Supplementary Figure Legends

Supplementary Figure 1. Generation of myeloid-specific ANT2 KO mice. (A) mRNA expression of Ant1 and Ant2 in bone marrow-derived monocytes of WT and ANT2 MKO mice (n=4 mice/group). (B) Ant2 mRNA expression in bone marrow-derived monocytes isolated from WT and ANT2 MKO mice during M-CSF-induced macrophage differentiation (n=3 mice/group). (C) mRNA expression of Ant1 and Ant2 in BMDMs of WT and ANT2 MKO mice (n=4 wells/group). (**D**) *Ant2* mRNA expression in eWAT (left; n=6 mice/group) and primary adipocytes (middle; n=6 mice/group) and SVCs (right; n=3 mice/group) isolated from eWAT of WT and ANT2 MKO mice. (E) mRNA expression of Ant1 and Ant2 in ATMs isolated from eWAT of WT and ANT2 MKO mice (n=4 mice/group). (F) mRNA expression of Ant1 and Ant2 in whole brain of WT and ANT2 MKO mice (n=6 mice/group). (G) Semiquantitative PCR analysis of Ant2 exon2 and 3 deletion in genomic DNAs purified from whole brain of WT and ANT2 MKO mice. Schematic diagram of the genomic DNA PCR strategy is illustrated on top. (H) Body weight of NCD WT and ANT2 MKO mice (n=5 WT and 5 KO mice). (I) eWAT Mass of NCD WT and ANT2 MKO mice (n=5 WT and 5 KO mice). (J) Average adjocyte size in eWAT of WT and ANT2 MKO mice (n=5 WT and 5 KO mice). (K) Liver Mass of NCD WT and ANT2 MKO mice (n=5 WT and 5 KO mice). (L) H & E staining of eWAT sections of NCD WT and ANT2 MKO mice. eWAT samples harvested from 5 WT and 5 KO individual mice were analyzed and representative pictures are shown. (M) H & E staining of liver sections of NCD WT and ANT2 MKO mice. Representative pictures are shown. eWAT samples harvested from 5 WT and 5 KO individual mice were analyzed and representative pictures are shown. (N) OGTT in NCD WT and ANT2 MKO mice (n=6 WT and 8 KO mice). (O) Fasting (6h) plasma insulin levels in NCD WT and ANT2 MKO mice (n=6 WT and 8 KO mice). (P) Body weight changes after HFD in WT and ANT2

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MKO NCD WT and ANT2 MKO mice (n=6 WT and 8 KO mice). **P*<0.05; ***P*<0.01; ****P*<0.001; all error bars represent SEM.

Supplementary Figure 2. Insulin-stimulated Akt phosphorylation in liver, skeletal **muscle, and eWAT of HFD WT and ANT2 MKO mice.** (**A**) Western blot analysis of total and phosphorylated (Ser473) Akt was performed in total lysates of liver, skeletal muscle (quadriceps), and eWAT of HFD WT and ANT2 MKO mice. (**B**) Relative band intensity in panel A was measured, plotted, and presented.

Supplementary Figure 3. ANT2 depletion does not affect myeloid development or macrophage differentiation, and obesity induced increased Ant2 expression in ATMs. (A-B) Flow cytometry analysis of the time course changes in macrophage differentiation of hematopoietic stem cells isolated from WT and ANT2 KO mice, stimulated by M-CSF in vitro (A). The proportion of CD11b⁺ F4/80⁺ macrophages during the course of BMDM differentiation is plotted in panel B (n=3 wells/time point). (C-E) Flow cytometry analysis of myeloid cells in spleen (C-left and E) and mesenteric lymph node (C-right and D) of WT and ANT2 MKO mice. The proportion of each of myeloid subsets is plotted in panel C (n= 5 mice/group). (F) Gating strategy for the flow cytometry analysis in Figure 2C. (G-H) Flow cytometry analysis of different CD4⁺ T cell subsets in HFD WT and ANT2 MKO mice (n= 7 mice per group). (G) The proportion of different CD4⁺ T cell subsets among total SVCs are plotted and presented. (H) Gating strategy for different CD4⁺ T cell subsets. (I-N) Single cell RNA-seq analysis of Ant2 expression in different subsets of adipose tissue macrophages and monocytes. UMAP projections of identified graph-based adipose tissue macrophage (I) and monocyte (J) clusters from scRNA-seq data derived from CD45⁺ cells sorted from the stromal vascular fraction of eWATs of NCD and HFD WT mice are shown in

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panels of I and J. k-nearest neighbor graph algorithm was applied to identify 6 clusters of adipose tissue macrophages and monocytes as illustrated and color-coded in panel I. Distribution and expression levels of *Ant2* in each of the adipose tissue macrophages (L) and monocytes (N) are presented as heat maps in panels L and N. Expression levels of *Ant2* in different ATM subsets expressing *Itgax*⁺ (encoding CD11c) and *Cd9*⁺ are plotted in a bar graph (M). n= 4 NCD and 4 HFD (18 weeks) mice. (**O**) *Ant1* and *Ant2* mRNA expression in WT BMDMs treated with or without LPS or IL-4/IL-13 for 24h (n=4 wells/group). (**P**) mRNA expression of *Ant1* and *Ant1* in ATMs isolated from NCD and HFD WT mice (n=4 mice/group). **P* < 0.05, ***P* < 0.01; all error bars represent SEM.

Supplementary Figure 4. Analysis of WT and ANT2 KO BMDMs. (**A**) Gating strategy for the flow cytometry analysis of BMDMs treated with or without LPS. (**B**) Quantitative changes in TLR2, TLR4, and TRAF6 expression relative to actin expression in Figure 4F Western blot images were calculated and plotted. (**C**) mRNA expression of TLRs and downstream signaling molecules in WT and ANT2 KO BMDMs (n=4 wells/group). (**D**) Western blot analysis of TRAF6 expression in the cytoplasmic and mitochondrial fraction of WT and ANT2 KO BMDMs treated with or without for 6 h. (**E**) Quantitative changes in the protein expression relative to GAPDH expression in panel D images were calculated and plotted.

Supplementary Figure 5. Gating strategies for flow cytometry analysis of ATMs. (A) Gating strategy for flow cytometry analysis of ATMs in Figure 5B. (B) mRNA expression of chemokine receptor genes in WT and ANT2 KO monocytes. *P < 0.05, **P < 0.01; all error bars represent SEM. (C) Gating strategy for flow cytometry analysis of ATMs in Figures 5C, 5D, and 5E. Supplementary Figure 6. OCR, PGC1 α expression, and mitophagy in WT and ANT2 KO BMDMs treated with or without LPS or PA. (A) Basal OCR was measured in WT and ANT2 KO BMDMs treated with or without LPS for 24h, in the presence or absence of acute PA treatment (n= 5 wells/group). (B) Oligomycin-insensitive (uncoupled) OCR in WT and ANT2 KO BMDMs treated with or without LPS for 24h, in the presence or absence of acute PA treatment (n= 5 wells/group). (C) PGC-1 α expression in WT and ANT2 KO BMDMs treated with PA or LPS for 24h. (D) Quantitative measurement of mitophagy using mtKeimared in WT and ANT2 KO BMDMs treated with or without LPS for 24. Representative pictures are shown on the left. The ratio between red and green fluorescence was calaculated and ploted on the right. (E) Electron microscopy analysis of autophagosome formation in WT and ANT2 KO BMDMs treated with or without PA or LPS for 24h. Representative pictures are shown on the left. The number of autophagosome in a given cellular area is plotted on the right. **P* < 0.05, ***P* < 0.01, ****P*<0.001; all error bars represent SEM.

Supplementary Figure 7. Relative band intensity in the Western blot images in Figure 7D.

Supplementary Figure 8. Inflammatory and mitophagic protein expression in WT and ANT2 KO BMDMs. (A) Relative band intensity of the Western blot images in Figure 8A. (B) Western blot analysis of inflammatory and mitophagic protein expression in WT and ANT2 KO BMDMs treated with or without PA or LPS, in the presence or absence of MitoTEMPO for 30 min. (C) Relative band intensity of the Western blot images in Figure 8C. (D) Western

blot analysis of HIF-1 α in WT and ANT2 KO BMDMs treated with or without H₂O₂ for 1 or 4h. (E) Relative band intensity of the Western blot images in Figure 8F.



Supplementary Figure 1













F



Gating strategy for flow cytometry analyses of ATMs





Η

Gating strategy for flow cytometry analyses of SVCs









THA THA TRAIS TRAIGECSIL

7117





Gating strategy for flow cytometry analysis of PKH67⁺ ATMs





С

В



Gating strategy for flow cytometry analysis of Ki67^{+/-} or active Caspase3⁺ ATMs (HFD)











CHIPPPS

ctile pes

cripps

0

CHI6105

CHIPPPS

C416605

CK12P25

0

CH16165

Supplementary Figure 8

Supplementary Table 1. Fast gene set enrichment analysis in CD11c+ ATMs isolated from HFD ANT2 MKO and WT ATMs

	Gene Ranks	NES*	Adj P value**
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	Imagene 1000	3.12	8.9e-29
HALLMARK_OXIDATIVE_PHOSPHORYLATION	18 Bar - 11 Bar - 19 - 19 - 19 - 19 - 19 - 19 - 19 - 1	2.48	3.8e-14
HALLMARK_ADIPOGENESIS		2.38	2.4e-12
HALLMARK_HYPOXIA		2.21	2.3e-09
HALLMARK_XENOBIOTIC_METABOLISM	Man iferenza (1997) - 1997 - 199	2.19	1.3e-08
HALLMARK_GLYCOLYSIS		2.12	4.6e-08
HALLMARK_APICAL_JUNCTION	Minimum and a second	2.19	5.3e-08
HALLMARK_FATTY_ACID_METABOLISM	IN mark and and an and a second a second	2.16	1.1e-07
HALLMARK_CHOLESTEROL_HOMEOSTASIS	HIMMMAN - FU - FO - MARK - FO	2.33	5.2e-07
HALLMARK_PEROXISOME	1800 (1800 - 1800 - 1990) - 1990 (1990) - 19900 (1990) - 1990 (1990) - 19900 (1990) - 19900 (1990) - 1990 (1990) -	2.25	6.3e-07
HALLMARK_PI3K_AKT_MTOR_SIGNALING		-0.92	7.0e-01
HALLMARK_SPERMATOGENESIS	0	-1.04	4.3e-01
HALLMARK_IL6_JAK_STAT3_SIGNALING	Т. 1. Билик — м. 1. или — ок. 1. т. т. т. т. т. т. т. т. на т. на т. 1. ни в	-1.20	1.9e-01
HALLMARK_INFLAMMATORY_RESPONSE	1. mm.110	-1.45	7.4e-03
HALLMARK_KRAS_SIGNALING_DN		-1.65	2.8e-03
HALLMARK_G2M_CHECKPOINT	111011 11 00.000 - 101 0000 - 000 10000 - 00000 - 00000 - 00000 - 00000 - 00000 - 00000 - 0000	-1.57	1.6e-03
HALLMARK_ALLOGRAFT_REJECTION		-1.59	1.3e-03
HALLMARK_E2F_TARGETS		-1.60	5.2e-04
HALLMARK_INTERFERON_ALPHA_RESPONSE	· · · · · · · · · · · · · · · · · · ·	-2.34	5.7e-08
HALLMARK_INTERFERON_GAMMA_RESPONSE		-2.26	1.7e-10
	5000 10000		

RNA-seq analysis was performed in CD11c⁺ ATMs isolated from ANT2 MKO and WT control mice fed HFD, and the resulting data were subjected to fast gene set enrichment analysis. Positive NES values indicate that the majority of genes implicated in the corresponding pathway or gene network generally showed increased expression in HFD ANT2 KO ATMs compared with HFD WT ATMs, whereas negative NES values indicate that the majority of genes implicated in the corresponding pathway or gene network generally showed increased expression in HFD ANT2 KO ATMs compared with HFD WT ATMs, whereas negative NES values indicate that the majority of genes implicated in the corresponding pathway or gene network generally showed decreased expression in HFD ANT2 KO ATMs compared with HFD WT ATMs. The gene rank plot shows fold changes in the expression of each of the genes that are implicated in the corresponding pathway or gene network. Thus, fold changes of the most highly increased genes are plotted on the left, whereas, fold changes of the most highly decreased genes are plotted on the right.

.*NES, normalized enrichment score. ** Adj P value, BH adjusted P value.

REAGENT or RESOURCE SOURCE **IDENTIFIER** Antibodies Anti-HIF-1α Abcam Cat# ab2185; RRID: AB 302883 Anti-ANT1 Cat# ab102032; RRID: AB 10710263 Abcam Anti-ANT2 Cell signaling Cat# 14671S; RRID:AB 2798562 Anti-NFkB p65, phospho (Ser536) Cell signaling Cat# 3033S; RRID:AB 331284 Cell signaling Anti-SAPK/JNK Cat# 9252S; RRID:AB 2250373 Anti-phospho SAPK/JNK, (Thr183/Tyr185) Cell signaling Cat# 9255S; RRID:AB 2307321 Anti-SQSTM1/p62 (D6M5X) Cell signaling Cat# 23214S; RRID:AB 2798858 Cell signaling Anti-LC3 Cat# 4108S; RRID:AB 2137703 Anti-Parkin Abcam Cat# ab77924; RRID: AB 1566559 Cat# ab15494; RRID:AB 301903 Anti-Parkin Abcam Anti-PINK1 Abcam Cat# ab23707; RRID:AB 447627 Anti-Mitofusin 2 Cat# ab56889; RRID:AB 2142629 Abcam **Total OXPHOS Rodent Antibody Cocktail** Abcam Cat# ab110413; RRID:AB 2629281 Cell signaling Cat# 4685; RRID: AB 2225340 Anti-Akt Anti-phospho Akt (S473) Cell signaling Cat# 4060; RRID: AB 2315049 Anti-_β-Actin Sigma Cat# A2228; RRID:AB 476697 Anti-α-Tubulin Abcam Cat# ab4074; RRID:AB 2288001 Anti-CD45 Brilliant Violet 605 BioLegend Cat# 103139, RRID: AB 2562341 Anti-CD11b PerCP-Cyanine5.5 Thermo Fisher Cat# 45-0112-82, RRID: AB 953558 Anti-CD11b APC-Cyanine7 BioLegend Cat# 101226, RRID: AB 830642 Anti-CD11b PE Thermo Fisher Cat# 12-0112-82, RRID: AB 2734869 Anti-F4/80 PE-Cyanine7 Thermo Fisher Cat# 25-4801-82, RRID: AB 469653 Anti-F4/80 PE BioLegend Cat# 123110, RRID: AB 893486 Anti-CD11c APC Cat# 17-0114-82, RRID: AB 469346 Thermo Fisher Anti-Ki67 FITC Thermo Fisher Cat# 11-5698-82, RRID: AB 11151330 Anti-Ki67 PE Thermo Fisher Cat# 12-5698-82, RRID: AB 11150954 Anti-FoxP3 PE Thermo Fisher Cat# 12-5773-80, RRID: AB 465935 Anti-CD170 (Siglec-F) Brilliant Violet 421 Cat# 155509, RRID: AB 2810421 BioLegend Anti-CD3 PerCP-Cyanine5.5 BioLegend Cat# 100218, RRID: AB 1595492 BioLegend Anti-CD4 APC-Cyanine7 Cat# 100525, RRID: AB 312726 Anti-CD8 Alexa Fluor 488 BioLegend Cat# 100723, RRID: AB 389304 Anti-IL-4 Brilliant Violet 421 BioLegend Cat# 504120, RRID: AB 2562102 Thermo Fisher Anti-IL-17A PE-Cyanine7 Cat# 25-7177-80, RRID: AB 10717952 Anti-IFNy APC Thermo Fisher Cat# 17-7311-82, RRID: AB 469504 Anti-Ly6C PE Thermo Fisher Cat# 560592, RRID: AB 1727556 Anti-Ly6G PerCP-Cyanine5.5 BioLegend Cat# 127616, RRID: AB 1877271 Anti-CD16/CD32 Thermo Fisher Cat# 14-0161-86, RRID: AB_467135 Sigma Cat# GLNA 934V Rabbit IgG Jackson Cat# 115-035-003, RRID: Mouse IgG Immuno AB 10015289 Research

Sigma

Cat# P9767

Chemicals, Peptides, and Recombinant Proteins

Palimitic acid

Supplementary Table 2. Detailed Information of The Reagents And Resources

LPS from <i>E.coli</i> O127:B8	Sigma			
	NI NI Pal	Cat# L3129		
	Norvo Nordisk			
50% Dextrose	Hospira	Cat# 0409-6648-02		
IL-4	PeproTech	Cat# 214-14		
IL-13	PeproTech	Cat# 210-13		
MitoTEMPO	Cayman	Cat# 16621		
Collagenase from Clostridium histolyticum	Sigma	Cat# C1764		
60% high-fat diet	Research Diets	Cat# D12492		
Trizol™ Reagent	ThermoFisher	Cat# 15596026		
SMARTScribe Reverse Transcriptase	Clontech	Cat# 639537		
RBC lysis buffer	eBioscience	Cat# 00-4333-57		
Lipofectamine 2000	ThermoFisher	Cat# 11668030		
Lipofectamine RNA iMAX	ThermoFisher	Cat# <u>13778150</u>		
Recombinant Mouse M-CSF	Biolegend	Cat# 576406		
TransIT®-LT1 Transfection Reagent	Mirus	Cat# MIR2300		
Endotoxin-low Bivine Serum Albumin	Sigma	Cat# A8806		
LIVE/DEAD™ Fixable Cell Stain Kit	ThermoFisher	Cat# L34966		
PKH67 Fluorescent Cell Linker Kits	Sigma	Cat# MINI67-1KT		
ROS Detection Reagent	ThermoFisher	Cat# C6827		
MitoSOX Red mitochondrial superoxide	ThermoFisher	Cat# M36008		
indicator for live-cell imaging				
Mitochondria Isolation Kit for Cultured cells	ThermoFisher	Cat# 89874		
UK5099	Sigma	Cat# PZ0160		
BPTES	Sigma	Cat# SML2472		
Etomoxir	Sigma	Cat# E1905		
Oligomycin	Sigma	Cat# 75351		
DNP	Sigma	Cat# 34334		
Myxothiazol	Sigma	Cat# T5580		
Cyclosporine A	TOCRIS	Cat# 59865-13-3		
TRO 19622	TOCRIS	Cat# 22033-87-0		
Critical Commercial Assays				
Citrate Synthase Activity Colorimetric	BioVision	Cat# K318-100		
Caspase-Glo® 3/7 Assav System	Promega	Cat# G8092		
RNeasy Micro Kit	Zvmo research			
Insulin ELISA kit	ALPCO	Cat# 80-INSHU-E01.1		
MitoProbe™ Transition Pore Assav Kit	ThermoFisher	Cat# M34153		
MitoProbe™ JC-1 Assay Kit for Flow	ThermoFisher	Cat# M34152		
Cytometry				
Experimental models. Cell Lines	ATOO			
	ATCC	ATCC [®] CL-173 [™]		
Recombinant DNA				
mKeima-Red-Mito-7	Addgene	Cat# 56018 ;		
		http://n2t.net/addgene:56018; RRID:Addgene_56018		

CA-HIF1α	Addgene	Cat # 44028 ; http://n2t.net/addgene:44028 ; RRID:Addgene_44028
Software and Algorithms		
GraphPad Prism v.8	GraphPad Software	GraphPad Prism, RRID: SCR_002798
Seahorse Wave v.2.2.0	Agilent	Seahorse Wave, RRID: SCR_014526
FlowJo	FlowJo	FlowJo, RRID: SCR_008520
ImageJ	NIH	https://imagej.nih.gov/ij/

	,	•	
Gene	Symbol and Full Name	Forward primer, 5' - 3'	Reverse primer, 5' - 3'
	Hypoxia-inducible	CAAGATCTCGGCGAAGCAA	GGTGAGCCTCATAACAGAAGCTTT
Hif1a	factor 1-alpha		
Hif2a	Hypoxia-inducible	TAAAGCGGCAGCTGGAGTAT	ACTGGGAGGCATAGCACTGT
TIIIZa		ATCACAAACCCAACTTCCACAC	<u> </u>
Glut4	Glucose transporter 4	ATGAGAAACGGAAGTTGGAGAG	GIGGGIGCGGCIGCC
Adipoq	AdipoQ, also known as Adiponectin and Acrp30	TGTTCCTCTTAATCCTGCCCA	CCAACCTGCACAAGTTCCCTT
Tnf	Tumour necrosis factor alpha	GAAATGCCACCTTTTGACAGTG	TGGATGCTCTCATCAGGACAG
Ccl5	Regulated on activation, normal T cell expressed and secreted	TGCCCTCACCATCATCCTCAC	GGCGGTTCCTTCGAGTGACA
lfng	Interferon gamma	ACAGCAAGGCGAAAAAGGATG	TGGTGGACCACTCGGATGA
Ant1	Adenine nucleotide translocase 1	GAATGCTCCCAGATCCCAAGAAT	AAAGGATAGGAAGTCAGGCCA
Ant2	Adenine nucleotide translocase 2	AGAGTGTGACAGCCGTTGC	ACCTTTGAAGAAAGCGTTGGC
116	Interleukin 6	GCTACCAAACTGGATATAATC	CCAGGTAGCTATGGTACTCCA
Tgfb	Transforming growth factor beta	GTGGAAATCAACGGGATCAG	ACTTCCAACCCAGGTCCTTC
ltgax	Integrin alpha-X protein	CTGGATAGCCTTTCTTCTGCT	GCACACTGTGTCCGAACTC
Nos2	Inducible nitric oxide synthase	CTCAGCCCAACAATACAAGAT	TGTGGTGAAGAGTGTCATGCA
Arg1	Arginase 1	CTCCAAGCCAAAGTCCTTAGA	AGGAGCTGTCATTAGGGACAT
<i>II10</i>	Interleukin 10	CCAAGCCTTATCGGAAATGA	TTTTCACAGGGGAGAAATCG
36B4	60S Acidic Ribosomal Protein P0	AGATGCAGCAGATCCGCAT	GTTCTTGCCCATCAGCACC
Primers	used for mouse genotyp	ing	
Cre	Cre recombinase	TGCAAGTTGAATAACCGGAAA	CTAGAGCCTGTTTTGCACGTT
Primer		ACTCAACCTAGGGCCTTGTG	GGGAGCATTCCTGAAAAATAA
set 1			
Primer set 2		ACTCAACCTAGGGCCTTGTG	GACTTACCCTCCACGACAGC
Primers	used for mtDNA content	assays	
mtDNA	Mitochondrial DNA	CCCAGCTACTACCATCATTCAAG T	GATGGTTTGGGAGATTGGTTGATG T
18S	18S ribosomal RNA	AGTCCCTGCCCTTTGTACACA	GATCCGAGGGCCTCACTAAAC

Supplementary Table 3. PCR Primer Sequences

Full unedited gel for Figure. 11





Full unedited gel for Figure. 1K



Full unedited gel for Figure. 3G



Full unedited gel for Figure. 3J



Full unedited gel for Figure. 1J

Full unedited gel for Figure. 6D







Full unedited gel for Figure. 7C



Full unedited gel for Figure. 7F



Full unedited gel for Supplementary Figure. 2A



Full unedited gel for Supplementary Figure. 4D



Full unedited gel for Supplementary Figure. 6C



Full unedited gel for Supplementary Figure. 8B



Full unedited gel for Supplementary Figure. 8D

