

Supplementary Material for

Microbiome structure influences infection by the parasite *Crithidia bombi* in bumble bees

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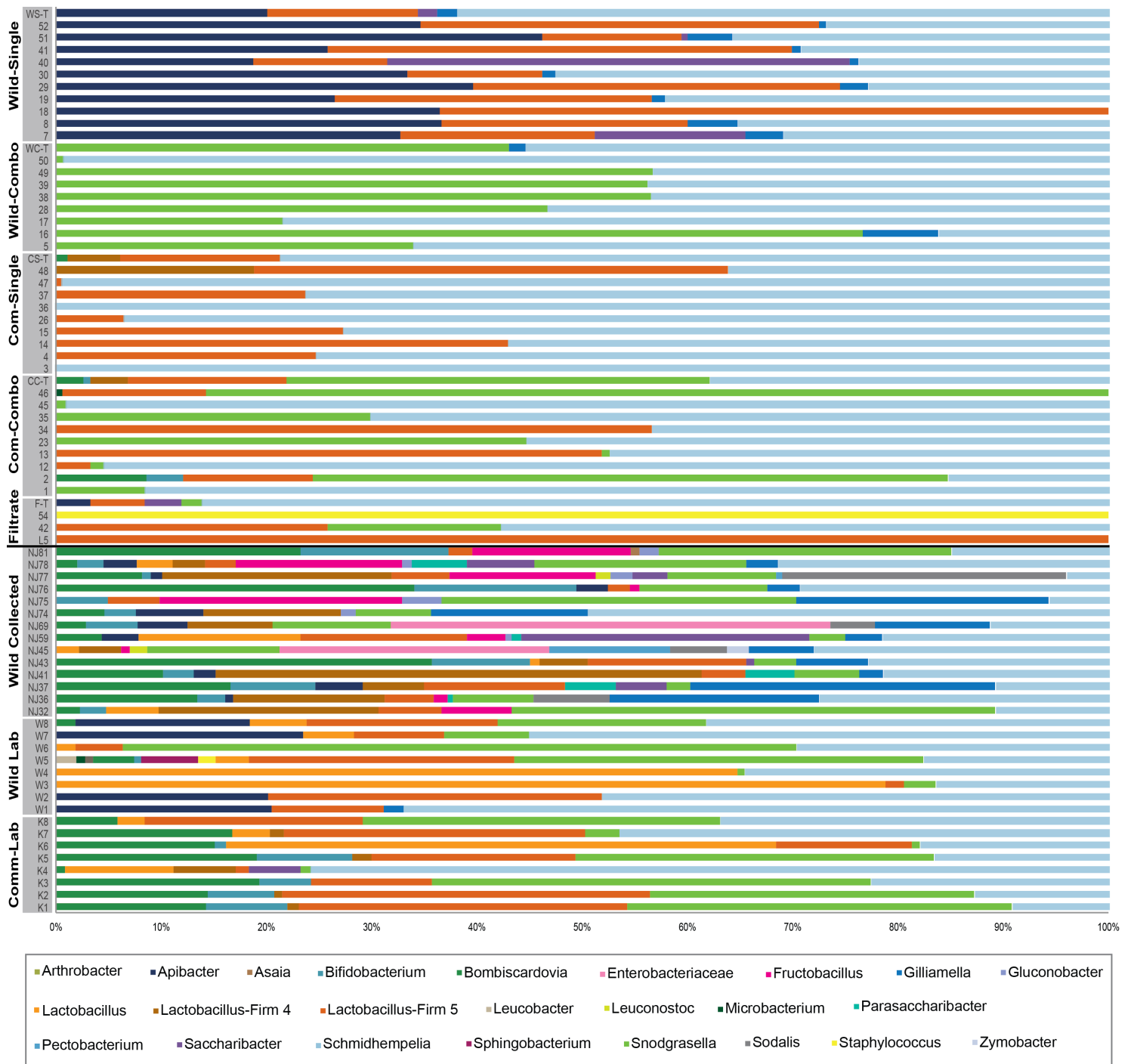


Figure S1. Microbiome composition of all samples, including that of the microbiota treatment inoculums (Wild-Single, Wild-Combo, Commercial-Single, Commercial-Combo, Filtrate), and samples from wild-collected bees and lab-raised bees from wild and commercial (Koppert) sources.

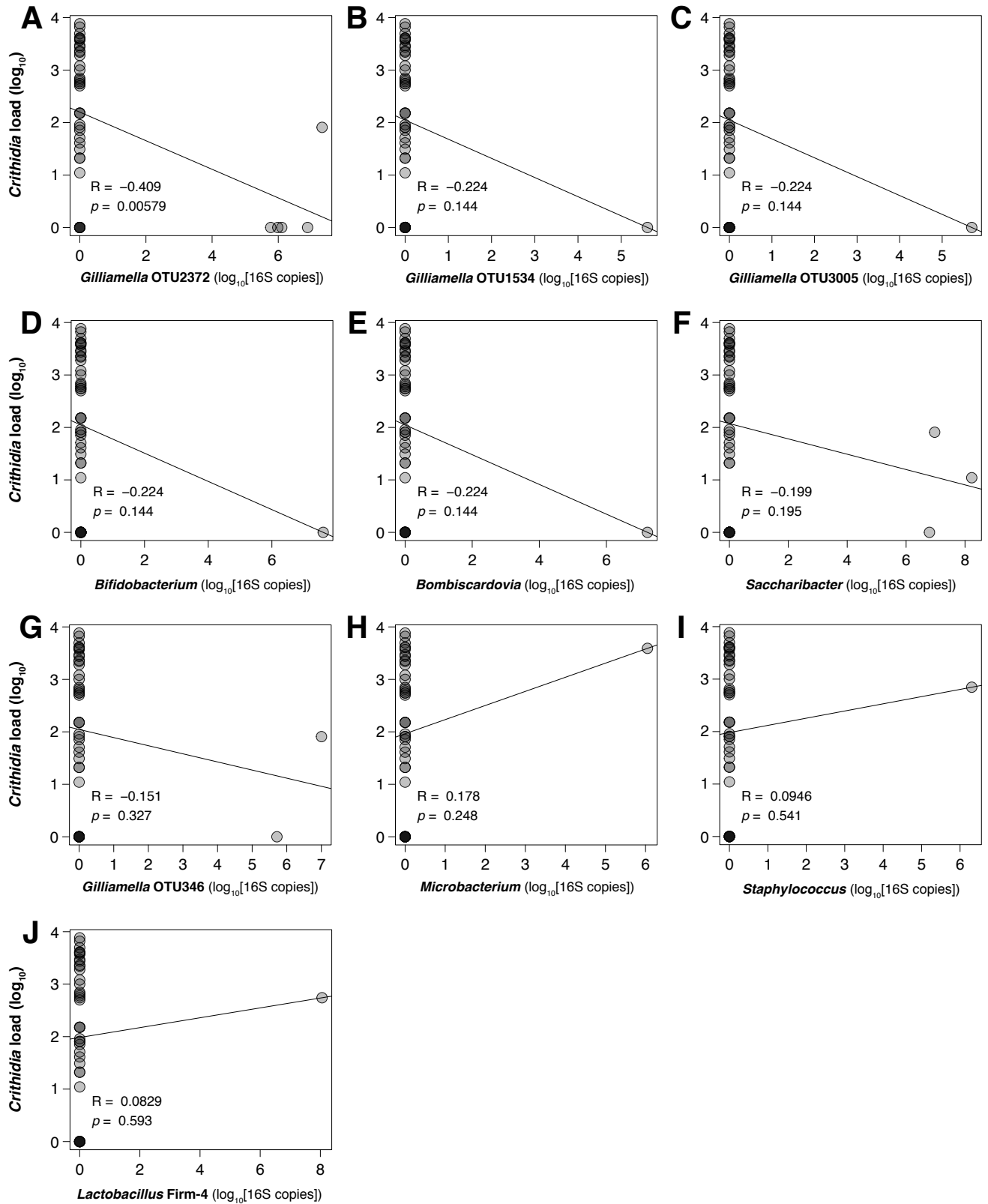


Figure S2. Additional correlations between *C. bombi* infection load and microbial phylotypes. Pearson correlation statistics shown. *C. bombi* load expressed as number of cells per 10 μ L.

Table S1. Correlations between *Crithidia* load and microbiome metrics within the experimental treatment groups.

<i>Crithidia</i> load correlation	Pearson		Spearman	
	R	p-value	R	p-value
OTUs at 97% identity	-0.553	0.0000999	-0.567	0.0000608
Shannon's H	-0.552	0.000103	-0.561	0.0000740
Bacterial load	-0.451	0.00114	-0.473	0.000596
<i>Apibacter</i>	-0.617	0.00000824	-0.578	0.0000405
<i>Lactobacillus</i> Firm-5	-0.549	0.000114	-0.529	0.000226
<i>Gilliamella</i> OTU3348	-0.322	0.0328	-0.365	0.0149
<i>Snodgrassella</i>	0.197	0.199	0.168	0.277
<u>without wild-single treatment</u>				
OTUs at 97% identity	-0.425	0.0123	-0.329	0.0577
Shannon's H	-0.274	0.117	-0.296	0.0887
Bacterial load	-0.279	0.853	-0.324	0.0444
<i>Apibacter</i>	-	-	-	-
<i>Lactobacillus</i> Firm-5	-0.304	0.0807	-0.286	0.101
<i>Gilliamella</i> OTU3348	-0.320	0.0652	-0.349	0.0428
<i>Snodgrassella</i>	-0.0867	0.626	-0.0925	0.603