Suppl Figure 1. Association and genotyping of *Nudt7* and *Acot12* knockout mice. (A) Correlation between Nudt7 and Acot12 regulating  $\beta$ -oxidation and coenzyme A homeostasis. (B) Genotyping of *Nudt7*-/- *Acot12*-/- dKO mice.

Suppl Figure 2. H&E staining of tibialis anterior (TA) muscle in 12- and 20-month-old dKO mice and peroxisomal gene profile of TA muscle in 12- and 20-month-old dKO mice (n = 5).

Suppl Figure 3. Cell proliferation in WT, Nudt7<sup>-/-</sup>, Acot12<sup>-/-</sup>, and dKO iMACs (n = 4).

Suppl Figure 4. *In vitro* characteristics of WT, *Nudt7<sup>-/-</sup>*, *Acot12<sup>-/-</sup>*, and dKO iMACs. (A) Cell proliferation in WT and dKO iMACs (n = 4). (B) Apoptotic cell death in WT and dKO iMACs (n = 3). (C) Mitotracker staining. Scale bar = 10  $\mu$ m. (D) BODIPY<sup>493/508</sup> staining. Scale bar = 20  $\mu$ m. (E) Oil red O staining (n = 3). Quantification of Oil red O staining. (F) Expression level of genes in lipid metabolism. \*P < 0.05; \*\*P < 0.01; \*\*\* P < 0.001; \*\*\*\* P < 0.0001.

Suppl Figure 5. Enrichment signaling in dKO iMACs. (A) List of overlapped genes among dKO iMACs, GSE 16464, and OA cartilage (H200-3). (B) Top canonical pathway in dKO iMACs compared with WT.

Suppl Figure 6. Immunohistochemistry of FOXM1 in DMM cartilage of dKO mice introduced with *lenti-HA-Nudt7, lenti-HA-Acot12*, or both (n = 6). \*P < 0.05; \*\*P < 0.01; \*\*\* P < 0.001.

Suppl Figure 7. Translational level of *FoxM1* in WT and dKO mice with or without introduction of *FoxM1*.

Suppl Figure 8. **Profile of lysosomal, mitochondrial, and peroxisomal genes. (A)** In *Nudt7<sup>-/-</sup>* (N7KO), *Acot12<sup>-/-</sup>* (A12KO), dKO (ANdKO); **(B)** In *FoxM1*-overexpressed iMACs (n = 3).

Suppl Figure 9. Transfection efficiency of three *siFoxM1* (n = 3).

Suppl Figure 10. Accumulation of acetyl-CoA induces *FoxM1* and stimulates catabolic regulatory factors. (A) Senescence gene signature with exposure of sodium acetate (100  $\mu$ M and 1 mM) into iMACs. (B) Transcriptional level of *FoxM1* treated with sodium acetate in a dose-dependent manner (n = 3). (C) Expression levels of *Col2a1*, *Mmp13*, and *Adamts5* with treatment of sodium acetate (n = 3).

Suppl Figure 11. Fluorescence intensity of Rho@PAA-MnO<sub>2</sub> in senescence sensor after treatment with 0.5% or 1% H<sub>2</sub>O<sub>2</sub>.

Suppl Figure 12. Senescence sensing images of WT, *Nudt7<sup>-/-</sup>, Acot12<sup>-/-</sup>,* and dKO passaged (P4 to P9) iMACs treated with 1mM H<sub>2</sub>O<sub>2</sub>.

Suppl Figure 13. **Senescence signaling increases with OA progression. (A)** IVIS images of senescence sensing from DMM cartilage at one, four, six, and eight weeks after surgery. **(B)** Safranin O staining and immunohistochemistry of P16<sup>INK4a</sup> in DMM cartilage at one, four, six, and eight weeks after surgery.



В

ACOT12



WТ	Homo	
-	 	

N7+A12





	ACOX1		ABCD1	ABCD2	ABCD3	ABCD4	ACAA1	ACAD11	ACBD5	ACOT1	ACOT2	ACOT4	ACOT8	ACOX1		
	BAAT		ACOX2	ACOX3	ACSF3	ACSL1	ACSL3	ACSL4	ACSL5	ACSL6	AGPS	ALDH3A2	AMACR	BAAT		
	FAR1		CAT	CRAT	CROT	DAO	DDO	DECR2	DNAJC10	DNM1L	ECH1	EHHADH	EPHX2	FAR1		
	IDI1	6	FAR2	FIS1	GNPAT	GSTK1	HACL1	HAO1	HAO2	HMGCL	HSD17B4	IDE	IDH1	IDI1	1.0	
	PEX5	4	IDI2	MLYCD	Mosc2	MPV17	MVK	NOS2	NUDT12	PAOX	PECI	PECR	PEX1	PEX5	0.8	
ĺ	PEX5L		PEX10	PEX11A	PEX11B	PEX11G	PEX12	PEX13	PEX14	PEX16	PEX19	PEX26	PEX3	PEX5L	0.0	
	SCP2	 2	PEX6	PEX7	РНҮН	PIPOX	PMVK	PRDX1	PRDX5	PXMP2	PXMP3	PXMP4	RHOC	SCP2	0.2	
		0	SLC22A5	SLC25A17	SLC27A2	SOD1	SOD2	TRIM37	XDH						0	

ABCD1	ABCD2	ABCD3	ABCD4	ACAA1	ACAD11	ACBD5	ACOT1	ACOT2	ACOT4	ACOT8	ACOX1	
ACOX2	ACOX3	ACSF3	ACSL1	ACSL3	ACSL4	ACSL5	ACSL6	AGPS	ALDH3A2	AMACR	BAAT	
CAT	CRAT	CROT	DAO	DDO	DECR2	DNAJC10	DNM1L	ECH1	EHHADH	EPHX2	FAR1	
FAR2	FIS1	GNPAT	GSTK1	HACL1	HAO1	HAO2	HMGCL	HSD17B4	IDE	IDH1	IDI1	
ID12	MLYCD	Mosc2	MPV17	MVK	NOS2	NUDT12	ΡΑΟΧ	PECI	PECR	PEX1	PEX5	
PEX10	PEX11A	PEX11B	PEX11G	PEX12	PEX13	PEX14	PEX16	PEX19	PEX26	PEX3	PEX5L	
PEX6	PEX7	РНҮН	PIPOX	PMVK	PRDX1	PRDX5	PXMP2	PXMP3	PXMP4	RHOC	SCP2	
SLC22A5	SLC25A17	SLC27A2	SOD1	SOD2	TRIM 37	XDH						



Tukey's multiple comparisons test							
Hour	WT vs. NUDT7-/-	WT vs. ACOT12-/-	WT vs. dKO				
0	ns	ns	ns				
1	ns	ns	ns				
2	ns	ns	ns				
3	ns	ns	*				
4	ns	ns	**				
5	**	ns	****				
6	****	ns	****				
7	****	*	****				
8	****	**	****				
9	****	****	****				
10	****	****	****				



Acaca-

Abcd1-

Acadvl-AclyAcss1-Acss2-Cyp7a1Fasn-

Nr1h2-Nr1h3-Prkaa1-Scd1-

Lpl

Elovl4-ElovI5-Elovl6Sirt1-

10

0.0

ŵт

dKO

Α

	Upstream Regulator	dKO			GSE16464			H200-3 vs N122		
Symbol	Description	z-score	p-value	FC	z-score	p-value	FC	z-score	p-value	FC
let-7	microRNA	-5.529	0.000	#N/A	-3.578	0.000	#N/A	-3.592	0.000	#N/A
RB1	Retinoblastoma 1	-3.230	0.000	1.020	-2.297	0.071	1.074	-3.613	0.000	-1.005
TCF3	Transcription factor 3	-3.665	0.000	-1.040	-2.254	0.084	1.000	-3.492	0.000	1.342
mir-21	microRNA	-2.291	0.000	#N/A	-2.505	0.000	#N/A	-2.422	0.000	#N/A
NPPB	Natriuretic peptide B	-2.213	0.002	1.130	-2.213	0.104	-1.080	-2.258	0.000	1.019
HGF	Hepatocyte growth facotr	4.445	0.000	1.290	5.375	0.000	-1.026	3.251	0.000	-1.121
PTGER2	Prostaglandin E receptor 2	5.673	0.000	-1.070	3.081	0.156	1.184	4.493	0.000	-2.096
FOXM1	Forkhead box M1	5.454	0.000	3.450	2.967	0.001	1.240	4.927	0.000	2.042
ESR1	Estrogen receptor 1	6.118	0.000	-1.170	3.110	0.000	-1.211	6.609	0.000	-1.001





### Top Canonical pathway

	p-value
Cell cycle: G2M DNA Damage Checkpoint Regulation	1.6E-08
ATM signaling	7.31E-07
Cell Cycle Control of Chromosomal Replication	7.7E-07





Western blot Sample : WT, dKO-con, FoxM1 OE EV : pcDNA empty vector WB antibody : FOXM1













	p4	р5	p6	p7	p9	
ΜŢ						80   9   40   0   4   5   6   7   9   passage
Acot12 <sup>-/-</sup>						80 80 40 0 40 - 40 - 40 - 40 - 40 - 40 - 5 6 7 9 passage
Nudt7-/-						6 80 40- 40- 40- 4 5 6 7 9 passage
dKO						80 e 40- 0 4 5 6 7 9 passage

Α



P16INK4a

#### Gene Forward primer Reverse primer RN18S CCAGTAAGTGCGGGTCATAAG GGCCTCACTAAACCATCCAA Acot12 CTCAGTGCACAGTGGGATATAAG CTTCTCCAAGGTGGTGGTAATC Nudt7 GCCAGAGGAGGAAAGTTGTATT GTGGCTGTGTCATCTGTGT Col2a1 CTGGTTTGGAGAGACCATGAA GAGGAAAGTCATCTGGACGTTAG GAGACTTCTGCCTCTGGAATAG CTCCAGAAGGAATCCCACTAAC Acan Comp CGTGGGCTGGAAGGATAAA TACTAGCTCAGGACCCTCATAG Mmp3 GGACCAGGGATTAATGGAGATG TGAGCAGCAACCAGGAATAG Mmp9 TCTGTATGGTCGTGGCTCTAA GGAGGTATAGTGGGACAC Mmp13 CCCTGATGTTTCCCATCTATACC TTCATCGCCTGGACCATAAAG GCATTCCATGGTACAGGGTTA AGTTGACAGGGTTTCGGATG Adamts4 Adamts5 TGCCACAGACCCAACTAAAG CCATGGCTGATGACAGAGTT IL-6 GGGTTGCTTCTCTGTGTCTT GGTCGTCTTGCTTTCCTTCT TNFa TTGTCTACTCCCAGGTTCTCT GAGGTTGACTTTCTCCTGGTATG Ccl4 CCACTTCCTGCTGTTTCTCTTA CAAAGACTGCTGGTCTCATAGT GCCCACGTCAAGGAGTATTT CTTGAACCCACTTCTTCTCTGG Ccl5 IL-1b CCACCTCAATGGACAGAATATCA CCCAAGGCCACAGGTATTT CAGTGGACTCTGGGATCTATCT TGACATTCCAGTGCTCTTATGG Casp3 AGACCTTGGATGGCATTCTG CAGCCAGGAATCTGCTTGTA Casp9 Casp1 ACAAGGCACGGGACCTATG TCCCAGTCAGTCCTGGAAATG ATG3 GCTGGAGGTGAAGATGCTATTT TAGCCGTGGTGTCTGGTAATA ATG12 GCCTCGGAACAGTTGTTTATTT CAGGACCAGTTTACCATCACT JNK **TCCAGCACCCATACATCAAC** CTATTGTGTGCTCCCTCTCATC FAS AGACAGGATGACCCTGAATCTA CTTCAGCAATTCTCGGGATGTA Nf-kB GGATGACAGAGGCGTGTATTAG CCTTCTCTCTGTCTGTGAGTTG AGCCAGAAGGGACAGTAGAA CTCAGCCAAGCGGATGTAAA Acaca GTACAGTCTGGTGTCCATGTAG GGGTGTGATGATAGGGATGTT Abcd1 CTTTGCAGGGACTCAAGGAA CAAGCGAGCATACTGGGTATTA Acadvl CGGGAGGAAGCTGATGAATATG GTCAAGGTAGTGCCCAATGAA Acly GAGCATGAGCAGTGAAGACA CATGGCGGCATACAGTAGATAG Acss1 CACCTTCTGGCAAACAGAAAC CTACACCGAAGAATGGGAAAGA Acss2 CACCTTGAGGATGGTTCCTATAA TCAAAGGGTCTGGGTAGATTTC Cyp7a1 GACCTGGACCATTGCAGATAA GCCACACGAACAGGAGATAG Elovl4 GGTGTGTGGGGAAGGCAAATAC TGGAGAAGTAGTACCACCAGAG ElovI5 CCGAACTAGGTGACACGATATT TGTAGGAGTACCAGGAGTACAG Elovl6 AAGTTGCCCGAGTCAGAGAA TTCCAGACCGCTTGGGTAAT Fasn GCCCGAGGTTTCCACAAATA GCTGAAGTAGGAGTCGCTTATC Lpl CCACGTCACCCACTATTAAGG GCTCTAAGATGACCACGATGTAG Nr1h2 GTGGAAGACAGAACCTCAAGAT TGACTCCAACCCTATCCCTAA Nr1h3 GATCCTTTCCGGTGTGGATTAT GAAAGACCAAAGTCGGCTATCT Prkaa1 CAACTTCACCACGTTCTTCATC CCCGTCTCCAGTTCTCTTAATC Scd1 GGAACCTTTGCCTCATCTACA CACCTAGCCTATGACACAACTC Sirt1

## Supplementary Table 1. qRT-PCR primer sequences

Acox1	CGCACATCTTGGATGGTAGT	GGCTTCGAGTGAGGAAGTTATAG
Fabp4	GGATGGAAAGTCGACCACAATA	TGGCTCATGCCCTTTCATAA
Cd36	CTGGGACCATTGGTGATGAAA	CACCACTCCAATCCCAAGTAAG
BDNF	GGTCACAGTCCTAGAGAAAG	CAGCCTTCCTTGGTGTAA
BMP6	AGGACTGGATCATTGCAC	GTTGGTGGCATTCATGTG
CCL2	CTCAGCCAGATGCAGTTA	GTGATCCTCTTGTAGCTCTC
CDKN1A	AAGTGTGCCGTTGTCTCTTC	AGTCAAAGTTCCACCGTTCTC
CXCL1	GCTGGGATTCACCTCAAGAA	TGGCTATGACTTCGGTTTGG
CXCL2	GACAGAAGTCATAGCCACTCTC	GCCTTGCCTTTGTTCAGTATC
CXCL3	CAGAAGTCATAGCCACTCTC	CTTGCCGCTCTTCAGTAT
FGF2	TACCGGTCACGGAAATAC	GAAGAAACAGTATGGCCTTC
FGF7	GCGACACACCAGAAGTTA	CTGGGTCCCTTTCACTTT
ICAM1	GTACTGCTGGTCATTGTG	CCTGAGCCTTCTGTAACT
IGFBP2	AAGTCAGGCATGAAGGAG	TCCAGACTGAGGTGTTTG
IGFBP4	CGAACATCCCAACAACAG	CATCTTGCTCCGATCTCTA
IGFBP7	GTGCTGGTATCTCCTCTAAG	GGGCATCAACCACTGTAA
LMNB1	GGGCGTCAGATTGAGTAT	CTCCAGCTCTTCCTTGTA
MMP10	GTGGTGTTCCTGATGTTG	ATCCACACTCTGTCTTGG
MST1	CTTCCACTACAACATGAGC	CACAGACTCGAGTGGTATAG
TNFRSF11B	GAAACCCTTCCTCCAAAGTA	CAATGTCTTCCTCCTCACTG
TNFRSF1B	CTGTAGCATCCTGGCTATTC	TCTGGCTGAGATACGTAGAG
VEGFA	CTTTACTGCTGTACCTCCAC	CTGGTAGACATCCATGAACT
MEIS1	CCCTCTCTTAGCACTGATTT	CATTGAATGACTCTGACGAG
RHNO1	TTTGAGAGTCCACAGTCTTC	CTGAACAATGGCACTAAAGG
SMO	CCCATCAAGATCCATTTCTC	AAGATCTCAGCCTCCATTAG
SPIN4	CCCACTTTCCTCACTCATAG	GAGCACAGTACCTTTCCATT
ZC3H4	AGACCGTCAATGTCAATACC	ATCTGCTGGCTTCTGTAATC
CCND1	CAGAGGCGGATGAGAACAAG	GAGGGTGGGTTGGAAATGAA
DYNLT3	CAAGCATAGTGGAACAGTCT	CTGGCTGTGTGAAATCCATA
GBE1	CAAGAGCTATACGGACTACC	GTCTCTGATGACCTCCATAC
GDNF	CTGACCAGTGACTCCAATATG	GCTTGTTTATCTGGTGACCT
P4HA2	AAGCTCGCCAAGATTAAGAG	GTAGGCATTCACAGGATGAG
PLK3	GTCTGTTTGCCAAAGTTACC	ACCAAGCAGGAGACATTATC
PLXNA3	CCTTCTCCCATTGCTATTC	GTGAGTCAGAGTGGTATCT
RAI14	AAGATTCTTCCGGTCACAG	CCGAGTTGTCAATGTTCTC
SLC16A3	CTGCAGAAGCATTATCCAGA	ATTGAGCATGATGAGGGAAG
TAF13	CTGAAATGACTCACAAGGC	CTCTAGCAAACTTCCTTGG
TMEM87B	GACAAATCAGGACCTTTGG	GCCACTCTATGGTAAACTTC
TSPAN13	CTTGTTTAGCTCTGAATCGG	GCAGTTCAAATTCCTCTGG
UFM1	GCTAAAGTTTGCAGCAGAAG	ACATTCCCAGCAGTCTGT
FOXM1	AGGAGGACATAGCACACTTAGA	GGAGTTGGATAGCTCCTCTTTG
Cox2	CATCCCAGGCCGACTAAAT	TGGGCATAAAGCTATGGTTAGA
Cox4	AGTTGTACCGCATCCAGTTT	GCAGTGAAGCCAATGAAGAAC

Pmp70	CTTGCTTGTTTCTGGGCTATTC	CGTATCTGTATTCTCCTTCGTACTT
Cat	GATGGTAACTGGGATCTTGTGG	GTGGGTTTCTCTTCTGGCTATG
Lamp1	GACCCTGAAAGTGGAGAACAA	GGGCATCAGGAAGAGTCATATT
Lamp2	CTGACTCCTGTCGTTCAGAAAT	GGTGGGAGTTTGGTCTTCTT
Erfdh	AGCTACACGCTGTTCGAAATA	GGCTCCATTCCTCTCAATATCC
Etfb	GTGGTCACTGATGGTGTGAA	CTCCTTCACCAGTTTCTTCTCC
Decr1	CTGGGAACTATGGAGGAACTTG	CTTCCTCTCCACCGTCAAATC
Hadha	AGACATCGGAGCTGTCTTTG	CACTACCTTCTGAGCACCATAC
Hadhb	CCAAGAAGGCACAGGATGAA	AGGAAGGACGGATCCCATTA
Hadh	CTTGACTATGTTGGACTGGATACT	GGAAGGACTGGGCTGAAATAA
Acaa2	GACTTCTCTGCCACCGATTTA	TTGCCCACGATGACACTATC
Cpt2	CTCAGAAATCCAGGCACATCTA	CTCGGTTCTCACTGGTCAAATA
Acadm	GAGAAGAAGGGTGACGAGTATG	GGCTTTACTAGCGGGTACTTTA
Acads	CCCACAGCTCAGGTTAAGAA	GATGGAGTAGGCCAGGTAATC