1	SUPPLEMENTAL MATERIALS
2	Population dynamics of intestinal Enterococcus modulate Galleria mellonella
3	metamorphosis
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17	Running title: Gut bacteria modulate insect metamorphosis
18	Keywords: Microbiota alteration, Insect metamorphosis, Host-microbe interactions

SUPPLEMENTARY TABLES

20 21 Table S1. Primer Sequence details

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Primer name	Sequence 5'-3'	Reference	
Gallerimycin F	GAAGTCTACAGAATCACACGA	—— Lange <i>et al.</i> (2018)	
Gallerimycin R	ATCGAAGACATTGACATCCA		
Apolipophorin III F	AGACTTGCACGCCATCAAGA	$\frac{1}{2} \int dx dx dx dx dx dx dx dx$	
Apolipophorin III R	TGCATGCTGTTTGTCACTGC	Lange $et at. (2018)$	
Gloverin F	GTGTTGAGCCCGTATGGGAA	Longo et $al (2018)$	
Gloverin R	CCGTGCATCTGCTTGCTAAC	Lange <i>et al.</i> (2018)	
Cecropin-D F	CTGTTCGTGTTCGCTTGTGT	Lenge of rl (2019)	
Cecropin-D R	GTAGCTGCTTCGCCTACCAC	Lange $et at. (2018)$	
IMPI-F	TAGTAAGCAGTAGCATAGTCC	- Dub conduits of $al (2016)$	
IMPI-R	GCCATCTTCACAGTAGCA	Dubovskiy et al. (2016)	
β-Actin f	CCCTGTGCTGCTCACCGA	$-$ Lange et r_{l} (2018)	
β-Actin r	ACAGTGTGGGTGACCCCGTC	Lange <i>et al.</i> (2018)	

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SUPPLEMENTARY FIGURES LEGENDS

- Fig S1. Heatmap of gene expression of *G. mellonella* according to metamorphosis. Normalized counts obtained with DESeq transformed to hellinger distance were used to generate heatmaps showing overexpressed (red) and underexpressed (blue) genes for two developmental conditions (larva and pupae).
- Fig S2. Sparse Canonical Correlation analysis. Sparse canonical correlation analysis was performed to analyze the correlation between microbiome data and RNAseq expression in the larva and pupae stages of Galleria mellonella. The database was performed with taxon and gene lists that differ by more than 2-fold change, and analyzed using the iSFun package of the R program Gene ontology analysis was performed on the genetic data from the obtained data using Panther, and it was created as a heatmap through R program.
- Fig S3. Hemolymph protein profile analysis. In-gel chymotryptic digestion for each protein
 segment < 25 kDa on electrophoresis was analyzed with LC-ESI-Q-TOF-MS for protein
 profile analysis. The fasta sequence DB of "Ditrysia and antimicrobial" (including 20
 Galleria antimicrobial protein sequences) and the fasta sequence DB of "Lepidoptera"
 (including 17,496 Galleria sequence DB) are used as databases.
- Fig S4. Confirmation of the presence of Enterococcus spp in the intestine after vancomycin treatment. *E. innesii* (Eg^{refR}) and *E. mundtii* (Em^{refR}) marked with rifampicin antibiotics were used to confirm the removal of Gram-positive bacteria from the intestine after vancomycin treatment. After feeding each bacteria, the reduction of bacteria by antibiotic treatment was tested by culturing in rifampicin-TSA.
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45	References
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Enterobacter_cancerogenus		
Enteropacter_uc		
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Enterococcus_saccharolyticus_group		
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Enterococcus_dispar		
EU465963_s Enterococcus_gallinarum		
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Larvae Pupae



Time (min)



