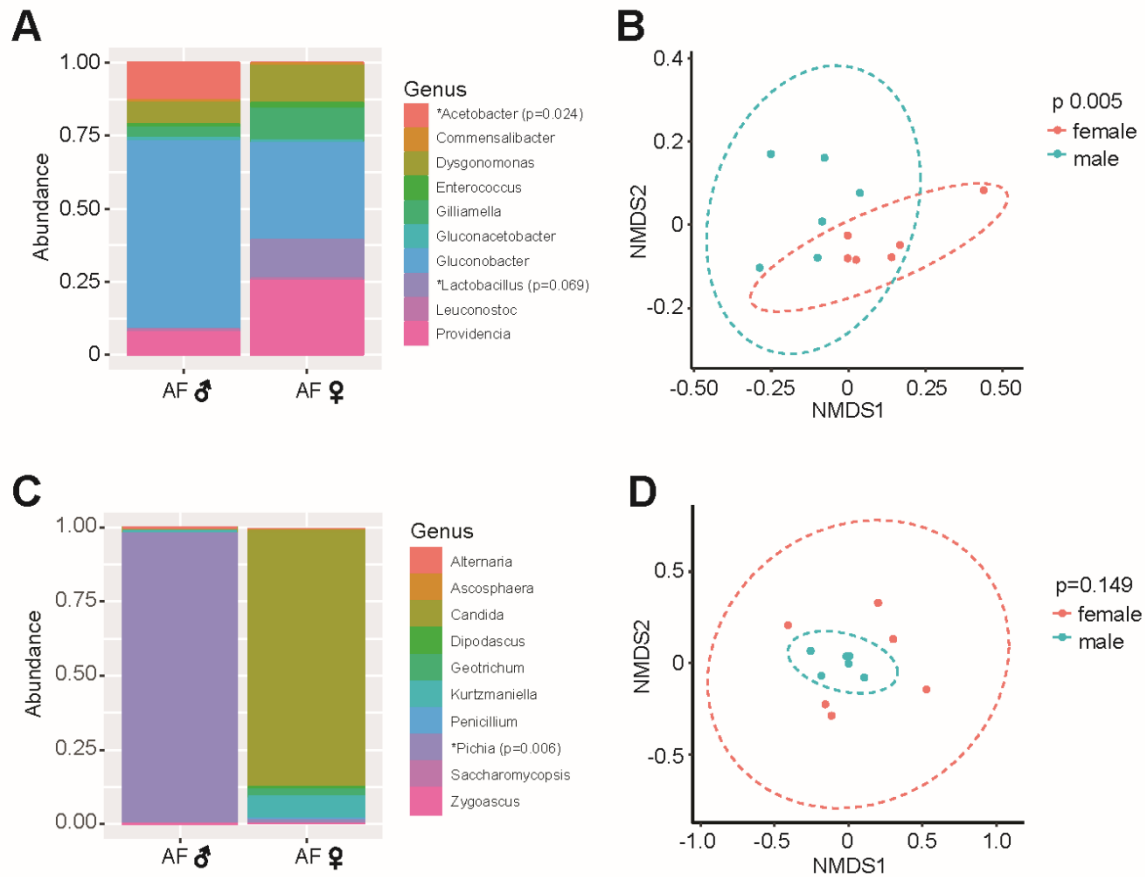


Supplemental Figure 1

A – F. Chao1 and Shannon α -diversity indices of bacterial (top row) and fungal communities (bottom row) in control and antimicrobial-treated flies. α -diversity was compared using a Wilcoxon rank-sum test, $n=6-8$ for all treatments; ns: not significant ($p>0.05$).



Supplemental Figure 2

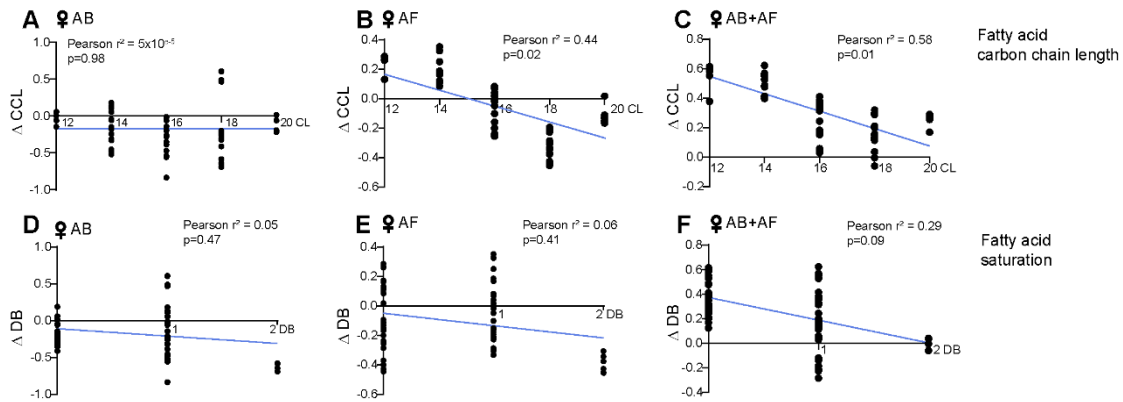
Comparison of male and female microbiome 16S and ITS high throughput sequencing amplicon profiles following antifungal treatment. Samples are comprised of flies that were treated for 21 and 35 days.

A. Scaled relative abundance plots for the 10 most abundant bacterial genera of males and females following antifungal (AF) treatment (n=6 per sex). The p values were determined using univariate multiple testing with an F test; *: abundance is significantly different between control and treatment conditions.

B. Non-multidimensional scaling plots (NMDS; based on Jaccard distances) of OTUs reveal distinct bacterial communities in males and females following AF treatment (ANOSIM, n=6 per sex). Ellipses represent significance at 0.05 confidence.

C. Scaled relative abundance plots for the 10 most abundant fungal genera of males and females following antifungal (AF) treatment (n=6 per sex). The p values were determined using univariate multiple testing with an F test; *: significantly different between control and treatment conditions.

D. Non-multidimensional scaling plots (NMDS; based on Jaccard distances) of OTUs show no significant separation in fungal composition between males and females (ANOSIM, n=6 per sex). Ellipses represent significance at 0.05 confidence.

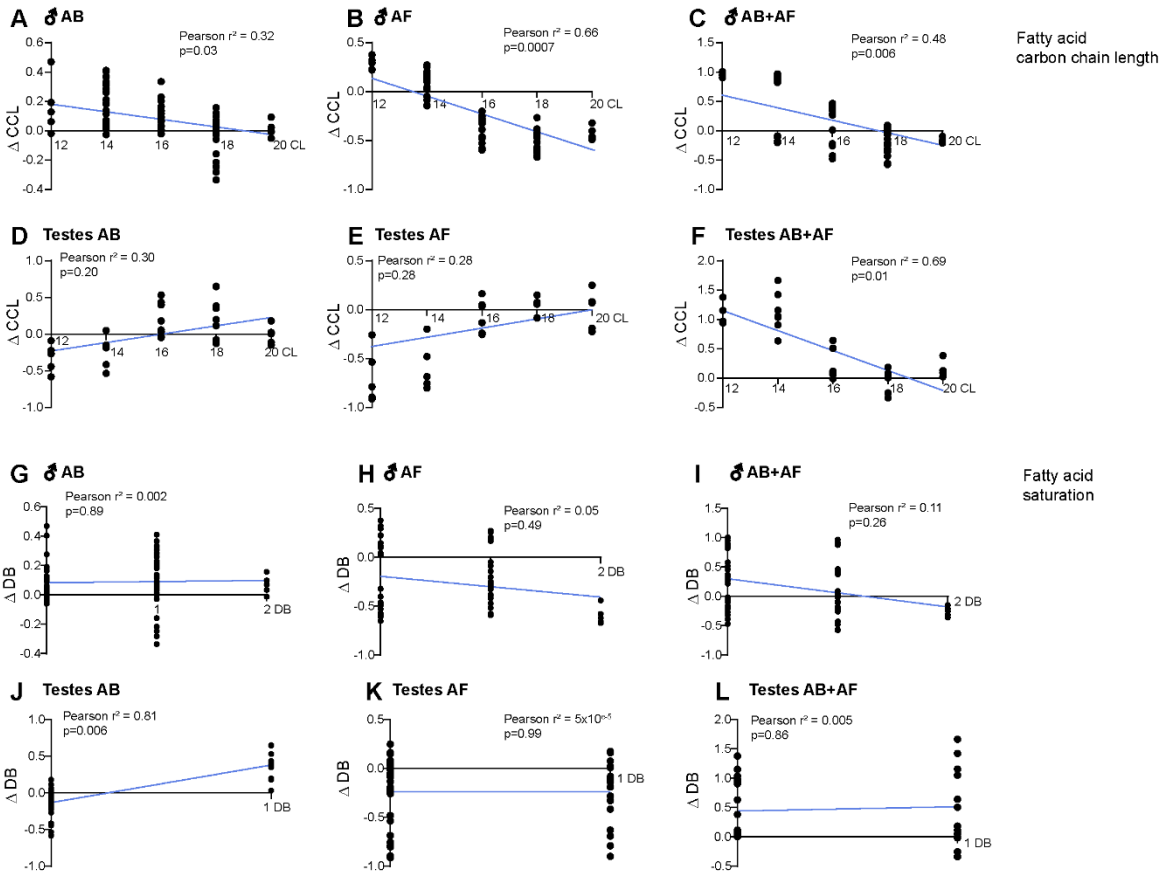


Supplemental Figure 3

Influence of microbiome composition on female whole body fatty acid carbon chain length and degree of saturation. The Pearson r^2 value and simple linear regression line are provided; n=3-5.

A – C. Change in whole body fatty acid carbon chain lengths (CCL) in antibacterial- (AB), antifungal- (AF), or AB+AF treated-females compared to controls.

D – F. Change in whole body fatty acid saturation levels in treated females compared to controls; DB: double bond number.



Supplemental Figure 4

Influence of microbiome composition on male whole body and testes fatty acid carbon chain length and degree of saturation. The Pearson r^2 value and simple linear regression line are provided; $n=3-5$.

A – C. Change in whole body fatty acid carbon chain lengths (CCL) in antibacterial (AB), antifungal (AF), or AB+AF treated-males compared to controls.

D – F. Change in testes fatty acid carbon chain lengths (CCL) in antibacterial- (AB), antifungal- (AF), or AB+AF-treated males compared to controls.

G – I. Change in whole body fatty acid saturation levels in treated males compared to controls; DB: double bond number.

J – L. Change in testes fatty acid saturation levels in treated males compared to controls; DB: double bond number.