

Table S1. Number of 16S rRNA operons per genome for each of the bacteria detected in this study.

Taxon	Reference	16S rRNA gene copy number*
<i>Gilliamella</i>	<i>Gilliamella apicola</i> wkB1	4
<i>Snodgrassella</i>	<i>Snodgrassella alvi</i> wkB2	4
<i>Lactobacillus</i> Firm-5	<i>Lactobacillus</i> sp. wkB8	4
<i>Bifidobacterium</i>	<i>Bifidobacterium asteroides</i> PRL2011	2
<i>Lactobacillus</i> Firm-4	<i>Lactobacillus</i> (genus)	4
<i>Frischella</i>	<i>Frischella perrara</i> PEB0191	4
<i>Bartonella</i>	<i>Bartonella</i> (genus)	2
Alpha 2.1	<i>Acetobacteraceae</i> (family)	4
<i>Fructobacillus</i>	<i>Leuconostocaceae</i> (family)	4
<i>Serratia</i>	<i>Serratia</i> (genus)	7
<i>Erwinia</i>	<i>Erwinia</i> (genus)	7
<i>Klebsiella</i>	<i>Klebsiella</i> (genus)	8
<i>Melissococcus</i>	<i>Melissococcus</i> (genus)	4
<i>Zymobacter</i>	<i>Zymobacter</i> (genus)	1
<i>Lactobacillus kunkeei</i>	<i>Lactobacillus</i> (genus)	4
<i>Gluconobacter</i>	<i>Gluconobacter</i> (genus)	4

*Operon number was determined using the reference genome for a given bee gut bacterial species when available. For numbers in bold, a complete genome was not available for the species, so the mean 16S rRNA operon copy for the bacterial genus or family was obtained from the rrnDB (<https://rrndb.umms.med.umich.edu/>) and used as an estimate of operon number.