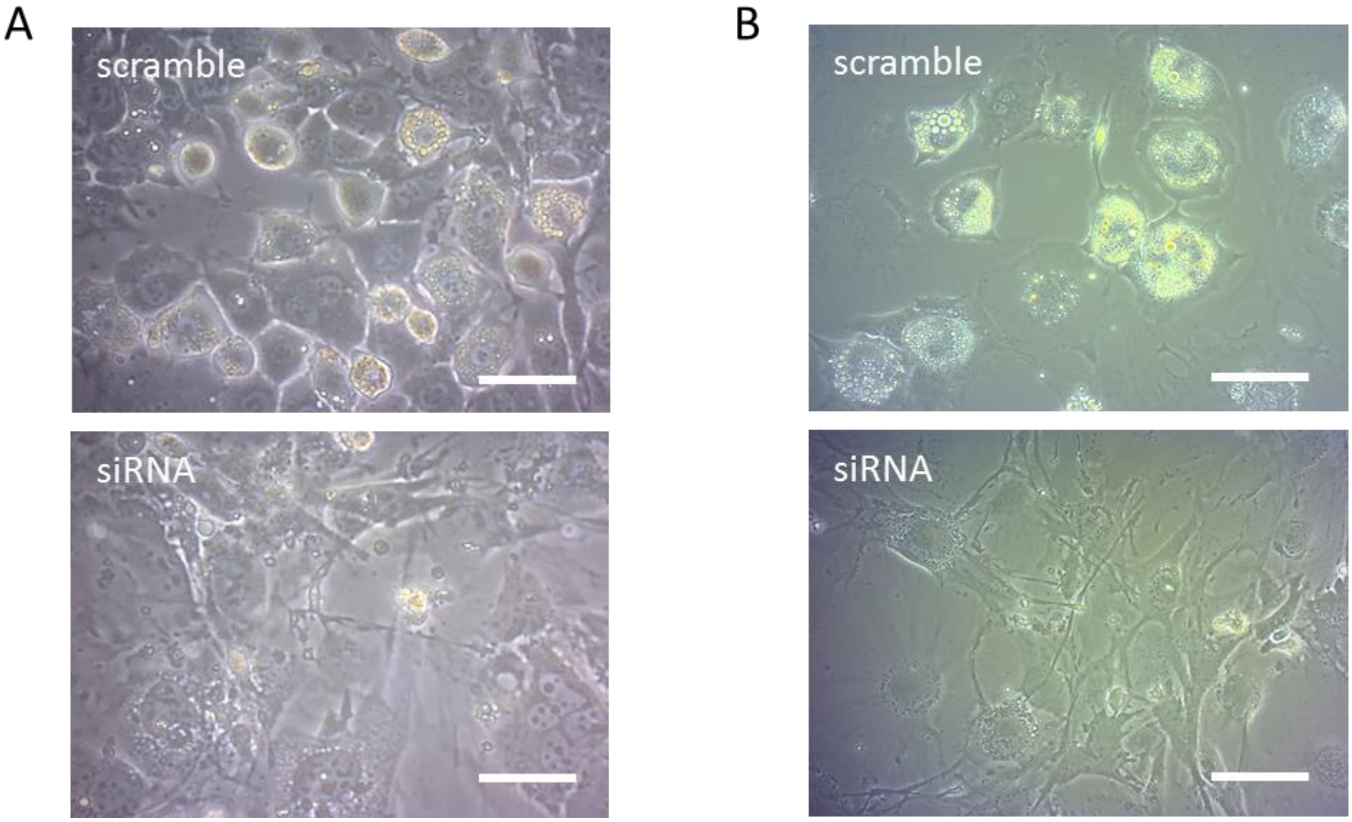
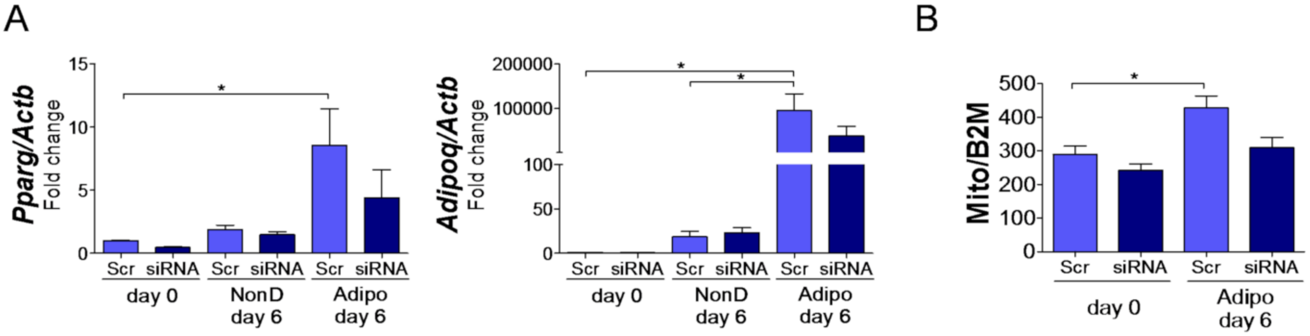
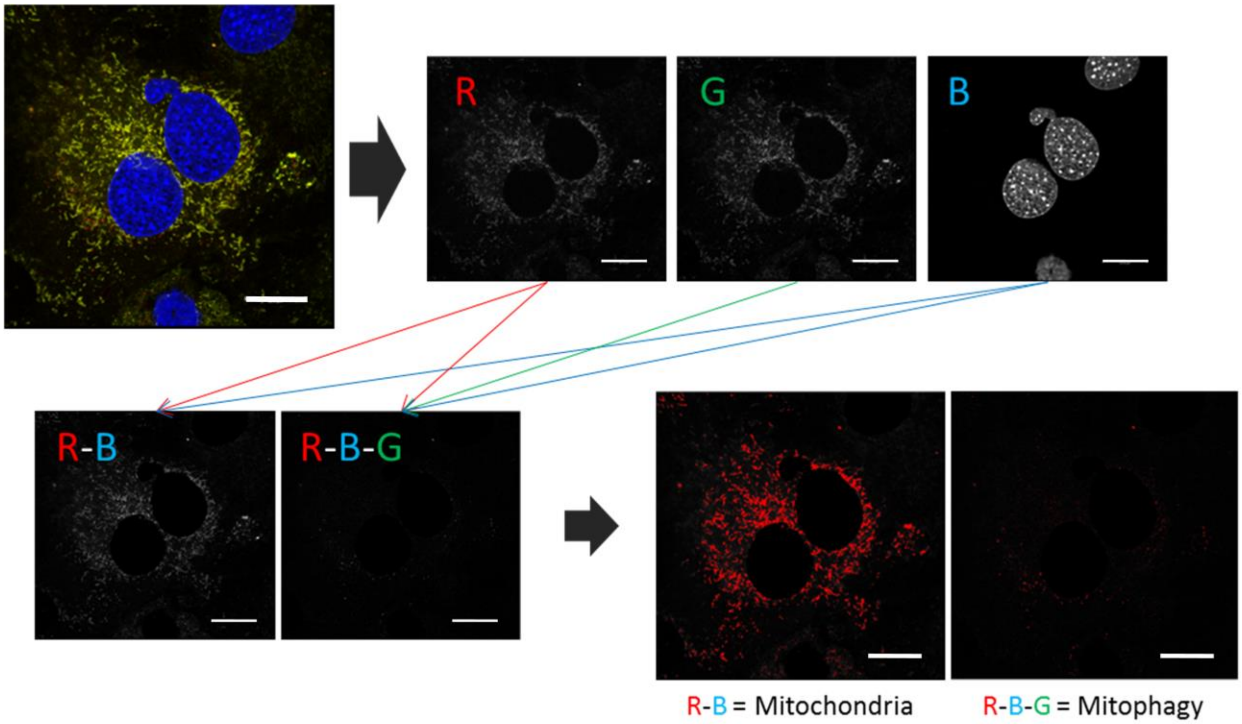
Supporting information 1. Cell morphology of 3T3-L1 cells and eMSCs with or without *Bcl2l13* knockdown after adipogenic differentiation. (A) 3T3-L1 cells, cultured in adipogenic medium for 6 days. Bar: 2µm. (B) eMSCs, cultured in adipogenic medium for 6 days. Bar: 5µm.



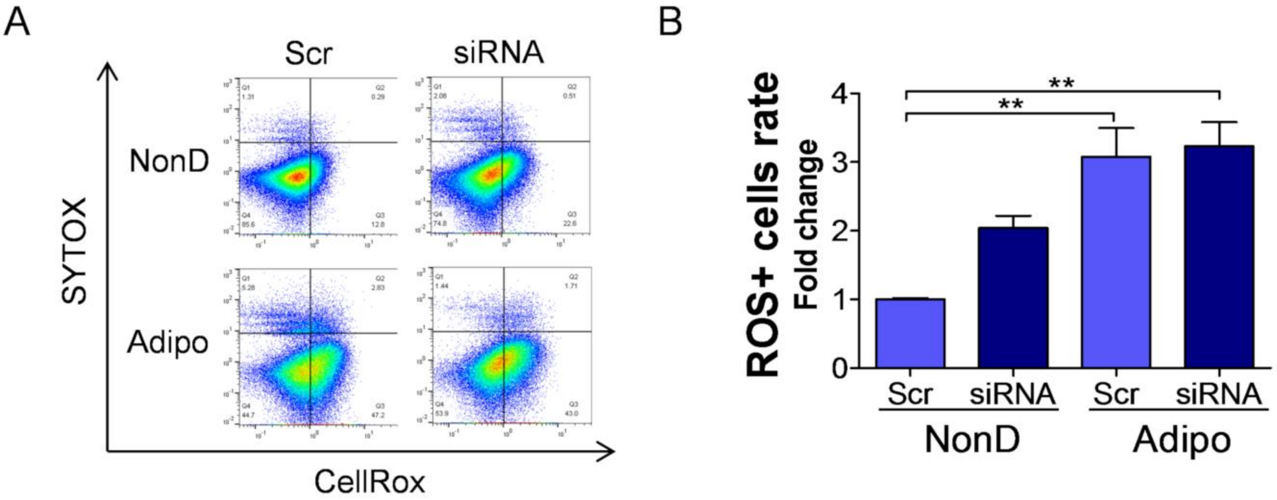
Supporting information 2. Adipogenic gene expression and mitochondrial DNA amount in eMSCs with *Bcl2l13* knockdown. eMSCs with transduction of scramble siRNA (Scr) or *Bcl2l13* siRNA were cultured in non-differentiation (NonD) or adipogenic (Adipo) medium for 6 days. (A) Relative mRNA levels of *Pparg* and *Adipoq*. The value for scramble on day 0 was set as 1. N = 3. (B) Mitochondrial/nuclear DNA ratio (Mt/N) shown by the rate of mitochondrial DNA (Mito) and β2-microglobulin (B2M). N = 3. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supporting information 3. Digital images of confocal microscope were processed by Image J software to calculate mitophagy/mitochondria ratio. R = Red, G = Green, and B = Blue channels. Each image was split to three color channels, subtracted blue from red (R-B, all mitochondria) or blue and green from red (R-B-G, mitophagy punctae). Finally, the threshold of red color was set. Bar: 23μm.



Supporting information 4. ROS production in *Bcl2l13* knockdown 3T3-L1 cells. 3T3-L1 cells with transduction of scramble siRNA (Scr) or *Bcl2l13* siRNA were cultured in non-differenatiation (NonD) or adipogenic (Adipo) medium for 6 days. (A) Flow cytometry analysis. X and Y-axis represents APC-A (CellRox positive = ROS productive cells) and VioGreen-A (SYTOX positive = dead cells), respectively. (B) Relative living ROS positive cells rate. The value for scramble on day 0 was set as 1. N = 3. ** $p < 0.01$.



Supporting information 5. Primer list for real-time PCR

Fragment	Forward primer	Reverse primer	Product size (bp)
Bcl2l13	agtggagactgcagtccatg	cgtgctcctccaggtacatc	149
Bnip3	tcctgggtagaactgcacttc	gctgggcatccaacagtattt	103
Bnip3l	atgtctcacttagtcgagccg	ctcatgctgtgcatccagga	240
Pink1	ttcttccgccagtcggtag	ctgcttctcctcgatcagcc	141
Prkn2	tcttccagtgtaaccaccgtc	ggcagggagtagccaagtt	115

Supporting information 6. Primer list for Mitochondria DNA quantification analysis

Fragment	Forward primer	Reverse primer	Product size (bp)
mMito	ctagaaaccccgaaaccaaa	ccagctatcaccaagctcgt	125
mB2M	atgggaagccgaacatactg	cagtctcagtgggggtgaat	177

Reference: Malik, A.N., Czajka, A., and Cunningham, P. (2016) Accurate quantification of mouse mitochondrial DNA without co-amplification of nuclear mitochondrial insertion sequences. *Mitochondrion* 29, 59-64