Supplemental Figure legends

Figure S1

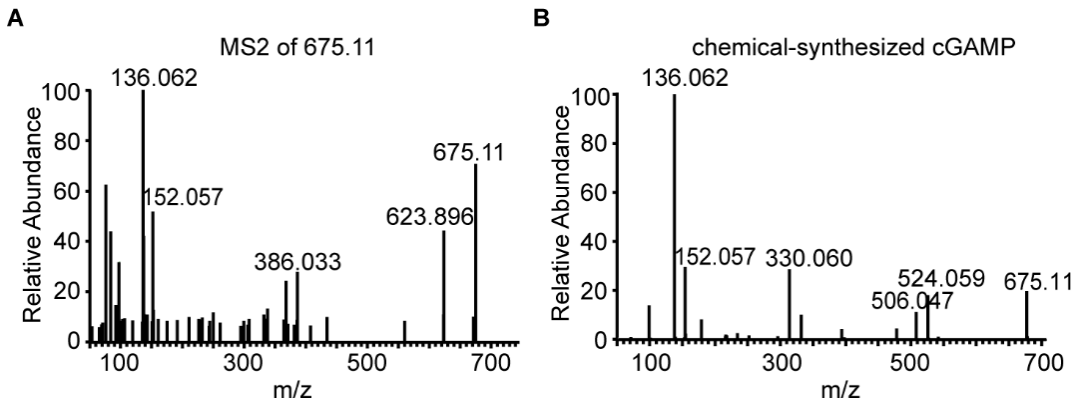

Figure S1. cGAMP was detected by full-scan LC-MS/MS.

The major ions in the CID MS2 spectra of the fragment of M/Z=675.11 derived from BmNPV-infected cells (A) and chemically synthesized cGAMP (B).

Figure S2

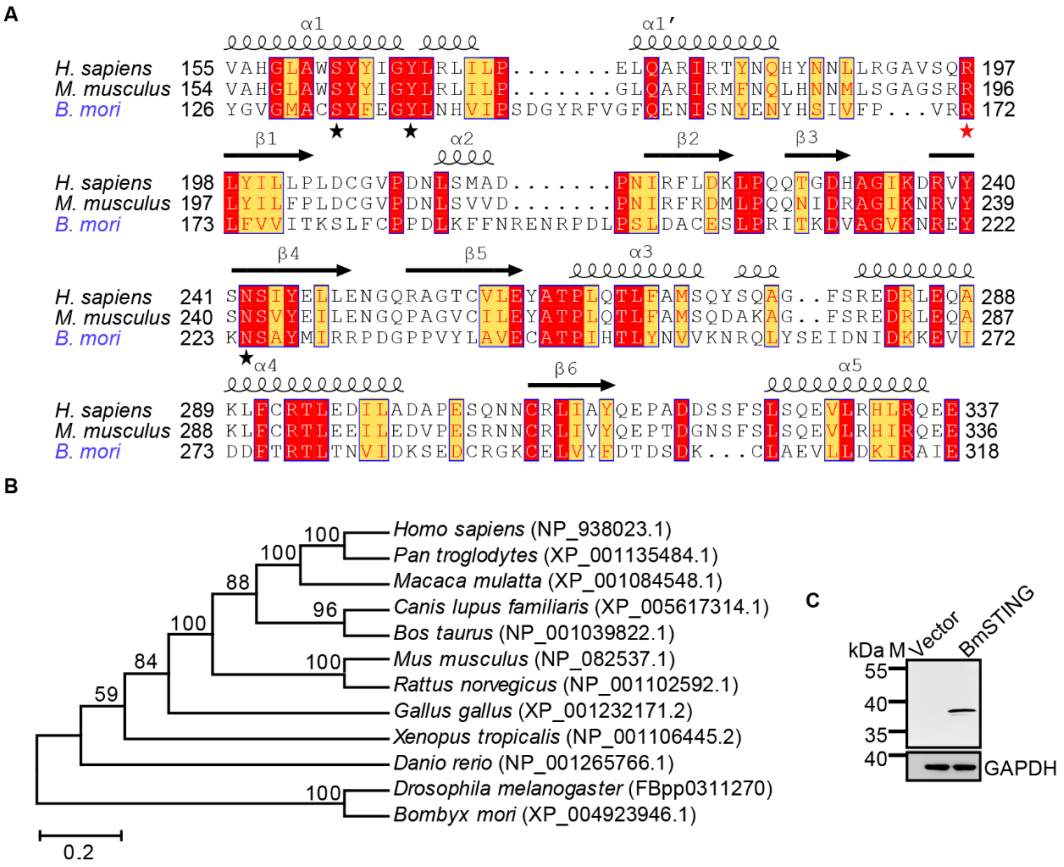

Figure S2. Sequence alignment and phylogenetic tree construction.

A, Multiple alignment of C terminus of STING sequences from *B. mori*126-318, *H. spaines*155-337 and *M. musculus*154-336. Identical positions are boxed in blue, strictly conservative positions in Red and block of similar residues in yellow. Black asterisks indicate residues directly involved in c-di-GMP and cGAMP binding; red asterisk indicates residue basis for the type I IFN expression. B, NJ phylogenetic tree of STINGs. The tree was based on multiple alignments of full-length STING amino-acid sequences from *B.mori* and other species. The tree is drawn to scale. C, BmSTING is a 37.9 kDa protein confirmed by immunoblot in BmE cells.

Figure S3

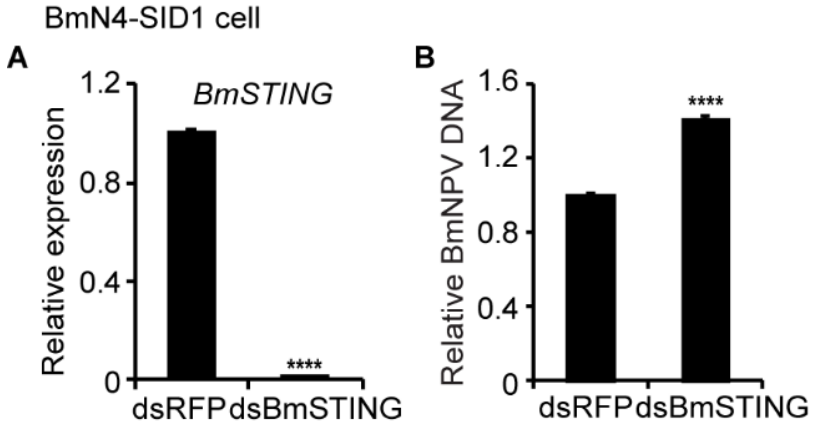

Figure S3. The abundance of the virus in BmN4-SID1 cells with BmSTING RNAi.
A, *BmSTING* mRNA level decreased after dsRNA transfection. B, Relative viral DNA level in cells treated with dsBmSTING or dsRFP determined by qRT-PCR.

Figure S4

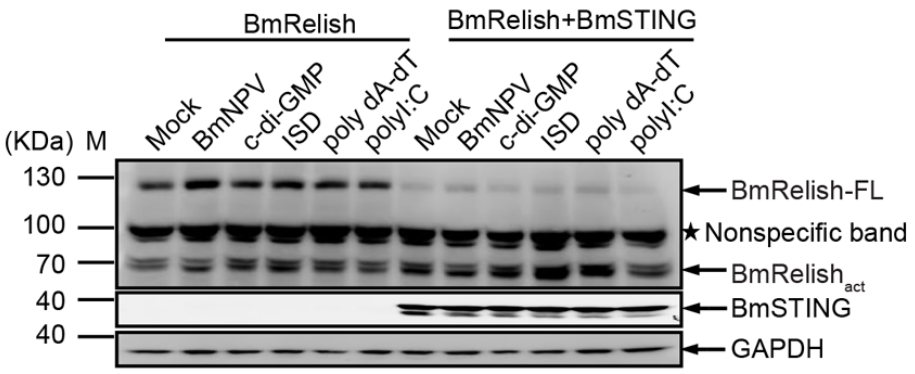

Figure S4. BmSTING ligands mediated the processing of Relish in BmE cells.
Cells overexpressing FL-Relish or co-overexpressing FL-Relish and BmSTING were stimulated with 3 μg/ml ISD, poly(dA-dT), poly(I: C), c-di-GMP, or BmNPV-GFP. Cleavage of Relish ($Relish_{act}$) was analyzed by immunoblotting.

Figure S5

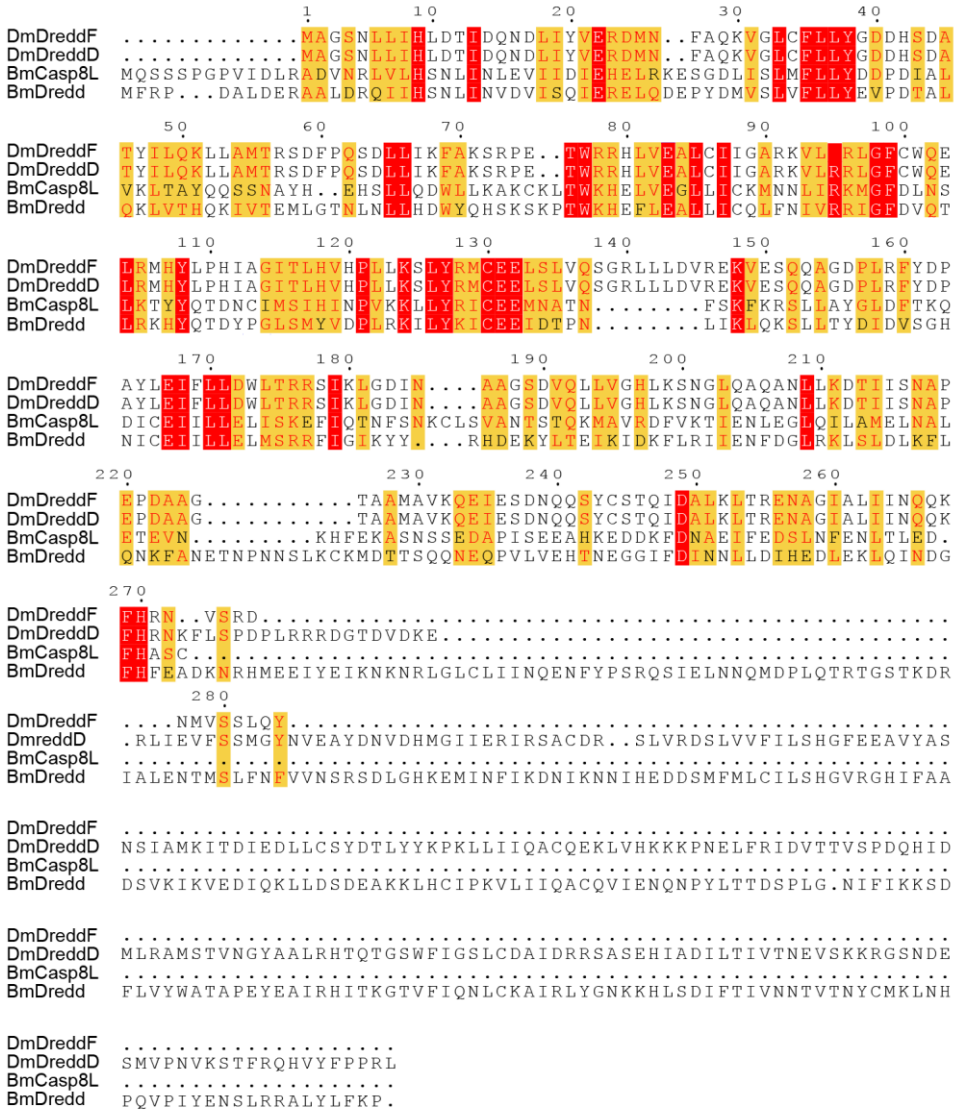

Figure S5. Sequence alignment between Casp8L and Dredd of *B.mori* and *Drosophila*. The amino acid sequences of BmCasp8L (XP_012552745.1), BmDredd (NP_001108337.1), DmDredd-F (NP_477250.3) and DmDredd-D (NP_477251.3) were aligned. Identical positions are boxed in red and strictly conservative positions in yellow.

Figure S6

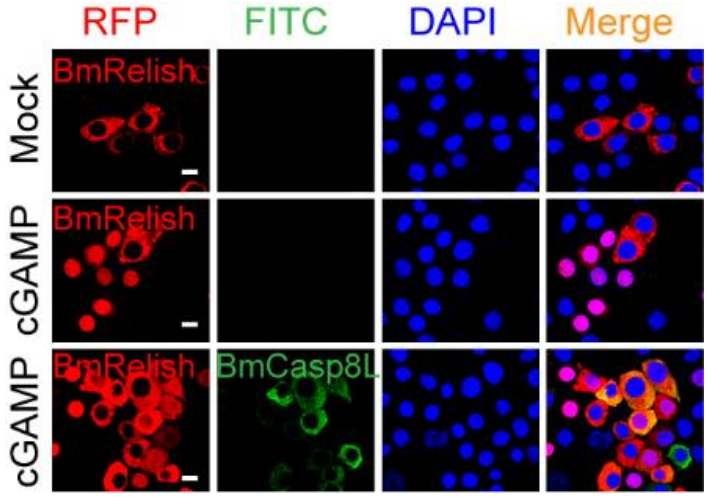

Figure S6. The translocation of BmRelish induced by cGAMP was attenuated by BmCasp8L.

BmE cells overexpressing BmRelish alone or co-expressing BmRelish and BmCasp8L were treated with cGAMP and subjected to fluorescence microscopic analysis (Scale bar = 10 μm).

Figure S7

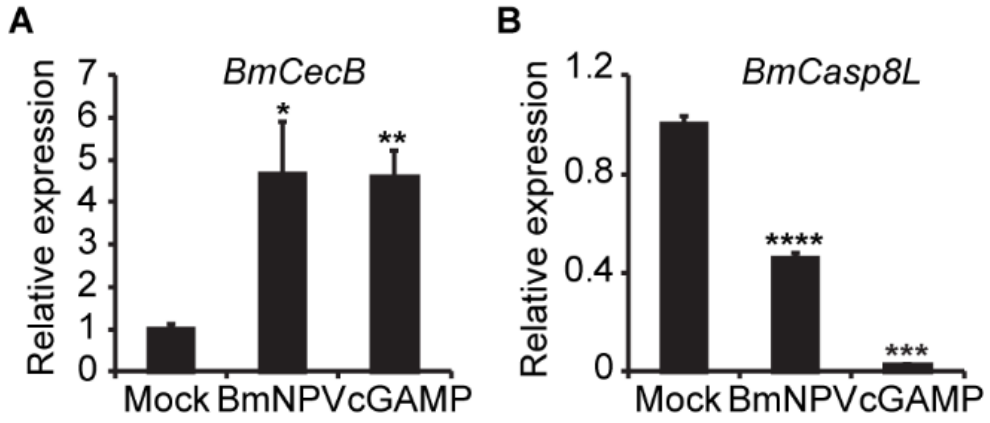

Figure S7. *BmCecB* was induced by BmNPV infection or cGAMP stimulation, but *BmCasp8L* was decreased.

BmE cells were treated with 3 μg/ml cGAMP or infected with BmNPV-GFP, thenthe mRNA levels of *BmCecB* (A) and *BmCasp8L* (B) were analyzed by qRT-PCR. Data are presented as the mean ± SEM. *$p < 0.05$, **$p < 0.01$ (Student's *t* test).

Table S1. Primers used in plasmid construction and qRT-PCR

Gene	Accession no.	Forward primer	Reverse primer
T7-BmSTING	XM_021346487	TAATACGACTCACTATAGGGTCGGAC	TAATACGACTCACTATAGGGAGTC

		GGCTACAGAC	GTCTATGACCTCCTTT
T7-DsRed	XM_015901630	TAATACGACTCACTATAGGGGTACGG CTCCAAGGTGTACG	TAATACGACTCACTATAGGGGGTG TAGTCCTCGTTGTGGG
BmSTING (HA tag)	XM_021346487	CGCGGATCCATGGCAGGCTTAAATG AGAC	AAATATGCGGCCGCCAGATCCTCT TCTGAGATGAGTTTTT
BmDredd (FLAG tag)	NM_001114865	GGAAGATCTATGTTCGACCTGACGC TTTA	TAAGAATGCGGCCGCTCACTTATC GTCCGTCATCCTTGTAATC
BmCasp8L (FLAG tag)	XM_012697291.2	CGCGGATCCATGGATTACAAGGATG ACGACGATAAGCAATCTTCGAGTCC TGG	AAATATGCGGCCGCCTAACAACTC GCATGAAA
BmSTING-RFP	XM_021346487	GCAGGCTTAAATGAGACTCATA	CCCTCGAGTTAGTCACGTTCCCTG CT
BmRelish-RFP	NM_001102465	TCTACAACTGCCAGTGATC	CCCTCGAGTTATAAGCTGGGTTGC TGCA
BmDredd-RFP	NM_001114865	TTTCGACCTGACGCT	CCCTCGAGTCATGGCTTAAATAAG TAAAGT
BmSTING (qPCR)	XM_021346487	AGCCGTCAACCGTCACTT	GAAAACCTACGAATCTGT
BmCecA (qPCR)	NM_001043997	TCGCTTGCCCTATGACG	TGAGCCCAGGTGGAAACT
BmCecB (qPCR)	NM_001043995.1	CCTATCCTTCGTCTTCGCTCT	TAGCTTTAGCCGAACCAAGG
BmGloverin (qPCR)	NM_001043465	TCGCGATATTCACGACTTTG	GCCTCCAGGCCCTAATACTC
BmLysozyme (qPCR)	NM_001043983	GTGCATGAGCTGAGGAAACA	AGTACCGGTCGTTGATCTGG
BmRelish (qPCR)	NM_001102465	GTCGTTGTTCCGGGCGTCC	TCCACACGCGGTGGCCATTC
BmCasp8L	XM_012697291.2	TTGGCAATGGAACTAAACGC	GTGCTTCTTCCGAAATAGGG

(qPCR)			
GAPDH	XM_012694444.2	CATTCCGCGTCCCTGTTGCTAAT	GCTGCCTCCTTGACCTTTTGC
(qPCR)			
GP64	AB253773	CCATCGTGGAGACGGACTA	CTCGCACTGCTGCCTGA
(qPCR)			
sgBmSTING-1	XM_021346487	AAGTGCATGCGCAATGTAGGCGTG	AAACCACGCCTACATTGCGCATGC
sgBmSTING-2	XM_021346487	AAGTGATATAAAATAATTAATAAT	AAACATTATTAATTATTTTATATC
sgBmSTING-3	XM_021346487	AAGTGAAAACTGAAAATCAAAAAA	AAACTTTTTTGATTTTCAGTTTTC