

Figure S1. Green fluorescence in the four transfected cell lines. Scale bar, 100  $\mu$ m. miR, microRNA; KD, knockdown; OE, over-expression.

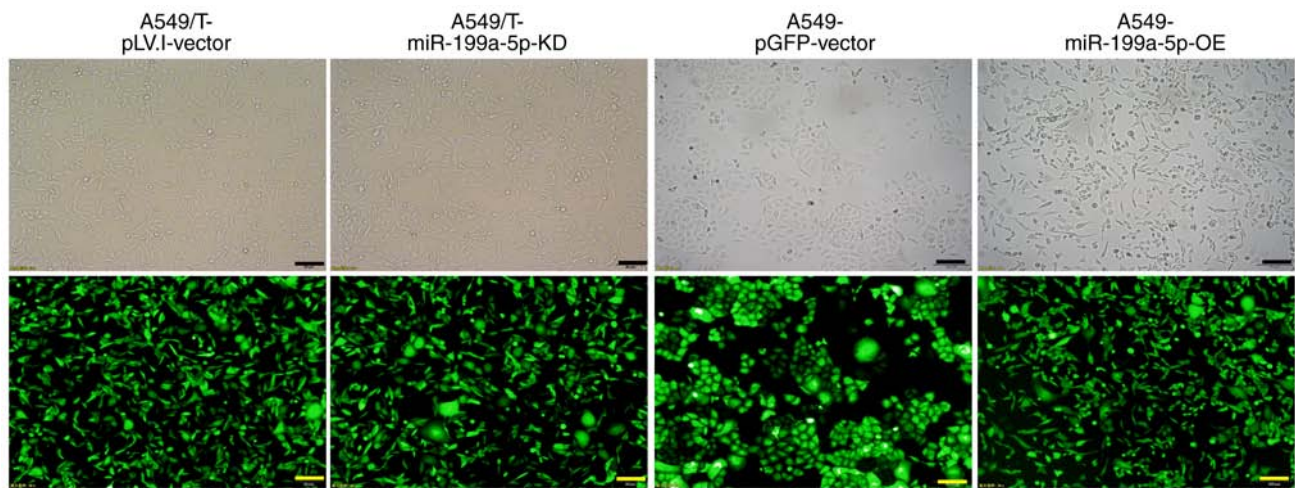


Figure S2. miR-199a-5p binds to ATG5 and decreases its mRNA expression levels. (A) The sequence of the miR-199a-5p binding site within the 3'-UTR of ATG5 was predicted by TargetMiner database. (B) Reverse transcription-quantitative PCR analysis of ATG5 mRNA expression levels in various cell lines. Data are presented as the FC value relative to A549 cells. The experiments were repeated three times. \*\*\*\* $P < 0.0001$ ; ns, not significant; ATG5, autophagy-related 5; FC, fold-change; miR, microRNA; KD, knockdown; OE, overexpression; UTR, untranslated region.

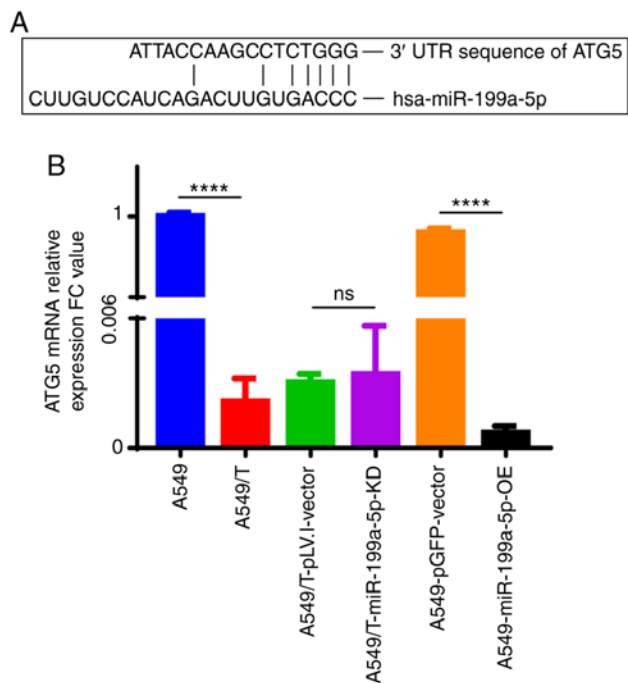


Figure S3. Effects of miR-199a-5p on ABCB1 regulation and cell proliferation. (A) The expression levels of ABCB1 protein in A549/T-miR-199a-5p-KD and A549-miR-199a-5p-OE cells with or without CQ treatment. (B) Proliferation of A549, A549/T, A549/T-miR-199a-5p-KD, A549-miR-199a-5p-OE, A549/T-pLV.I-vector and A549-pGFP-vector cells. \* $P < 0.05$  and \*\* $P < 0.01$ ; ns, not significant; miR, microRNA; KD, knockdown; OE, overexpression; ABCB1, ATP-binding cassette subfamily B member 1; CQ, chloroquine; OD, optical density.

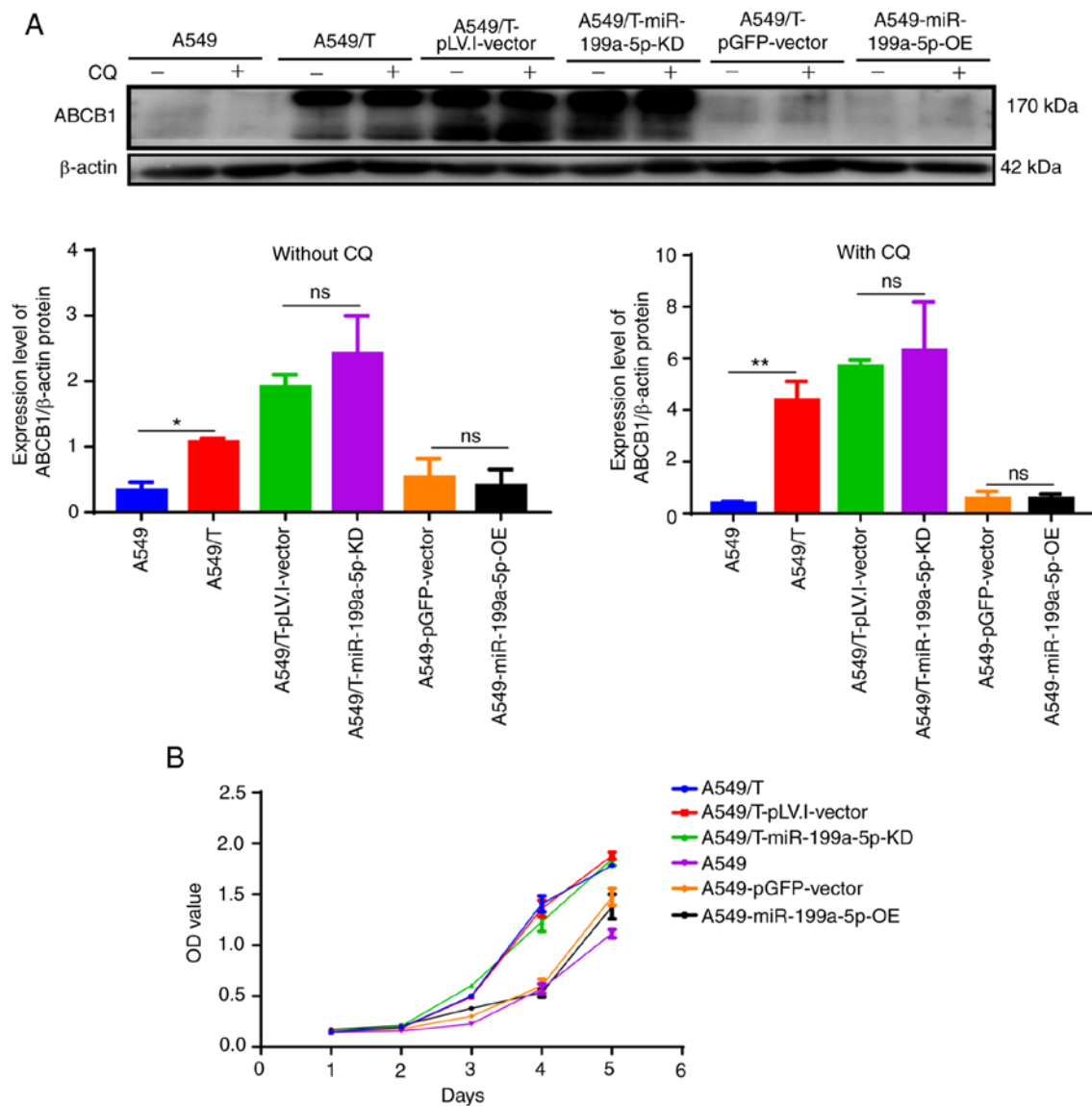


Figure S4. Cell survival curves. Cell survival was determined by the Cell Counting Kit-8 assay following treatment with  $\geq 8$  gradient concentrations of various chemotherapeutic agents for 72 h.

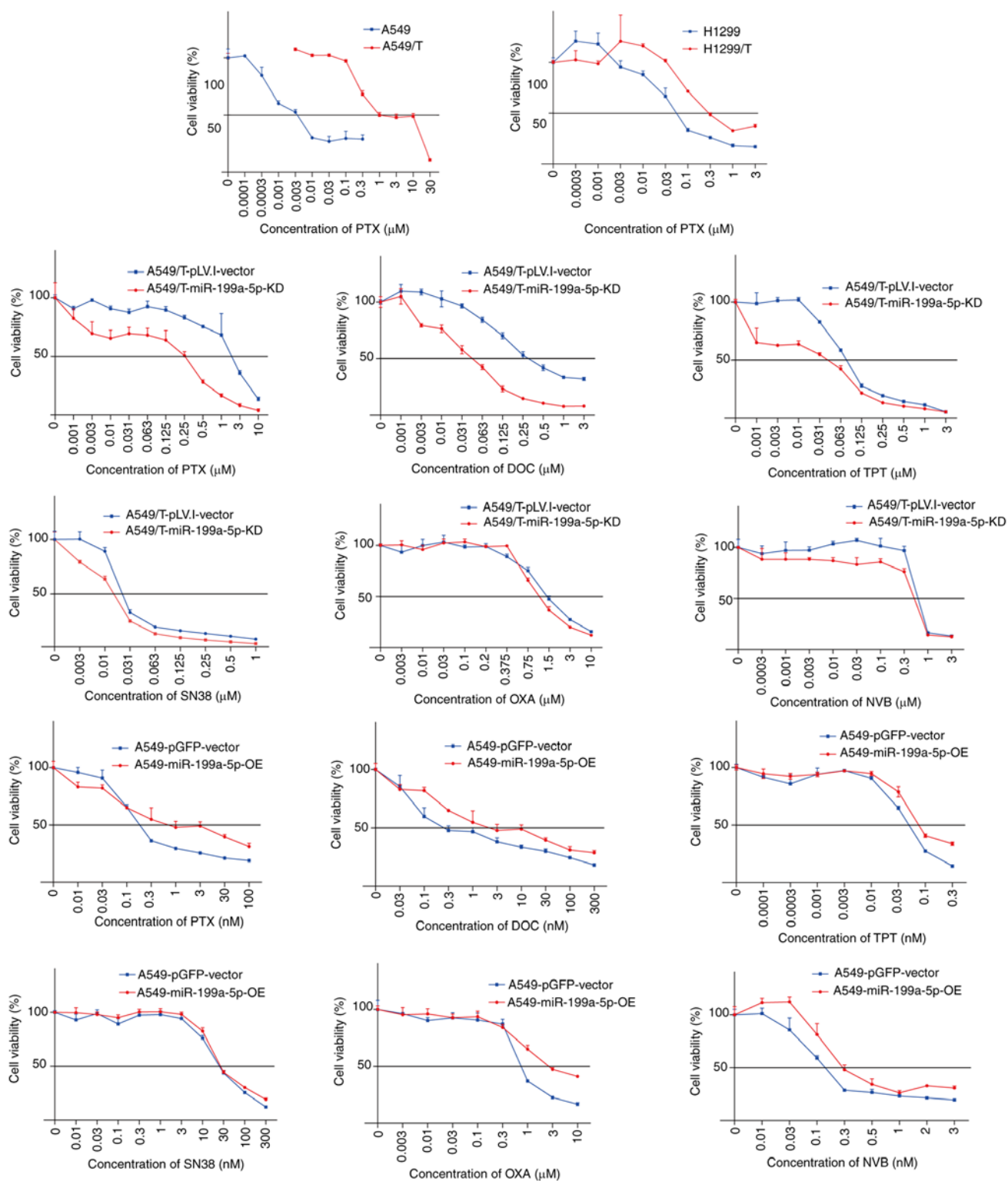


Table SI. Sequences used for quantitative PCR.

Target	Sequences (5'→3')
U6	F: AGAGAAGATTAGCATGGCCCCTG R: AGTGCAGGGTCCGAGGTATT
hsa-miR-199a-5p	F: CGCGCCCAGTGTTTCAGACTAC R: AGTGCAGGGTCCGAGGTATT
$\beta$ -actin	F: CTACCTCATGAAGATCCTGACC R: CACAGCTTCTCTTTGATGTCAC
p62/SQSTM1	F: TGATTGAGTCCCTCTCCCAGATGC R: CCGCTCCGATGTCATAGTTCTTGG
ATG5	F: GATGGGATTGCAAAATGACAGA R: GAAAGGTCTTTCAGTCGTTGTC
ATG7	F: TGTATAACACCAACACACTCGA R: GGCAGGATAGCAAAACCAATAG

miR, microRNA; SQSTM1, Sequestosome-1; ATG, autophagy-related.