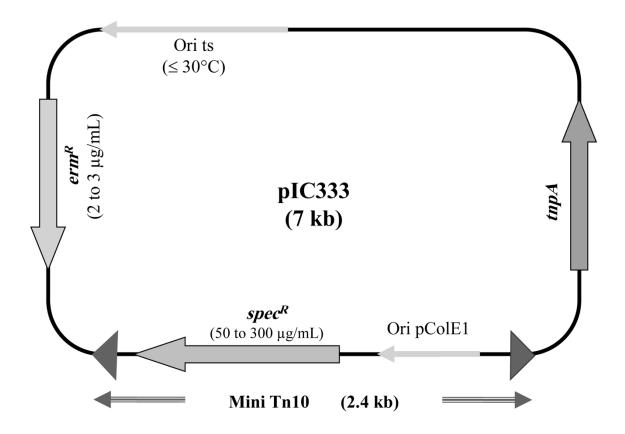


## Supplementary Material

Supplementary Figure 1. The loss of *Bacillus thuringiensis* flagellar filaments enhances the release of immunostimulatory fragments of peptidoglycan. (A) Wild-type (wt) and *relish* (Rel) mutant flies were injected with the supernatant of *Bt407*, *Bt407*Δ*fliK*, *Bt407*Δ*fliK*Ω*fliK* or *Bt407*Δ*fla* cultures. Relative *Diptericin (Dipt)* expression was measured by RT-qPCR 4 h upon the induction. Ribosomal protein 49 (Rp49) transcript was used as reference gene. Transcripts levels are compared to that triggered in wt flies injected with Muller Hinton broth (MH) as a control. (B) Autolysis rates of *Bt407*, *Bt407*Δ*fliK*, *Bt407*Δ*fliK*Ω*fliK*, *Bt407*Δ*fliK*Ω*fliK*, *Bt407*Δ*fliK*Ω*fliK* and *Bt407*Δ*fla* in the presence of Triton X-100. Autolysis rates were determined over a period of 3 h (180 min) in PBS at 37 °C, without shaking. Data obtained from three independent experiments are combined in single value (mean ± sd). Statistical tests were performed using the Mann-Whitney test within Prism software (ns: p > 0.05; \*\*\*\*: p < 0.0001).



Supplementary Figure 2. Map of the temperature sensitive plasmid pIC333. The plasmid pIC333 carries the Gram-positive thermosensitive replication origin of pE194 plasmid (Ori ts), a gene conferring resistance to erythromycin  $(erm^R)$ , a Tn10 transposase gene (tnpA) and the transposable element mini-Tn10. The mini-Tn10 (double grey arrow) is a 2.4 kb transposon flanked by inverted terminal repeat ends (dark grey triangles), containing a pColE1-type origin of replication (Ori pColE1) and a gene coding for resistance to spectinomycin  $(spec^R)$ . This transposon system was originally used to generate random *B. subtilis* mutants (Steinmetz & Richter, 1994).

Name	Nucleotide sequence $(5' \rightarrow 3')$	Restriction site
fliK-a	CGC <u>GGATCC</u> GAACGTGGTCGGGAAGTAAA	BamHI
fliK-b	CCAACTGTTGGCACGCTTTATTCCTCCAATATCATCCATTCATACACATTTTCAAATCCAG	None
fliK-c	CTGGATTTGAAAATGTGTATGAATGGATGATATTGGAGGAATAAAGCGTGCCAACAGTTGG	None
fliK-d	CATG <u>CCATGG</u> CGCATTGTCCATGTATTCCC	NcoI
CompfliK-a	CGC <u>GGATCC</u> GATGATATCGTTGAAGCGATACACC	BamHI
CompfliK-b	GGTAATACAGACTGTATCACCTGTTTTCATAGCCCCTTCC	None
CompfliK-c	GGAAGGGGCTATGAAAACAGGTGATACAGTCTGTATTACC	None
CompfliK-d	CCGGAATTCTTATTCCTCCAATAATCCCGC	EcoRI
E1	CGTTGGCCGATTCATTAATGC	None
E3	CGATATTCACGGTTTACCCAC	None
PU	CGCCAGGGTTTTCCCAGTCACGAC	None
PR	AGCGGATAACAATTTCACACAGGA	None
DiptRTFw	GCTGCGCAATCGCTTCTACT	None
DiptRTRv	TGGTGGAGTGGGCTTCATG	None
Rp49RTFw	GACGCTTCAAGGGACAGTATCTG	None
Rp49RTRv	AAACGCGGTTCTGCATGAG	None

Supplementary Table 2. Primers sequences used in this study.