

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

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SUPPLEMENTARY TABLES

20 **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	AGACTTGACGCCATCAAGA	Lange <i>et al.</i> (2018)
Apolipophorin III R	TGCATGCTGTTTGTCACTGC	
Gloverin F	GTGTTGAGCCCGTATGGGAA	Lange <i>et al.</i> (2018)
Gloverin R	CCGTGCATCTGCTTGCTAAC	
Cecropin-D F	CTGTTCGTGTTTCGCTTGTGT	Lange <i>et al.</i> (2018)
Cecropin-D R	GTAGCTGCTTCGCCTACCAC	
IMPI-F	TAGTAAGCAGTAGCATAGTCC	Dubovskiy <i>et al.</i> (2016)
IMPI-R	GCCATCTTCACAGTAGCA	
β -Actin f	CCCTGTGCTGCTCACCGA	Lange <i>et al.</i> (2018)
β -Actin r	ACAGTGTGGGTGACCCCGTC	

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SUPPLEMENTARY FIGURES LEGENDS

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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.

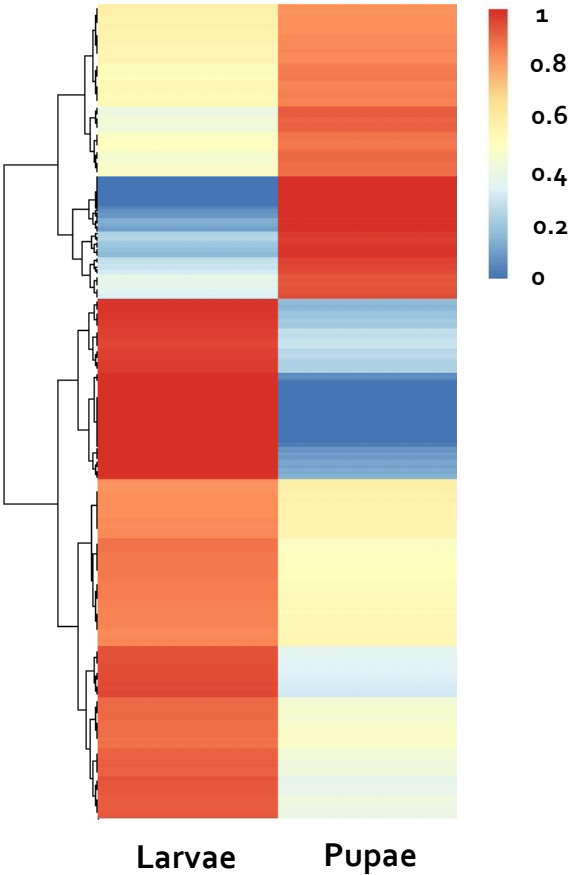
Fig S3. Hemolymph protein profile analysis. In-gel chymotryptic digestion for each protein segment < 25 kDa on electrophoresis was analyzed with LC-ESI-Q-TOF-MS for protein profile analysis. The fasta sequence DB of “Ditrysia and antimicrobial” (including 20 *Galleria* antimicrobial protein sequences) 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.

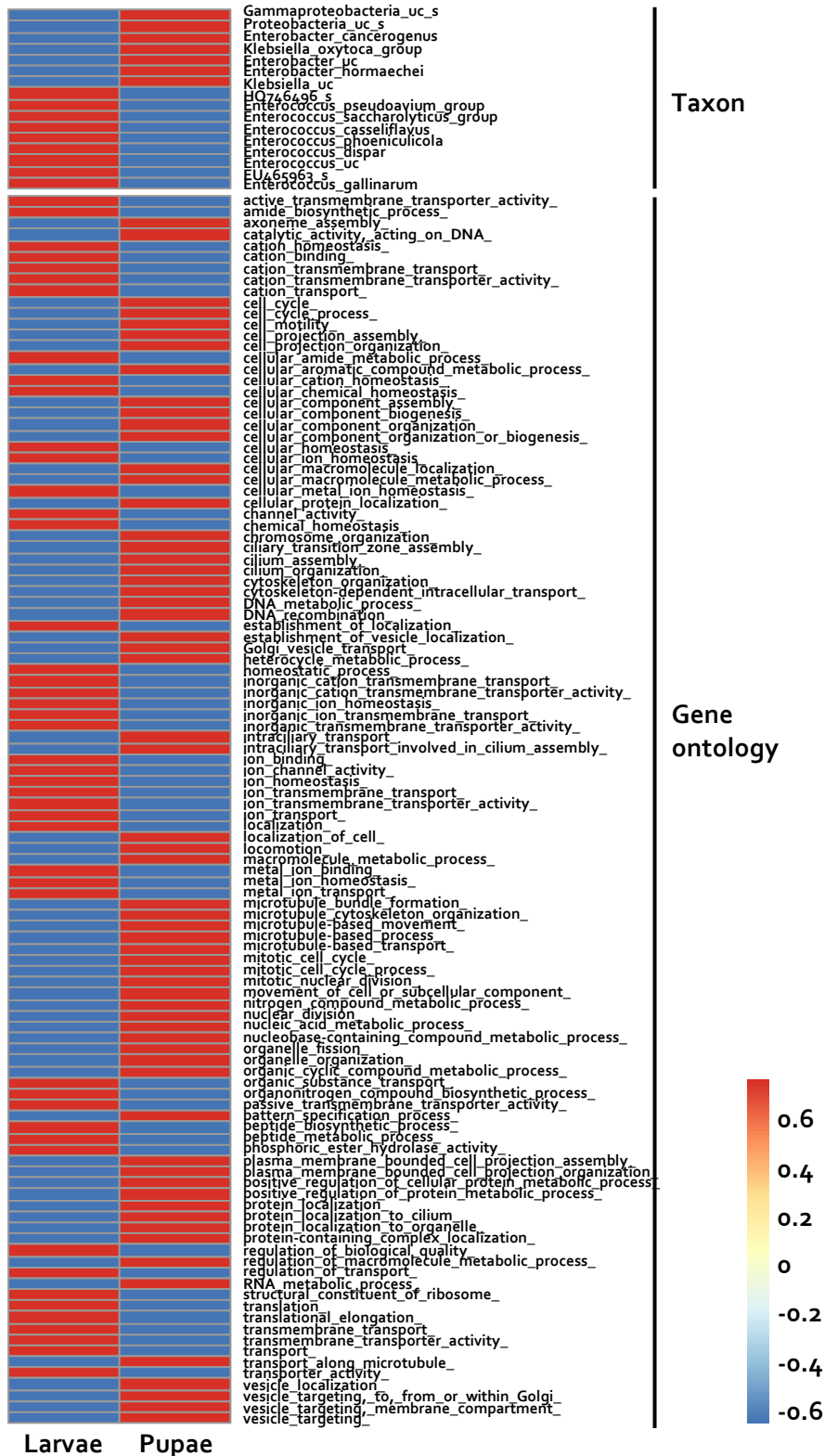
References

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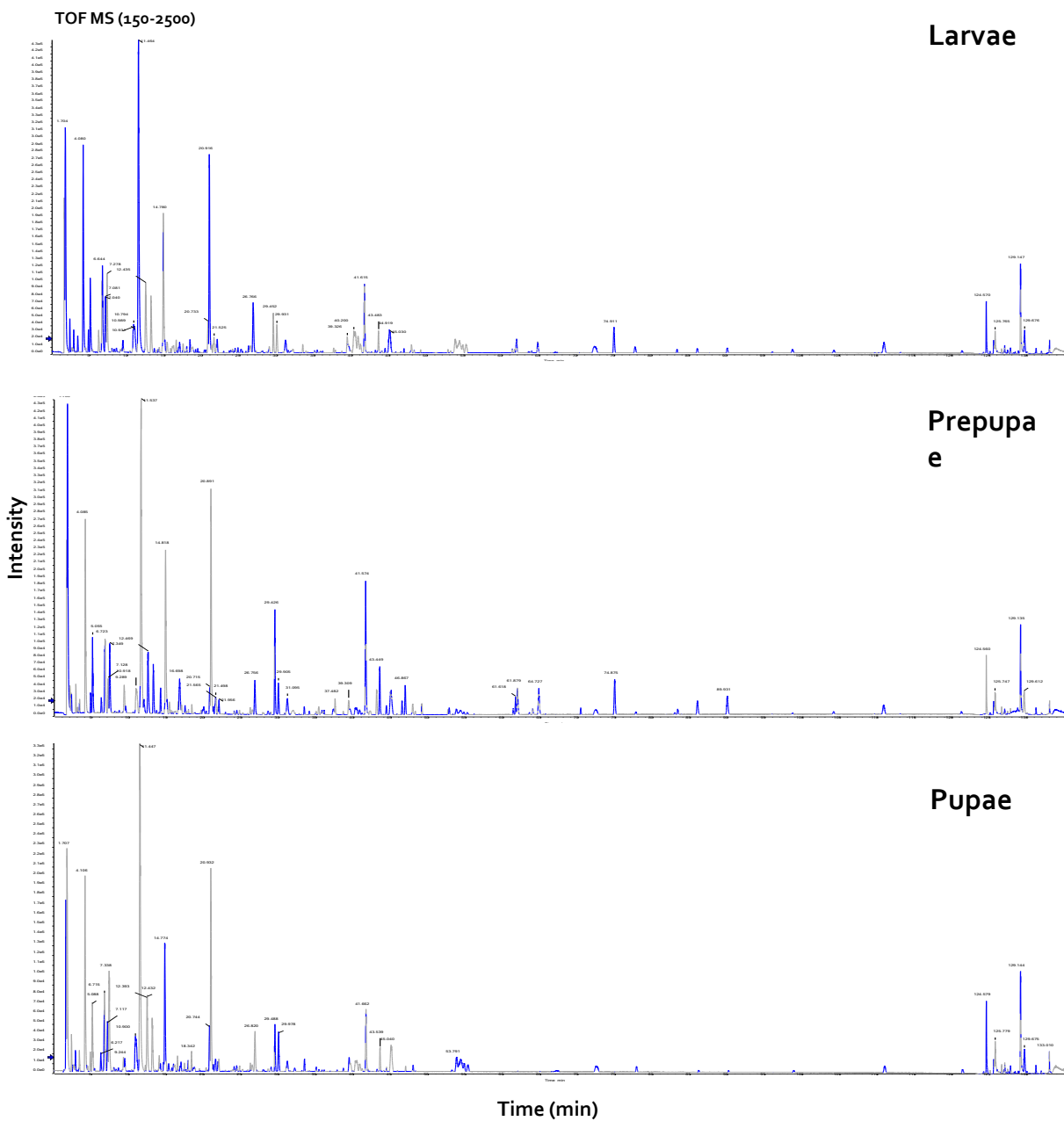
Supplementary Figure 1



Supplementary Figure 2

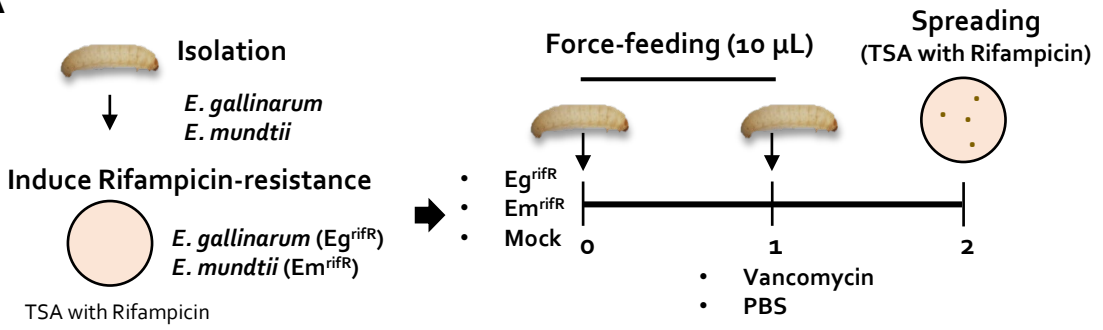


Supplementary Figure 3

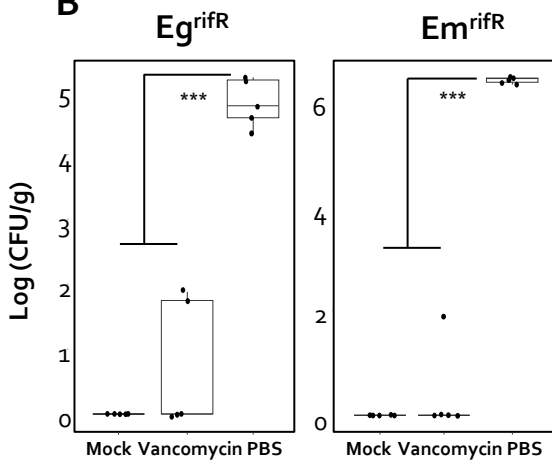


Supplementary Figure 4

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