



Figure S1. Growth curves of the *X. nematophila* dam-overexpressing strain (grey, triangles) and the control strain (black, circles).

Absorbance at 600nm was measured every 30 minutes during growth in LB at 28°C with shaking of the *X. nematophila* Dam-overexpressing strain and the control strain harboring an empty plasmid. Mean values +/- SDs of 3 independent biological replicates for each strain are shown.

Supp data for the Article:

Diverse roles for a conserved DNA-methyltransferase in the entomopathogenic bacterium *Xenorhabdus*

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Table S1: Primers used in this study.

Oligonucleotides	use	Sequence (5'- 3') ^a
Cp-dam0322-F	Cloning of <i>dam</i> gene	TGCT <u>GAA</u> TTACAATCTGCGGCTCTGAAAT
Cp-dam0322-R	Cloning of <i>dam</i> gene	TGGT <u>GGAT</u> CCCTGCATTGTTATCCCCGTTA
qRT-mreB-F	qRT-PCR on <i>mreB</i> gene	AATTCTGGTGGGCACTGTTC
qRT-mreB-R	qRT-PCR on <i>mreB</i> gene	GGATCGGCTTATCCAACAGA
qRT-recA-F	qRT-PCR on <i>recA</i> gene	ATTAATACTCTGGAGAGTTGATCG
qRT-recA-R	qRT-PCR on <i>recA</i> gene	AGTTTCTTATTCAACTCAGCAGCAG
qRT-hsdM-F	qRT-PCR on <i>XNC3v3_0283</i> MTase gene	CGCAAATTAGCTGATGAAAATAGAT
qRT-hsdM-R	qRT-PCR on <i>XNC3v3_0283</i> MTase gene	AGATATTCAAGGCATCACCCATT
qRT-dam-F	qRT-PCR on <i>XNC3v3_0322</i> MTase gene	CTGATCAATCTGTACAACACCGTAA
qRT-dam-R	qRT-PCR on <i>XNC3v3_0322</i> MTase gene	ATAGCAGTGTGGTTAAGGTAAAGA
qRT-MTase-1961-F	qRT-PCR on <i>XNC3v3_1961</i> MTase gene	ATCCAAAGCGTATTACAGAAGAAGA
qRT-MTase-1961-R	qRT-PCR on <i>XNC3v3_1961</i> MTase gene	AATACCAATAGCTTCATAGCCTTCC
qRT-MTase-2953-F	qRT-PCR on <i>XNC3v3_2953</i> MTase gene	TGTCAGATGAAAGAGCACCAGT
qRT-MTase-2953-R	qRT-PCR on <i>XNC3v3_2953</i> MTase gene	CGTTAAATCGTTACGTACCAAG
qRT-MTase-3497-F	qRT-PCR on <i>XNC3v3_3497</i> MTase gene	TTAACGTGCTGAACCACATTATCT
qRT-MTase-3497-R	qRT-PCR on <i>XNC3v3_3497</i> MTase gene	TTAGATCTTGGCATTGCTTGTAAATA
qRT-MTase-3873-F	qRT-PCR on <i>XNC3v3_3873</i> MTase gene	TGGAAAACAATTCTGGAATTAGAAA
qRT-MTase-3873-R	qRT-PCR on <i>XNC3v3_3873</i> MTase gene	ATTAGAAAGTAAATACGCAGTGTCC
qRT-flhD-F	qRT-PCR on <i>flhD</i> gene	CGTTTAGGTATTAGTGAATCGATGG
qRT-flhD-R	qRT-PCR on <i>flhD</i> gene	AGATGAGTAGACAGCAAAATACCTG
qRT-fliA-F	qRT-PCR on <i>fliA</i> gene	GTAGAACTCGATGACTTGCTTCAG
qRT-fliA-R	qRT-PCR on <i>fliA</i> gene	AACTCTTGCTCAAGTTACGGATG
qRT-fliZ-F	qRT-PCR on <i>fliZ</i> gene	GACAAAACCTGGAGTGAATTACAAG
qRT-fliZ-R	qRT-PCR on <i>fliZ</i> gene	GACGTCTAACGAACCACATACTC
qRT-fliC-F	qRT-PCR on <i>fliC</i> gene	GGTATCTCATTGCTCAGACTACC
qRT-fliC-R	qRT-PCR on <i>fliC</i> gene	TGTAGAGATA CGGTCAATTCTTCC
qRT-xaxA-F	qRT-PCR on <i>xaxA</i> gene	GAGACAGCAGGAAAATACTCAGAAG
qRT-xaxA-R	qRT-PCR on <i>xaxA</i> gene	TGATGGTGGTAGAGAGGTTATTGTC
qRT-xhIA-F	qRT-PCR on <i>xhIA</i> gene	GCTGTTGGCAGATAATTGCC
qRT-xhIA-R	qRT-PCR on <i>xhIA</i> gene	CGGATGTGAGTCAGGCTGACA
MSRE-2082-F	MSRE-PCR on region upstream from <i>XNC3v3_2082</i>	CAATAGAAGATATTACCTAATCAACC
MSRE-2082-R	MSRE-PCR on region upstream from <i>XNC3v3_2082</i>	GAAAGAAGTTCATTAGTCAATGACAG

^a Restriction enzyme sites are underlined