

Supplementary Table. 1

Gene	Forward Sequence (5'-3')	Reverse Sequence (5'-3')	Species
Sirt3	GCAGCTCCCAGTTTCTTCTTT	CACCATGACCACCACCCTCT	Human
PINK1	TCTAAGCCTCTGGGGTGAACA	AGCGTTTCACACTCCAGGTT	Human
Parkin	GTGTTTGTCAAGTTCAACTCCA	GAAAATCACACGCAACTGGTC	Human
Sirt3	TGCTTCTGCGGCTCTATACAC	GGTTTCACAACGCCAGTACAG	Mouse
PINK1	GCAATGCCGCTGTGTATGAAG	TGGAGGAACCTGCCGAGATAT	Mouse
Parkin	GGCTGCGGGTTTGTTTTCTG	GGCTTGGTGGTCTTCTTGATG	Mouse
miR-34b-3p	CAATCACTAACTCCACTGCCATAA	-	Human
miR-34b-5p	CGCTAGGCAGTGTCATTAGCTG	-	Human
miR-34c-3p	CTAACCACACGGCCAGGA	-	Human
miR-34c-5p	CAGGCAGTGTAGTTAGCTGATTG	-	Human
miR-34b-3p	CACTAACTCCACTGCCATCAAA	-	Mouse
miR-34b-5p	GGCAGTGTAATTAGCTGATTGTAAA	-	Mouse
miR-34c-3p	CTAACCACACAGCCAGGAAAA	-	Mouse
miR-34c-5p	CAGGCAGTGTAGTTAGCTGATTG	-	Mouse

Supplementary Figure S1

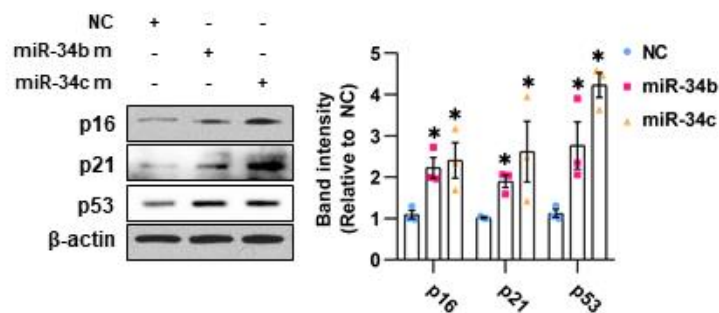


Figure S1. Western blot analysis of p16, p21, and p53 in HUVECs with NC or miR-34b m or miR-34c m. n≥3 per group, mean ± SEM, *P < 0.05 compared with NC group.

Supplementary Figure S2

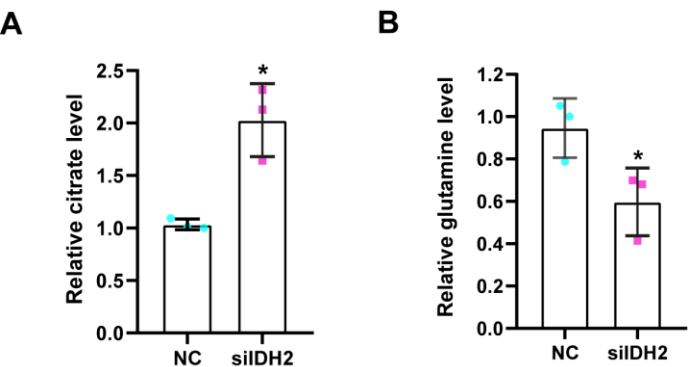


Figure S2. Relative intracellular levels of citrate (A), and glutamine (B) in HUVECs cells following treatment with NC or siIDH2. $n \geq 3$ per group, mean \pm SEM, * $P < 0.05$ compared with NC group.

Supplementary Figure S3

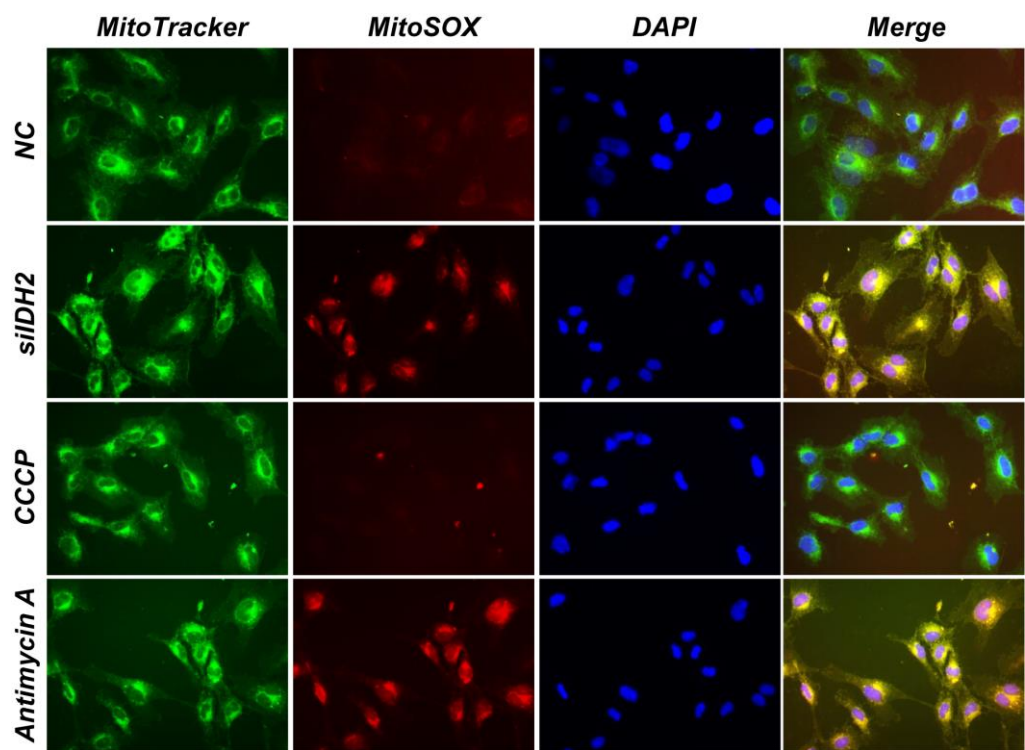


Figure S3. Representative micrographs of MitoTracker Green- and MitoSox Red-labeled HUVECs in the NC (Control) or siIDH2 (100 pmol) or CCCP (20 μ M, negative control) or Antimycin A (5 μ M, positive control) ; blue shows nuclei staining with DAPI.

Supplementary Figure S4

A

has-miR-34b 5' UAGGCAGUGUCAUUAGCUGAUUG 3'
has-miR-34c 5' AGGCAGUGUAGUUAGCUGAUUGC 3'
mmu-miR-34b 5' AGGCAGUGUAAUUAGCUGAUUGU 3'
mmu-miR-34c 5' AGGCAGUGUAGUUAGCUGAUUGC 3'

B

	3'..AUGUGACGGA..... 5'		3'..AUGUGACGGA..... 5'
human	5'.....GAGCTGCCTG... 3'	human	5'.....GCACTGCCCG... 3'
mouse	5'.....AGGCTGCCTT... 3'	mouse	5'.....AGACTGCCCT... 3'
rat	5'.....AGGCTGCCTT... 3'	rat	5'.....ACACTGCCCC... 3'
hamster	5'.....AGGCTGCCTT... 3'	hamster	5'.....CTGCTGCCTG... 3'
	<div style="border-top: 1px solid black; width: 150px; margin: 0 auto;"></div> Sirt3 3'-UTR		<div style="border-top: 1px solid black; width: 150px; margin: 0 auto;"></div> PINK1 CDS
	3'..AUGUGACGGA..... 5'		
human	5'.....ACACTGCCCT... 3'		
mouse	5'.....AGACTGCCCT... 3'		
rat	5'.....AGACTGCCTG... 3'		
hamster	5'.....AGACTGCCGT... 3'		
	<div style="border-top: 1px solid black; width: 150px; margin: 0 auto;"></div> Parkin CDS		

C

(716~730 bp)

WT-Sirt3-CDS 5'ATCCCTGCCTCAAA... 3'

miR-34b 3'.....UGUGACGGAU..... 5'

miR-34c 3'.. AUGUGACGGA..... 5'

wild type 5'.....CCCTGCCTCA..... 3'

mutation 5'..... CCTTCATCA..... 3'

D

(1414~1428 bp) (1120~1138 bp)

WT-PINK1-CDS 5'GCTGCTGCCTGGCT....CTGCACTGCCCGAG.. 3'

miR-34b 3'.....UGUGACGGAU..... 5'

miR-34c 3'.. ..AUGUGACGGA..... 5'

wild type 5'.....TGCTGCCTGG..... 3'

wild type 5'.....GCACTGCCCG..... 3'

mutation 5'.....TGCCGACCGG..... 3'

mutation 5'.....GTAGTCGCG..... 3'

E

(951~968 bp) (955~969 bp)

WT-Parkin-CDS 5'CCCCACACTGCCCTGG....CTCCCTGCCTTGTG... 3'

miR-34b 3'.....UGUGACGGAU..... 5'

miR-34c 3'.. AUGUGACGGA..... 5'

wild type 5'.....CCCTGCCTTG..... 3'

wild type 5'.....ACACTGCCCT..... 3'

mutation 5'..... CCCCGACCTG..... 3'

mutation 5'.....CCCCGGACCT..... 3'

Figure S4. (A) Sequence and seed site of human and mouse miR-34b/c. (B) Representative mode of miR-34b/c targeting the 3'-UTR or CDS region of Sirt3, PINK1, and Parkin. (C, D, E) Sequence mutation sites of Sirt3, PINK1, and Parkin CDS region.