

Figure S1. RT-qPCR analysis of GAM1 immune gene expression. Quantification of GAM1 in the gut of sugar-fed (SF) and blood-fed (BF) mosquito carrying a conventional (C) microbiota or treated with antibiotics (abx). Data show the average ratios of two independent replicates, and error bars represent the standard error. Tukey test were used to determine the confidence interval, ns non significative, * $p < 0.05$, ** $p < 0.01$.

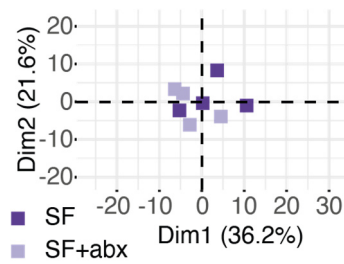


Figure S2. Principal Component Analysis (PCA) plot of the midgut metabolome. Only sugar-fed samples are included in the analysis.

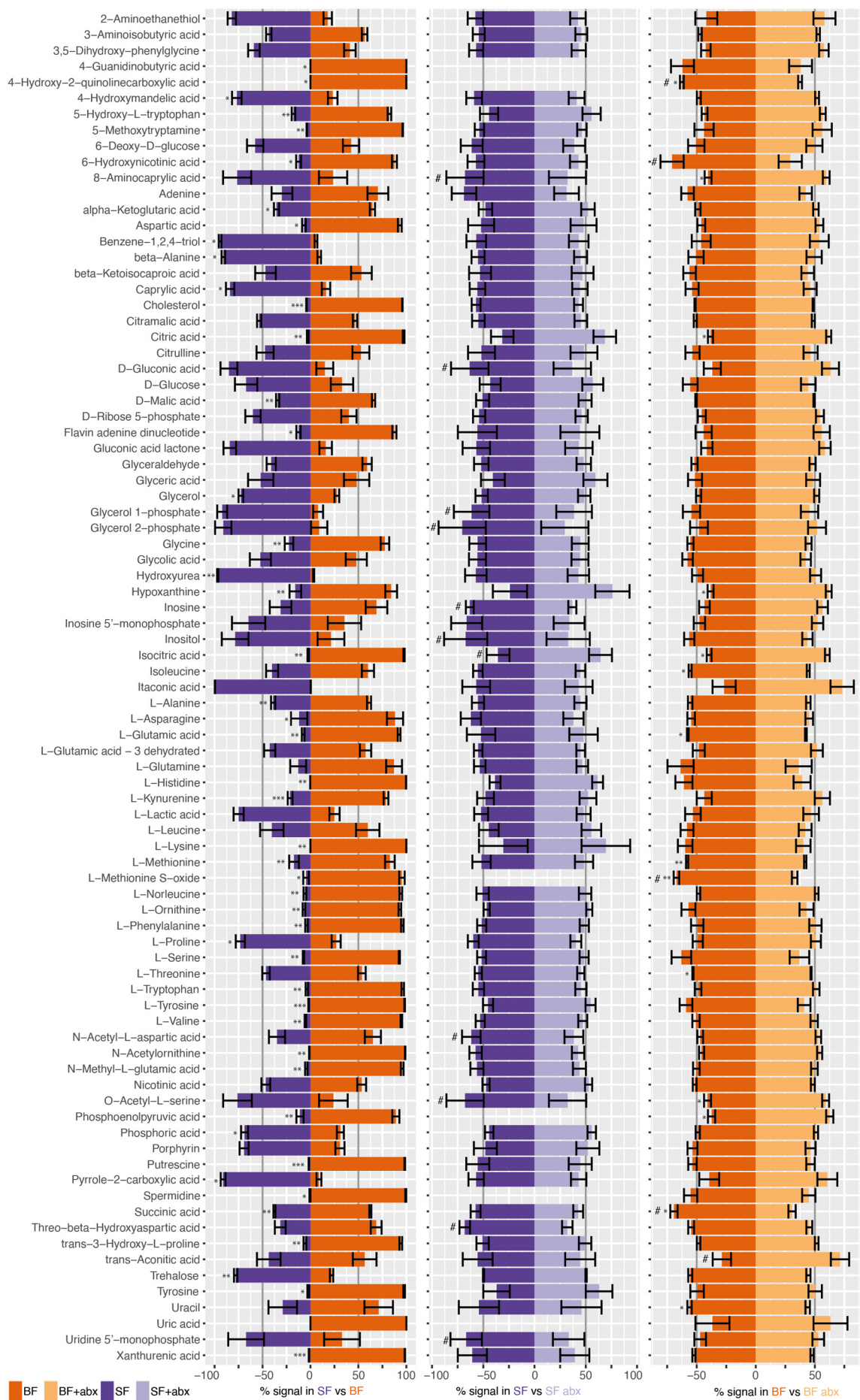


Figure S3. Bar charts representing the comparative percentage of signal from different conditions. Data represent the average percentage from 4 independent replicates and error bars show the standard error. t-test were used to determine statistical significance, * $-p < 0.05$, ** $-p < 0.01$, *** $-p < 0.001$. # indicate metabolites which are consistently regulated at least 1.7-fold (ratio >1.7 or <0.588) in at least 3 of the 4 replicates by the antibiotic treatment.

Table S1. Primers sequences for qPCR.

Primer name	Forward/ Reverse	Gene Name	ACOM #	Sequence
Cec1 F qPCR	F	<i>Cecropin1</i>	042420	TCATCTTTGTCGTGCTGGCA
CEC1 R qPCR	R	<i>Cecropin1</i>	042420	TCTTCAGCCGTCCCGCT
Gam1_F	F	<i>Gambicin 1</i>	024216	CTATCTCAACCGGAAGGGCG
Gam1_R	R	<i>Gambicin 1</i>	024216	GCCAAACTTTCGCTTGCAGT
PGRPLB_qPCR F	F	<i>PGRPLB</i>	033796	GAGTATGGTGTCCGGAATGG
PGRPLB_qPCR R	R	<i>PGRPLB</i>	033796	GGCCAGGTTTGTATCTCCTC
S7-F	F	<i>S7</i>	041783	GTGCGCGAGTTGGAGAAGA
S7-R	R	<i>S7</i>	041783	ATCGGTTTGGGCAGAA TGC
16s F qPCR	F	Generic bacterial 16S	N/A	TCCTACGGGAGGCAGCAGT
16s R qPCR	R	Generic bacterial 16S	N/A	GGACTACCAGGGTATCTAATCCTGTT