomycin
FCCP
Rotenone & Antimycin A
OCR (pmol / min)
Time (min)
E
Basal respiration
ATP production
Proton leak
Maximal respiration
Spare capacity

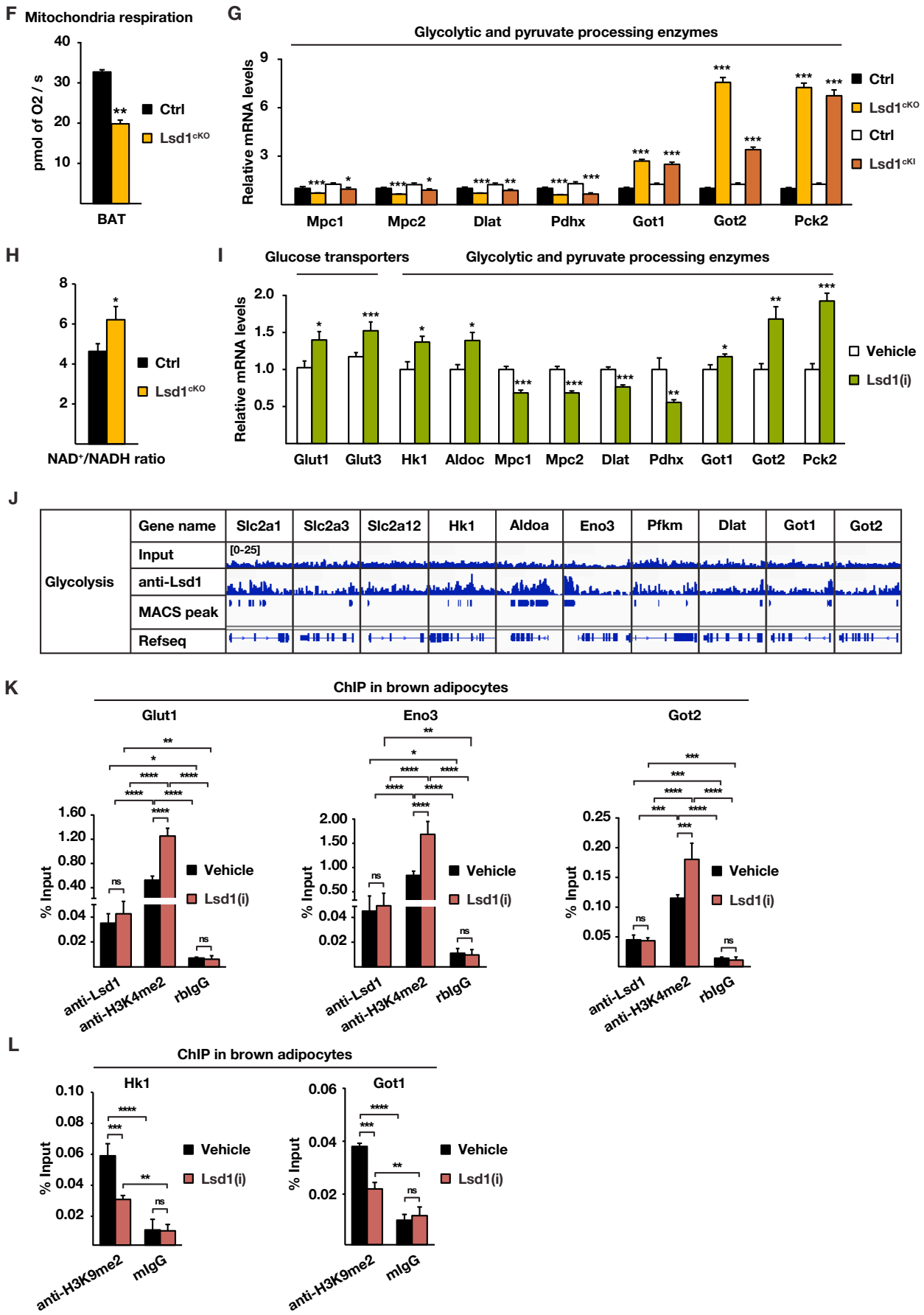


Figure S4 (related to Figure 4). Lsd1 represses glycolysis in BAT.
(A) Heatmaps depicting mRNA levels of genes involved in β-oxidation and oxidative phosphorylation (OXPHOS) in BAT of 10 week-old control (Ctrl) and Lsd1^{cKO} mice.

(B) Relative mRNA levels of genes encoding glucose transporters and glycolytic enzymes in BAT of Ctrl, $Lsd1^{cKO}$, and $Lsd1^{cKI}$ mice [mean + SEM, *p<0.05, **p<0.01, ***p<0.001, Ctrl (black bars) n = 9, $Lsd1^{cKO}$ (orange bars) n = 7, Ctrl (white bars) n = 7, and $Lsd1^{cKI}$ (red bars) n = 6].
(C) Glycolysis, maximal glycolytic capacity and glycolytic reserve deduced from extracellular acidification rate (ECAR) (mean + SEM, *p<0.05, n = 6).
(D-E) Oxygen consumption rate (OCR) of vehicle- or Lsd1(i) treated brown adipocytes determined by the Seahorse Extracellular Flux Analyzer (mean + SEM, *p<0.05, n = 9).
(F) Mitochondrial respiration of BAT extracts from Ctrl and $Lsd1^{cKO}$ mice assessed with a high-resolution respiratory Oxygraph-2K system (mean + SEM, **p<0.01, n = 5).
(G) Relative mRNA levels of genes encoding glycolytic and pyruvate processing enzymes in BAT of Ctrl, $Lsd1^{cKO}$, and $Lsd1^{cKI}$ mice [mean + SEM, *p<0.05, **p<0.01, ***p<0.001, Ctrl (black bars) n = 9, $Lsd1^{cKO}$ (orange bars) n = 7, Ctrl (white bars) n = 7, and $Lsd1^{cKI}$ (red bars) n = 6].
(H) Determination of the NAD^+/NADH ratio in BAT of Ctrl and $Lsd1^{cKO}$ mice at 10 weeks of age (mean + SEM, **p<0.01, ***p<0.001, n = 6).
(I) Relative mRNA levels of selected genes encoding glucose transporters, glycolytic, and pyruvate processing enzymes in BAT of mice treated with vehicle or Lsd1(i) [mean + SEM, *p<0.05, **p<0.01, ***p<0.001, Vehicle n = 6, Lsd1(i) n = 7].
(J) Localization of Lsd1 at the promoter of representative genes encoding glucose transporters, glycolytic and pyruvate processing enzymes in brown adipocytes.
(K-L) ChIP analysis to detect promoter occupancy performed with (K) anti-Lsd1 and anti-H3K4me2 antibody, or rbIgG or (L) anti-H3K9me2 antibody, or mIgG in brown adipocytes treated with vehicle or Lsd1(i). The precipitated chromatin was quantified by qPCR analysis with primers flanking Lsd1-binding sites in the indicated genes (mean + SEM, two-way ANOVA, ns: p>0.05, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001, n = 3).

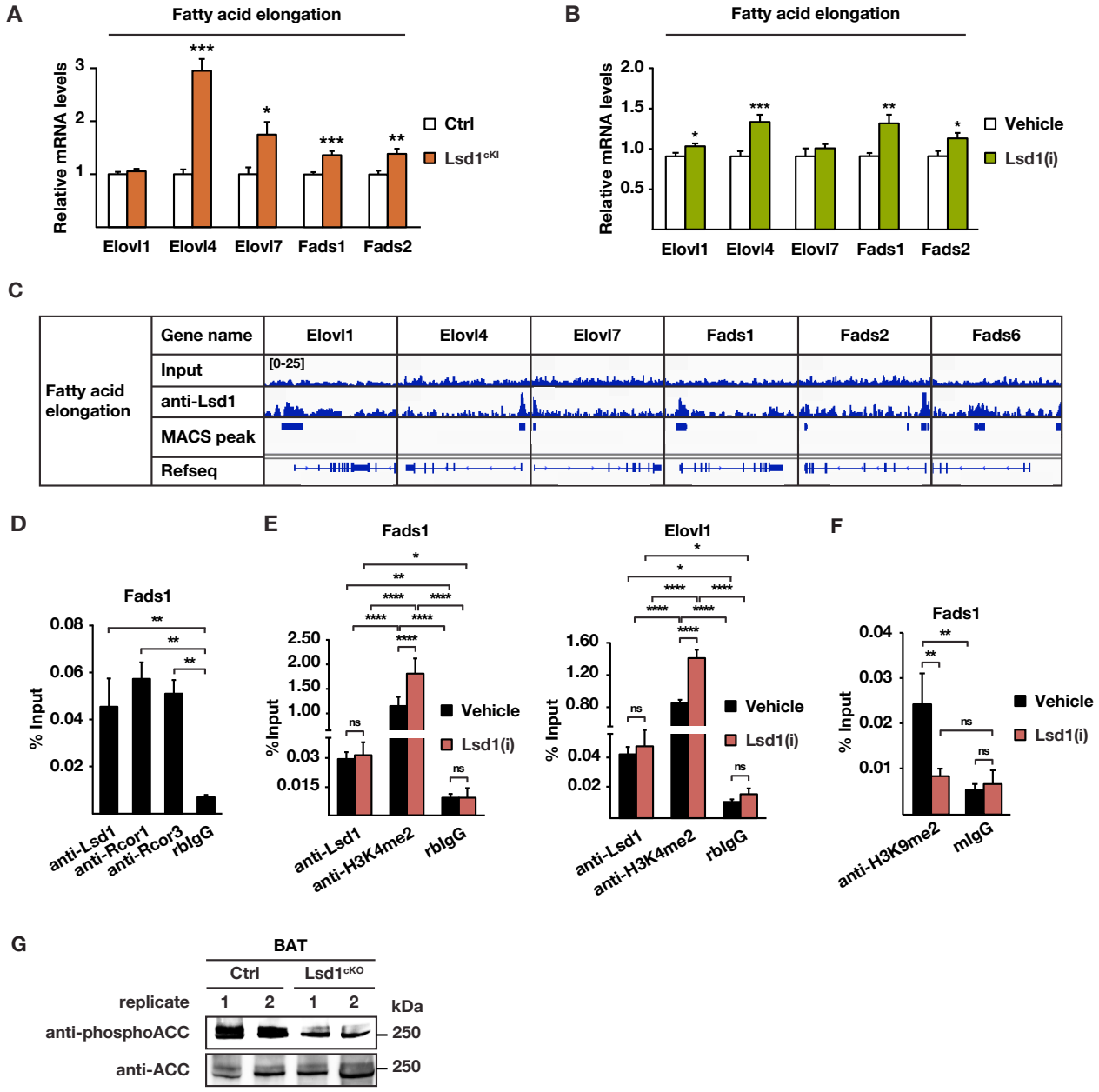


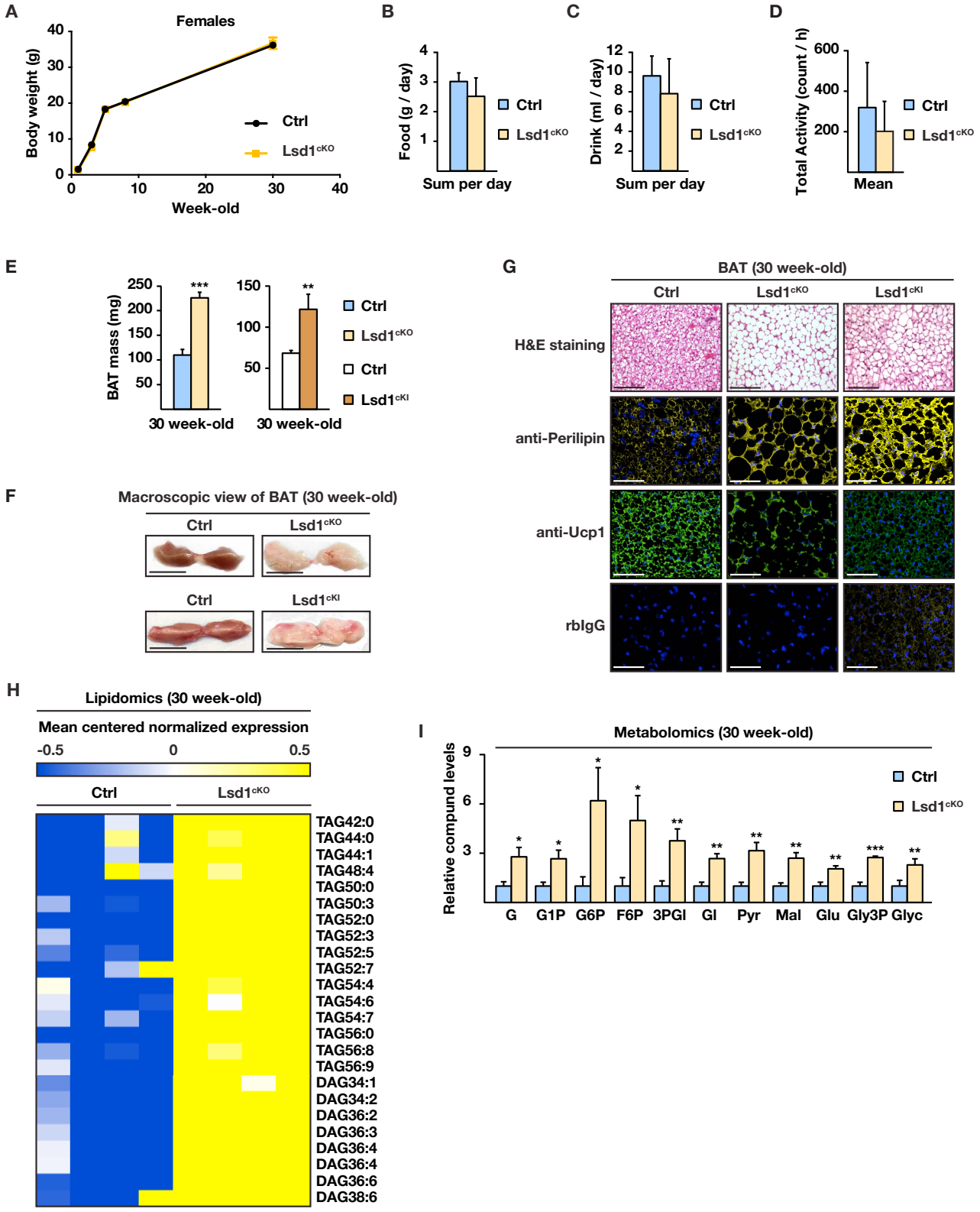
Figure S5 (related to Figure 5). Lsd1 limits fat accumulation in BAT.

(A-B) Relative mRNA levels of indicated enzymes involved in fatty acid elongation in BAT of (A) Ctrl and Lsd1^{cKI} mice and (B) mice treated with vehicle or Lsd1(i) [(A-B) mean + SEM, *p<0.05, **p<0.01, ***p<0.001; (A) Ctrl n = 7, Lsd1^{cKI} n = 6; (B) Vehicle n = 6, Lsd1(i) n = 7].

(C) Localization of Lsd1 at the promoter of representative genes encoding enzymes involved in fatty acid elongation in brown adipocytes.

(D-F) ChIP analysis to detect promoter occupancy performed with with (D) anti-Lsd1, anti-Rcor1, and anti-Rcor3 antibody or rbIgG in brown adipocytes, (E) anti-Lsd1 and anti-H3K4me2 antibody, or rbIgG, or (F) anti-H3K9me2 antibody, or mIgG in brown adipocytes treated with vehicle or Lsd1(i). The precipitated chromatin was quantified by qPCR analysis with primers flanking Lsd1-binding sites in the indicated genes (mean + SEM, (D) one-way ANOVA, (E-F) two-way ANOVA, ns: p>0.05, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001, n = 3).

(G) Western blot analysis of phosphor-ACC and total ACC in BAT of Ctrl and Lsd1^{cKO} mice.


A
Females
Body weight (g)
Week-old
Ctrl
Lsd1cKO
B
Food (g / day)
Sum per day
C
Drink (ml / day)
Sum per day
D
Total Activity (count / h)
Mean
E
BAT mass (mg)
30 week-old
30 week-old
Ctrl
Lsd1cKO
Ctrl
Lsd1cKI
F
Macroscopic view of BAT (30 week-old)
Ctrl
Lsd1cKO
Ctrl
Lsd1cKI
G
BAT (30 week-old)
Ctrl
Lsd1cKO
Lsd1cKI
H&E staining
anti-Perilipin
anti-Ucp1
rbIgG
H
Lipidomics (30 week-old)
Mean centered normalized expression
-0.5
0
0.5
Ctrl
Lsd1cKO
TAG42:0
TAG44:0
TAG44:1
TAG48:4
TAG50:0
TAG50:3
TAG52:0
TAG52:3
TAG52:5
TAG52:7
TAG54:4
TAG54:6
TAG54:7
TAG56:0
TAG56:8
TAG56:9
DAG34:1
DAG34:2
DAG36:2
DAG36:3
DAG36:4
DAG36:4
DAG36:6
DAG38:6
I
Metabolomics (30 week-old)
Relative compund levels
Ctrl
Lsd1cKO
G
G1P
G6P
F6P
3PGl
Gl
Pyr
Mal
Glu
Gly3P
Glyc

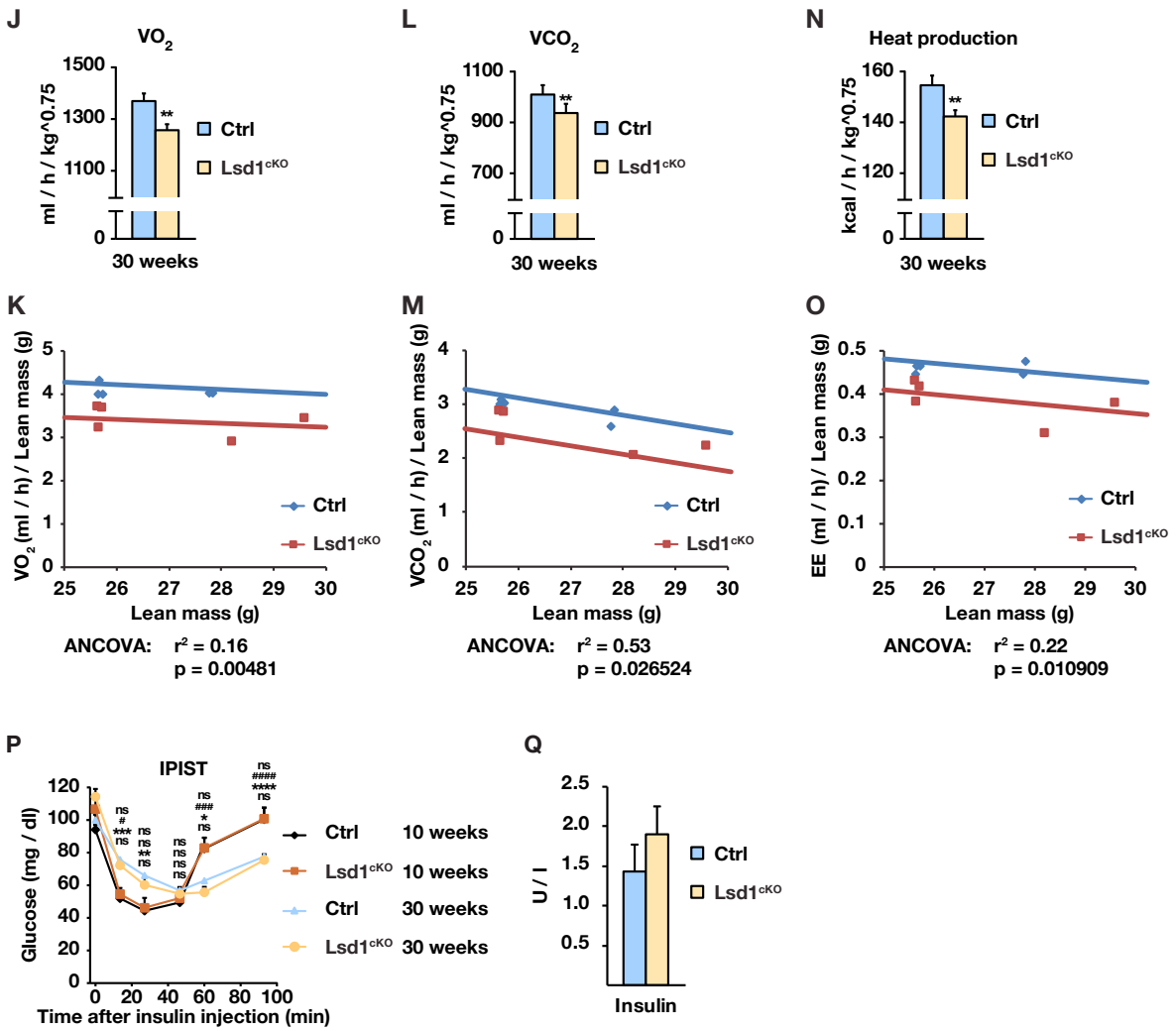


Figure S6 (related to Figure 6). Lsd1^{cKO} mice have a higher glucose uptake despite an increased body weight.
(A) Body weight of control and Lsd1^{cKO} female mice at indicated age (mean + SEM; two-way ANOVA with repeated measures; factor interaction: $p_{genotype/time}$: ns; Ctrl n = 6, Lsd1^{cKO} n = 6).
(B-D) (B) Food consumption, (C) drink consumption, and (D) total activity of 30 week-old control (Ctrl) and Lsd1^{cKO} mice (mean + SEM, Ctrl n = 9, Lsd1^{cKO} n = 7).
(E-F) (E) Mass and (F) macroscopic view of BAT of 30 week-old Ctrl, Lsd1^{cKO}, and Lsd1^{cKI} mice [(D) mean + SEM, **p<0.01, ***p<0.001, Ctrl n = 9, Lsd1^{cKO} n = 7, and Ctrl n = 7, Lsd1^{cKI} n = 6].
(G) H&E staining and perilipin or Ucp1 immunofluorescence of representative sections of BAT of 30 week-old Ctrl, Lsd1^{cKO}, and Lsd1^{cKI} mice. Nuclei were counterstained with DAPI. Rabbit IgG (rbIgG) was used as negative control.
(H) Lipidomic analysis of BAT from 30 week-old Ctrl and Lsd1^{cKO} mice (mean + SEM, n = 5).
(I) Relative abundance of indicated metabolites in BAT of Ctrl and Lsd1^{cKO} mice. G: glucose, G1P: glucose-1-phosphate, G6P: glucose-6-phosphate, F6P: fructose-6-phosphate, 3PGl: 3-phosphoglycerate, Gl: glycerate, Pyr: pyruvate, Mal: malate, Glu: glutamate, Gly3P: glycerol-3-phosphate, Glyc: glycerol (mean + SEM, n = 5, *p<0.05, **p<0.01, ***p<0.001).
(J-O) (J-K) VO_2, (L-M) VCO_2, and (N-O) energy expenditure of 30 week-old control and Lsd1^{cKO} mice represented related to the metabolic body weight (J, L, and N) (mean + SEM, *p<0.05, **p<0.01, Ctrl n = 8, Lsd1^{cKO} n = 7) or as a linear regression (K, M, and O) for which an ANCOVA analysis was performed.
(P) Intraperitoneal insulin sensitive test (IPIST) for 10 week-old or 30 week-old control and Lsd1^{cKO} mice starved for 6 hours prior to analysis (mean + SEM, two-way ANOVA, Ctrl 10 week-old vs Lsd1^{cKO} 10 week-old: ns p>0.05; Ctrl 10 week-old vs Ctrl 30 week-old: **p<0.01, ***p<0.001, ****p<0.0001; Lsd1^{cKO} 10 week-old vs Lsd1^{cKO} 30 week-old: # p<0.05, ### p<0.001, #### p<0.0001; Ctrl 30 week-old vs Lsd1^{cKO} 30 week-old: ns p>0.05; Ctrl n = 8, Lsd1^{cKO} n = 7).
(Q) Serum insulin levels of 30 week-old control (Ctrl) and Lsd1^{cKO} mice (mean + SEM, Ctrl n = 9, Lsd1^{cKO} n = 7).
Scale bars: (F) 7 mm, (G) H&E staining 100 µm, immunofluorescence 20 µm.

Supplemental Tables

Table S1 (related to Figure 1). mRNA ratios [represented as log(fold change), logFC] for BAT- (yellow) and WAT-selective (bleu) genes in BAT and WAT of 10 week-old control mice (BAT / WAT) and in BAT of 10 week-old Lsd1^{cKO} and control mice (cKO / Ctrl).

Table S2 (related to Figure 3). List of the 163 Lsd1 interacting proteins identified by immunoprecipitation followed by mass-spectrometry. The calculation of log2-value is described in Materials and Methods.

Gene	Sense	Primer 5'-3'
***Lsd1* WT/L2**	fw	CCTCAGTAGGCCTGGTTTGT
***Lsd1* WT/L2**	rev	TTGGTTTTGGTTGACCCTTC
***Lsd1* L-**	fw	CCGTGGAAATTCGTGCACTC
***Lsd1* L-**	rev	GCAGGCGGTTTGAAATGTATTC
***Lsd1* WT/KI**	fw	CCAGCTGCTTGTTGGTGC
***Lsd1* WT/KI**	rev	TGGAGTGAAGTGGTTACCTGC
Ucp1-Cre	fw	CCTCTGCACTGGCACTACCT
Ucp1-Cre	rev	TCTTCTTCTTGGGCACCATC

Table S3 (related to Figure S1). Primers used for genotyping

Gene	Sense	Primer 5'-3'
Tbp	fw	GAAGCTGCGGTACAATTCCAG
Tbp	rev	CCCCTTGTACCCTTCACCAAT
36b4	fw	GCGTCCTGGCATTGTCTGT
36b4	rev	GCAAATGCAGATGGATCAGCC
Hprt	fw	AGGGCATATCCAACAACAAACTT
Hprt	rev	GTTAAGCAGTACAGCCCCAAA
Lsd1	fw	GTGTTCTGGGACCCAAGTGT
Lsd1	rev	TAATGCCAGCAGCTTCTCCT
Bmp4	fw	GCTGGAATGATTGGATTGTGG
Bmp4	rev	ATGGCATGGTTGGTTGAGTTG
Egfr	fw	ACACTGCTGGTGTTGCTGAC
Egfr	rev	CCCAAGGACCACTTCACAGT
Pdk3	fw	TTTGAGAGGCTGCCAGTTTT
Pdk3	rev	CGTCTCTGGTTGACTTGCAG
Fads1	fw	AAGGCCAACCACCTCTTCTT
Fads1	rev	ACTGACAGGTGCCCAAAGTC
Apoe	fw	GGTTCGAGCCAATAGTGGAA
Apoe	rev	TATTAAGCAAGGGCCACCAG
Klhl13	fw	AGAATTGGTTGCTGCAATACTCC
Klhl13	rev	AAGGCACAGTTTCAAGTGCTG
Rtn1	fw	TCCGCATCTACAAGTCCGTT
Rtn1	rev	AAAAGCCTCCGTAGCTCCTT
Bmp1	fw	CAAGGCCCACTTCTTCTCAG
Bmp1	rev	TTGTGTTCACAGCCAGCTTC
Wls	fw	ATTTGACTGGACCTGGATGC
Wls	rev	TTCCAGTACCCTGCAATGTG
Ucp1	fw	TGGCAAAAACAGAAGGATT
Ucp1	rev	CGAGTCGCAGAAAAGAAGC
Slc27a2	fw	ATGCCGTGTCCGTCTTTTAC
Slc27a2	rev	CGATGATGATTGATGGTTGC
Acadm	fw	GGATGACGGAGCAGCCAATG
Acadm	rev	ATACTCGTCACCCTTCTTCT
Oplah	fw	CTTCACGCACGTCTCCTTGT
Oplah	rev	GCATCTGCACAGGCCGTAT
Acadl	fw	TTGGTGGGGACTTGCTCTCA
Acadl	rev	CTGTTCTTTTGTGCCGTAAT
Cox6a1	fw	TGCTCAACGTGTTCCTCAAG
Cox6a1	rev	TAAGGGTCCAAAACCAGTGC
Prdm16	fw	CCCCCAACGCTCTCGGATCC
Prdm16	rev	CCGAAGCAGCGGTTGCACAG
Cox17	fw	ATAGTTGCTTTCGCCTGGAA
Cox17	rev	ACAAAGTAGGCCACCACGTC
Elovl1	fw	TTCCAACTTCGAGGCTTCAT
Elovl1	rev	GCTCAATGACCTTGGAAAGC
Elovl4	fw	ACTATGGGCTGACTGCGTTC
Elovl4	rev	TTCCGGTTTTTGACTGCTTC
Elovl7	fw	TCATCCTGGGCCTCTATGTC
Elovl7	rev	ACCATCCTCATTGCTCTTGG
Fads2	fw	GCTCTCAGATCACCGAGGAC
Fads2	rev	AGTGCCGAAGTACGAGAGGA

Gene	Sense	Primer 5'-3'
Hk1	fw	TGGACAAAGGGATTCAAAGC
Hk1	rev	CTCCACCATCTCCACGTTTT
Pfkm	fw	GCTGTGGTCCGAGTTGGTAT
Pfkm	rev	CTCTCGGAAGTCCTTGCATC
Fbp1	fw	CCATCATAATCGAACCTGAG
Fbp1	rev	CTTCTCAGAAGGCTCATCAG
Aldoc	fw	CTGCTCAAGCCCAATATGGT
Aldoc	rev	CTTCACTCTGACCCCCAGAC
Pgam2	fw	ACACCTCCATCAGCAAGGAC
Pgam2	rev	GGGCTGCAATAAGCACTCTC
Eno3	fw	CTCCGAGATGGAGACAAAGC
Eno3	rev	CGTCCAGCTCAATCATGAAC
Ldha	fw	AGACAAACTCAAGGGCGAGA
Ldha	rev	CAGCTTGCAGTGTGGACTGT
Mpc1	fw	ACTTTCGCCCTCTGTTGCTA
Mpc1	rev	AAGTCGTCCTCCCTGAATGA
Mpc2	fw	TGTTGCTGCCAAAGAAATTG
Mpc2	rev	GCTAGTCCAGCACACACCAA
Dlat	fw	TCCAAAGCGAGAGAGGGTAA
Dlat	rev	AGCACCGATTGCCAGAATAC
Pdhx	fw	ATTCCCAAGGATGTCAGTGC
Pdhx	rev	CAGCTGGACTTAAGCGGAAC
Got1	fw	GCTGACTTCTTAGGGCGATG
Got1	rev	TAGCAATAGGGCCGAATGTC
Got2	fw	TTGATCCGTCCCCTGTATTC
Got2	rev	TTAGGCCGGTGAAACAGAAC
Pck2	Fw	GGGGTACCACTGGTGTACGA
Pck2	rev	TCTCTCCGGAACCAATTGAC
Glut1	fw	TCAACACGGCCTTCACTG
Glut1	rev	CACGATGCTCAGATAGGACATC
Glut3	fw	TTCTGGTCGGAATGCTCTTC
Glut3	rev	AATGTCCTCGAAAGTCCTGC
Glut12	fw	ACTATCCCAGCAACCCTCCT
Glut12	rev	AAACTCCTCCAGGGACTGGT
Ndufa6	fw	GTCACAGACCCCAGAGTGGT
Ndufa6	rev	TAACATGCACCTTCCCATCA
Sdha	fw	ACACAGACCTGGTGGAGACC
Sdha	rev	GGATGGGCTTGGAGTAATCA
Uqcrc1	fw	GACAACGTGACCCTCCAAGT
Uqcrc1	rev	ACTGGTACATAGGCGCATCC
Cox8b	fw	GAACCATGAAGCCAACGACT
Cox8b	rev	GCGAAGTTCACAGTGGTTCC
Atp5b	fw	GAGGGATTACCACCCATCCT
Atp5b	rev	CATGATTCTGCCCAAGGTCT
Cpt1b	fw	CAGCTGGCTGGTTGTTGTCA
Cpt1b	rev	TTGTCGGAAGAAGAAAATGC
Pgc1a	fw	AAGTGTGGAACTCTCTGGAACTG
Pgc1a	rev	GGGTTATCTTGGTTGGCTTTATG
Cox2	fw	CAGTCCCCTCCCTAGGACTT
Cox2	rev	TTTCAGAGCATTGGCCATAGAA
Fasn	fw	AGGATATGGAGAGGGCTGGT
Fasn	rev	ACCCAAGCATCATTTTCGTC

Table S4. Primers used for qPCR analysis

Gene	Sense	Primer 5'-3'
Acadm	fw	CTTCGTGTTGTGCCTGTGTT
Acadm	rev	GCCACTTCTCTCCAGTCACC
Oplah	fw	CAGGGGGAAAGTAGGAAAGG
Oplah	rev	CCAGGCTTGTGTGTCTGTGT
Cox6a1	fw	TTGCGAGCTTTTCTGGTTTT
Cox6a1	rev	GGGCACAACGGAAGAGAATA
Unrelated1	fw	AATGCCTCTCACGCTCAACT
Unrelated1	rev	AAGTGTGTGCCATCCTTTCC
Pdk3	fw	TTCCTTAAAGCCCCGGTAAC
Pdk3	rev	GGGAGGTCTAGAGCCCCTAA
Fads1	fw	ACGGTGAGAGCGGACAATAG
Fads1	rev	ATCCAACCCATGCTTGAGAC
Bmp1	fw	GTCTCTGTCGCTGTCCTTCC
Bmp1	rev	TTCTCAGCTCGGCTTCTAGC
Wls	fw	CTGGCTGTGGCTTGTGTAAA
Wls	rev	GGACAAGAGGCAAAAGCAAC
Unrelated2	fw	AGCCAGGGCTACACAGAGAA
Unrelated2	rev	AGATTCCTGCACCAAAGTGG
Slc2a1	fw	ATCAGAAAGGGACACGGATG
Slc2a1	rev	AAATCCTCCCGAGGAAAGAA
Slc2a12	fw	CTAGACCCAAATCCCGTTGA
Slc2a12	rev	CGCCGAAGAGGAACATTTTA
Hk1	fw	AAACTAGGCGGCTTCACAGA
Hk1	rev	GGGGACCATGAGCTCTTACA
Eno3	fw	GCGGAGAGAGTTACCGAGTG
Eno3	rev	TTCCTGCGTGAAGCCTAAGT
Got1	fw	CCGCAGTGAGCTTAAAGACC
Got1	rev	AGTCGGAAGGTTGTGATTGG
Got2	fw	GTAAGACGGCAGTGGATGGT
Got2	rev	CTTGCGAGTTTCCATGACCT
Elovl1	fw	CAGCCCTTAGTAGGCACAGC
Elovl1	rev	CACCCAGCTTCTTCTTGAGG

Table S5. Primers used for ChIP-qPCR analysis

Supplemental Experimental Procedures

Generation of conditional *Lsd1* knock-out and knock-in mice

All experiments were performed in C57/Bl6N background. The targeting strategy for the conditional deletion of the first exon of *Lsd1* (*Lsd1*^{tm1Schüle}) is available upon request (Zhu et al., 2014). Briefly, conditional *Lsd1* mice were mated with *Ucp1-Cre* mice to selectively ablate *Lsd1* in brown adipose tissue (Figures S1A and S1B). Homozygous conditional mice were used as controls. Mice were genotyped with primers for detection of conditional *Lsd1* alleles and *Cre* recombinase (Table S3).

Lsd1 knock-in (KI) mice were generated by Taconic [C57BL/6-Kdm1a$^{tm2931(K662A,\ W752A,\ Y762S)Arte}$]. The targeting vector has been engineered as follows (Figure S1F). Wild-type *Lsd1* exons 15 to 19, including the complete 3‘ untranslated region (UTR), were flanked by *loxP* sites. An additional polyadenylation signal (hGHpA: human Growth Hormone polyadenylation signal) was inserted between the 3’ UTR and the distal *loxP* site in order to prevent downstream transcription of the mutated *Lsd1* exons 15 to 19. The size of the *loxP*-flanked region is 5.1 kb. Exons 15 to 19, including the splice acceptor site of intron 14, were duplicated and inserted downstream of the distal *loxP* site. Intron 15 was removed from the wild-type and the duplicated region in order to create a fusion of exon 15/16. K662A mutation was introduced into the duplicated exon 15, W752A and Y762S mutations were introduced into the duplicated exon 18. A second hGHpA cassette was inserted downstream of the duplicated 3‘ UTR. Positive selection markers were flanked by *FRT* (Neomycin resistance) and *F3* (Puromycin resistance) sites, and inserted into intron 14 and downstream of the second hGHpA, respectively. The targeting vector has been generated using BAC clones from the C57BL/6J RPCIB-731 BAC library and transfected into the Taconic Artemis C57BL/6N Tac ES cell line. Homologous recombinant clones were isolated using double positive (NeoR and PuroR) selection (in order to increase the efficiency of co-integration of both *loxP* sites and the point mutations). The conditional KI allele was obtained after Flp-mediated deletion of the selection markers. This allele expresses wild-type Lsd1 protein. The presence of the first hGHpA cassette downstream of the wild-type exon 19 should prevent transcription of the mutated exons 15 to 19. Conditional *Lsd1*$^{KI/KI}$ mice were crossed to *Ucp1-Cre* mice to selectively express mutated Lsd1 in brown adipose tissue (Lsd1^{cKI} mice). Homozygous conditional *Lsd1*$^{KI/KI}$ mice were used as controls. Mice were genotyped with primers for detection of conditional KI alleles and *Cre recombinase* (Figure S1G and Table S3).

RNA preparation, qRT-PCR, and RNA sequencing (RNA-seq)

RNA was isolated with TRIzol Reagent (Invitrogen) and processed as described (Duteil et al., 2014). Data were analyzed using the standard curve method (Bookout et al., 2006). *36b4*, *Hprt*, or *β-actin* were used for normalization. Primer sequences are given in Table S4.

RNA samples were sequenced by the standard Illumina protocol to create raw sequence files (.fastq files). We annotated these reads to the mm10 build of the mouse genome using TopHat version 2. The aligned reads were counted with the homer software (analyze RNA) and DEGs were identified using EdgeR and DESeq version 1.8.3. Differentially regulated genes (reads > 50, $p < 0.01$) were further used for pathway analysis in WebGestalt (Heinz et al., 2010; Wang et al., 2013).

Protein analyses

Western blot analysis, co-immunoprecipitation assays, gel filtration, and mass spectrometry experiments were performed as described (Duteil et al., 2014; Metzger et al., 2016). For gel filtration, brown adipocytes were harvested and suspended in isolation buffer (10 mM HEPES-KOH, pH 7.9, 1.5 mM $MgCl_2$, 10 mM KCl, 0.5 mM DTT, and complete protease inhibitor cocktail, Roche), allowed to swell on ice for 10 min, and pelleted. Isolated nuclei were resuspended in 20 mM HEPES-KOH, pH 7.9, 25 % glycerol, 420 mM NaCl, 1.5 mM $MgCl_2$, 0.2 mM EDTA, 0.5 mM DTT, and complete protease inhibitor cocktail, incubated on ice for 20 min and centrifuged at 14,000 r.p.m. for 10 min. Nuclear complexes were separated by gel filtration on a Superose 6^{TM} 10/300 GL column (GE Healthcare) using the ÄKTA pure 25 system (GE Healthcare). The void volume was 7.2 mL. 60 fractions of 300 µL were collected from an elution volume of 4.8 mL. The gel filtration buffer was composed of 50 mM KCl, 50 mM $NaCH_3COOH$, pH 7.2 including protease inhibitors and phosphatase inhibitors (Roche Diagnostics). Column calibration was done using carbonic anhydrase (26 kDa), bovin serum albumin (66 kDa), alchol dehydrogenase (150 kDa), ☙-amylase (200 kDa), apoferritin (443 kDa), and thyroglobulin (669 kDa) as markers according to the method provided by the supplier. Western blot membranes were decorated using following antibodies: anti-Lsd1 [3544 , Schüle laboratory (Duteil et al., 2014), 1/1000], anti-Ucp1 (Abcam, ab10983, 1/1000), anti-Apoe (Santa Cruz, M-20, 1/200), anti-Nrf1 (Abcam, ab55744, 1/500), anti-Hdac1 (Abcam, ab7028-50, 1/1000), anti-Hdac2 (Santa Cruz, sc-7899, 1/2500), anti-Rcor1 (Abcam, ab32631, 1/400), anti-Rcor3 (Abcam, ab76921, 1/2000), anti-Arid1a (Santa Cruz, sc-373784, 1/200), anti-phosphoAcc (Cell signaling, 11818, 1/1000), anti-Acc (Cell signaling, 3676, 1/1000), anti-β-Tubulin (Sigma, T6074, 1/10000), and anti-β-Actin (Sigma, A1978, 1/10000). Secondary antibodies conjugated to horseradish peroxidase (GE Healthcare) were detected using an enhanced chemiluminescence detection system (GE Healthcare). For immunoprecipitation assay, 500 mg of

protein extracts were incubated with 5 µg of anti-Lsd1 (Sigma, L-4481) and processed as described (Metzger et al., 2010). Mass spectrometry experiments were performed as described (Metzger et al., 2016). Lsd1 antibodies used for immunoprecipitation were Sigma L-4481 (Ab3 in Figure S3F), and the two Lsd1 antibodies 20752 and 3544 (Ab1 and Ab2 in Figure S3F, respectively) that we previously characterized (Duteil et al., 2014). The number of peptides obtained for each protein after Lsd1 immunoprecipitation was subtracted from the number of peptides obtained with IgG. The resulting number was then normalized to the number of Lsd1 peptides on a log2 basis. The calculation of log2-value is presented in Table S2. GO cellular component analysis was performed using the Panther algorithm (Ashburner et al., 2000).

Primary cell isolation and cell culture

BAT was cut in small pieces and incubated with 2 mg/ml collagenase I (CLS-1, Worthington) for 45 min. The cell suspension was filtered through a 150 µm nylon mesh and the stromal-vascular fraction (SVF) was isolated by low-speed centrifugation. For FACS analysis, the erythrocyte-free SVF was incubated with a mix of antibodies against different surface markers as described previously (Duteil et al., 2014; Wu et al., 2012) and sorted using an Aria flow cytometer (BD Biosciences). Dead cells were removed using DAPI staining (1/10000). Primary adipocytes were cultured in DMEM High Glucose containing 20 % fetal calf serum (FCS) and 2 % of 1 M Hepes buffer in dishes coated with collagen. Alternatively, preiBA cells were cultured in DMEM containing sodium pyruvate and glutamine (GIBCO 11995-065) supplemented with 10 % FCS. Differentiation of primary adipocytes and preiBA cells was induced by treatment of confluent cells with an adipogenic mixture consisting of 850 nM insulin (Gibco), 1 µM dexamethasone (Calbiochem), 1 µM rosiglitazone (Cayman), 125 nM indomethacin (Sigma), 1 nM T3 (Sigma), and 500 µM isobutylmethylxanthine (Serva) in the presence of 10 % FCS. The differentiation medium was replaced 2 days later with medium supplemented with 10 % FCS, 850 nM insulin, and 1 nM T3 for 2 days. Subsequently, cells were cultured in the same medium for 4 more days and considered as differentiated. Differentiated cells were transfected with 1 mM siRNA against Lsd1, Nrf1, Rcor1, Rcor3, or unrelated control (Invitrogen) using Lipofectamine RNAimax (Invitrogen) according to the manufacturer's instructions. siRNA oligonucleotide sequences were as follows:
Lsd1 siRNA: 5'-CCCAAAGAUCCAGCUGACGUUUGAA-3';
Nrf1 siRNA: 5'-UAUGGUAGCCAUGUGUUCAGUUUGG-3';
Rcor1 siRNA: 5'-GCGCAGUCAAGAACGAGACAAUCUU-3';
Rcor3 siRNA: 5'-UCCCAGAUGCCAAAUUGGAUGAAUA-3';
unrelated control siRNA: 5'-UUCUUAGCAAGACUGGUCUCUAGGG-3'.
Lsd1 inhibitor QC6688 was applied to differentiated cells at 100 nM (in EtOH) for 3 days. EtOH was used as a vehicle. Brown adipocytes were either harvested and snap-frozen for RNA, protein, and chromatin immunoprecipitation experiments, fixed for 1 h with 4 % PFA and stained with Oil Red O, or fixed for 5 min with 1 % PFA for chromatin immunoprecipitation experiments (see bellow).

Chromatin immunoprecipitation (ChIP) and ChIP sequencing (ChIP-seq)

Chromatin immunoprecipitation experiments were performed using anti-Lsd1 (20752, Schüle laboratory), anti-Nrf1 (Abcam, ab55744), anti-Rcor1 (Abcam, ab32631), anti-Rcor3 (Abcam, ab76921), H3K9me2 (Diagenode, Mab-154-050), or H3K4me2 (Diagenode, CS-035-100) antibodies, or a rabbit IgG negative control on protein G-Sepharose 4B (GE Healthcare) essentially as described (Metzger et al., 2008). For ChIP experiments, ChIPed DNA was processed by qPCR analyses with the primers described in Table S5. For ChIP-seq analysis, libraries were prepared from Lsd1-immunoprecipitated DNA according to standard methods. ChIP-seq libraries were sequenced using a HiSeq 2000 (Illumina) and mapped to the mm10 reference genome using bowtie 2 (Langmead et al., 2009). Data were analyzed using the peak finding algorithm MACS 1.41 (Zhang et al., 2008) using input as control. All peaks with a FDR greater than 0.3 % were excluded from further analysis. The uniquely mapped reads were used to generate the genome-wide intensity profiles, which were visualized using the IGV genome browser (Thorvaldsdottir et al., 2012). HOMER (Heinz et al., 2010) was used to annotate peaks, to calculate overlaps between different peak files, and for motif searches. The genomic features (promoter, exon, intron, 3' UTR, and intergenic regions) were defined and calculated using Refseq and HOMER.

Histological and immunofluorescence analysis

Tissues were fixed in 10 % buffered formalin and embedded in paraffin. 5 µm paraffin sections were deparaffinised and rehydrated. Hematoxylin and eosin staining was performed as described (Duteil et al., 2014). For immunofluorescence analyses, rehydrated sections were boiled in antigen unmasking solution (Tris buffer pH 9) for 20 min, cooled to room temperature, washed 3 times with PBS, 0.1 % Triton-X100 for 5 min, blocked for 1 h in 5 % FBS (Gibco, 10270-106) in PBS, 0.1 % Triton-X100, and incubated overnight at 4°C with anti-Lsd1 (1/1000), anti-Ucp1 (Abcam, ab10983, 1/500), or anti-Perilipin (Abcam, ab3526, 1/400) antibodies. Slides were then incubated with secondary antibody conjugated to Alexa488 (Invitrogen, 1/400) and mounted in aqueous

medium (Fluoromount-G, SouthernBiotech, 0100-01) with DAPI (Sigma, D-9542, 1/1000). Ultrastructural analyses were performed as described (Duteil et al., 2014).

Measuring activities of metabolic enzymes

Glucose uptake, hexokinase, phosphofructokinase, enolase, lactate dehydrogenase, glutamate oxaloacetic transaminase, NAD^+/NADH ratio, hormone-sensitive lipase, LPL, and fatty acid synthase activities were assessed by the Glucose Uptake Assay Kit (ab136955, abcam), Hexokinase Colorimetric Assay Kit (MAK091, Sigma), the Phosphofructokinase Colorimetric Assay Kit (MAK093, Sigma), the Enolase Activity Colorimetric/Fluorometric Assay Kit (K691-100, Bio Vision), the Lactate Dehydrogenase Activity Assay Kit (Sigma, MAK066), the Glutamate-oxaloacetate transaminase kit (K753-100, Bio Vision), the NAD/NADH Assay Kit (ab65348, abcam), the Lipase Activity Assay Kit (MAK046, Sigma), the LPL Activity Assay kit (MAK109, Sigma), and Fatty Acid Synthase ELISA kit (ABIN425666, antibodies-online), respectively. All activities were measured using 20-50 mg of BAT according to the manufacturer recommendations.

Metabolomic and lipidomic analyses

Tissue samples were grinded with a Retsch MM440 instrument and further extracted as described in (Giavalisco et al., 2009). LC-MS measurements were performed using a Waters ACQUITY UPLC system coupled to a Thermo-Fisher QExactive mass spectrometer. Lipophilic compounds were separated using a C8 and hydrophilic compounds using a C18 reverse phase column, respectively. The mobile phase composition and electrospray parameters are described in (Giavalisco et al., 2009). Chromatograms were recorded in survey MS mode (Mass Range [100 - 1500]) for hydrophilic compounds and in DDA MS/MS (40 eV collision energy) mode for lipophilic compounds. GC-MS measurements were performed as follows. An aliquot of lower polar extraction phase was dried and the dry residue was sequentially derivatized by methoxyamine/MSTFA and injected onto DB35 GC column (Agilent Technologies GC machine) coupled to Leco Pegasus HT mass spectrometer with EI ionization source. Gas elution was performed for two minutes at 85 °C with a further temperature gradient of 15 °C per minute untill a final temperature of 360 °C was reached.

Peak-picking and background removal of the LC-MS data from measurements of hydrophilic extraction phase was accomplished with the Genedata REFINER MS® 7.5 software. Chromatogram alignment and filtering were completed using in-house R-based software. Filtering included removal of isotopic peaks, in-source fragments, and additional lower intense adducts of the same analyte. The annotation of the content of the sample was accomplished by matching the extracted data from the chromatograms with our library of reference compounds in terms of accurate mass and retention time, and the most abundant adduct was used for relative quantification of a metabolite. For GC-MS data of the same extraction phase NetCDF files were exported from the Leco Pegasus software to "R". The package TargetSearch was used to transform retention time to retention index (RI), to align the chromatograms, extract the peaks, and annotate them by comparing the spectra and the RI to the Golm metabolome database. A unique mass was used to relatively quantify each identified metabolite. For those metabolites, which were annotated in both GC-MS and LC-MS data the value with smallest deviation was kept.

Peak-picking of the LC-MS/MS data from measurements of the lipophilic extraction phase was accomplished with the Genedata REFINER MS® 7.5 software without alignment. Identification of lipid species was performed using output.mgf files with dedicated in-house R-based software. Acyl composition of di- and triacylglycerols was established from the [Acyl + NH4] neutral loss in positive ion mode using a pre-formed library of accurate masses for all possible precursor and fragment peaks.

Mitochondrial respiration

10 mg (wet weight) of BAT were minced and incubated in Mir05 with 50 µg/mL Saponin for 30 min at 37 °C to permeabilize the cell membrane. Mir05 is composed of 0.5 mM EGTA, 3 mM $MgCl_2$, 60 mM K-lactobionate, 20 mM Taurine, 10 mM KH_2PO_4, 20 mM HEPES, 110 mM Sucrose, and 1 g/L BSA fatty acid free. Respiration of permeabilized brown adipocytes was measured by high-resolution respiratory using Oxygraph-2K (OROBOROS INSTRUMENTS, Innsburk, Austria) at 37 °C in 2 mL glass chambers. For each experiment, one control mouse and one $Lsd1^{cKO}$ mouse were processed in parallel in the 2 chambers. Mitochondrial respiration was assessed in Mir05 buffer supplemented with 5 mM glutamate and 2 mM malate substrates to activate mitochondrial complex I. After stabilization of mitochondrial respiration, 10 mM succinate were added to activate complex II. Maximal respiration rate was then recorded. 0.5 µM rotenone were finally added to inactivate mitochondrial complex I and measure complex II specific activity. Respiration rates were expressed in pmol / s and reported to 1 mg of tissue. Results presented correspond to maximal mitochondrial respiration rate. Alternatively, mitochondrial respiration was analyzed using 100 µM palmitoyl-L-carnitin as substrate.

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Gene	logFC (BAT / WAT) Ctrl	logFC BAT cKO / Ctrl	Pvalue BAT cKO / Ctrl
Elovl3	5.03299562	-1.62	0.001219151
Ucp1	5.00670672	-1.30	1.30077E-14
Slc27a2	4.37326691	-0.69	6.43585E-05
Ttn	4.29867521	2.43	0.000865337
Cox8b	4.29718081	-0.55	0.000291991
Atp2a1	4.0289958	2.26	0.001667186
Neb	3.96631771	2.37	0.000921791
Acot11	3.83873439	-1.38	1.43858E-12
Myh4	3.7381612	2.13	0.002877973
Tnnt3	3.7380522	2.22	0.001649781
Pvalb	3.72418941	2.19	0.001981397
Kng2	3.72363221	0.59	0.000241961
Myh1	3.41451981	2.15	0.003594862
Myot	3.3878186	2.44	0.000506074
Trdn	3.24837761	2.42	0.00077337
Pygm	3.15693339	2.17	0.000361333
Xirp2	3.1539427	2.14	0.002667801
Elovl6	3.0406506	-1.03	4.75194E-06
Eno3	2.9917913	1.89	0.000221154
Ckm	2.99007899	2.28	0.001188043
Casq1	2.97852901	2.17	0.002159524
Tmod4	2.9119845	1.77	9.63957E-06
Klhl41	2.8879419	2.43	0.000549249
Gys2	2.860137	-0.72	0.000121841
Gyk	2.8223806	-1.13	6.02382E-11
Actn2	2.8101819	2.58	5.44997E-05
Myh2	2.8034711	2.92	0.000331045
Klhl31	2.7929658	2.13	0.002638979
Acta1	2.6715471	2.22	0.002026685
Ryr1	2.6494346	2.50	0.000549159
Actn3	2.6337787	2.28	0.000905087
Tnni1	2.5870373	2.64	0.001651905
Smpx	2.5510228	2.18	0.001558461
Myl1	2.5452367	1.35	8.46766E-06
Tnnc2	2.5245382	2.28	0.001155315
Tbx15	2.4851201	1.49	2.56286E-06
Mb	2.4654502	2.46	0.000290047
Letmd1	2.4425538	-0.88	5.57259E-09
Hfe2	2.4289734	2.20	0.002099998
Mybpc2	2.2732745	2.16	0.002949454
Lmod2	2.2409907	2.54	0.000324037
Srl	2.2243066	1.43	2.73232E-05
Acadl	2.1468803	-0.45	0.0032486
Xrcc6	2.1438778	-0.69	0.000114925
Ampd1	2.1435778	2.44	0.000454238
Nrap	2.1091306	2.57	8.3254E-05
Txlnb	2.0677527	2.45	5.25504E-10
Des	2.055763	1.43	3.24022E-05
Cox5a	2.040698	-0.49	0.001196991
Myom2	2.0159153	2.23	0.002659321
Fam195a	2.0115126	-0.91	1.90933E-09
Plin5	2.0099523	-0.47	0.001420747

Gmpr	1.9825364	0.68	0.00014563
Slc25a48	1.9666641	-0.53	0.001142606
Myf6	1.9282471	2.25	0.000268158
Ndufa1	1.9269462	-0.54	0.000763618
Adra1a	1.9211102	-0.76	4.30516E-05
Etfdh	1.8947846	-0.57	0.000145712
1110001J03Rik	1.8905052	-0.46	0.001313185
Cacna1s	1.8715755	2.48	0.00043397
Pfkm	1.8460598	0.82	4.38404E-05
Asb5	1.8120707	2.40	0.000192744
Ankrd2	1.7627584	2.93	8.48464E-06
Pygl	1.7574803	-0.77	0.000114572
Sgcg	1.7155958	2.35	0.000784189
Sdhd	1.6973534	-0.45	0.002776772
Abcd3	1.6866076	-0.71	2.9521E-05
Mpc1	1.661639	-1.06	1.20683E-08
Adcy10	1.6608713	-1.24	0.000241208
Spata22	1.6560036	-0.61	0.008874902
Rmnd1	1.6449246	-0.38	0.008719637
Rorc	1.6432967	0.50	0.000850651
Ndufb5	1.6432544	-0.51	0.000586518
Ak1	1.6194486	0.77	2.20633E-05
Nr4a1	1.6194294	1.83	6.13833E-08
Acaca	1.6139319	-0.59	0.008281571
Ndufb8	1.6124303	-0.44	0.003666094
Lrpprc	1.6110574	-0.63	3.99638E-05
S100b	1.6078772	0.57	0.000574459
Lrrc2	1.5968932	3.03	5.21862E-05
Uqcr10	1.5763753	-0.45	0.003043739
Hk2	1.565692	-0.79	1.16303E-05
Adrbk2	1.5632039	-0.67	0.000115754
Gbe1	1.5480882	-0.68	1.24887E-05
Cox6a1	1.5214636	-0.63	5.4922E-05
Ndufaf4	1.5154105	-0.45	0.00386484
Abra1	1.5102565	2.33	0.000130738
Pdk1	1.5094381	-0.77	1.02644E-05
Dnajc15	1.5044648	-0.56	0.000206354
Mrpl47	1.4848642	-0.43	0.006890769
H2-Q10	1.478339	0.89	5.24408E-05
Taco1	1.470753	-0.40	0.005326922
Dnaja3	1.4693509	-0.49	0.000906621
Dnajc28	1.4661216	-0.51	0.000479307
Mrpl34	1.4604883	-0.81	6.27865E-08
Cyc1	1.4563158	-0.41	0.007200329
Gapdh	1.4482808	0.92	2.77478E-05
Crls1	1.4178434	-0.60	0.000407998
Tmem143	1.3877961	-0.42	0.005153249
Decr1	1.3641582	-0.48	0.001690793
Idh3g	1.362291	-0.43	0.004820943
Impa2	1.3616334	-0.53	0.004500228
Pdhx	1.3562688	-0.83	9.17093E-08
Acadm	1.3534738	-0.72	2.46911E-06
Dhrs11	1.3515689	-0.48	0.003640452
Ndufs6	1.3508479	-0.44	0.002538835

Slc25a51	1.3482817	-0.52	0.000922129
Vat1l	1.3447501	2.65	1.47501E-23
Atp5j2	1.3325927	-0.44	0.003275362
Echdc1	1.3278418	-0.74	1.30912E-05
Gpd1	1.3261119	-0.64	5.48676E-05
Ndufb9	1.3139325	-0.45	0.003220105
Slmo2	1.3120885	-0.77	1.1809E-06
Oplah	1.3037535	-0.50	0.000733205
Cox4i1	1.3014376	-0.44	0.004233073
Alpk3	1.3013005	2.31	5.28232E-05
Timm44	1.2976149	-0.48	0.001125659
Ndufv2	1.2943616	-0.42	0.005774662
Ifi27	1.2923955	-0.80	1.39289E-07
Prdm16	1.2827252	-0.62	0.007518191
Chkb	1.263494	-0.40	0.006127324
Timm9	1.2634205	-0.91	9.62456E-11
Ptcd3	1.2628892	-0.55	0.000140782
Hsd17b12	1.2612536	-0.78	6.87377E-06
Uck1	1.260333	-0.45	0.002615142
Samm50	1.254787	-0.45	0.002788801
Uqcrb	1.247245	-0.49	0.00115042
Ptges2	1.2245397	-0.45	0.002625114
Bckdha	1.2224938	-0.58	0.000112944
Amacr	1.217493	-0.45	0.001123573
Nat8l	1.1977957	-0.51	0.000948558
Atpaf2	1.1964137	-0.72	1.15585E-06
Tfb2m	1.1924828	-0.71	7.18473E-07
Mtor	1.1913036	-0.85	1.11471E-07
Syngr1	1.1834583	-0.68	1.67645E-05
Usp2	1.1779407	0.75	8.13367E-07
Slc15a5	1.1737574	-1.75	0.000677963
Pla2g7	1.1642939	0.61	0.000191588
Taldo1	1.1560384	-0.67	6.6006E-05
Cox10	1.1406282	-0.52	0.000712683
D10Jhu81e	1.1367016	-0.42	0.005363498
Yars2	1.0970882	-0.47	0.000744108
Pcyt2	1.0903566	-0.77	8.85287E-07
Slc25a32	1.0836581	-0.82	4.60934E-06
Fam96a	1.0835492	-0.43	0.002196928
Rilp	1.0734653	-0.57	0.000180862
Snx10	1.0695383	-0.42	0.009359112
Mmaa	1.0644134	-0.54	0.000253186
Mtif2	1.0612006	-0.46	0.001335321
Mrpl9	1.0555778	-0.38	0.009654965
Akr1b10	1.0505579	1.03	1.41222E-10
Atp6v0a2	1.0503636	-0.65	1.55922E-05
Abcb8	1.0373427	-0.54	0.00029628
Plin2	1.0364955	-0.89	4.12728E-06
Mrpl39	1.0347274	-0.41	0.003638033
Dhrs7	1.0312138	-0.73	1.82953E-06
Mfsd7b	1.0213425	0.71	0.000922663
Ptcd2	1.0197239	-0.40	0.006229583
Mrs2	1.0134	-0.58	0.000705498
Mc5r	1.006574	-1.54	9.30733E-05

Cbr4	1.0038152	-0.48	0.000695764
Cox11	1.0007593	-0.42	0.002623094
Nav2	0.987369401	-0.54	0.004743848
Rnf182	0.987129201	0.63	0.001231806
Cox17	0.9796465	-0.69	6.95036E-06
Agpat3	0.9787027	-0.52	0.000629523
Tbrg4	0.966252101	-0.54	0.00040421
Mrpl51	0.9658004	-0.46	0.001967628
Mrps5	0.9609215	-0.37	0.006716725
Poldip2	0.952709201	-0.58	9.12042E-05
Mkks	0.948025101	-0.53	0.000160747
Bcs1l	0.939809799	-0.52	0.000157574
Lynx1	0.933017399	1.28	8.69779E-11
Mtch2	0.914093999	-0.55	0.000225575
Ccbl2	0.9100549	-0.42	0.008997386
Mab21l2	0.906294399	-0.99	1.31096E-05
L2hgdh	0.903796099	-0.59	0.000254156
Ndufv3	0.8984114	-0.62	3.58306E-05
Gm5069	0.889656301	-0.51	0.005086202
Mrpl3	0.8889495	-0.43	0.003035069
Cspg4	0.8881896	-0.82	1.46654E-06
C330018D20Rik	0.887993101	-0.38	0.008057152
Csrp3	0.869814699	2.55	0.000423532
Cecr2	0.8697951	0.37	0.009857474
Fbxo44	0.865014	0.46	0.002179536
Decr2	0.8518547	-0.50	0.001055388
Hebp2	0.848965599	0.83	0.006420287
Igsf21	0.844494601	-0.99	4.29991E-08
Mrpl2	0.839864299	-0.44	0.002410305
Hhatl	0.839524499	2.12	0.001515449
Cyp1a1	0.8091394	-1.36	7.00504E-06
Mrpl35	0.794774499	-0.47	0.001048432
Mrpl19	0.786392299	-0.48	0.001380077
Ppdpf	0.778606001	-0.75	7.50806E-07
Txnrd2	0.777910399	-0.56	0.000205836
Supv3l1	0.766875801	-0.47	0.001351881
Lipt1	0.763724801	-0.81	4.4759E-07
Clpx	0.750698699	-0.48	0.001132879
Tpte	0.745887201	-0.74	0.007787397
Acn9	0.7209527	-0.75	0.000118817
Sars2	0.715647901	-0.55	0.00066782
Ccbl1	0.6703475	0.45	0.005196054
Mrpl45	0.650774401	-0.44	0.002508633
Myom2	2.0159153	2.23	0.002659321
Fam195a	2.0115126	-0.91	1.90933E-09
Plin5	2.0099523	-0.47	0.001420747
Gmpr	1.9825364	0.68	0.00014563
Slc25a48	1.9666641	-0.53	0.001142606
Myf6	1.9282471	2.25	0.000268158
Ndufa1	1.9269462	-0.54	0.000763618
Adra1a	1.9211102	-0.76	4.30516E-05
Etfdh	1.8947846	-0.57	0.000145712
1110001J03Rik	1.8905052	-0.46	0.001313185
Cacna1s	1.8715755	2.48	0.00043397

Pfkm	1.8460598	0.82	4.38404E-05
Asb5	1.8120707	2.40	0.000192744
Ankrd2	1.7627584	2.93	8.48464E-06
Pygl	1.7574803	-0.77	0.000114572
Sgcg	1.7155958	2.35	0.000784189
Sdhd	1.6973534	-0.45	0.002776772
Abcd3	1.6866076	-0.71	2.9521E-05
Mpc1	1.661639	-1.06	1.20683E-08
Adcy10	1.6608713	-1.24	0.000241208
Spata22	1.6560036	-0.61	0.008874902
Rmnd1	1.6449246	-0.38	0.008719637
Rorc	1.6432967	0.50	0.000850651
Ndufb5	1.6432544	-0.51	0.000586518
Ak1	1.6194486	0.77	2.20633E-05
Nr4a1	1.6194294	1.83	6.13833E-08
Acaca	1.6139319	-0.59	0.008281571
Ndufb8	1.6124303	-0.44	0.003666094
Lrpprc	1.6110574	-0.63	3.99638E-05
S100b	1.6078772	0.57	0.000574459
Lrrc2	1.5968932	3.03	5.21862E-05
Uqcr10	1.5763753	-0.45	0.003043739
Hk2	1.565692	-0.79	1.16303E-05
Adrbk2	1.5632039	-0.67	0.000115754
Gbe1	1.5480882	-0.68	1.24887E-05
Cox6a1	1.5214636	-0.63	5.4922E-05
Ndufaf4	1.5154105	-0.45	0.00386484
Abra1	1.5102565	2.33	0.000130738
Pdk1	1.5094381	-0.77	1.02644E-05
Dnajc15	1.5044648	-0.56	0.000206354
Mrpl47	1.4848642	-0.43	0.006890769
H2-Q10	1.478339	0.89	5.24408E-05
Taco1	1.470753	-0.40	0.005326922
Dnaja3	1.4693509	-0.49	0.000906621
Dnajc28	1.4661216	-0.51	0.000479307
Mrpl34	1.4604883	-0.81	6.27865E-08
Cyc1	1.4563158	-0.41	0.007200329
Gapdh	1.4482808	0.92	2.77478E-05
Crls1	1.4178434	-0.60	0.000407998
Tmem143	1.3877961	-0.42	0.005153249
Decr1	1.3641582	-0.48	0.001690793
Idh3g	1.362291	-0.43	0.004820943
Impa2	1.3616334	-0.53	0.004500228
Pdhx	1.3562688	-0.83	9.17093E-08
Acadm	1.3534738	-0.72	2.46911E-06
Dhrs11	1.3515689	-0.48	0.003640452
Ndufs6	1.3508479	-0.44	0.002538835
Slc25a51	1.3482817	-0.52	0.000922129
Vat1l	1.3447501	2.65	1.47501E-23
Atp5j2	1.3325927	-0.44	0.003275362
Echdc1	1.3278418	-0.74	1.30912E-05
Gpd1	1.3261119	-0.64	5.48676E-05
Ndufb9	1.3139325	-0.45	0.003220105
Slmo2	1.3120885	-0.77	1.1809E-06
Oplah	1.3037535	-0.50	0.000733205

Cox4i1	1.3014376	-0.44	0.004233073
Alpk3	1.3013005	2.31	5.28232E-05
Timm44	1.2976149	-0.48	0.001125659
Ndufv2	1.2943616	-0.42	0.005774662
Ifi27	1.2923955	-0.80	1.39289E-07
Prdm16	1.2827252	-0.62	0.007518191
Chkb	1.263494	-0.40	0.006127324
Timm9	1.2634205	-0.91	9.62456E-11
Ptcd3	1.2628892	-0.55	0.000140782
Hsd17b12	1.2612536	-0.78	6.87377E-06
Uck1	1.260333	-0.45	0.002615142
Samm50	1.254787	-0.45	0.002788801
Uqcrb	1.247245	-0.49	0.00115042
Ptges2	1.2245397	-0.45	0.002625114
Bckdha	1.2224938	-0.58	0.000112944
Amacr	1.217493	-0.45	0.001123573
Nat8l	1.1977957	-0.51	0.000948558
Atpaf2	1.1964137	-0.72	1.15585E-06
Tfb2m	1.1924828	-0.71	7.18473E-07
Mtor	1.1913036	-0.85	1.11471E-07
Syngr1	1.1834583	-0.68	1.67645E-05
Usp2	1.1779407	0.75	8.13367E-07
Slc15a5	1.1737574	-1.75	0.000677963
Pla2g7	1.1642939	0.61	0.000191588
Taldo1	1.1560384	-0.67	6.6006E-05
Cox10	1.1406282	-0.52	0.000712683
D10Jhu81e	1.1367016	-0.42	0.005363498
Yars2	1.0970882	-0.47	0.000744108
Pcyt2	1.0903566	-0.77	8.85287E-07
Slc25a32	1.0836581	-0.82	4.60934E-06
Fam96a	1.0835492	-0.43	0.002196928
Rilp	1.0734653	-0.57	0.000180862
Snx10	1.0695383	-0.42	0.009359112
Mmaa	1.0644134	-0.54	0.000253186
Mtif2	1.0612006	-0.46	0.001335321
Mrpl9	1.0555778	-0.38	0.009654965
Akr1b10	1.0505579	1.03	1.41222E-10
Atp6v0a2	1.0503636	-0.65	1.55922E-05
Abcb8	1.0373427	-0.54	0.00029628
Plin2	1.0364955	-0.89	4.12728E-06
Mrpl39	1.0347274	-0.41	0.003638033
Dhrs7	1.0312138	-0.73	1.82953E-06
Mfsd7b	1.0213425	0.71	0.000922663
Ptcd2	1.0197239	-0.40	0.006229583
Mrs2	1.0134	-0.58	0.000705498
Mc5r	1.006574	-1.54	9.30733E-05
Cbr4	1.0038152	-0.48	0.000695764
Cox11	1.0007593	-0.42	0.002623094
Nav2	0.987369401	-0.54	0.004743848
Rnf182	0.987129201	0.63	0.001231806
Cox17	0.9796465	-0.69	6.95036E-06
Agpat3	0.9787027	-0.52	0.000629523
Tbrg4	0.966252101	-0.54	0.00040421
Mrpl51	0.9658004	-0.46	0.001967628

Mrps5	0.9609215	-0.37	0.006716725
Poldip2	0.952709201	-0.58	9.12042E-05
Mkks	0.948025101	-0.53	0.000160747
Bcs1l	0.939809799	-0.52	0.000157574
Lynx1	0.933017399	1.28	8.69779E-11
Mtch2	0.914093999	-0.55	0.000225575
Ccbl2	0.9100549	-0.42	0.008997386
Mab21l2	0.906294399	-0.99	1.31096E-05
L2hgdh	0.903796099	-0.59	0.000254156
Ndufv3	0.8984114	-0.62	3.58306E-05
Gm5069	0.889656301	-0.51	0.005086202
Mrpl3	0.8889495	-0.43	0.003035069
Cspg4	0.8881896	-0.82	1.46654E-06
C330018D20Rik	0.887993101	-0.38	0.008057152
Csrp3	0.869814699	2.55	0.000423532
Cecr2	0.8697951	0.37	0.009857474
Fbxo44	0.865014	0.46	0.002179536
Decr2	0.8518547	-0.50	0.001055388
Hebp2	0.848965599	0.83	0.006420287
Igsf21	0.844494601	-0.99	4.29991E-08
Mrpl2	0.839864299	-0.44	0.002410305
Hhatl	0.839524499	2.12	0.001515449
Cyp1a1	0.8091394	-1.36	7.00504E-06
Mrpl35	0.794774499	-0.47	0.001048432
Mrpl19	0.786392299	-0.48	0.001380077
Ppdpf	0.778606001	-0.75	7.50806E-07
Txnrd2	0.777910399	-0.56	0.000205836
Supv3l1	0.766875801	-0.47	0.001351881
Lipt1	0.763724801	-0.81	4.4759E-07
Clpx	0.750698699	-0.48	0.001132879
Tpte	0.745887201	-0.74	0.007787397
Acn9	0.7209527	-0.75	0.000118817
Sars2	0.715647901	-0.55	0.00066782
Ccbl1	0.6703475	0.45	0.005196054
Mrpl45	0.650774401	-0.44	0.002508633

Gene	logFC (BAT / WAT) Ctrl	logFC BAT cKO / Ctrl	Pvalue BAT cKO / Ctrl
Pcbd1	-3.2632882	2.66	6.91251E-15
Ear12	-3.1882655	1.60	0.001345952
Chrdl1	-3.0824307	0.42	0.158089413
Nnat	-2.9569817	1.07	0.002900348
Fmod	-2.8289014	1.26	3.62849E-05
Apcdd1	-2.697608	1.35	2.70798E-07
Sucnr1	-2.6807593	-0.80	0.000214181
Gpr133	-2.5279137	0.98	0.002061336
Efemp1	-2.5165729	1.67	4.32858E-19
Thbs1	-2.3937744	1.41	0.000383235
Lyz1	-2.3666866	1.08	0.001513277
Emp1	-2.3386909	0.69	0.000679098
Fgf10	-2.3332402	0.86	0.007962201
Ccnd2	-2.2759691	1.13	3.60936E-07
Steap2	-2.2725703	2.41	1.47612E-08
Fn1	-2.2089048	0.80	0.00161554
Hn1l	-2.1950607	0.60	0.002371773
Boc	-2.1045359	0.66	0.00138771
Cxx1c	-2.1010332	1.39	1.40543E-10
F13a1	-2.0909058	0.68	0.003246755
Bmp4	-2.087984	1.60	0.000204112
Hmgcs2	-2.0595371	0.77	0.003388908
Slit3	-2.0560716	0.85	1.62673E-06
Heph	-2.0215497	1.16	1.42052E-08
Casp12	-2.0171042	1.95	1.36468E-05
Sfrp1	-1.9836814	0.73	0.0051609
Colec12	-1.9790154	0.62	0.006992329
Prps2	-1.9749816	1.43	1.00007E-11
Ptprj	-1.9516001	0.74	0.00101842
Adcy5	-1.9248017	1.68	4.61458E-09
Fam115a	-1.8842348	0.71	8.78633E-06
Tmem176b	-1.8751872	0.78	5.77284E-05
Fmo2	-1.861151	0.60	0.003432056
Abat	-1.8572421	1.61	1.02114E-11
Htra3	-1.856199	-0.53	0.008711887
H2-Aa	-1.8300556	0.86	1.64451E-05
Cpne2	-1.825423	0.94	1.17082E-05
Adamts2	-1.8099403	0.90	3.0872E-06
Clec10a	-1.801191	0.95	0.006797953
Iqgap2	-1.8002544	1.28	0.000142675
Cd74	-1.7964949	0.75	9.36636E-05
Csf1r	-1.7939702	0.72	0.001301145
Gca	-1.7809689	1.56	7.49693E-08
Myof	-1.7765789	0.85	7.9087E-05
Ptplad2	-1.758685	1.13	0.00041861
Slc7a8	-1.7559865	1.18	0.000244908
Cybb	-1.7477015	1.00	8.00961E-05
Podn	-1.7455875	0.78	1.31991E-05
Gas6	-1.7398867	0.76	3.64392E-06
H2-Ab1	-1.7224157	0.80	2.92728E-05
Egfr	-1.7170061	0.76	0.007273341
Mfap5	-1.7147097	0.65	0.005430528

Cacng7	-1.7029779	2.49	2.37841E-25
Pam	-1.6958376	0.71	2.16573E-06
Rab32	-1.6949296	0.80	0.005007434
Lyz2	-1.6946569	0.86	5.63966E-06
Fcgr2b	-1.6904109	0.84	0.004663405
Man1a	-1.6762105	0.60	0.00078319
Serpinb6b	-1.6759304	0.94	0.000692819
Cd53	-1.6745447	0.79	0.001751235
Phgdh	-1.6650659	2.39	3.66785E-14
Ptgis	-1.6644072	-1.17	2.22663E-05
Ecm1	-1.6630135	0.65	0.008539541
Cyp1b1	-1.6619105	0.67	0.001565518
Gstm6	-1.6597105	1.48	0.006412047
Plekhh2	-1.6430072	0.95	0.000687894
Prrg3	-1.6427554	0.86	7.73085E-05
Plxnb2	-1.6374546	1.10	3.81317E-13
Ehd3	-1.6335227	1.09	4.02615E-09
Pdk3	-1.630637	1.38	1.8465E-05
Cd109	-1.6289039	1.09	0.004117425
Dennd2d	-1.6178842	0.76	2.48536E-05
Fads1	-1.6097298	1.01	3.86998E-09
App	-1.6094279	0.47	0.003291249
Pld4	-1.6055948	0.92	0.000443276
Slc39a8	-1.6020375	0.99	5.47767E-05
Mgl2	-1.5999588	0.60	0.007446619
Dab2	-1.5979973	0.52	0.004862248
Pdpn	-1.5968793	1.24	0.000763324
Dse	-1.5865287	0.71	0.004312348
Tmem176a	-1.5726527	0.77	0.002521389
Ifi205	-1.5650766	1.08	0.001937943
Kirrel	-1.5646327	1.28	2.84002E-16
Dock2	-1.5417345	0.91	0.000233977
C1ra	-1.5328077	0.77	5.74342E-05
Bicc1	-1.5196078	0.97	0.000200363
Sec24d	-1.5181492	1.23	9.01972E-13
Trim14	-1.5126389	1.09	0.002736008
Cd34	-1.5093328	0.75	6.10875E-05
Prss23	-1.5021808	1.08	2.11513E-07
Ace	-1.4968087	0.63	0.004743775
Ttc39c	-1.4889196	1.92	2.14847E-07
Ifi27l2a	-1.4845255	0.97	0.006008309
Axl	-1.4811205	0.56	0.002014481
C1qc	-1.4799747	0.76	0.004311418
Pcdh7	-1.4781911	1.27	1.07775E-06
Tgfbi	-1.4701542	0.96	2.54523E-08
Rtn4rl1	-1.4600119	0.71	8.13357E-05
Fcgr3	-1.45902	1.12	0.000305893
Mapre2	-1.4509218	0.73	5.57891E-07
Tmem98	-1.4501452	0.76	0.003739779
Smoc1	-1.4486338	-0.71	6.82216E-05
Cd55	-1.4480843	1.21	4.46471E-08
Serpine1	-1.434145	1.72	0.000102421
Cfp	-1.4292959	0.88	0.000739243
Sgpp1	-1.425625	1.58	1.21054E-15

Apoe	-1.4243036	1.12	3.46767E-07
Car5b	-1.4230693	-0.58	0.005910039
Hip1	-1.419519	0.53	0.00019298
Tmem159	-1.4125741	0.88	1.19837E-07
Cxx1b	-1.4094375	0.59	0.002098172
Arhgap20	-1.4039676	1.81	7.33166E-09
Gnb4	-1.403389	0.58	0.000919177
Tshz2	-1.4031634	0.52	0.000667147
Maml2	-1.3687247	0.60	0.003781347
Klhl13	-1.3685794	0.98	1.63152E-06
Tmem100	-1.3441655	1.10	0.00011237
Hexb	-1.3441595	0.76	2.95439E-06
C1qb	-1.3434335	0.85	0.000238207
Tlr7	-1.3384951	1.14	0.000550698
Lrrc1	-1.3363496	0.89	0.003659618
Itgam	-1.3355582	1.01	0.002419667
Pros1	-1.3290567	0.76	5.55856E-06
CERS4	-1.3279382	0.80	9.59367E-06
Snhg11	-1.3156262	1.04	5.35634E-05
Lxn	-1.3144108	0.73	0.005465613
Atp6v0e2	-1.3117689	2.01	1.47396E-19
Fstl1	-1.3105889	0.53	0.002158467
Ptpn13	-1.3051403	0.90	7.46245E-05
Smo	-1.3024697	0.39	0.008391824
Srd5a3	-1.2949306	0.74	2.31986E-05
Anln	-1.2945037	1.06	0.000418922
Ctso	-1.2929783	0.72	6.1891E-07
Fbln2	-1.2879139	0.47	0.002621783
Prcp	-1.2808394	0.86	4.20623E-06
Atp11a	-1.279251	0.59	0.001376971
Synpo2	-1.2629384	1.68	1.09795E-06
Eya2	-1.2507573	1.08	0.000877488
Elovl1	-1.2451779	0.58	0.003744028
Serpinb8	-1.2442648	0.77	0.082574509
Ppap2c	-1.2434412	0.75	0.000165668
Tfpi	-1.2171798	0.91	2.71726E-05
Cyba	-1.2157924	0.61	0.004478316
Evi2b	-1.2126059	0.95	0.00095874
Ppic	-1.2095604	0.50	0.001847521
Lcp1	-1.2055832	0.98	4.01097E-05
H2-Eb1	-1.2030441	0.76	0.000144106
Mnda	-1.1950333	1.36	0.000395361
H2-DMa	-1.1893782	0.95	6.66248E-05
Ptprc	-1.1870171	0.75	0.001219214
Asph	-1.179157	1.65	1.86081E-06
Csf1	-1.1755465	0.42	0.015455663
Dnm1	-1.1695897	1.56	1.04817E-16
Slit2	-1.1695762	1.97	7.66845E-08
Sfxn3	-1.1653741	0.63	0.000661851
Txndc16	-1.1630145	1.11	2.19701E-11
Casp4	-1.1620865	1.10	0.006626183
Serpinb9	-1.1597133	0.96	1.15962E-06
Eid1	-1.1554107	0.60	3.32117E-05
Prps1	-1.1540246	0.63	2.85839E-05

Far1	-1.1514514	0.60	0.000201917
Myo1d	-1.1460858	0.47	0.001897662
Rtn1	-1.1278124	0.59	0.148985842
Ctps2	-1.1177141	0.48	0.00137068
Auts2	-1.1164624	0.66	0.003243919
Cidec	-1.1149929	-0.58	0.000169423
Zfp521	-1.1091669	0.64	0.00217312
Fam114a1	-1.1086302	0.79	1.48287E-06
Lox	-1.1077419	0.97	3.77468E-08
Ifit3	-1.0934234	1.14	0.000371353
Slc38a1	-1.0904852	1.01	0.00675152
Atpif1	-1.0863163	0.85	1.73432E-06
Lrp1	-1.0830362	0.46	0.003519888
Plekha2	-1.0814814	0.59	0.000492622
Scrn1	-1.0807957	1.50	6.58021E-06
Tgfb1i1	-1.069295	0.71	0.000472183
Spata6	-1.0635971	0.78	0.000142054
Plek	-1.0627387	0.99	0.000816917
Sdc2	-1.0595868	0.90	5.75892E-10
Itga5	-1.0508873	0.59	0.004694932
Mctp1	-1.0457396	1.14	0.009148741
Unc93b1	-1.0425978	0.56	8.90212E-05
Bmp1	-1.0394927	0.45	0.003405471
Arhgef3	-1.0388377	0.49	0.002821286
B3galnt1	-1.0371377	1.04	1.49433E-07
Gcnt2	-1.0356267	0.83	1.53316E-05
Ahnak	-1.0210975	0.27	0.103718087
Cetn4	-1.0187829	1.43	3.62303E-05
Itm2c	-1.0173682	0.44	0.003346468
Renbp	-1.015341	1.03	3.45505E-05
Grb10	-1.0133894	0.71	1.42904E-06
Slc2a3	-1.009352	1.22	1.07945E-06
Sh3d19	-1.0070267	0.80	1.13155E-05
Plekho2	-1.0053907	0.69	0.006327041
Cd44	-1.0002924	1.60	5.03805E-09
Bgn	-0.9964489	0.63	0.000558543
Ifih1	-0.9872261	0.87	5.67972E-05
Lhfp	-0.9798497	0.94	8.38236E-09
Dst	-0.9769494	0.51	0.001315379
Adamts1	-0.9738518	0.61	0.002220279
Fgfrl1	-0.9717172	-0.40	0.008724028
Selp	-0.9715214	1.13	0.000791975
Pld2	-0.9665379	0.83	4.0213E-07
Ezr	-0.9616136	1.67	1.59897E-15
Loxl2	-0.9497986	0.86	1.23413E-06
Me2	-0.9461683	0.66	0.000552627
Wls	-0.9431341	0.52	0.000430198
Mocs1	-0.9365457	-0.37	0.007652592
Tmem63a	-0.9363129	0.79	6.37798E-08
Gstz1	-0.9300304	-1.03	3.90614E-08
Vcam1	-0.9272603	1.28	7.41971E-10
Prkcb	-0.9136873	1.64	1.41968E-10
Sigmar1	-0.9128917	-0.62	2.30741E-06
Cers5	-0.9084227	0.49	0.000467117

Rcn1	-0.8944038	0.80	3.48452E-06
Parp8	-0.8913668	1.29	9.5952E-07
Ptprs	-0.8901032	0.74	9.88337E-07
Rab3il1	-0.889673	0.58	0.004467803
Clstn1	-0.8871496	1.20	4.31155E-14
Casc4	-0.8861973	0.99	0.001516623
Inhbb	-0.8850116	1.10	0.000133655
Fam26e	-0.8753365	1.14	0.001383832
Tll1	-0.8685642	1.47	2.86782E-05
Reps2	-0.8681077	1.16	8.10545E-06
Sgcd	-0.8674877	-0.69	0.000182621
Slc16a9	-0.8637977	0.79	0.006966135
Aff3	-0.8627653	1.31	1.68149E-06
Ywhab	-0.8597608	-0.52	0.0011487
Acvr1b	-0.8584101	0.82	2.05486E-05
Mmp23	-0.8557028	2.63	4.39552E-12
Zfp503	-0.8549957	0.47	0.006835861
Cd9	-0.8528665	0.47	0.002324542
Enpp5	-0.850783	0.75	2.39983E-06
Rp2h	-0.8436587	0.49	0.003611452
Glis2	-0.831506	0.83	1.97817E-06
Bid	-0.8281165	1.12	3.77747E-07
Arrb2	-0.8144297	0.56	0.003866736
Prkcd	-0.8085257	0.80	2.99806E-07
Lima1	-0.8009701	0.51	0.000745142
Abhd3	-0.7974874	0.83	8.92425E-05
Ubqln2	-0.7951526	0.38	0.007266709
Tspan6	-0.789328	1.02	1.89565E-06
Mmp11	-0.7768243	0.84	0.000653698
Zfp36	-0.7530988	0.74	1.90995E-05
Kctd17	-0.7040395	0.84	3.58109E-06
H2-K1	-0.7027553	0.69	0.000782314

Gene Name	iBAT #1 RT_sigma	iBAT #1 RT_20752	iBAT #1 RT_3544	iBAT #2 RT_sigma
Acadvl	-0.3883163	-0.5800329	-0.496947	-0.09023653
Aco2	-0.2922752	-0.6236091	-0.4084727	0.00957801
Acsl1	-0.5353679	-0.4501629	-0.3581361	-0.4029019
Actn2	-0.4438484	-0.6261941	-0.6624517	-1.052506
Actn3	-0.3604366	-0.6450114	-0.479862	-0.7816935
Actn4	-0.6256494	-0.7483979	-0.6643844	-0.7579146
Ago1	-0.8110184	-1.314279	-1.084085	-0.6660813
Ahnak	-0.8747633	-1.256509	-1.28186	-0.6690966
Alb	-0.05583907	0.01365764	0.01478262	0.03700713
Atp2a1	-0.2921241	-0.6323434	-0.4819327	-0.3129884
Atp2a2	-0.2921241	-0.6323434	-0.4819327	-0.3129884
Arid1a	-0.08900774	-0.5258144	-0.659574	-0.1102102
Arid1b	-0.3523777	-1.093886	-0.5898302	-0.2860602
Atp1a2	-0.3549446	-0.6107828	-0.5742555	-0.275806
Atp2a1	-0.2921241	-0.6323434	-0.4819327	-0.3129884
Bckdk	-0.1966897	-0.946576	-0.8023846	-0.06159862
C1qb	-0.4520436	-0.5045292	-0.09168123	-0.7171543
C4a	-0.8001008	-0.5521382	-0.3688629	-0.5961118
C4b	-0.8001008	-0.5521382	-0.3688629	-0.5961118
Capza1	-0.287835	-0.4419247	-0.3455427	-0.2212606
Capza2	-0.287835	-0.4419247	-0.3455427	-0.2212606
Capzb	-0.4638188	-0.6525056	-0.5761456	-0.3594868
Cav1	-0.1880986	-0.1741314	-0.5350763	0
Cbln1	-0.004836856	-0.0280243	-0.009899932	0.1808323
Ccar1	-0.5140755	-0.5353574	-1.068944	-0.3559406
Cenpv	0.00017524	-0.6645953	-0.4190575	0.1071896
Ckm	-0.7981196	0.01545044	-0.6925843	0.1361754
Cltc	-0.4251396	-1.262034	-0.5140082	-1.063484
Col12a1	-0.931327	-0.9500378	-0.75741	-0.6779628
Ctbp1	0	-0.6808621	-0.4866112	-0.3154609
Decr1	-0.3086893	-0.486864	-0.3860468	-0.1580123
Dhx15	-0.7497139	-1.157112	-0.9698685	-0.5352843
Dhx30	-0.6723918	-1.530371	-1.321589	-0.8678795
Dnah8	-0.3829494	-0.4666509	-0.3522546	-0.2234299
Dsg1	-0.7499167	-0.8521296	-0.6364253	-0.707042
Eftud2	-0.6834896	-1.11932	-1.133739	-0.6811364
Ehd2	-0.4506841	-0.4170976	-0.6984921	-0.2675602
Eif2c1	-0.3681405	-0.7441542	-0.5806117	-0.3299747
Eif2c2	-0.3681405	-0.7441542	-0.5806117	-0.3299747
Eif3a	-0.864806	-0.9787945	-1.151595	-0.850413
Eprs	-0.8242722	-1.017607	-1.045566	-1.128805
Etfa	-0.6145682	-0.6057222	-0.257863	-0.02368202
Etfb	-0.5389953	-0.7355291	-0.5754987	-0.02894978

Ewsr1	-0.1879804	-0.4653937	-0.3295601	0.04327382
Fam120a	-0.5269114	-1.039406	-0.9247171	-0.4882108
Flna	-1.015279	-1.402458	-1.96773	-0.5801722
Flnc	-0.9039878	-1.883428	-1.469525	-1.335867
Fus	-0.5832061	-0.2446321	-0.2599145	0.1047635
Fxr1	-0.2592673	-0.9373453	-1.071335	-0.1083686
Gapvd1	-0.1758094	-0.4517279	-0.6491773	-0.165848
Grpel1	-0.6391264	-0.7512214	-0.5501289	-0.2015136
Gse1	-0.7565958	-0.4223372	-0.4478257	-0.416043
H1f0	-0.004761708	-0.09468618	-0.1608015	-0.01502967
H2afy	-0.1913771	-0.3390428	-0.3474742	-0.3230024
Hadha	-0.1115446	-0.2029531	-0.2103002	-0.04293215
Hdac1	-0.04793421	-0.07376998	-0.02793523	0.09259167
Hdac2	-0.2004447	-0.2267146	-0.1720608	-0.003193208
Hist1h1b	-0.2141557	-0.4704448	-0.6498817	-0.1407114
Hist1h1c	0.04704401	-0.1591087	-0.1416709	0.1512033
Hist1h1d	0.04704401	-0.1591087	-0.1416709	0.1512033
Hist1h1e	0.04704401	-0.1591087	-0.1416709	0.1512033
Hmg20a	-0.3963653	-0.2881045	-0.2116844	-0.1557073
Hmg20b	-0.3733076	-0.2985787	-0.1984215	-0.04221777
Hnrnpc	-0.464015	-0.6011477	-0.4961514	-0.0972729
Hnrnpl	-0.585185	-0.7733757	-1.019509	-0.375183
Hnrnpm	-0.6125332	-0.8203249	-1.355044	-0.3711668
Hnrnpu	-0.2116165	-0.5270439	-0.5808382	-0.2092191
Hnrnpul1	-0.4163414	-0.4380846	-0.6206637	-0.2097301
Hp1bp3	-0.4028034	-0.7621231	-0.7912167	-0.3335544
Hspa5	-0.1837423	-0.2402291	-0.3119965	0.01991695
Hspa8	0.01523791	-0.07476712	-0.1189337	0.1481507
Hspa9	0.05897238	0.09021259	0.03605989	0.2013869
Hspd1	-0.1737511	-0.09213846	-0.1695795	0.03659488
Idh3g	-0.8238413	-0.9254951	-0.6214814	-0.1793599
Immt	-0.5006976	-0.5778042	-1.145005	-0.3476781
Jup	-0.9049305	-0.706477	-0.5972651	-1.118993
Kdm1a	0	0	0	0
Kiaa1967	-0.5754926	-0.3216162	-0.6451902	-1.027574
Krba2	-0.1682866	-0.3326304	-0.3954299	-0.04837067
Lmna	-0.2069054	-0.2497106	-0.341518	-0.3854574
Matr3	-0.7197468	-0.8396777	-0.8152295	-1.213017
Msn	-0.5684367	-0.9325637	-0.9283072	-0.8744669
Mvp	-0.6247543	-0.7688698	-0.6512609	-0.4362738
Ndufs1	-0.8227475	-0.9013417	-1.147869	-0.3929055
Nid1	-0.8785174	-1.018988	-0.899685	-0.9735618
Ogdh	-0.8236445	-0.6794458	-0.5877734	-0.2060802
Pabpc1	0.02722535	-0.3124042	-0.1385092	0.1578334

Pabpc4	-0.1784664	-0.663475	-0.8717744	-0.06724621
Pcca	-0.3818632	-0.4493131	-0.5052677	-0.244701
Pdha1	-0.2690412	0.004669503	-0.003473843	0.04860311
Phf21a	-0.301107	-0.3441512	-0.3122578	-0.09347589
Polr2c	-0.07826819	-0.2980327	-0.1770162	-0.9861981
Prdx2	-0.4274741	-0.3296407	-0.2377049	-0.5343488
Prdx5	0	-0.525737	-0.02057568	-0.1488544
Prss3	-0.5351159	-0.2184262	-0.0700607	-0.3371474
Ptrf	-0.08143234	-0.2280257	-0.2180305	0.05505516
Puf60	-0.6555162	-0.6540925	-0.8019684	-0.1939352
Rars	-0.7641873	-0.9099689	-1.396419	-0.6040787
Rbm14	-0.3009858	-0.006790438	-0.416018	-0.1162465
Rbm25	-0.5601862	-0.8091035	-0.9580131	-0.3458638
Rcor1	-0.1976248	-0.2603815	-0.149796	-0.1132797
Rcor3	-0.09575633	-0.1302709	-0.0200171	0.05606446
Rpl10a	-0.06364728	-0.4680292	-0.5296854	0.06708981
Rpl11	-0.2270781	-0.3730546	-0.2468935	-0.151543
Rpl12	-0.1468108	-0.3406093	-0.5258903	-0.000119877
Rpl13	-0.09571093	-0.6210494	-0.4301498	0.02137143
Rpl13a	-0.1545748	-0.3462456	-0.3986406	-0.03134305
Rpl23a	-0.1351674	-0.4408669	-0.3806198	0.006722422
Rpl26	-0.1682866	-0.3326304	-0.3954299	-0.04837067
Rpl26l1	-0.1682866	-0.3326304	-0.3954299	-0.04837067
Rpl28	-0.1852606	-0.2860173	-0.3391092	-0.04906915
Rpl3	-0.284537	-0.5577257	-0.6438671	-0.04657642
Rpl35	-0.07831657	-0.1930454	-0.09778711	0.06492347
Rpl6	-0.2517053	-0.4449267	-0.6220434	-0.01278414
Rpl7	-0.1068241	-0.3977499	-0.3702097	-0.02561517
Rpl7a	-0.09216257	-0.6027485	-0.328146	0.1187773
Rpl9	-0.3252298	-0.8815523	-0.4168038	-0.05473371
Rplp0	-0.1353806	-0.5785624	-0.2176241	0.06465051
Rplp0p6	-0.1353806	-0.5785624	-0.2176241	0.06465051
Rps13	-0.2015272	-0.3802991	-0.515866	-0.02780311
Rps16	-0.3420297	-0.7414965	-0.4197353	-0.2365459
Rps17	-0.1353806	-0.5785624	-0.2176241	0.06465051
Rps17l	-0.1353806	-0.5785624	-0.2176241	0.06465051
Rps2	-0.1900599	-0.9359135	-0.4621983	-0.04328806
Rps23	-0.1708637	-0.3752507	-0.8542188	-0.3097058
Rps26	-0.1792898	-0.5305853	-0.3481225	-0.8871301
Rps26p11	-0.1792898	-0.5305853	-0.3481225	-0.8871301
Rps6	-0.2986415	-1.124867	-0.6966897	-0.3414119
Rps8	-0.1048821	-0.4388111	-0.467578	0.08253728
Rps9	-0.1834177	-0.3926111	-0.3061523	-0.264093
Rreb1	-0.574889	-0.6129221	-0.5520176	-0.4937714

Sdpr	-0.4283737	-0.6830711	-0.4232179	-0.3160163
Sf3a1	-0.8781345	-1.548262	-0.9996454	-0.714281
Sfpq	-0.1997253	-0.6514781	-0.4629481	-0.1356116
Slc25a20	-0.8108977	-0.940626	-0.4078523	-0.4527915
Smarca2	-0.1494508	-0.6907336	-0.7764553	-0.2778496
Smarca4	-0.1206736	-0.6285487	-0.7354307	-0.1996505
Smarcb1	-0.1594838	-0.6370735	-0.6828822	0.01623803
Smarcc2	-0.05363349	-0.4717082	-0.4755208	-0.08631209
Smarcd2	-0.1399883	-0.6088396	-0.1578427	0.03631919
Syncrip	-0.5695168	-1.043652	-1.256688	-0.2767502
Tgm2	-0.5200006	-0.5968542	-0.6609853	-0.7050746
Tkt	-0.6570694	-0.7198516	-0.8696296	-0.1310863
Tln1	-1.171525	-1.773526	-1.649486	-0.8339005
Tnnt3	-0.1489985	-0.2670093	-0.1943828	-0.01297475
Tns1	-0.2473553	-0.9107477	-1.054703	-0.3583288
Top1	-0.5919017	-0.7273327	-0.7307827	-0.7614627
Tpi1	-0.4595308	-0.4712717	-0.4189129	-0.05876035
Tpm1	-0.07184944	-0.4242442	-0.1514647	-0.06664144
Tpm2	-0.20948	-0.350767	-0.2691243	-0.2065137
Tpm4	-0.20948	-0.350767	-0.2691243	-0.2065137
Ttn	-0.7454253	-1.291933	-1.143244	-1.222757
Ubap2l	-0.2567465	-0.8889427	-0.4542627	-0.3355739
Upf1	-0.4562762	-0.9479432	-0.9415284	-0.5762373
Vcl	-0.9740413	-0.9159472	-1.350749	-0.9813634
Vcp	-0.6386583	-0.9324558	-1.138961	-0.3766549
Vdac1	-0.5550604	-0.7067438	-0.5060412	-0.5549354
Vdac2	-0.4420542	-0.5126742	-0.3952686	-0.2962379
Wdr33	-0.4934459	-0.6189083	-0.5277464	-0.758649
Wdr91	-0.1338701	-0.3635526	-0.4197537	-0.1198129
Zmym2	-0.330241	-0.4289301	-0.1937661	-0.4698442
Zmym3	-0.8206886	-0.8081326	-0.6513423	-1.111327
Znf217	-0.8534035	-0.7260347	-0.6198554	-0.7806929

iBAT #2 RT_3544
-0.2464462
-0.06308283
-0.4538497
-0.7853426
-0.5705298
-0.5859577
-0.8246079
-0.7003253
-0.0509293
-0.370185
-0.370185
-0.9329161
-0.5647836
-0.492982
-0.370185
-0.4935552
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-0.5716137
-0.3567643
-0.3567643
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-0.5622394
-0.7769057
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-0.9761487
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-0.7291013
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-0.232245
-0.6489222
-0.3067251
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-0.1919405
-0.1774687
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