

Table S1. Sequences of oligonucleotide primers for qRT-PCR.

Gene Names	Sequence (5' → 3')	NCBI Reference Sequence	Amplicon size (bp)
GAPDH1	GTCGGAGTGAACGGATTTGGC CTTGCCGTGGGTGGAATCAT	NM_001289745.3	150
Occludin	GACAGACTACACAACTGGCGG TGTA CTCTGCAGGCCACTG	NM_001302926.2	662
N-Cad	CTTCATGCTGGTGGTGTCTTGG CACAGTCTTTGGCAGGGCTCAG	NM_000165.5	149
Claudin1	CCATCGTCAGCACCGCACTG CGACACGCAGGACATCCACAG	NM_001244539.1	107
ZO-1	CCTGAGTTTGATAGTGGCGTTGA AAATAGATTTCTGCCCCAATTCC	XM_003353439.2	269
SIRT1	ACTCTCCCTCTTTTAGACCAAGC AAACCTGGACTCTCCATCGG	NM_001145750.2	149
PGC-1 α	ACCAGGACTCTGTATGGACTGA TGAGGGCAATCCGTCTTCAT	NM_213963.2	299
Nrf1	GGCGGGAGGACCTTTTGTAT ACTGTTGCCCTGTACCAAC	XM_021079000.1	163
SIRT3	TGTGGTGTCTGTTTCATCTGTTG CTTCCACAGACACCTGAGGC	NM_001110057.1	136
TFAM	GCTCTCCGTTTCAGTTTTCGCG GGAAGTTCCCTCCACAGCTC	NM_001130211.1	187
OPA1	ACAGAGGATGGTGCTTGTTGAC CAGTATGATGGCGTTGGGATT	XM_047448216.1	130
Mfn1	AGAAAGCACAAAGCACAGGGGATG CACTGCTGACTGCGAGATACTC	XM_011512963.4	126
Mfn2	GCCACACCACCAACTGCTTCC TCTTGACGCTCCTCTTCTCCTCTG	XM_047436156.1	96
Drp1	TCTGAATCTGGTGGGCATGATTGC CTCCGCAGTAAAGGACTCGAAGTG	XM_001928848.6	91
Fis1	CTACCCAAAGGGAGCAAAGAG GTCCAATGAGTCCAGCCAGTC	NM_016068.3	250
Clpp	CGCTTATGACATCTACTCAC GGGCTTCTTGTTGCTTTC	XM_003480818.4	130

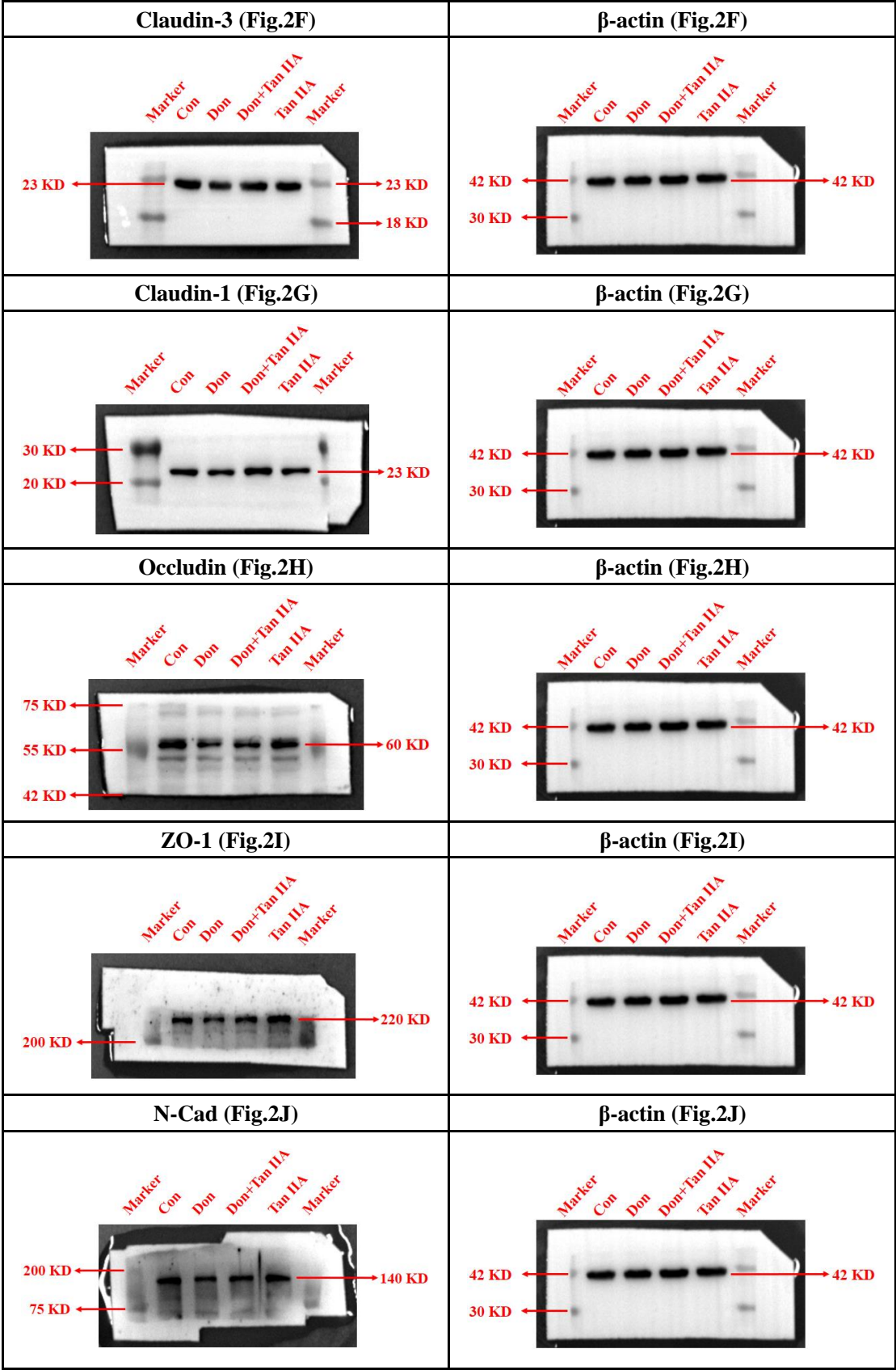
Gene Names	Sequence (5' → 3')	NCBI Reference Sequence	Amplicon size (bp)
HSP10	GCAGCTGAAACGGTAACCAA TCCACCCTTTCCTTTAGAGCC	NM_214307.1	111
HSP60	CGGATGCTGTAGCCGTTACT ATCCCCAGCCTCTTCGTTTG	NM_001254716.1	191
Htra-2	GGCCGCGAAGTACCTATCTC GCGTTGGTAACAATGAGCCC	XM_021087326.1	71
ATF4	AGTCCTTTTCTGCGAGTGGG CTTCCACAGACACCTGAGGC	NM_001110057.1	80
Parkin	GTGGTTCTGCGGTGGATTCTGAG TTRACTGCCTGTGGTTCTTTGGGAAG	NM_001044603.2	104
PINK1	CAGGAGCGGTCCCAAGCA GTCATCACAGTGGCGAGGC	NM_032409.3	246
LC3	TGCCCTCAGACCGGCCTTTCAAGCA TCCTTCTCCTGCTCATAGATGTCCG	XM_047440559.1	310
FUNDC-1	GGCAGCACCTGAAATCAACA GCCTAGCAAAAAGCCTCCCA	XM_003135038.4	100
BNIP3	GACTCGCCAGGTTACAGACA CAGTGACGTGCTTAGGACCC	XM_003359404.4	80
Beclin1	GGTTGGATCAGGAGGAAGCT TGTCCACTGTGCCAAATGTG	NM_001044530.1	181
Atg5	AGAAACCTAGAGAGGGCCACA TCTTCCTAGTCAAACAACGTCA	NM_001037152.2	111
P62	CGATGGCGATGTCGTATGTG TTGCTGTGCTCCTTGTGAATG	XM_003123639.4	244

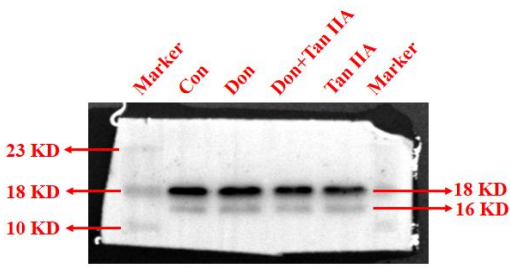
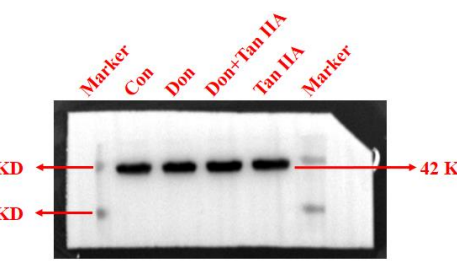
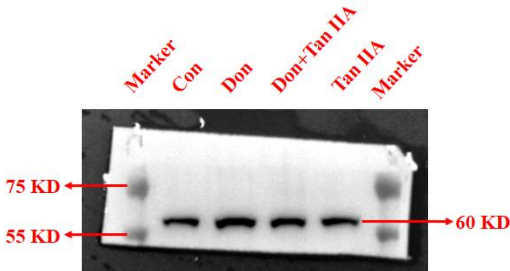
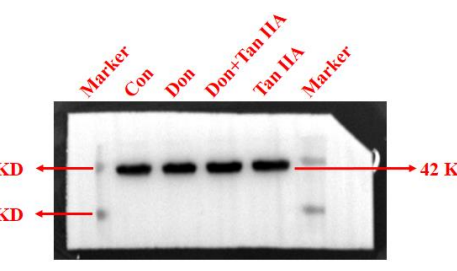
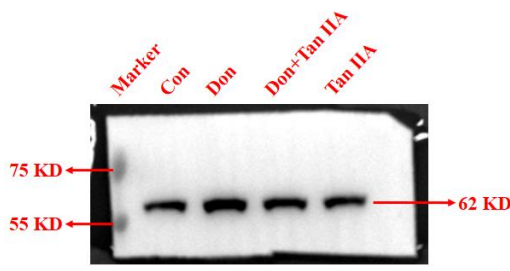
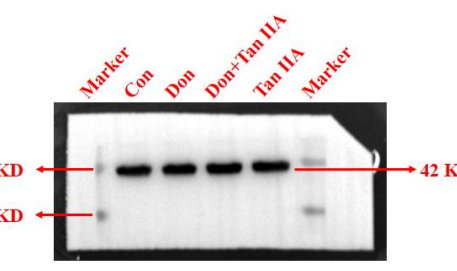
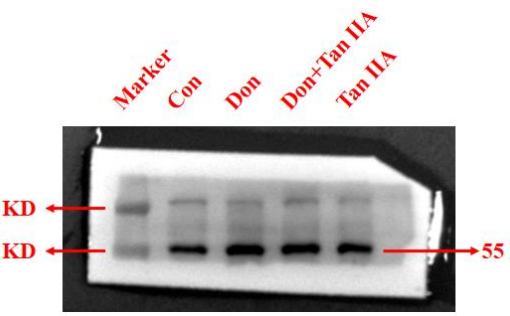
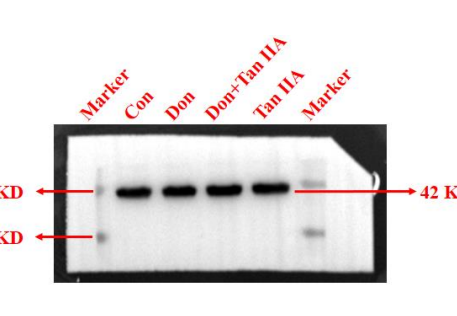
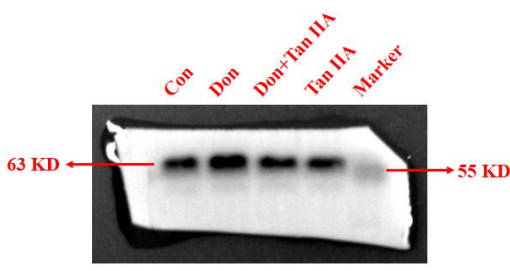
Table S2. Total Variance Explained of PCA

Component	Total Variance Explained (Mitophagy)					
	Initial Eigenvalues			Extraction Sums of Squared Loadings		
	Total	% of Variance	Total	% of Variance	Total	% of Variance
1	7.315	91.432	91.432	7.315	91.432	91.432
2	.284	3.548	94.980	.284	3.548	94.980
3	.145	1.818	96.797			
4	.096	1.201	97.998			
5	.073	.912	98.910			
6	.055	.684	99.594			
7	.032	.406	100.000			
8	-.1539E-16	-1.924E-15	100.000			

Extraction Method: Principal Component Analysis (PCA).

Figure S1. Original western blot gels used in the study



<p>LC3 I/II (Fig.6A)</p> 	<p>β-actin (Fig.6A)</p> 
<p>Beclin1 (Fig.6B)</p> 	<p>β-actin (Fig.6B)</p> 
<p>P62 (Fig.6C)</p> 	<p>β-actin (Fig.6C)</p> 
<p>Parkin (Fig.6D)</p> 	<p>β-actin (Fig.6D)</p> 
<p>PINK1 (Fig.6E)</p> 	<p>β-actin (Fig.6E)</p> 