

- Supplementary figures and information

Detailed composition of the fly food medium

amounts per liter			
Water	-	1000	mL
agar	-	10	g
sucrose	-	15	g
glucose	-	30	g
cornmeal	-	15	g
wheat germ-		10	g
soy flour	-	10	g
molasses	-	30	g
Yeast	-	35	g
Propionic acid	-	5	mL
tegosept	-	2	g
ethanol	-	10	mL

- Primers targeting V4V6 region.

Forward primer:

GTGCCAGCMGCCGCGGTAA

Reverse primer:

CGACRRCCATGCANCACT

- Primers targeting ITS1 region.

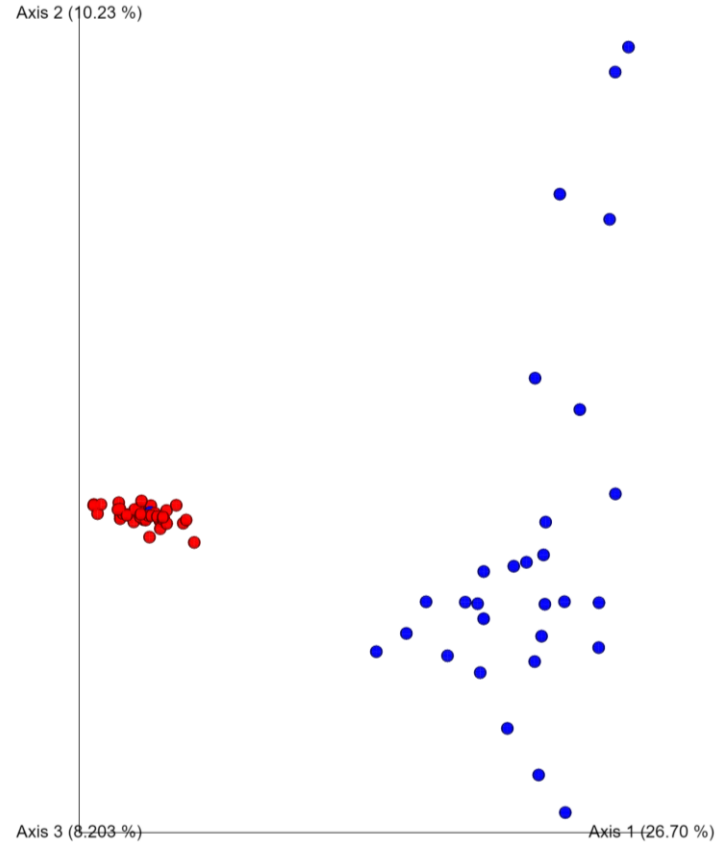
Forward primer:

CTTGGTCATTAGAGGAAG*TAA

Reverse primer:

GCTGCGTTCTTCATCGA* TGC

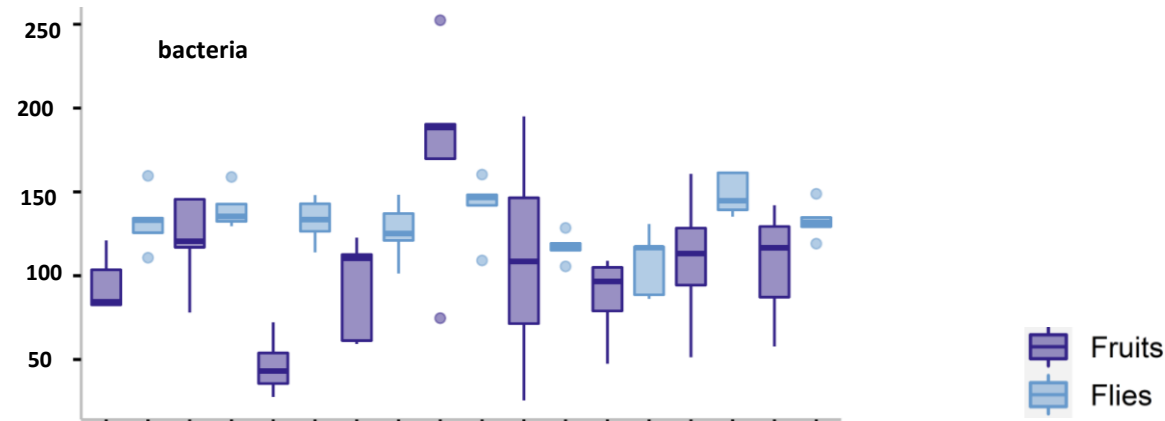
Weighted UniFrac metric



Example of the community pattern of wild fly-fruit samples following pairing of both reads
Blue: fruits, Red: wild flies
Description: Reads were paired following truncation at 230 bp with rest of the parameters as default in QIIME platform.

S1a

Phylogenetic diversity



S1b

Shannon diversity

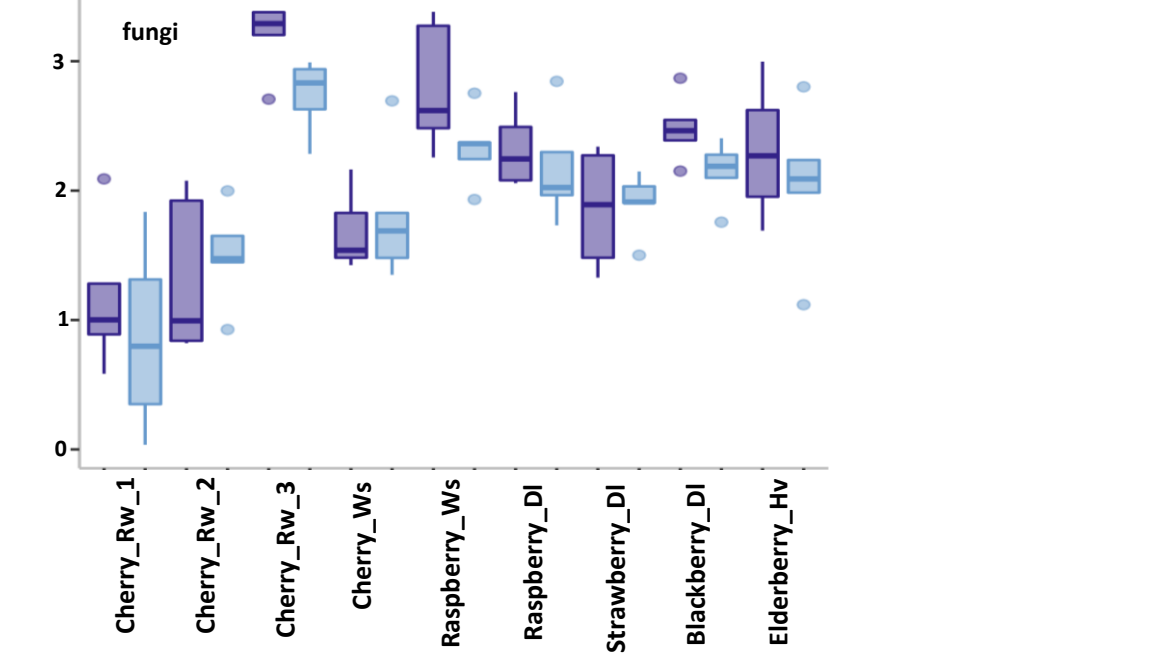


Figure S1a & S1b: Phylogenetic diversity of bacterial communities in fruit and wild fly samples (p-value<0.05) & Shannon diversity of fungal communities in fruit and wild fly samples (p-value <0.001)

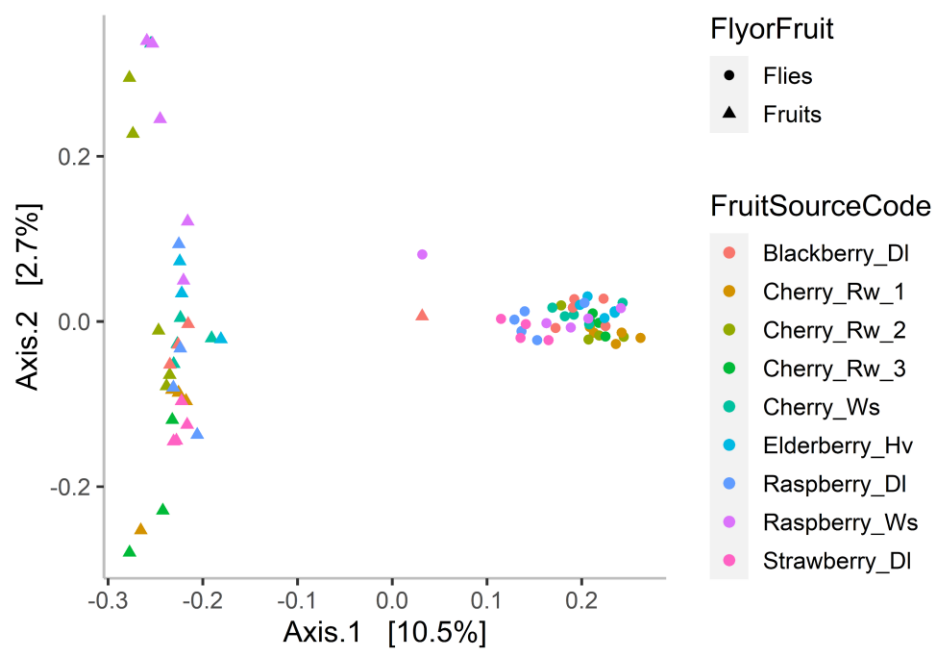


Figure S2: Unweighted UniFrac metrics of bacterial communities in fruits and wild flies (p-values=0.001)

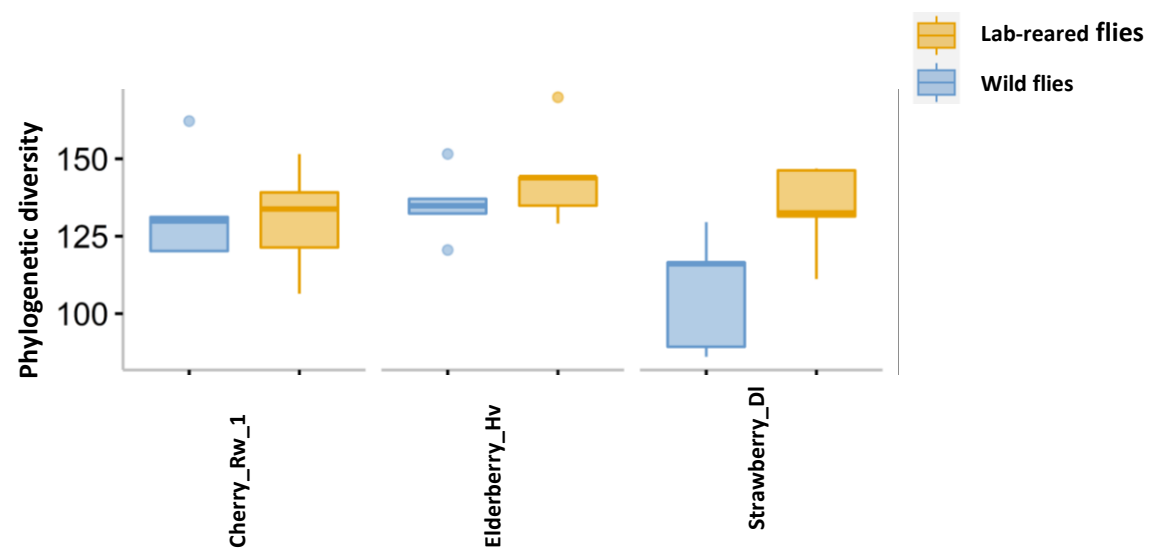


Figure S3: Faith's phylogenetic diversity of bacterial communities in lab-reared and wild flies (p-values=0.1)

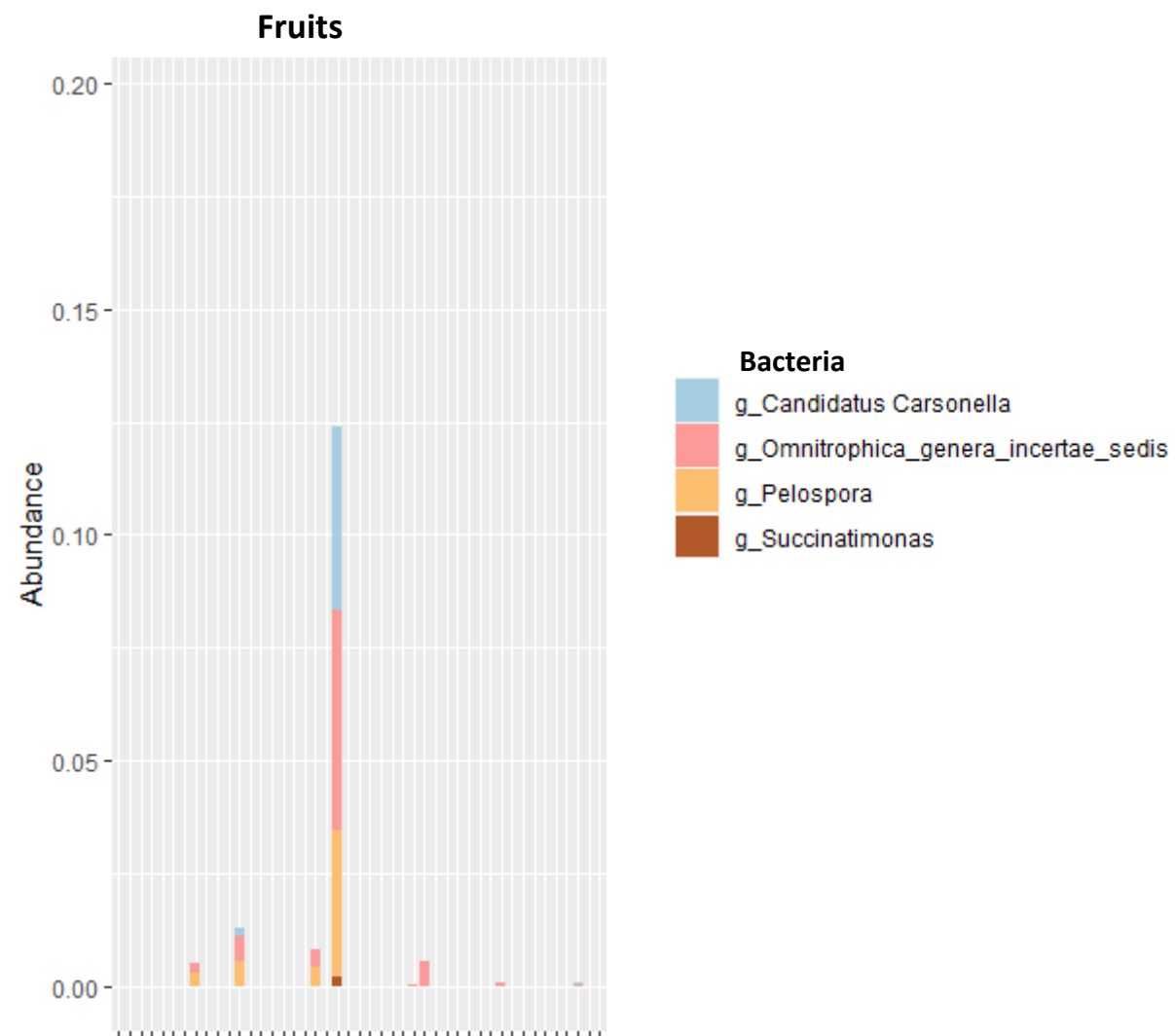


Figure S4: Core bacteria as observed in the fruit samples

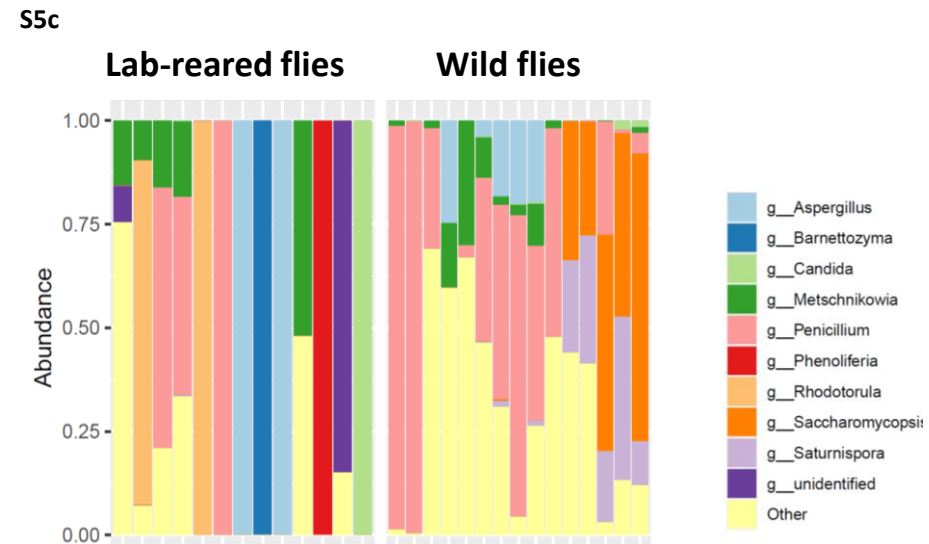
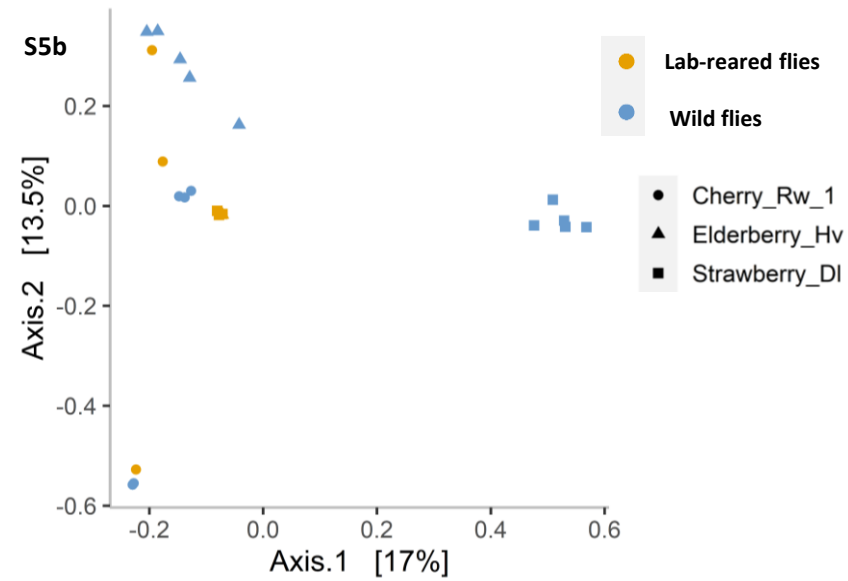
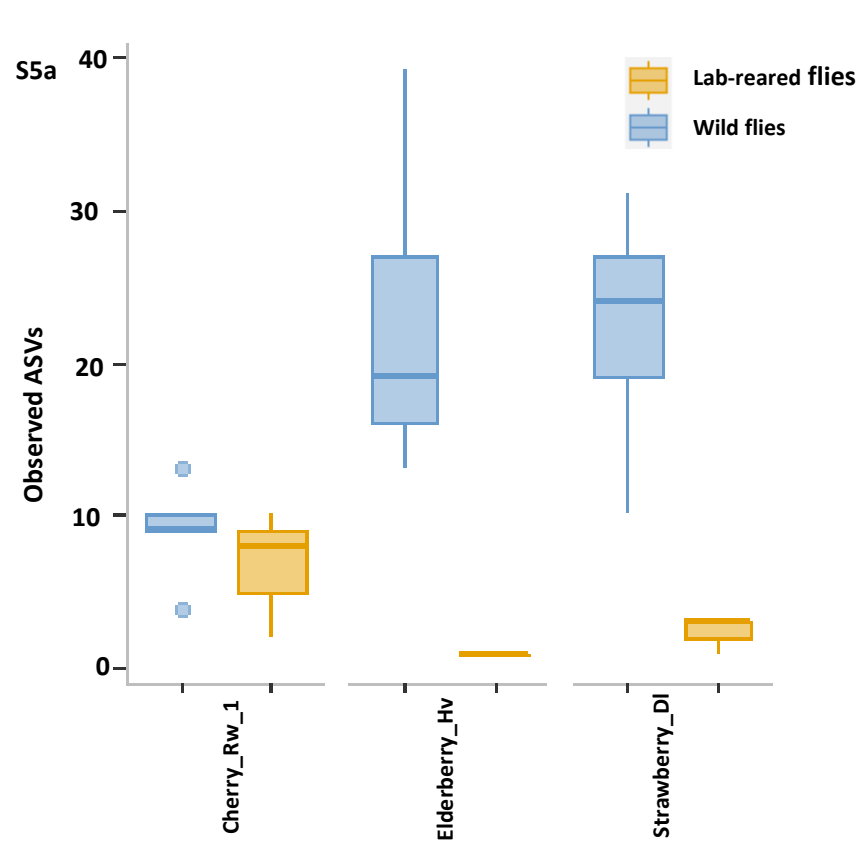


Figure S5: Fungal communities in lab-reared as well as the wild flies. Observed ASVs in lab-reared and wild flies ($\chi^2=11.19$, p -value<0.001; S5a). Bray Curtis plot shows beta diversity (non-significant) of the fungal communities across lab-reared and wild flies (PERMANOVA, p -value=0.06; S5b). Top 10 abundant fungi as noted across the lab-reared and wild flies (S5c).