

Supplementary Materials

Chronic Fatty Acid Depletion Induces Uncoupling Protein 1 (UCP1)

Expression to Coordinate Mitochondrial Inducible Proton Leak

in a Human-Brown-Adipocyte Model

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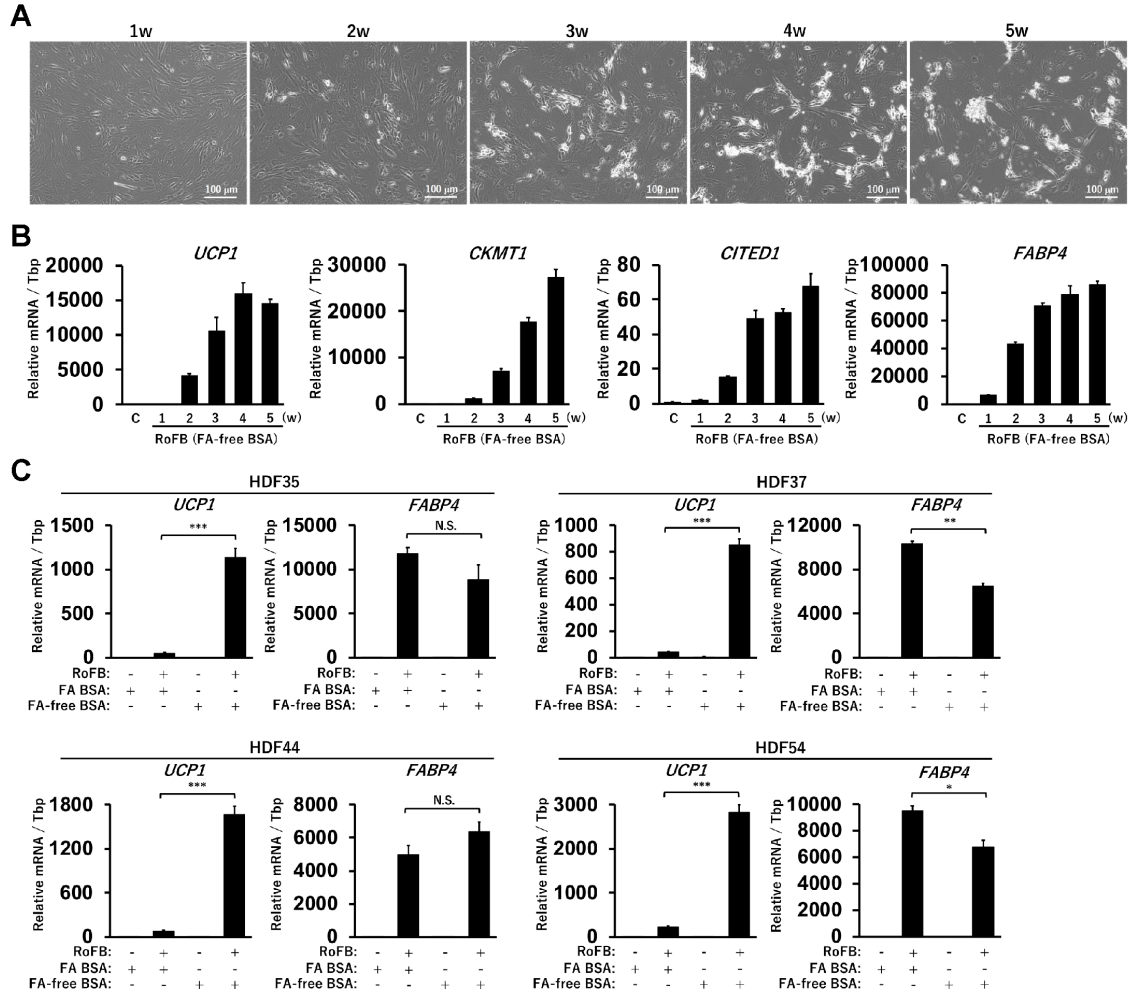


Figure S1. Characterization of ciBAs converted under FA-free conditions. (A) Representative pictures of ciBAs converted by RoFB and FA-free BSA for up to 5 weeks. (B) The time course of the expression of *UCP1*, *CKMT1*, *CITED1*, and *FABP4* was measured using qRT-PCR. “C” indicates the control fibroblasts cultured by the medium only. (C) The four lines of human dermal fibroblasts (HDFs) derived from different subjects aged 35, 37, 44, and 54 were converted into ciBAs by either FA-binding BSA or FA-free BSA for 3 weeks. The expression of *UCP1* and *FABP4* was quantitated using qRT-PCR. Data represent mean \pm SD ($n = 3$). Student’s t-test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, N.S.; not significant.

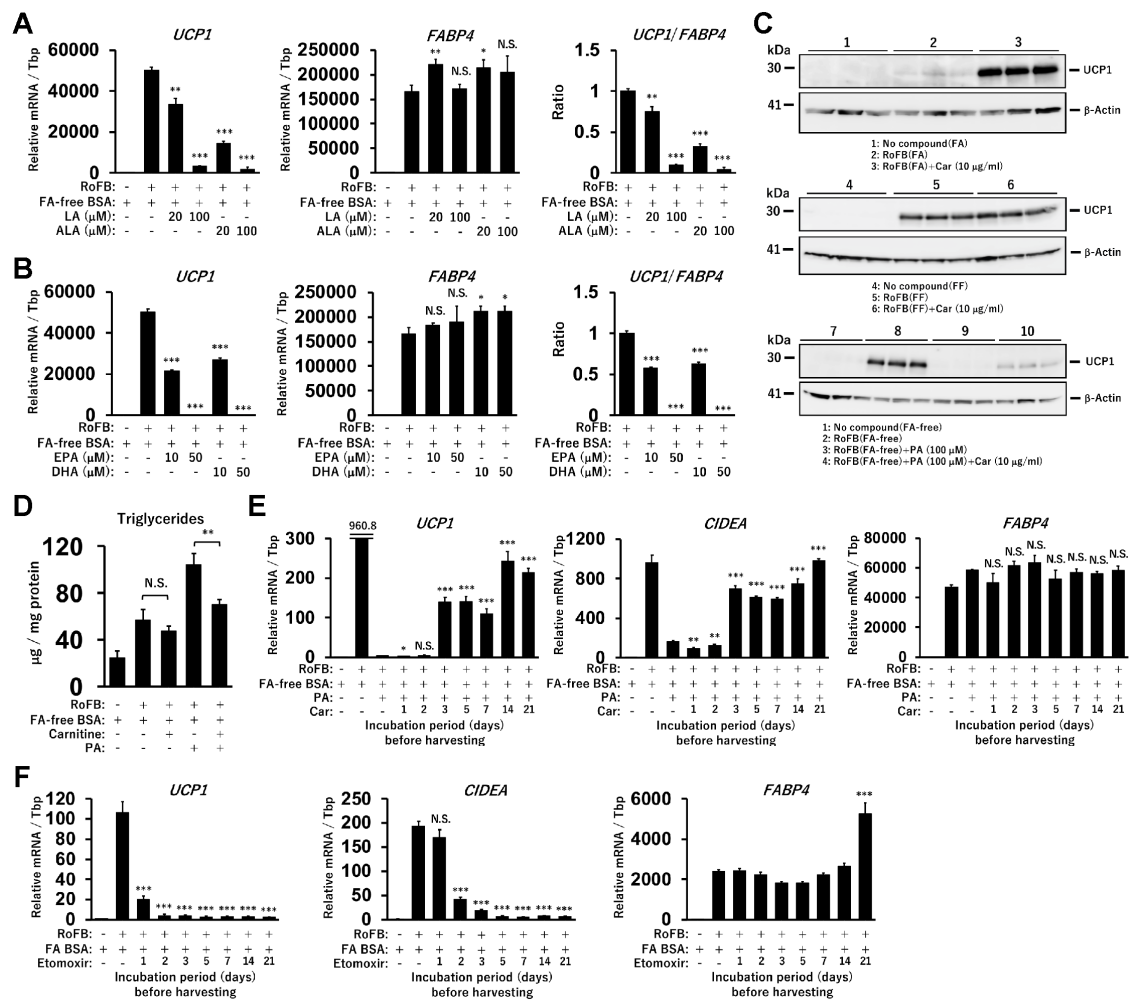


Figure S2. Regulation of *UCP1* expression by the treatment with various FAs and carnitine. (A) The expression of *UCP1* and *FABP4* mRNA and the ratio were quantified using qRT-PCR in ciBAs treated with either linoleic acid (LA) or α -linolenic acid (ALA) (20 and 100 μ M). (B) The expression was quantified in ciBAs treated with either eicosapentaenoic acid (EPA) or docosahexaenoic acid (DHA) (10 and 50 μ M). (C) The UCP1 and β -Actin proteins were immunoblotted in ciBAs treated with carnitine or PA. The quantification of the band intensities is shown in Figure 2F by densitometry using ImageJ software. (D) Cellular triglyceride content was measured in ciBAs converted by FA-free BSA under the treatment with carnitine and PA. (E) The expression of *UCP1*, *CIDEA*, and *FABP4* was measured using qRT-PCR in ciBAs treated with FA-free BSA, PA (100 μ M), and carnitine (10 μ g/ml) for different incubation periods (days) before harvesting the cells on day 21. (F) The expression was measured in ciBAs treated with

FA-binding BSA and etomoxir (50 μ M) for different incubation periods (days) before harvesting the cells on day 21. Data represent mean \pm SD ($n = 3$). Student's t-test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, N.S.; not significant.

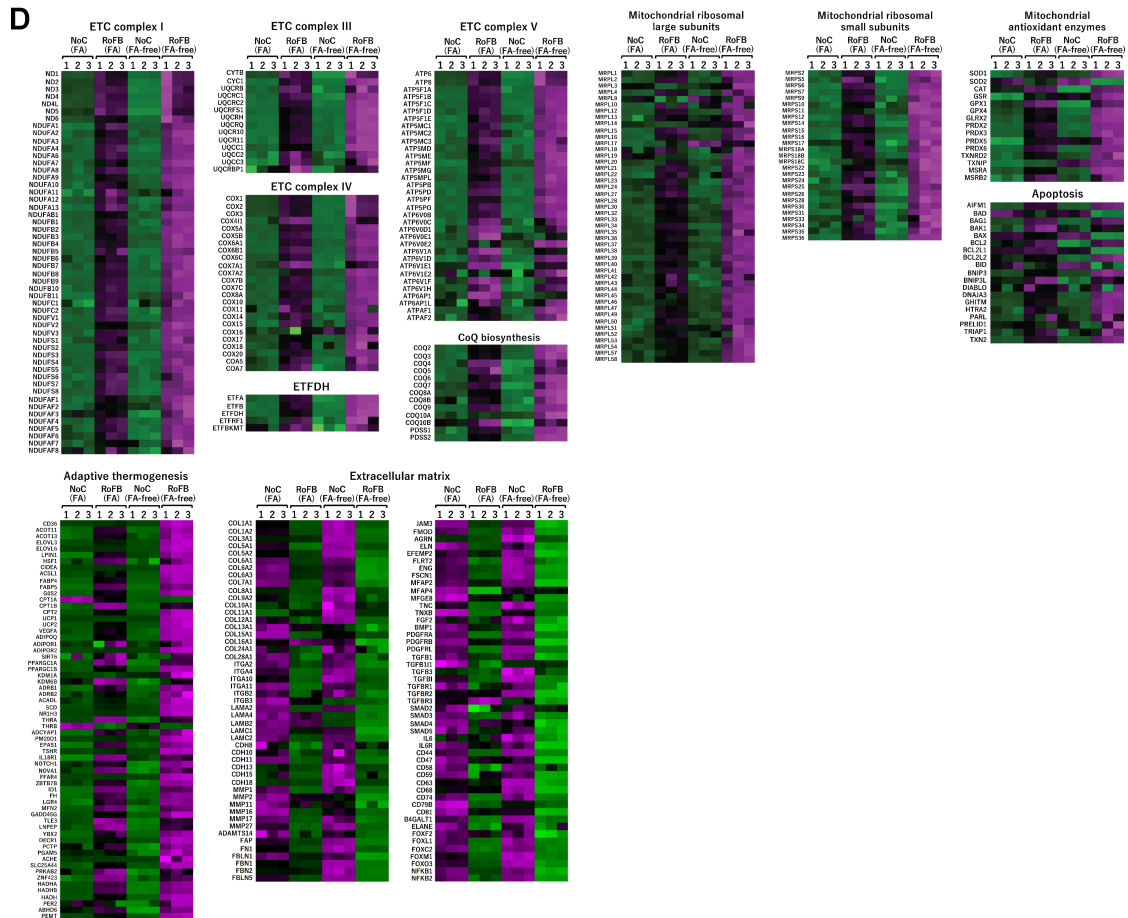
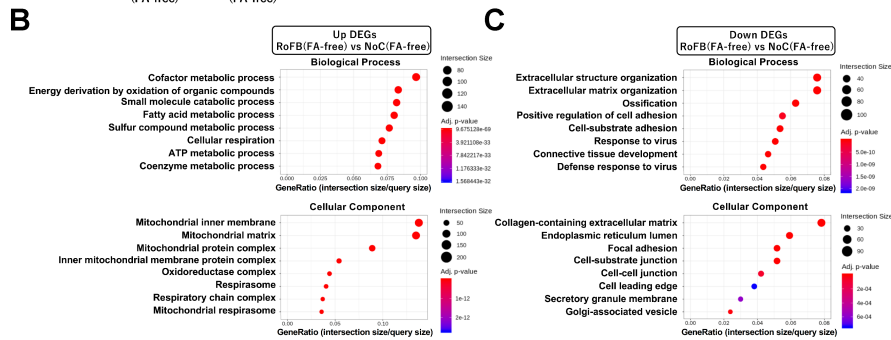
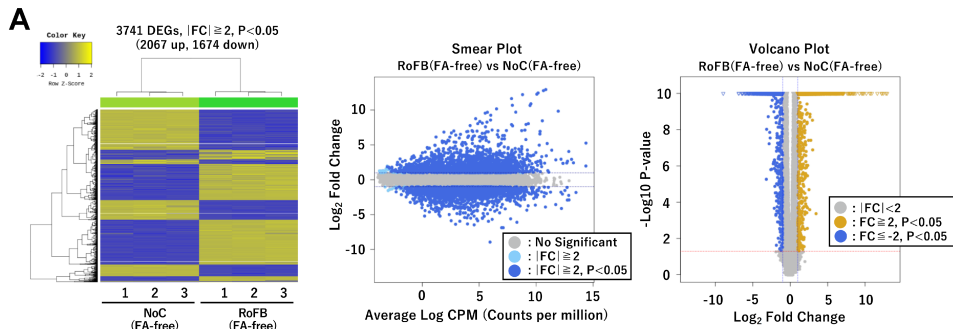


Figure S3. Comparison of genome-wide transcriptional analysis in ciBAs converted by either FA BSA or FA-free BSA. (A) Heatmap and hierarchical clustering analysis represent 3741 differentially expressed genes (DEGs) ($|\text{fold change (FC)}| \geq 2$, $p < 0.05$) between RoFB(FA-free) ciBAs and NoC(FA-free) control fibroblasts. Smear and Volcano plots indicate logarithmic fold change, P -value, and counts per million (CPM) between RoFB(FA-free) and NoC(FA-free). (B,C) Gene ontology (GO) enrichment analysis was performed in 2067 upregulated DEGs (B) and 1674 downregulated DEGs (C). The top 10 GO terms are represented in the category of biological process and cellular component. (D) Heatmaps represent transcriptional profiles in functional groups related to the electron transfer chain (ETC) complex, mitochondrial ribosomal subunits, antioxidant enzymes, apoptosis, adaptive thermogenesis, and extracellular matrix in NoC(FA), RoFB(FA), NoC(FA-free), and RoFB(FA-free). The color scale shows z-scored fragments per kilobase of transcript per million mapped sequence reads (FPKM) representing mRNA levels of each gene in green (lower expression) and magenta (higher expression).

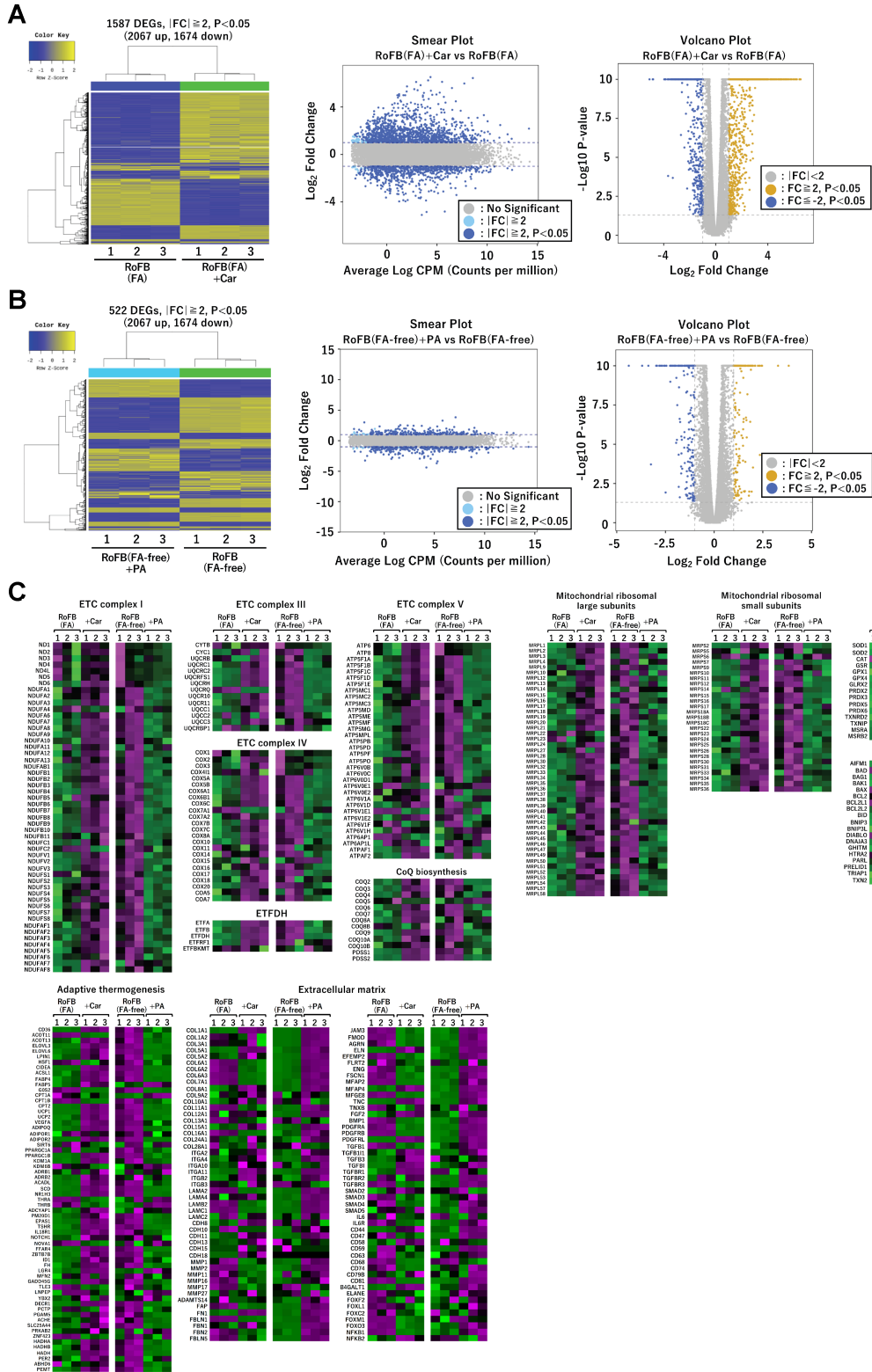


Figure S4. Comparison of genome-wide transcriptional analysis in ciBAs treated with either carnitine or PA. (A) Heatmap and hierarchical clustering analysis represent 1587 DEGs ($|\text{FC}| \geq 2$, $p < 0.05$) between RoFB(FA) and RoFB(FA)+Car. Smear and Volcano plots indicate logarithmic FC, P-value, and CPM between them. (B) 522 DEGs were detected between RoFB(FA-free) and RoFB(FA-free)+PA. (C) Heatmaps represent transcriptional profiles in the functional groups, as indicated, between RoFB(FA) and RoFB(FA)+Car and between RoFB(FA-free) and RoFB(FA-free)+PA. The color scale shows z-scored FPKM representing mRNA levels of each gene in green (lower expression) and magenta (higher expression).

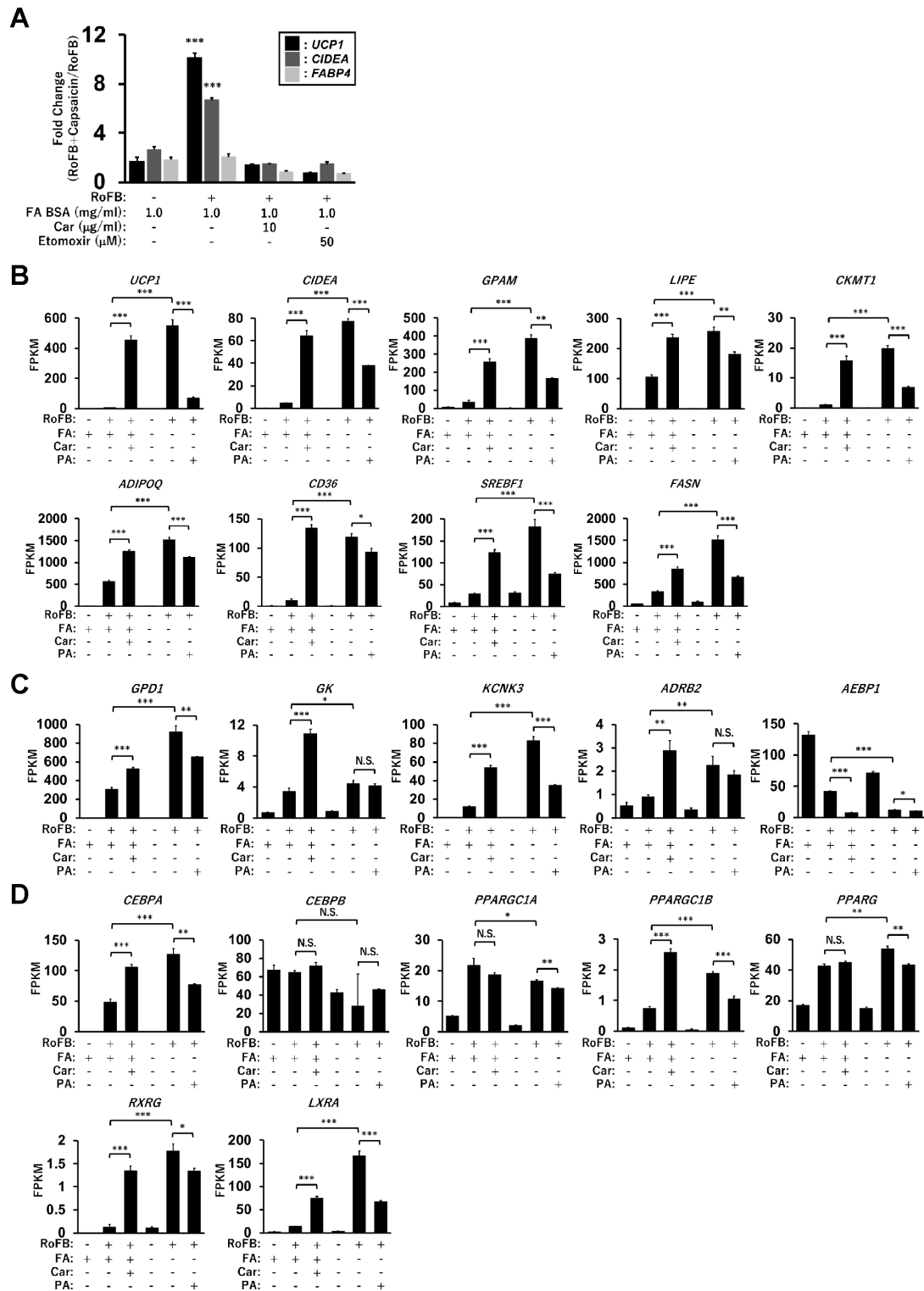


Figure S5. RNA-Seq results on the expression of lipid metabolic genes and transcription factors. (A) The fold change of *UCP1*, *CIDEA*, and *FABP4* expression by capsaicin was quantified in ciBAs treated with either carnitine (10 µg/ml) or etomoxir

(50 μ M). **(B,C)** The FPKM values of *UCP1*, *CIDEA*, *GPAM*, *LIPE*, *CKMT1*, *ADIPOQ*, *CD36*, *SREBF1*, and *FASN* **(B)**, as well as *GPD1*, *GK*, *KCNK3*, *ADBR2*, and *AEBP1* **(C)** were depicted from the RNA-Seq results to compare corresponding qRT-PCR results in Figures 4E and 4F. **(D)** The FPKM values of *CEBPA*, *CEBPB*, *PPARGC1A*, *PPARGC1B*, *PPARG*, *RXRG*, and *LXRA* were also depicted to compare corresponding qRT-PCR results in Figure 4G. Data represent mean \pm SD ($n = 3$). Student's t-test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, N.S.; not significant.

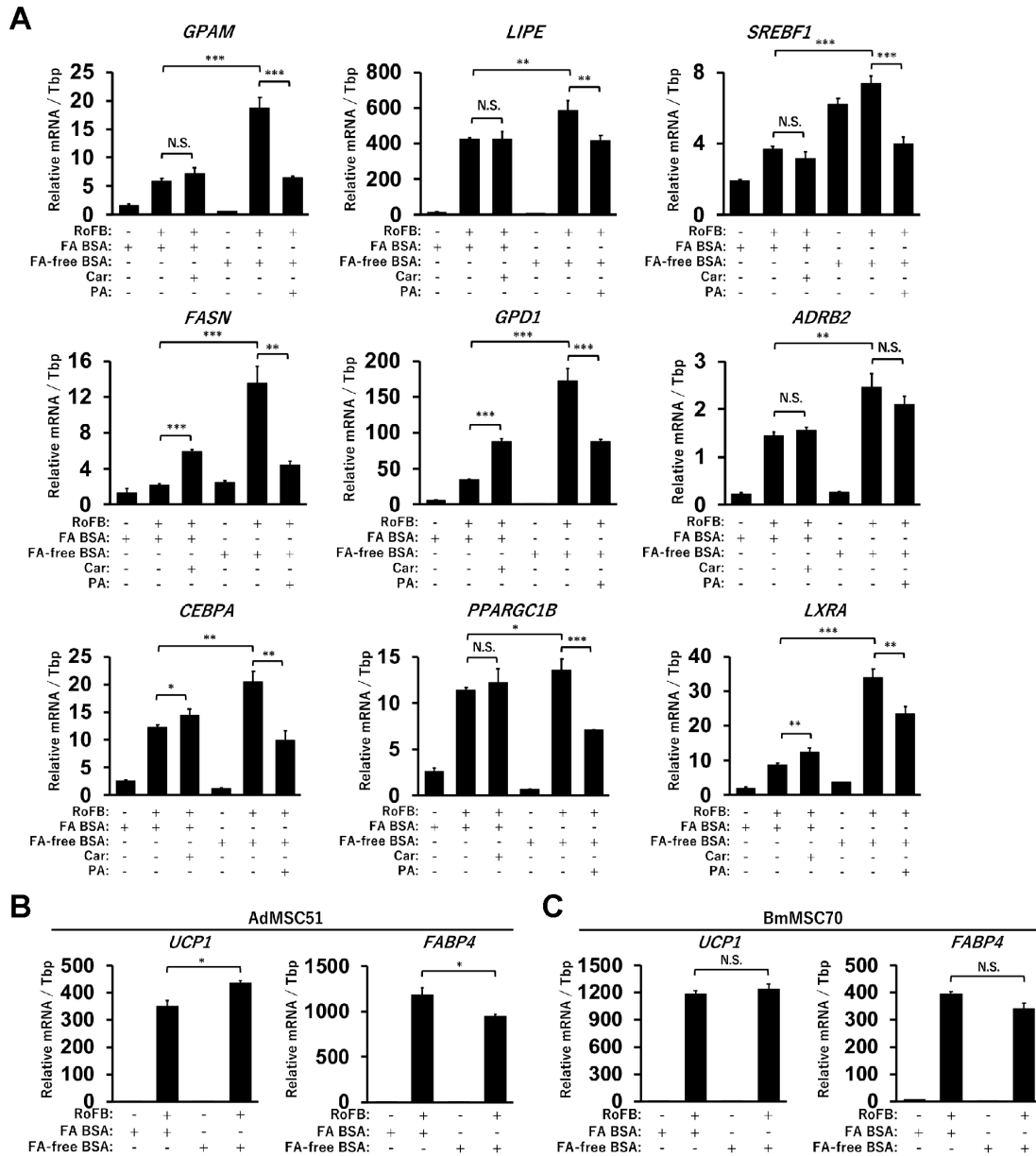


Figure S6. Characterization of adipocytes derived from hTERT A41BAT-SVF cells and AdMSC. (A) The expression of *GPAM*, *LIPE*, *SREBF1*, *FASN*, *GPD1*, *ADRB2*, *CEBPA*, *PPARGC1B*, and *LXRA* was quantified using qRT-PCR in A41BAT-SVF adipocytes differentiated under various conditions, as indicated. (B,C) The expression of *UCP1* and *FABP4* was quantified in mature adipocytes differentiated from human MSCs derived from adipose tissue (AdMSC51) (B) and bone marrow (BmMSC70) (C). The information on the MSCs is listed in Table S3. Data represent mean \pm SD ($n = 3$). Student's t-test: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, N.S.; not significant.

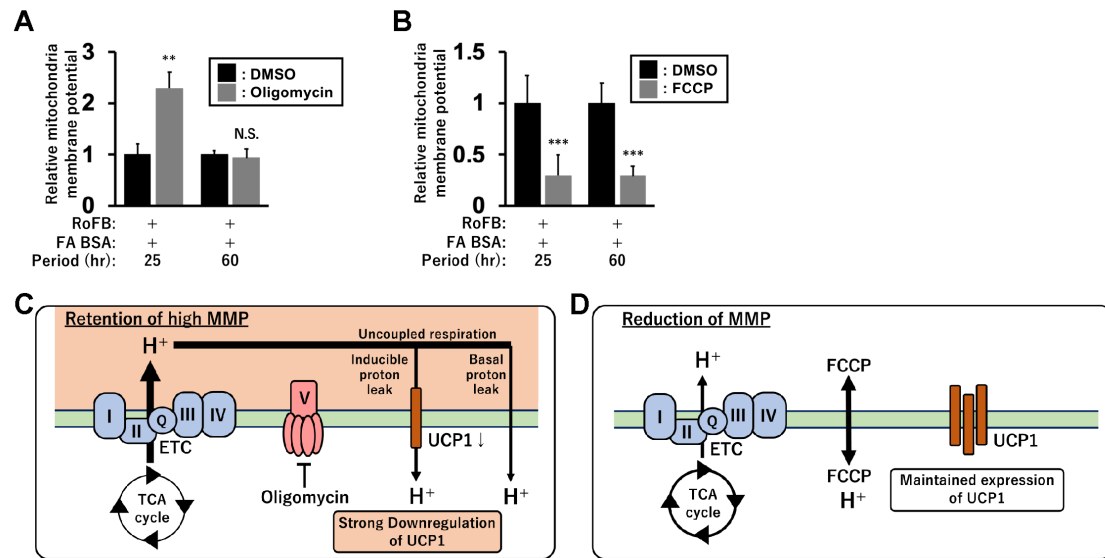
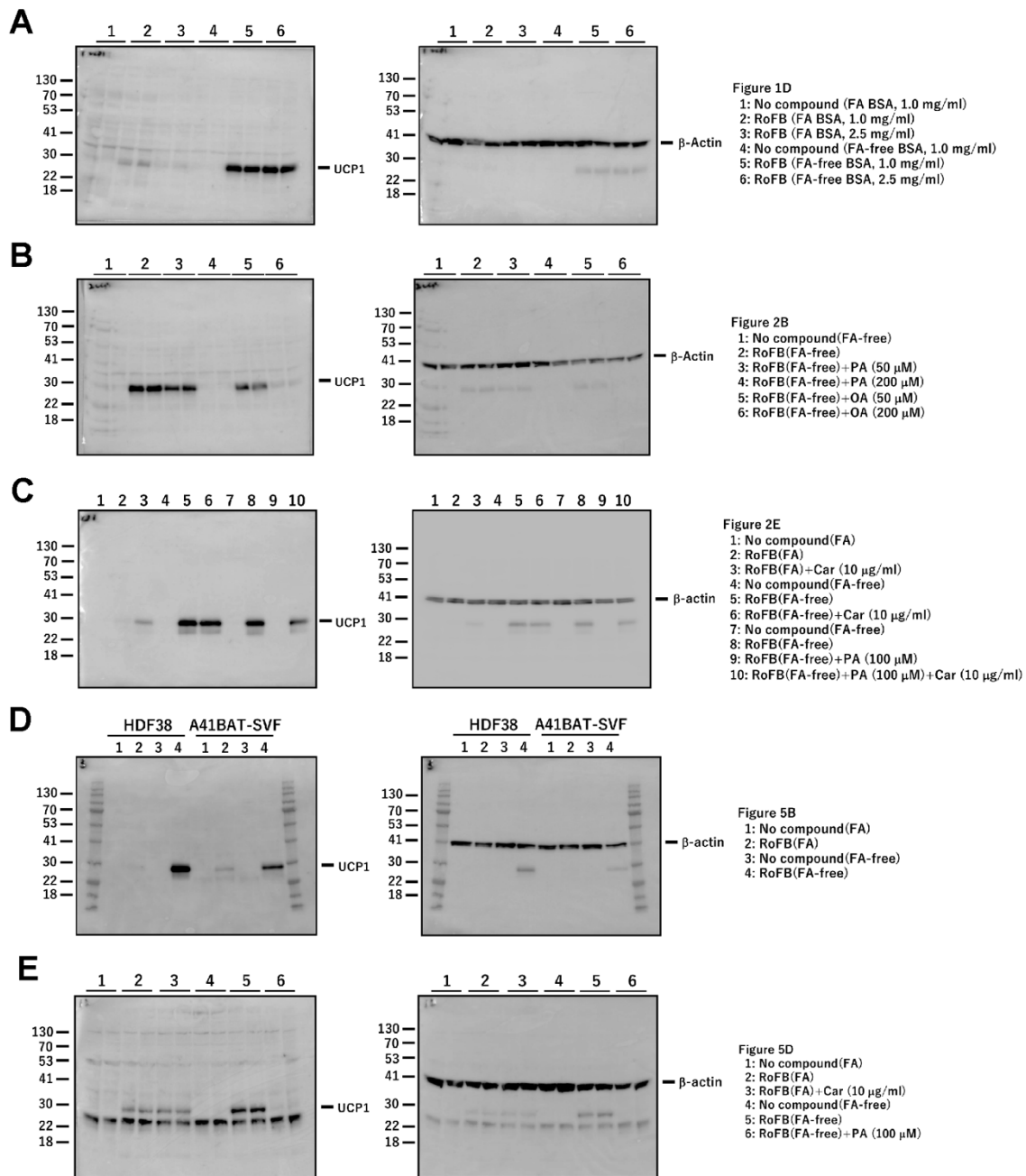


Figure S7. Effects of oligomycin and FCCP on mitochondria membrane potential (MMP) in ciBAs. (A) Relative MMP levels were measured in ciBAs, 1 and 36 h after the treatment with either DMSO or oligomycin. The period (hr) follows the illustration in Figure 7E. The area of staining of MT-1 dye was quantified using ImageJ software. (B) Relative MMP levels were similarly measured in ciBAs 1 and 36 hours after the treatment with either DMSO or FCCP. (C,D) Schematic presentations represent a possible status of mitochondrial inner membrane in the treatment with oligomycin (C) or FCCP (D). Oligomycin leads to the retention of MMP at a high level by inhibiting the dissipation of a proton gradient. In this condition, *UCP1* expression was strongly downregulated likely to avoid an excess amount of inducible proton leak by UCP1. The uncoupler FCCP reduces MMP by releasing a proton gradient across mitochondrial inner membrane. In this condition, *UCP1* expression was maintained.



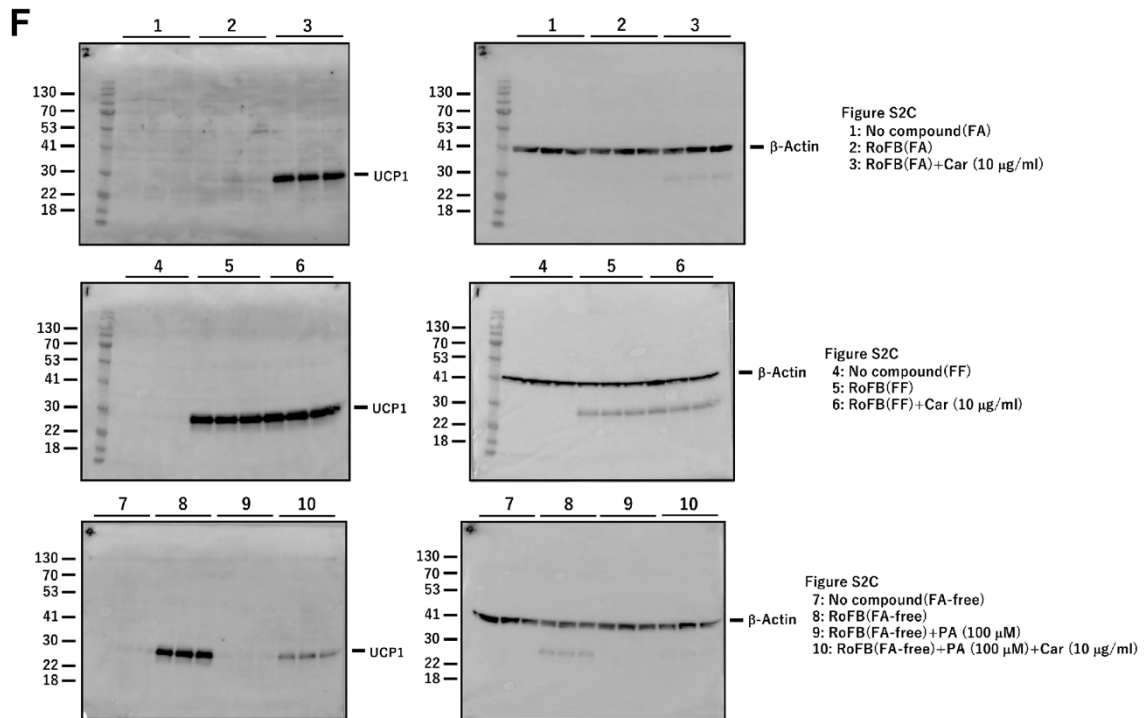


Figure S8. Original images of full-length western blots. They are shown for Figure 1D (A), Figure 2B (B), Figure 2E (C), Figure 5B (D), Figure 5D (E), and Figure S2C (F).

Table S1. List of 137 fatty acid depletion-activated genes (FADAGs) in ciBAs. The fold changes were calculated from the expression levels between RoFB(FA) and RoFB(FA-free).

Gene name	Description	Fold Change	Adjusted p-value
<i>SLC2A5</i>	Solute carrier family 2 member 5	143.58	0.00E+00
<i>TF</i>	Transferrin	111.23	8.16E-240
<i>PDZD2</i>	PDZ domain containing 2	91.76	0.00E+00
<i>SHISA9</i>	Shisa family member 9	58.31	6.67E-243
<i>THRSP</i>	Thyroid hormone responsive	24.93	0.00E+00
<i>PLA2G2A</i>	Phospholipase A2 group IIA	22.94	7.12E-193
<i>ME1</i>	Malic enzyme 1	20.83	0.00E+00
<i>ALDH5A1</i>	Aldehyde dehydrogenase 5 family member A1	19.87	7.64E-220
<i>MARCO</i>	Macrophage receptor with collagenous structure	17.78	1.25E-224
<i>APOC1</i>	Apolipoprotein C1	17.42	1.09E-242
<i>TMEM37</i>	Transmembrane protein 37	17.10	1.19E-227
<i>CACNA2D4</i>	Calcium voltage-gated channel auxiliary subunit alpha2delta 4	16.37	3.28E-68
<i>SORL1</i>	Sortilin related receptor 1	14.64	9.29E-152
<i>ACSS2</i>	Acyl-CoA synthetase short chain family member 2	14.27	0.00E+00
<i>PRRT4</i>	Proline rich transmembrane protein 4	14.10	3.06E-244
<i>LBHD1</i>	LBH domain containing 1	13.77	3.82E-69
<i>NR1H3</i>	Nuclear receptor subfamily 1 group H member 3	13.72	1.00E-280
<i>ALDH1L1</i>	Aldehyde dehydrogenase 1 family member L1	13.71	0.00E+00
<i>ETNK2</i>	Ethanolamine kinase 2	13.58	2.09E-249
<i>GLYCK</i>	Glycerate kinase	13.50	4.31E-45
<i>GPAM</i>	Glycerol-3-phosphate acyltransferase, mitochondrial	11.99	5.86E-190
<i>SULT1B1</i>	Sulfotransferase family 1B member 1	11.87	1.76E-39
<i>CLMN</i>	Calmin	11.71	0.00E+00
<i>ACLY</i>	ATP citrate lyase	11.70	0.00E+00
<i>SCARB1</i>	Scavenger receptor class B member 1	11.44	9.37E-125
<i>ABCC2</i>	ATP binding cassette subfamily C member 2	11.31	2.59E-180
<i>RIMS4</i>	Regulating synaptic membrane exocytosis 4	10.94	1.34E-67
<i>DHRS9</i>	Dehydrogenase/reductase 9	10.84	3.99E-103
<i>TSHR</i>	Thyroid stimulating hormone receptor	10.82	2.41E-210
<i>SLC29A4</i>	Solute carrier family 29 member 4	10.40	1.90E-248
<i>CD14</i>	CD14 molecule	9.51	6.85E-98
<i>PNPLA3</i>	Patatin like phospholipase domain containing 3	9.32	3.56E-221
<i>RBP4</i>	Retinol binding protein 4	9.22	3.00E-192
<i>LOC100130872</i>	Uncharacterized LOC100130872	9.04	1.56E-40

<i>FADS2</i>	Fatty acid desaturase 2	8.31	1.05E-237
<i>ACSL5</i>	Acyl-CoA synthetase long chain family member 5	8.27	4.10E-131
<i>GFOD1</i>	Glucose-fructose oxidoreductase domain containing 1	7.81	2.13E-131
<i>SYN2</i>	Synapsin II	7.70	8.74E-216
<i>KCNK3</i>	Potassium two pore domain channel subfamily K member 3	7.55	2.72E-297
<i>HCP5</i>	HLA complex P5	7.50	2.42E-23
<i>STBD1</i>	Starch binding domain 1	7.49	1.09E-05
<i>IQGAP3</i>	IQ motif containing GTPase activating protein 3	7.44	1.03E-34
<i>SCD</i>	Stearoyl-CoA desaturase	7.25	1.67E-217
<i>OASL</i>	2'-5'-oligoadenylate synthetase like	7.06	1.86E-105
<i>SREBF1</i>	Sterol regulatory element binding transcription factor 1	6.99	8.96E-171
<i>ARRB1</i>	Arrestin beta 1	6.92	3.27E-232
<i>FAR2</i>	Fatty acyl-CoA reductase 2	6.88	5.15E-240
<i>COL5A3</i>	Collagen type V alpha 3 chain	6.86	1.25E-290
<i>SCCPDH</i>	Saccharopine dehydrogenase (putative)	6.81	2.05E-301
<i>INSIG1</i>	Insulin induced gene 1	6.75	3.04E-213
<i>NES</i>	Nestin	6.67	8.35E-24
<i>LPCAT3</i>	Lysophosphatidylcholine acyltransferase 3	6.45	3.91E-252
<i>PKD1</i>	Pyruvate dehydrogenase kinase 1	6.40	9.15E-81
<i>TSPAN1</i>	Tetraspanin 1	6.35	3.46E-23
<i>FGR</i>	FGR proto-oncogene, Src family tyrosine kinase	6.30	1.37E-159
<i>MAFF</i>	MAF bZIP transcription factor F	6.19	1.54E-147
<i>ELOVL3</i>	ELOVL fatty acid elongase 3	6.00	8.77E-145
<i>TM7SF2</i>	Transmembrane 7 superfamily member 2	5.95	2.79E-154
<i>PTK2B</i>	Protein tyrosine kinase 2 beta	5.87	8.61E-234
<i>LPL</i>	Lipoprotein lipase	5.79	3.47E-230
<i>SLC4A4</i>	Solute carrier family 4 member 4	5.78	5.25E-117
<i>AATBC</i>	Apoptosis associated transcript in bladder cancer	5.78	3.21E-21
<i>NXPH4</i>	Neurexophilin 4	5.78	3.59E-21
<i>OLMALINC</i>	Oligodendrocyte maturation-associated long intergenic non-coding RNA	5.74	6.04E-149
<i>ABLIM2</i>	Actin binding LIM protein family member 2	5.70	1.61E-88
<i>GPR153</i>	G protein-coupled receptor 153	5.57	9.86E-124
<i>ACSM3</i>	Acyl-CoA synthetase medium chain family member 3	5.56	3.35E-37
<i>DGAT2</i>	Diacylglycerol O-acyltransferase 2	5.47	5.00E-127
<i>NCAM2</i>	Neural cell adhesion molecule 2	5.40	1.62E-34
<i>ECHDC1</i>	Ethylmalonyl-CoA decarboxylase 1	5.31	2.84E-213
<i>FLVCR1-DT</i>	FLVCR1 divergent transcript	5.29	5.45E-11
<i>IFI27</i>	Interferon alpha inducible protein 27	5.23	1.58E-14
<i>FASN</i>	Fatty acid synthase	5.18	4.50E-133
<i>EPHB2</i>	EPH receptor B2	5.18	7.43E-79
<i>EPB41L4A</i>	Erythrocyte membrane protein band 4.1 like 4A	5.13	4.54E-12

<i>PLEKHH1</i>	Pleckstrin homology, MyTH4 and FERM domain containing H1	5.05	1.40E-129
<i>ELOVL5</i>	ELOVL fatty acid elongase 5	5.04	1.14E-203
<i>PLCD4</i>	Phospholipase C delta 4	4.99	7.48E-23
<i>CKMT2</i>	Creatine kinase, mitochondrial 2	4.95	1.27E-136
<i>STX11</i>	Syntaxin 11	4.86	2.08E-134
<i>PCBD1</i>	Pterin-4 alpha-carbinolamine dehydratase 1	4.78	2.55E-141
<i>TSPAN13</i>	Tetraspanin 13	4.76	8.38E-150
<i>SLC2A6</i>	Solute carrier family 2 member 6	4.71	7.23E-99
<i>HMGS1</i>	3-hydroxy-3-methylglutaryl-CoA synthase 1	4.65	1.25E-55
<i>CABLES1</i>	Cdk5 and Abl enzyme substrate 1	4.65	7.29E-195
<i>RPH3AL</i>	Rabphilin 3A like (without C2 domains)	4.59	1.56E-22
<i>CD9</i>	CD9 molecule	4.57	4.93E-133
<i>LINC01128</i>	Long intergenic non-protein coding RNA 1128	4.52	1.61E-37
<i>LETM1</i>	Leucine zipper and EF-hand containing transmembrane protein 1	4.52	4.68E-205
<i>C1orf54</i>	Chromosome 1 open reading frame 54	4.42	1.88E-30
<i>ADIPOR2</i>	Adiponectin receptor 2	4.34	1.36E-237
<i>ADIRF</i>	Adipogenesis regulatory factor	4.30	1.48E-83
<i>UBASH3B</i>	Ubiquitin associated and SH3 domain containing B	4.30	4.10E-143
<i>RIPOR2</i>	RHO family interacting cell polarization regulator 2	4.27	2.48E-09
<i>ACSL4</i>	Acyl-CoA synthetase long chain family member 4	4.13	1.02E-66
<i>FAM83D</i>	Family with sequence similarity 83 member D	4.06	2.15E-04
<i>ANK3</i>	Ankyrin 3	4.05	1.86E-33
<i>CLSTN3</i>	Calsyntenin 3	4.00	6.73E-60
<i>DENND3</i>	DENN domain containing 3	4.00	2.28E-120
<i>ZFAT</i>	Zinc finger and AT-hook domain containing	4.00	3.34E-160
<i>RASSF2</i>	Ras association domain family member 2	4.00	2.95E-55
<i>MECR</i>	Mitochondrial trans-2-enoyl-CoA reductase	3.99	1.60E-104
<i>AGPAT2</i>	1-acylglycerol-3-phosphate O-acyltransferase 2	3.99	2.42E-107
<i>DHCR7</i>	7-dehydrocholesterol reductase	3.98	6.07E-114
<i>KIAA1671</i>	KIAA1671	3.93	3.84E-46
<i>ABCA4</i>	ATP binding cassette subfamily A member 4	3.86	6.26E-12
<i>SLC19A1</i>	Solute carrier family 19 member 1	3.86	2.33E-87
<i>BRINP2</i>	BMP/retinoic acid inducible neural specific 2	3.82	1.26E-25
<i>LDB3</i>	LIM domain binding 3	3.74	1.85E-19
<i>PRKCD</i>	Protein kinase C delta	3.70	2.13E-126
<i>NKILA</i>	NF-kappaB interacting lncRNA	3.69	1.41E-08
<i>OSBPL11</i>	Oxysterol binding protein like 11	3.63	5.82E-113
<i>LRRC2</i>	Leucine rich repeat containing 2	3.57	4.69E-08
<i>SPIRE2</i>	Spire type actin nucleation factor 2	3.56	9.59E-20
<i>SULT4A1</i>	Sulfotransferase family 4A member 1	3.51	6.48E-08
<i>GCH1</i>	GTP cyclohydrolase 1	3.48	1.05E-21

<i>KCNQ3</i>	Potassium voltage-gated channel subfamily Q member 3	3.43	3.31E-63
<i>DIAPH3</i>	Diaphanous related formin 3	3.42	7.71E-09
<i>CDK15</i>	Cyclin dependent kinase 15	3.36	5.65E-68
<i>FLVCR2</i>	Feline leukemia virus subgroup C cellular receptor family member 2	3.23	3.88E-57
<i>MAPK8IP2</i>	Mitogen-activated protein kinase 8 interacting protein 2	3.19	6.93E-34
<i>DMTN</i>	Dematin actin binding protein	3.14	3.95E-48
<i>EGR3</i>	Early growth response 3	2.95	4.32E-09
<i>EXOSC10-AS1</i>	EXOSC10 antisense RNA 1	2.86	5.81E-03
<i>PRPS2</i>	Phosphoribosyl pyrophosphate synthetase 2	2.78	1.55E-55
<i>CLDN7</i>	Claudin 7	2.70	2.30E-02
<i>NETO2</i>	Neuropilin and tolloid like 2	2.64	3.03E-04
<i>GRK3</i>	G protein-coupled receptor kinase 3	2.61	2.15E-43
<i>CMYA5</i>	Cardiomyopathy associated 5	2.56	1.86E-38
<i>MAP6</i>	Microtubule associated protein 6	2.48	1.74E-02
<i>GKAP1</i>	G kinase anchoring protein 1	2.47	4.59E-08
<i>AKAP1</i>	A-kinase anchoring protein 1	2.46	1.01E-75
<i>BLM</i>	BLM RecQ like helicase	2.39	3.27E-10
<i>TAF1A-AS1</i>	TAF1A antisense RNA 1	2.39	1.19E-06
<i>BRIP1</i>	BRCA1 interacting protein C-terminal helicase 1	2.31	3.01E-03
<i>AGAP11</i>	ArfGAP with GTPase domain, ankyrin repeat and PH domain 11	2.16	7.38E-13
<i>IFI30</i>	IFI30 lysosomal thiol reductase	2.01	1.19E-05

Table S2. Top 15 GO terms for 137 FADAGs.

Category	Term name	P-value	Benjamini
GOTERM_BP_FAT	Lipid metabolic process	1.10E-16	2.90E-13
GOTERM_BP_FAT	Cellular lipid metabolic process	3.30E-15	4.50E-12
GOTERM_BP_FAT	Lipid biosynthetic process	2.30E-14	2.10E-11
GOTERM_BP_FAT	Thioester metabolic process	3.40E-12	1.90E-09
GOTERM_BP_FAT	Acyl-CoA metabolic process	3.40E-12	1.90E-09
GOTERM_BP_FAT	Fatty acid metabolic process	1.10E-11	5.10E-09
GOTERM_BP_FAT	Monocarboxylic acid metabolic process	5.20E-11	2.00E-08
GOTERM_BP_FAT	Coenzyme metabolic process	8.30E-11	2.80E-08
GOTERM_BP_FAT	Triglyceride metabolic process	1.60E-10	4.90E-08
GOTERM_BP_FAT	Small molecule biosynthetic process	2.10E-10	5.80E-08
GOTERM_BP_FAT	Coenzyme biosynthetic process	4.00E-10	9.80E-08
GOTERM_BP_FAT	Fatty acid biosynthetic process	4.70E-10	1.10E-07
GOTERM_BP_FAT	Monocarboxylic acid biosynthetic process	6.90E-10	1.20E-07
GOTERM_BP_FAT	Acylglycerol metabolic process	7.10E-10	1.20E-07
GOTERM_BP_FAT	Acyl-CoA biosynthetic process	7.60E-10	1.20E-07

Table S3. Information on human dermal fibroblasts (HDFs) and mesenchymal stem cells (MSCs) used in this study.

Abbreviation	Lot#	Passage	BMI	Age	Gender	Ethnicity	Site
HDF38	DFM090214A	2	23.1	38	Male	Caucasian	Abdomen
HDF35	DFM102715B	3	33.9	35	Female	Hispanic	Abdomen
HDF37	DFM111714A	3	33.1	37	Female	African-American	Abdomen
HDF44	DFM101014C	2	31.8	44	Female	African-American	Breast
HDF54	DDFM052010B	3	21.3	54	Female	African-American	Abdomen
AdMSC46	394Z027.1	2	Unknown	46	Female	Caucasian	Abdomen
AdMSC51	423Z037.1	2	24	51	Female	Caucasian	Breast
BmMSC70	429A022	2	Unknown	70	Male	Caucasian	Femoral head

Table S4. Sequences and product size of primers used for qRT-PCR.

Gene	Sense primer	Antisense primer	Product size
<i>TBP</i>	CCTAAAGACCATTGCACTTCGTG	GTGGTTCGTGGCTCTCTTATC	93
<i>UCP1</i>	TCTACGACACGGTCCAGGAG	GAATACTGCCACTCCTCCAGTC	104
<i>FABP4</i>	GCCAGGAATTTGACGAAGTCA	CCCATTCTGCACATGTACCAG	93
<i>CIDEA</i>	AAGGCCACCATGTATGAGATGTAC	ACAGGAACCGCAGCAGACTC	91
<i>GPAM</i>	GATCGCATTATCGAAGGTCCTAC	TTGCTACACTCCACAGGCTCTC	79
<i>LIPE</i>	CTCAGTGTGCTCTCCAAGTG	CTTCTGGTCTGAGTTGGAGTG	76
<i>CKMT1</i>	AGCAGGAATGGCTCGAGAC	ATCCTCCTCATTACCCAGATC	88
<i>ADIPOQ</i>	CTGGTGAGAAGGGTGAGAAAG	GTTTCACCGATGTCTCCCTTAG	64
<i>CD36</i>	CAACCTATTGGTCAAGCCATCAG	TGTTTGCCTTCTCATCACCAATG	119
<i>SREBF1</i>	CCTGGTCTACCATAAGCTGCAC	CTGCACACTCTGCCAGGTTC	110
<i>FASN</i>	CCTTCGAGGTGTCAGAGAAC	TTTCCGGGTGGTCAAGAG	93
<i>GPD1</i>	CTGACCTGATCACTACCTGCTATG	GCAACTCTTCTCCAGCTGCTC	99
<i>GK</i>	GATTTGTCTGCCGTCACGATG	CCAACCCATTGACTTCATCACAG	108
<i>KCNK3</i>	CCATCACCGTCATCACCAC	CAGCGCGTAGAACATGCAG	86
<i>ADRB2</i>	CTGCTGTGACTTCTTCACGAAC	AGACCCTGGAGTAGACGAAGAC	101
<i>AEBP1</i>	AACGCCACCATCTCTGTGAG	CAAGATTCGCCAGTAATCACCAC	75
<i>CEBPA</i>	AACATCGCGGTGCGCAAGA	AGCTCCAGCACCTTCTGCT	74
<i>PPARGC1A</i>	AGGTCAAGATCAAGGTCTCCAG	GGTGTCTGTAGTGGCTTGACTC	79
<i>PPARGC1B</i>	AGTGTTTGGTGAGATTGAGGAGTG	AGAACACCGGTAGGTGATGAAG	85
<i>PPARG</i>	TGGAATTAGATGACAGCGACTTG	CTTCAATGGGCTTCACATTGAG	93
<i>RXRG</i>	GGCCTACACCAAGCAGAAGTATC	CAAGCCAATGGAACGCAGAG	88
<i>LXRA</i>	CAGATTGCCCTGCTGAAGAC	AGGGTTGTACCTCCGAGATG	69
<i>CITED1</i>	TGGCACCTCACCTGCGAAG	GCAGAATGGCCACTGCTTTG	98