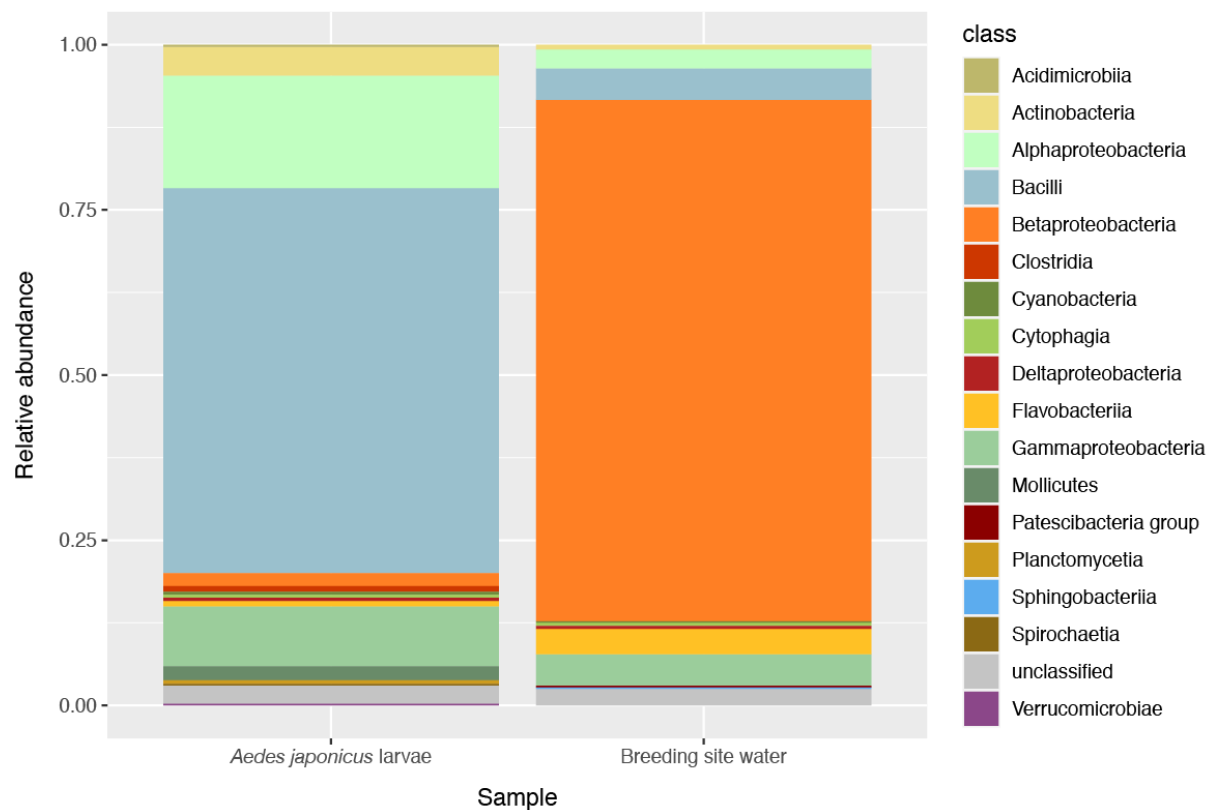
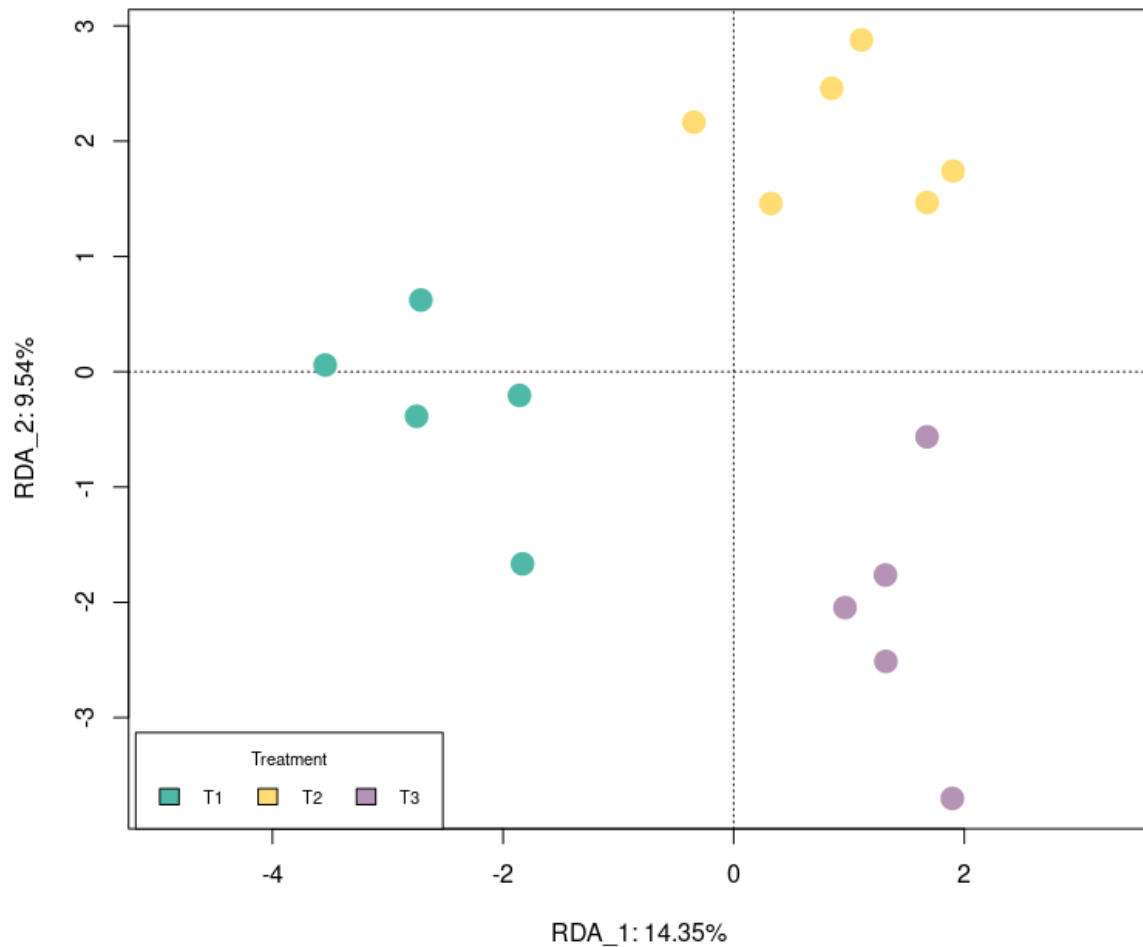


Supplementary Material



Supplementary Figure 1. Barplot of the relative abundance of bacterial classes in *Aedes japonicus* larvae and in the breeding site water. *Klebsiella* represented 1% of the Gammaproteobacteria reads in both samples. Twelve larval midguts were lysed individually overnight and pooled during DNA isolation, directly on a DNeasy Mini spin column (QIAGEN DNeasy Blood & Tissue Kit). The pooled midgut DNA sample was eluted in 80 μ l AE buffer. Metagenomics library preparation and paired-end (150 bp) sequencing was performed on an Illumina NovaSeq6000 instrument by Novogene. Raw sequence reads can be found at the European Nucleotide Archive (accession number PRJEB45737). Trimmed reads were uploaded to the Kaiju web server (v1.7.3) for taxonomic classification and searched against the non-redundant database (NCBI BLAST nr+euk; last updated: 2017-05-16). Results were downloaded and stacked bar plots representing the bacterial class level were created with R (version 4.0.5) and the package ggplot2 (version 3.3.3).



Supplementary Figure 2. Constrained ordination (RDA) showing the clustering profile among samples from each experimental treatment with regard to their affiliation. From the total variance based on Jaccard dissimilarities within the metabolite presence and absence matrix, a total of 23.89% is represented within the two constrained axes shown, distributing as follows: RDA_1(14.35%) and RDA_2(9.54%). Treatment 1 (green) included samples that served as experimental control (T₁). Treatment 2 (yellow) comprised breeding sites visited by an ovipositing female (T₂). Treatment 3 (purple) comprised breeding sites set up with manually deposited eggs (T₃).

Supplementary Table 1. Genomes used to search metabolic pathways displayed in Figure 2.

Strain	Accession No.
<i>Acinetobacter</i> sp. Ag1	LBMZ00000000
<i>Acinetobacter</i> sp. Ag2	LBNA00000000
<i>Acinetobacter</i> sp. AR2-3	MJIQ00000000
<i>Asaia</i> sp. SF2.1	AYXS00000000
<i>Chromobacterium</i> sp. Panama	QARX01000001
<i>Elizabethkingia anophelis</i> Ag1	CP007547
<i>Elizabethkingia anophelis</i> As1	LFKT00000000
<i>Elizabethkingia anophelis</i> R26	ANIW01000054
<i>Elizabethkingia anophelis</i> AR6-8/AR4-6	CP023403/CP023404
<i>Enterobacter</i> sp. Ag1	AKXM00000000
<i>Klebsiella</i> sp. MC1F	JAGTYC000000000
<i>Leucobacter</i> sp. Ag1	LAYO00000000
<i>Lysinibacillus</i> sp. AR18-8	MDGU00000000
<i>Microbacterium</i> sp. Ag1	LBCR00000000
<i>Microbacterium</i> sp. AR7-10	MJIR00000000
<i>Pantoea</i> sp. Ae16	MDJQ00000000
<i>Pseudomonas</i> sp. Ag1	AKVH01000000
<i>Pseudomonas stutzeri</i> AR9-4	MDGV00000000
<i>Serratia fonticola</i> AeS1	MDJO00000000
<i>Serratia</i> sp. Ag1	JQEI00000000
<i>Serratia</i> sp. Ag2	JQEI00000000
<i>Serratia marcescens</i> strain Ano1	MJVB00000000
<i>Serratia marcescens</i> strain Ano2	MJVC00000000
<i>Serratia marcescens</i> As1	CP010584
<i>Sphingobacterium</i> sp. Ag1	LBGU00000000
<i>Sphingomonas</i> sp. Ag1	LAZX00000000
<i>Staphylococcus equorum</i> AR8-13	MDJP00000000
<i>Staphylococcus hominis</i> As1	LFKQ00000000
<i>Staphylococcus hominis</i> As2	LFKR00000000
<i>Staphylococcus hominis</i> As3	LFKS00000000
<i>Stenotrophomonas maltophilia</i> As1	LFKU00000000.
<i>Thorsellia anophelis</i> DSM 18579	FOHV01000000

Supplementary Table 2. Quantification of metabolites from each sample in the network displayed in Figure 3. Also shown are the m/z ratios and retention times of each metabolite. The network and associated metadata can be accessed at <https://gnps.ucsd.edu/ProteoSAFe/status.jsp?task=47c0d4e60d3d41c7ac9e738004711e55>

Supplementary Table 3. Pairwise PERMANOVA assessing if the variance captured by the Jaccard dissimilarities among samples from each treatment were significant and what is the effect size (R^2) that could be attributed to the conditions (biotic or abiotic) represented by each experimental group we proposed as a decoupling of the oviposition and larval development events. Treatment 1 included samples that served as experimental control. Treatment 2 comprised breeding sites visited by an ovipositing female. Treatment 3 comprised breeding sites set up with manually deposited eggs.

	Treatment 2	Treatment 3
Treatment 1	0.2464 **	0.3007 **
Treatment 2	--	0.2120 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1