

## Supplementary Materials

**Supplemental Table S1**

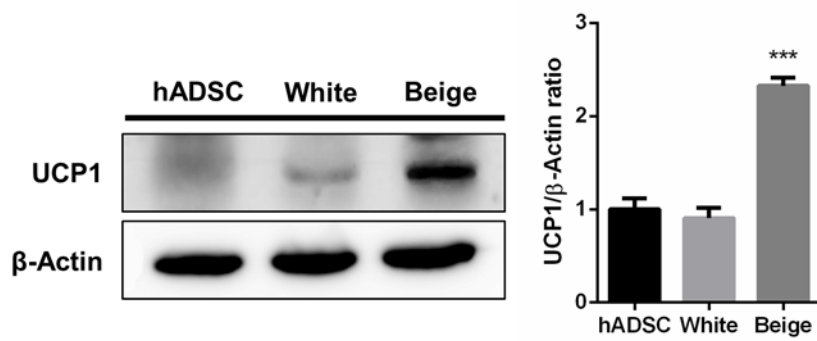
**Table S1.** The used primer sequences for quantitative PCR (5'-3').

Gene	Forward	Reverse	Accession no.
<i>GAPDH</i>	GGAAGGTGAAGGTCGGAGTC	GAAGGGGTCATTGATGGCAAC	NM_001256799
<i>CEBPA</i>	GTCGGTGGACAAGAACAGCAA	CATTGTCACTGGTCAGCTCCA	NM_001279
<i>PPARG</i>	GACCCAGAAAGCGATTCTTC	TCCATTACGGAGAGATCCACG	NM_001330615
<i>ADIPOQ</i>	TTGCCTACCACATCACAGTCT	TTACGCTCTCCTTCCCCATAC	NM_001177800
<i>FASN</i>	TCAGCCGCCATCTACAACATC	CAGCACCACATCCTCAAACAC	NM_004104
<i>UPC1</i>	ACTTGGTGTCGGCTCTTATCG	CCGTGCTCCTTCGTTAGTGA	NM_021833
<i>SAMM50</i>	CTGTCAAGTGGGAAGGCGTAT	ATGGCGTGCGAAAGAGATGAT	NM_015380
<i>PPARGC1A</i>	ACCCACCACTCCTCCTCATAA	GTCTTCCTTTCCTCGTGTCCA	NM_001330751
<i>DIO2</i>	GTCCTCCATCAGGTTTTAGCAA	CTCACCCAATTTACCATCCA	NM_000793
<i>ELOVL3</i>	CAGTGAGGATGTGGGGCATT	ATGATGAAGGCTGTGTCTCCG	NM_152310
<i>CIDEA</i>	TGGGAGACAACACGCATTTCA	TCATACATGGTGGCCTTCACG	NM_001279
<i>CIDEC</i>	AAGTCCCTTAGCCTTCTCTACC	CCTTCCTCACGCTTCGATCC	NM_001199551
<i>PAT2</i>	GACATCAAGGCCAGCATAAGC	GACGAGGCGAATGGACAGAT	NM_181776
<i>SLC25A20</i>	AGACACAGCCACCGAGTTTG	TCCCCAAACCAAACCCAAAGA	NM_000387
<i>FABP3</i>	ACCAAGCCTACCACAATCATCG	CAAGTTTCCCTCCATCCAGTGT	NM_001320996
<i>PK4</i>	TCAGCCTTCCCTTACACCAAT	AAACCAGCCAAAGGAGCATTC	NM_002612
<i>CITED1</i>	CCTCACCTGCGAAGGAGGA	GGAGAGCCTATTGGAGATCCC	NM_001144885
<i>CYCS</i>	TGGGTGATGTTGAGAAAGGCA	TGGCGGCTGTGTAAGAGTATC	NM_018947
<i>COX7A1</i>	GAGTGCGCGAGAAACAGAAG	CCCAGCCAAGGGAGTACAAG	NM_001864
<i>TFAM</i>	ATGGCGTTTCTCCGAAGCAT	TCCGCCCTATAAGCATCTTGA	NM_001270782
<i>CPT1B</i>	ACCAGGATCTGGGCTATGTGT	TACCGCTGAATTGTGGCTGAC	NM_001145134
<i>CPT2</i>	CAGCAGCCAAAGGGATCATCT	TACCCAACACCAAAGCCATCA	NM_000098
<i>MFN1</i>	AAATGCTCAAAGGGTGCTCCT	AGATGTAACGGACGCCAATCC	NM_033540
<i>MFN2</i>	CTGTCTGGGACCTTTGCTCAT	TGCAGGTACTGGTGTGTGAAC	NM_001127660
<i>OPA1</i>	AAGGGTCTGCTTGGTGAGCT	CTTGCGCTTCTGTTGGGCATA	NM_001354663
<i>DNM1L</i>	TGCCGTGAACCTGCTAGATG	GCCTTTGGCACACTGTCTTG	NM_001278463
<i>DNM2</i>	CCCCGACATGGCCTTTGAAG	GAGCTTCTCGGCACACTTTT	NM_001005360
<i>MFF</i>	GCCTCATCAGTCCACCCAAC	CTGGCACCAGACCATGACTT	NM_001277061

**Supplemental Table S2****Table S2.** The used shRNA sequences for knock down of SAMM50.

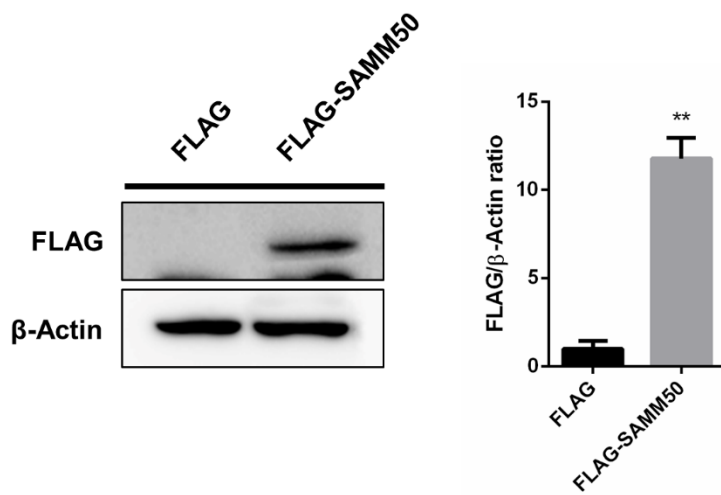
Clone ID	Target sequences	Oligonucleotide sequence
TRCN000 0229422	5'-CATCGCTCG GTTGGAAGTTAA-3'	F: 5'-CCGGCATCGCTCGGTTGGAAGTTAACTCGAGTTAAGTTCCAACC GAGCGATGTTTTTG-3' R: 5'-AATTCAAAAACATCGCTCGGTTGGAAGTTAACTCGAGTTAAGTT CCAACCGAGCGATG-3'
TRCN000 0229420	5'-GAGATTAAC GGGCAGTTATAA-3'	F: 5'-CCGGGAGATTAACGGGCAGTTATAACTCGAGTTATAACTGCCC GTTAATCTCTTTTTG-3' R: 5'-AATTCAAAAAGAGATTAACGGGCAGTTATAACTCGAGTTATAA CTGCCCGTTAATCTC-3'

## Supplemental Figure S1



**Figure S1.** Western blot analysis was performed to examine the protein levels of UCP1 in the human adipose-derived stem cells, white adipocytes, and beige adipocytes. The protein levels of UCP1 was quantified using ImageJ software. Results are shown as mean  $\pm$  SEM ( $n = 3$ ). \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.005$  compared to the hADSC and White groups.

Supplemental Figure S2



**Figure S2.** Western blot analysis was performed to examine the protein levels of FLAG in the FLAG and the human adipose-derived stem cells infected FLAG-tagged SAMM50 using lentivirus. The protein levels of FLAG was quantified using ImageJ software. Results are shown as mean  $\pm$  SEM ( $n = 3$ ). \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.005$  compared to the FLAG group.