**Table S1** Primer sequences

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
circRNA.0007127	GTCGACAGTGACTACCATGA	CCACCACGTCTCCCTATCTT
CNOT2	GGGTATTTTGCCTATGAATCCT	CTGTTCACAGTAAAAGGCTGT
CASP8	AGAGTCTGTGCCCAAATCAAC	GCTGCTTCTCTCTTTGCTGAA
CASP3	TTCAGAGGGGATCGTTGTAG	CAAGCTTGTCGGCATACTGTTT
	AAGTC	CAG
FADD	ATTAATGCCTCTCCCGCACC	TCTCTGCTTCGCTCCGATTC
CASP6	AGGTGGATGCAGCCTCCGTTTA	ATGAGCCGTTCACAGTTTCCCG
Bad	CCCAGAGTTTGAGCCGAGTG	CCCATCCCTTCGTCGTCCT
Bax	CCCGAGAGGTCTTTTTCCGAG	CCAGCCCATGATGGTTCTGAT
U6	${\tt CTCGCTTCGGCAGCACATATACT}$	ACGCTTCACGAATTTGCGTGTC
GAPDH	GAAGATGGTGATGGGATTTC	GAAGGTGAAGGTCGGAGTC

Table S2 The full length of hsa\_circ\_0007127 circRNA mature sequence

Hsa\_circ\_0007127 circRNA Mature Sequence. Length: 490 nt.

The letters marked red and green indicate back splice junction.

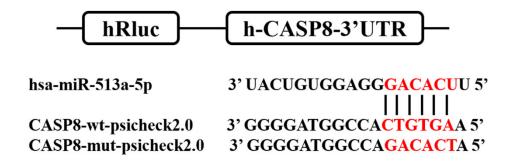


Fig. S1 The binding sequence of miR-513a-5p and the wild-type or mutant vector in the luciferase reporting system. *CASP8*-wt-psicheck2.0 and *CASP8*-mut-psicheck2.0 represent the wild-type vector and mutant vector, respectively.

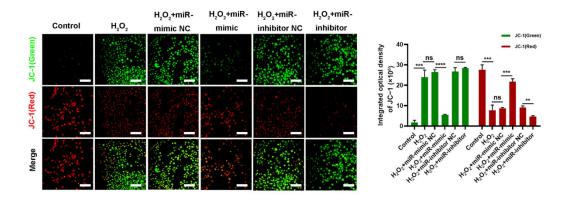


Fig. S2 Early apoptosis was observed using the JC-1 probe (scale bar=40  $\mu$ m). Data were shown as mean±standard error of the mean (SEM), n=3. \*\* P<0.01, \*\*\* P<0.001, \*\*\*\* P<0.0001. ns: not significant.

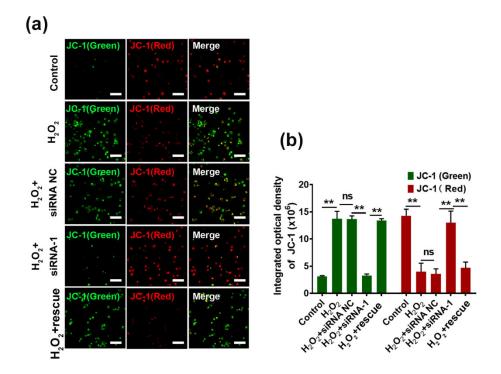


Fig. S3 (a) JC-1 fluorescent probes were used to detect early cell apoptosis in K-562 cells in the different treatment groups. (b) The ratio of red fluorescence to green fluorescence was quantified (scale bar=40  $\mu$ m). Data were shown as mean±standard error of the mean (SEM), n=3. \*\*\* P<0.01. ns: not significant.