Description of Supplementary Files

File name: **Table S1. Numbers of mosquitoes selected for DNA extraction and 16S rRNA sequencing.** Mosquitoes were allocated to a concentration/time group based on the concentration of deltamethrin to which they were exposed, the period of follow up post exposure and whether they survived exposure. A selection from each group were pooled in groups of three and sequenced.

File name: **Table S2. Summary statistics of raw sequencing outputs and resulting data following denoising with Dada2 and filtering**.

File name: **Table S3. Relative abundances of bacterial species present in mosquitoes, grouped by age and resistance status.** Taxa are annotated to genus or lowest possible taxonomic level (square brackets).

File name: **Table S4. Beta diversity outputs, showing no significant difference between rarefied and non-rarefied data.** Samples which fail to meet the rarefaction depth are excluded from analysis, therefore the sample sizes of rarefied data are reduced.

File name: **Table S5. Differential rankings for features and taxa present in 2-3 day old** *An. coluzzii,* **as computed by Songbird.**

File name: **Figure S1. Quality plots for forward and reverse untrimmed reads, generated in Qiime2.** Low quality forward reads resulted in sequence loss due to failure of strands to merge during denoising, therefore only the reverse reads were used for downstream analysis.

File name: **Figure S2. Box plots showing Shannon index of diversity and Faith's Phylogenetic Diversity in 2-3 day old** *An. coluzzii.* Upper and lower limits of boxes represent first and third quintiles of the median (dark horizontal line).

File name: **Figure S3. Stacked bar plot showing relative abundance of taxa present in 2 day old and 5 day old** *An. coluzzii* **grouped by resistance phenotype.** Taxa are annotated to genus or lowest possible taxonomic level. Taxa present at less than 1% abundance are grouped together and coloured in grey.
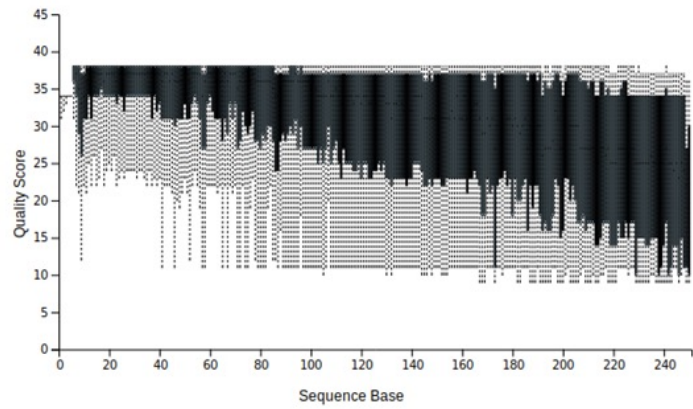
File name: **Figure S4. Songbird model.** Blue line is trained on the dataset and is a predictor of model accuracy in contrast to the null hypothesis (orange). Illustrates the accuracy of model prediction and proportion of variance in microbial composition explained by resistance phenotype.

File name: **Figure S5. Volcano plot of differentially abundant bacterial taxa in 2-3 day old** *An. coluzzii*, as computed by analysis of composition of microbiomes (ANCOM).

Table S1: Numbers of mosquitoes selected for DNA extraction and 16S rRNA sequencing. Mosquitoes were allocated to a concentration/time group based on the concentration of deltamethrin to which they were exposed, the period of follow up post exposure and whether they survived exposure. A selection from each group were pooled in groups of three and sequenced.

Resistance phenotype	Description	Concentration /time group	Age at death	Number of individuals	Number selected for sequencing (#pools)
Susceptible	Knocked-down at 60 minutes post exposure to the diagnostic dose (1x) deltamethrin.	Susceptible	2-3 days	97	87 (29)
Resistant	Survivors at 60 minutes post exposure to 5x deltamethrin	5xRes60	2-3 days	83	30 (10)
	Survivors at 60 minutes post exposure to 10x deltamethrin	10xRes60	2-3 days	89	21(7)
	Survivors at 72 hours post exposure to 5x deltamethrin	5xRes72	5-6 days	24	24(8)
	Survivors at 72 hours post exposure to 10x deltamethrin	10xRes72	5-6 days	33	12 (4)
	Survivors at 72 hours post exposure to diagnostic dose (1x) deltamethrin	1xRes72	5-6 days	55	36 (12)
Controls	Mosquitoes from control bottle which were alive 60 minutes after the initiation of bioassay	ControlA60	2-3 days	57	42 (14)
	Mosquitoes from control bottle which were alive 72 hours after the initiation of bioassay	ControlA72	5-6 days	69	30 (10)
Blanks	70% Ethanol which underwent same DNA extraction and 16S rRNA sequencing as samples	Ethanol blank	N/A	1	1 (1)
	Sterile, RNAse free water which underwent same DNA extraction and 16S rRNA sequencing as samples	Water blank		3	3 (1)

Forward Reads

Reverse Reads

Shannon Index of Diversity

Faith's Phylogenetic Diversity