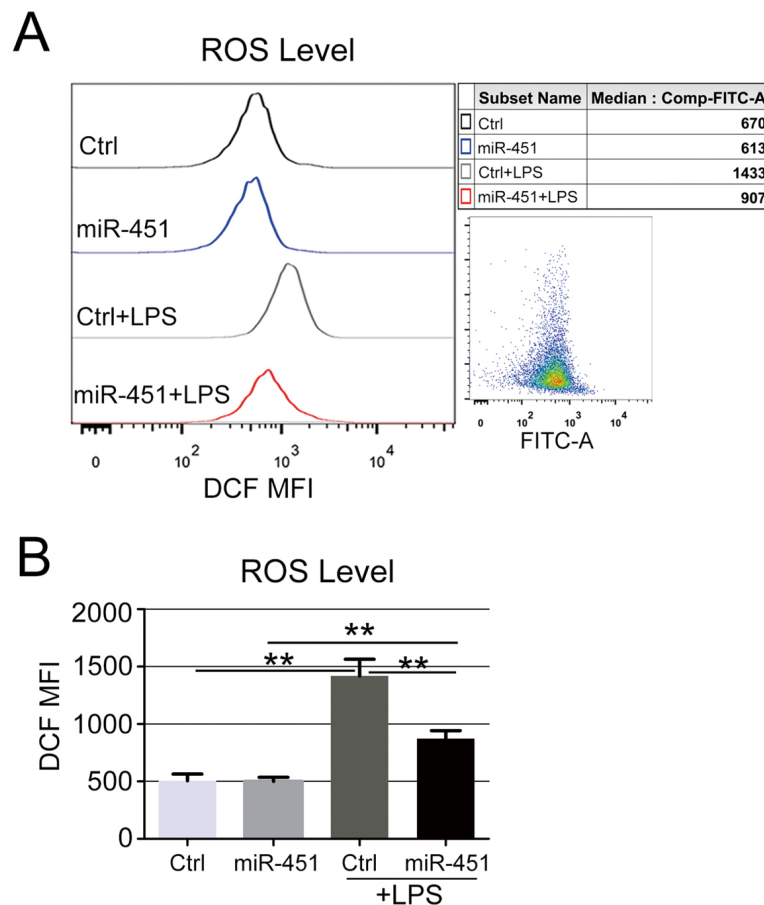


**Table S1** Primer sequences for qRT-PCR

Gene	Forward	Reverse
<i>miR-451</i>	AAACCGTTACCATTACTGAGT	Universal
<i>miR-144</i>	TACAGTATAGATGATGACT	Universal
<i>U6</i>	CGCTTCGGCAGCACATATAC	Universal
<i>mus-GAPDH</i>	AATGGTGAAGGTCGGGTGTGA	CTCCTGGAAGATGGTGATGG
<i>mus-Bax</i>	GGTTTCATCCAGGATCGAGCA	CGTCAGCAATCATCCTCTGCA
<i>mus-Bcl2</i>	GCTACCGTCGTGACTTCGC	CCCCACCGAAGCTCAAAGAAGG
<i>has-Bax</i>	AGCGACTGATGTCCCTGTCTCC	AGATGGTGAGTGAGGCGGTGAG
<i>has-Bcl2</i>	TCGCCCTGTGGATGACTGAGTAC	ACAGCCAGGAGAAATCAAACAGAGG
<i>has-Cat</i>	AATGAAAAACAGTCGTGTACCG	CCTTCTGCAACTGATCTACTGA
<i>has-Gpx1</i>	ACAAGCGCTTCTACTTAGATGT	GTAGTGTCTATGAAGTCGCC
<i>hsa-GAPDH</i>	GTCATGGGTGTGAACCATGA	ACTGTGGTCATGAGTCCTC

qRT-PCR, quantitative real-time PCR.



**Figure S1** *MiR-451* overexpression decreases intracellular reactive oxygen species (ROS) levels after lipopolysaccharide (LPS) stimulation. A549 cells were transfected with *miR-451* mimic and miR-NC. (A) ROS levels were determined by flow cytometry and measured by the mean fluorescence intensity (MFI) of dichloro-dihydro-fluorescein (DCF). (B) Quantitative analysis of MFI for DCF. \*\* $P < 0.01$ .