Methodology

The total RNA from kidney samples was purified using TRIzols Reagent (Life Technologies, USA). In a two-step RT-PCR experiment, 1μg of total RNA was reverse-transcribed into single-stranded complementary DNA using the QuantiTects Reverse Transcription Kit (Qiagen, USA) and a random primer hexamer. Maximas SYBR Green/Fluorescein qPCR Master Mix was used to amplify C-DNA amplicons through specific primers.

Table S1. Beclin1, p62, ATG5, LC3II genes primer sequences.

Gene	primer sequences	References
Beclin-1	5′-ATACTGTTCTGGGGGTTTGCG-3′ 5′-GTCTCTCCTTTTTCCACCTCTTC-3′.	(Liu, Huang, Liu, Song, & Xiao, 2020)
P62	5′- AGG GAA CAC AGC AAG CT -3′ 5′- GCC AAA GTG TCC ATG TTT CA -3′	(Crippa et al., 2013)
GAPDH	5′-TGACAACTTTGGTATCGTGGAAGG-3′; 5′-AGGCAGGGATGATGTTCTGGAGAG-3′.	(Yang, Yu, Liu, Yang, & Tao, 2020)
LC3II	5′-AACATGAGCGAGTTGGTCAAG-3′; 5′-GCTCGTAGATGTCCGCGAT-3′;	
ATG5	5′CCAAGCTTCTAATACGACTCACTATAGG GAGAATGACAGATGACAAAGATGTGC-3′ 5′-TCAATCTGTTGGCTGGGGGACA-3′	(Kim et al., 2014)

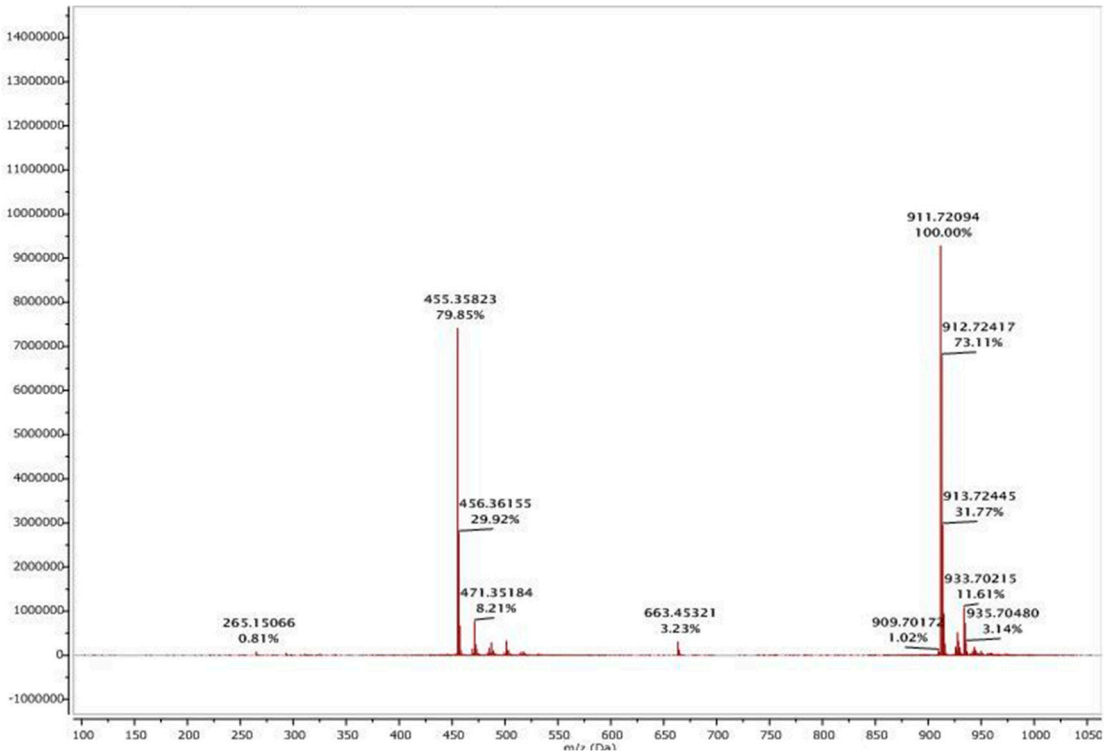

Figure S1. The HR-ESI-MS of BA.

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