

Appendix 1: Primer sequences

Target genes	Control
GAPDH	Forward 5'-GCAAGAGCACAAGAGGAAGA-3' Reverse 5'-ACTGTGAGGAGGGGAGATTC-3'
Bax	Forward 5'-GCTGGACATTGGACTTCCTC-3' Reverse 5'-ACCACTGTGACCTGCTCCA-3'
Bcl2	Forward 5'-GGATGCCTTTGTGGAAGTGT-3' Reverse 5'-TCACTTGTGGCCCAGATAGG-3'
mTOR	Forward 5'-TGTGATGGCTGTGAAGATCC-3' Reverse 5'-TATTCACCTCCTGCCTCACC-3'
Atg5	Forward 5'-CAATCCCATCCAGAGTTGCT-3' Reverse 5'-CCAGAAAAAGACCTTTCTGCAC-3'
Beclin 1	Forward 5'-CGGTTTTTCTGGGACAACAA-3' Reverse 5'-AAAAACGTGTCTCGCCTTTC-3'
MLKL	Forward 5'-AGAGCTCCAGTGGCCATAAA-3' Reverse 5'-TACGCAGGATGTTGGGAGAT-3'
RIP1	Forward 5'-GCACAGCAAAGACCTTACG-3' Reverse 5'-TTGTTCAAAGCCATGTGAG-3'
RIP3	Forward 5'-CAAGGAGGGACAGAAATGGA-3' Reverse 5'-TTGTGGAACCTTGCTCCTCTT-3'

Appendix 2. The results obtained from MTT assay, colony formation and Annexin V/PI method in NIH-3T3 treated cells

Groups	Control	Blank-ME	AJE	AJE-ME
Viability (%)	99.01± 0.07	101 ± 0.09	99.2 ± 0.53	98.2 ± 1.4
Colony numbers	1.13 ± 0.14	1.16 ± 0.13	1.05 ± 0.07	1.17 ± 0.15
Early apoptosis (%)	1.21 ± 0.39	1.08 ± 0.23	1.24 ± 0.22	1.15 ± 0.31
Late apoptosis (%)	1.49 ± 0.14	1.67 ± 0.24	1.36 ± 0.12	1.41 ± 0.23
Necrosis (%)	0.56 ± 0.08	0.39 ± 0.05	0.43 ± 0.11	0.53 ± 0.06

Values are expressed as mean ± SD (n=5).