Supplementary Materials

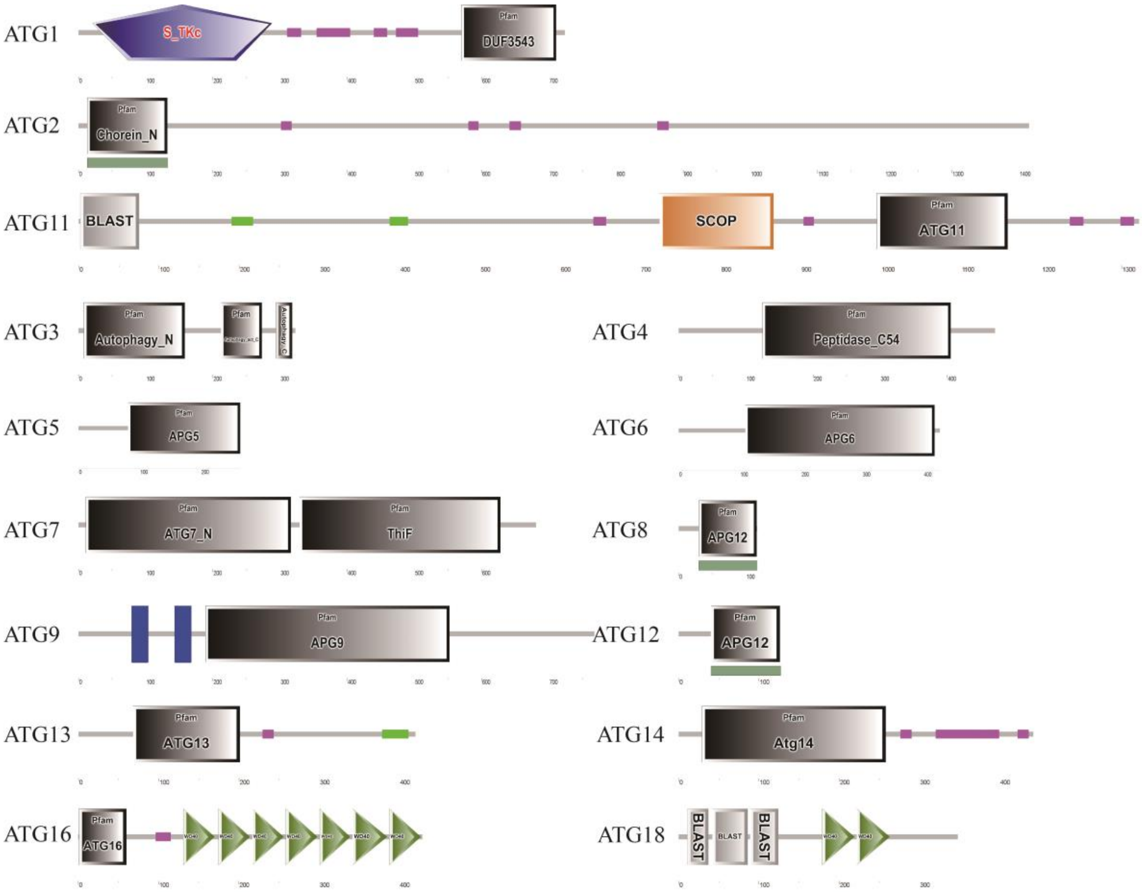

Figure S1. Fifteen autophagy-related genes in *Bombyx mori* have their conserved domains as predicted by SMART (http://smart.embl-heidelberg.de/).

Table S1. Function of autophagy-related genes.

Atg genes	Aliases	Complexes	Function
Atg1	ULK	ULK complex (induction of autophagy)	Phosphorylates Atg9(1) and Atg6(2) as a Ser/Thr kinase; regulates autophagy
Atg11	Atg17/FIP200		Mediates mTor signaling to autophagy with ULK-Atg13(3)
Atg13	APG13		Interaction with Atg1(4) and regulates localization to the PAS(5)
Atg9	APG9/CVT6	ATG9L complex	Recruitment of PI3K complex(6) and Atg proteins(1)
Atg6	VPS30/Beclin1	ATG14L complex(apg-specific PI(3)K complex)	Component of class III PI3K complexes(7); binds Atg14 and Rubicon(8, 9)
Atg14	APG14		Localizes on the ER to induce autophagy(10)
Atg2	APG2	Atg2-Atg18 complex	Localizes to some membranous structure and is essential for autophagy(11)
Atg18	WIPI		Binds to Atg16L1 and recruits ATG16 complex to APS(12)
Atg5	APG5	Atg16L1 complex (as E3-like enzyme for LC3-PE)	Conjugates to Atg12 to form ATG16L1 complex(13); involves in sequestration(14)
Atg7	APG7		Mediates the conjugation of Atg5 and Atg12 as an E1-like enzyme(15)
Atg12	APG12		Conjugates to Atg5 to form ATG16L1 complex(13)
Atg16	APG16/CVT11		Forms a 2:2:2 complex with Atg12-Atg5 as E3-like enzyme for LC3-PE
Atg8	LC3	ATG8-II ubiquitin-like conjugation system	Marker and closure of isolated membrane(16); quantification of autophagy activity(17)
Atg3			Mediates LC3 conjugating to PE as a E2-like enzyme with Atg7(18)
Atg4			Cleaves the C-terminal arginine of Atg8(19) and Mediates LC3 deconjugating from the outer autophagosomal and LAP phagosome membrane(20)
Atg7			Mediates LC3 conjugating to PE as a E1-like enzyme with Atg3(18)

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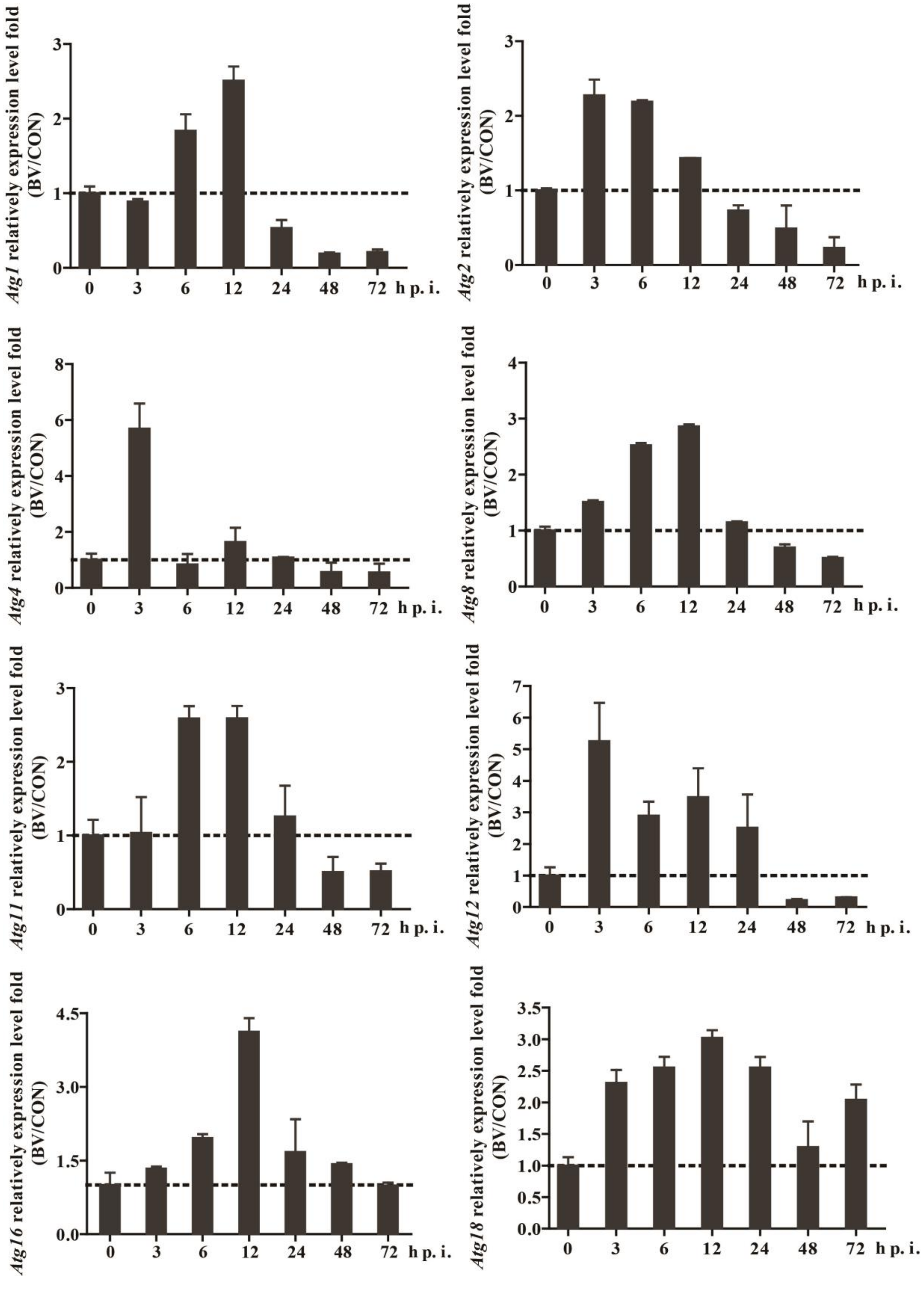

Figure S2. BmNPV infection caused the expression level change of autophagy-related genes. *Atg1*, *2*, *4*, *8*, *11*, *12*, *16*, and *18* expression-level fold changes to control are listed after infection.

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ATG3    22.2%

TGGCCGGTTACTTGACACCGGTGTTGAAGGTACGTTTATCACGATCATTATTAATTACATACATATTGAAATT
TGGCCGGTT---------------------GTGTTGAAGGTACGTTTATCACGATCATTATTAATTACATACATATTGAAATT
TGGCCGG-------------------------------------------------------------------------------------------------------CATACATATTGAAATT
TGGCCG--------------------------------------------------------------------------------------------------------------------------------------------
TGGCCGGTT-----TTGACACCGGTGTTGAAGGTACGTTTATCACGATCATTATTAATTACATACATATTGAAATT
TGGCCGG-------------------------------------------------------------------------------------------------------------------------TTGAAATT
TGGCCGGTT---------------------------------------------------------------------------------------------------------------------TTGAAATT

ATG4    33%

CTCATACCCCACTGACAAACGCTCGAGACAATGCTGAAGATTCAATTGA
CTCATACCCCAC--GACAAACGCTCGAGACAATGCTGAAGATTCAATTGA
CTCATACCCCAC--------AAACGCTCGAGACAATGCTGAAGATTCAATTGA
CTCATACCC---------------------CGCTCGAGACAATGCTGAAGATTCAATTGA
CTCATACCCCACTG------------------CGAGACAATGCTGAAGATTCAATTGA
CTCATACCCCAC----------AACGCTCGAGACAATGCTGAAGATTCAATTGA
CTCATACCCCAC-----------------------------ACAATGCTGAAGATTCAATTGA

ATG5    25%

TTTTCCATCCCATATTTCTCGAAGTACCTCCCTGTCGTTGGCCATAAGGG
TTTTCCATCCCAT----TTCTCGAAGTACCTCCCTGTCGTTGGCC----AAGGG
TTTTCCATCC--A--ATTTCTCGAAGTACCTCCCTGTCGTTGGCCATAAGGG
TTTTCCATCC--A----- ----------GAAGTACCTCCCTGTCGTTGGCCATAAGGG
TTTTCCAT------------------------------------CTCCCTGTCGTTGGCCATAAGGG
TTTTCCATC--------------------GAAGTACCTCCCTGTCGTTGGCCATAAGGG

ATG7    22.2%

AATATTTGTTTGGTAGTTTCCTTTAATTTGTCTACTTCTAATTTCATTTCAGTGAGGGTATGCCAGAATGA
AATATTTGTTTGGTAGTTTCCTTTAATTTGTCTACTTCTAATTTCATT---------- ------------------------------ -GA
AATATTTGTTTGGTAGTTTCCTTTAATTTGTCTTG--------------------- ---------------------------------------------  A
AATATTTGTTTGGTAGTTTCCT---------------------------------------------------------------------------------------ATGA
AATATTTGTTTGGTAGTTTCCTTTAATTTGTCTACTTCTAATTTCATT------------------------------------------GA
AATATTTGTTTGGTAGTTTCCTTTAATTTGTCTACTTCTATG--------------------------------------------------------A
AATATTTGTTTGGTAGTTTCCTTTAATTTGTCTACTTCTAATTTCATT------------------------------------------TGA

ATG9    25%

CCTTTAGGTGGATTGGCTGACAATGTGAACATAACGTCGCCTAAAGGCAGTGTAGATGCTGATCATGAAGATTACAGTAAGGTGATCATCCACGAAGTGC
CCTT--AGGTGGATTGGCTGACAATGTGAACATAACGTCGCCTAAAGGCAGTGTAGATGCTGATCATGAAGATTACAGTAAGGTGATCATCCACGAAGTGC
CCTT----------GGATTGGCTGACAATGTGAACATAACGTCGCCTAAAGGCAGTGTAGATGCTGATCATGAAGATTACAGTAAGGTGATCATCCACGAAGTGC
CTTTAG-----TGGATTGGCTGACAATGTGAACATAACGTCGC-TAAAGGCAGTGTAGATGCTGATCATGAAGATTACAGTAAGGTGATCATCCACGAAGTGC
CCTGGAT------------TGGCTGACAATGTGAACATAACGTCGCCTAAAGGCAGTGTAGATGCTGATCATGAAGATTACAGTAAGGTGATCATCCACGAAGTGC
CCTAAG---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------TGC

ATG12   42%

AAACTCCATAATCCATCCAATAGGCTTTTCAGCATCAACAGCCCATTTTTTTTTCTTC
AAACTCCATAATCCATCCAATA-----CTTTTCAGCATCAACAGCCCATTTTTTTT--CTTC
AAACTCCATAATCCATCCAATA-------------------CATCAACAGCCCATTTTTTTTTCTTC
AAACTCCATAATCCATCCAATA---GCTTTTCAGCATCAACAGCCCATTTTTTTT--CTTC
AAACTCCATAATCCATCCAATA-------------------------CAACAGCCCATTTTTTTTTCTTC
AAACTCCATAATCCATCCAATAAG---------------CATCAACAGCCCATTTTTTTTTCTTC
AAACTCCATAATCCATCCGATA---------------------ATCAACAGCCCATTTTTTTTTCTTC
AAACTCCATAATCCATCCAAT---------------------------------------------ATTTTTTTTTCTTC
AAACT---------------------------------GGCTTTTCAGCATCAACAGCCCATTTTTTTTTCTTC
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Figure S3. Knockout efficiency of autophagy-related genes was analyzed through PCR and ligated into the pMD19-T vector for sequencing using M13 primers. *Atg3*, *4*, *5*, *7*, *9*, and *12* are knocked down through the CRISPR/Cas9 gene editing system.