

Table S1. Primers used in this study.

Honey bee			Annealing temperature (°C)	Reaction efficiency (logarithmic dilution)	Study
Gene	Forward 5'-3'	Reverse 5'-3'			
<i>actin</i>	TGCCAACACTGTCCTTTCTG	AGAATTGACCCACCAATCCA	55.0	1.01	[1]
<i>npf</i>	GAACTTTTGGGTGAGCACGAA	ACGTGACAAGGTCGAGTATCGA	60.0	0.94	[2]
<i>snpfR</i>	AATTGCGCATTGAGCGATGTT	CCGAGGAACGTGTACAATGGT	60.0	0.92	[2]
<i>AstA</i>	GTCTCCGAGTATAAGAGGCTACC	TGTATTGTCTTCGTTTACCAAGCC	55.0	0.98	[3]
<i>AstC</i>	CCTGTTACAGAAACAAATCG	TATTTGCCAAAGCAAGAGA	55.0	1.04	[3]
<i>AstCC</i>	GAGCAACAAACGHTAAAGATGG	TTCTCTTGAAACACGTCACAG	55.0	0.89	[3]
<i>AstAR</i>	CGACGATAATGGTGC	CTAAATGATGTCACCGG	55.0	1.13	[3]
<i>AstCR</i>	CGAGTTTTAGGACRAGGAC	TCTGCTCCTTCGGCTCCATTG	55.0	0.90	[3]
Microbiota			Annealing temperature (°C)		Study
Gene	Forward 5'-3'	Reverse 5'-3'			
<i>Lactobacillus Firm 5 16S rRNA</i>	GCAACCTGCCCTWTAGCTTG	GCCCATCCTKTAGTGACAGC	60.0	0.98	[4]
<i>Lactobacillus Firm 4 16S rRNA</i>	AGTCGAGCGCGGGAAGTCA	AGCCGTCTTTCAACCAGCACT	60.0	0.97	[4]
<i>Bifidobacterium 16S rRNA</i>	ATGCAAGTCGAACGGGATCC	CATCCCATRCCGGTAAACCC	60.0	0.99	[4]
<i>Gilliamella 16S rRNA</i>	CTTTGTTGCCATCGGTTAGGCC	CCGCTTGCTCTCGCGAGG	60.0	0.89	[5]

<i>Snodgrassella</i> 16S rRNA	CTTAGAGATAGGAGAGTGCCTT	AACTTAATGATGGCAACTAATGACAA	60.0	1.08	[4]
<i>Lactobacillus</i> <i>Firm 5 ackA</i>	GGTGTTCCTGAAGTAGGCGT	GAGCAGCGCGTCCTACAATA	62.0	0.95	[6]
<i>Bifidobacterium ackA</i>	GGCGAAAACCGTCCTAGTCA	CGGTCTCATGGTCGTGGATG	62.0	1.18	[6]
<i>Gilliamella ackA</i>	GCGCCATAACGACGAATACC	TCGTGAAGCTTTTGCCGAGT	62.0	0.87	[6]
<i>Lactobacillus</i> <i>Firm 5 ldh</i>	GTTGTTGTGATCACCGCTGG	AGGGAAGTACCTGTCCCAAT	62.0	0.90	[6]
<i>Bifidobacterium ldh</i>	AAGGGGTCAACACCCACATC	TTGCTTGCCGTCTCCTTGAG	62.0	1.21	[6]
<i>Gilliamella ldh</i>	TAGCTTGCGCGAATCAACTG	CAATCACACGGTGACGAGGT	62.0	0.93	[6]
<i>Lactobacillus Firm 4</i> <i>hbd</i>	ATCGATGTGACCGTGGCTTT	CATCAACGGCCTGAGGAGAA	60.0	0.88	This study
<i>Bifidobacterium</i> <i>hbd</i>	TCGATGCTGGGCTGAACAAT	TTGCTGGCGAAGATGGTCTT	60.0	0.91	This study

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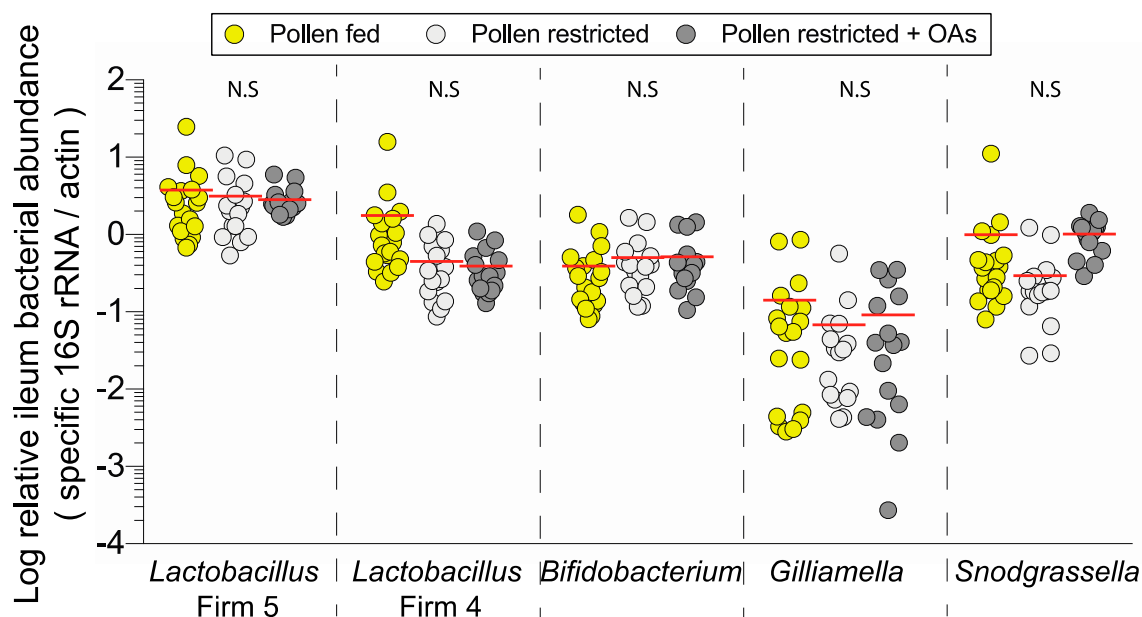


Figure S1. Relative ileum species-specific 16S rRNA abundance in honey bees subjected to different diet treatments. Each point represents a pooled sample from an independent cage ($n = 16$ – 19 cages). Black horizontal lines indicate the mean. No significant differences were detected.

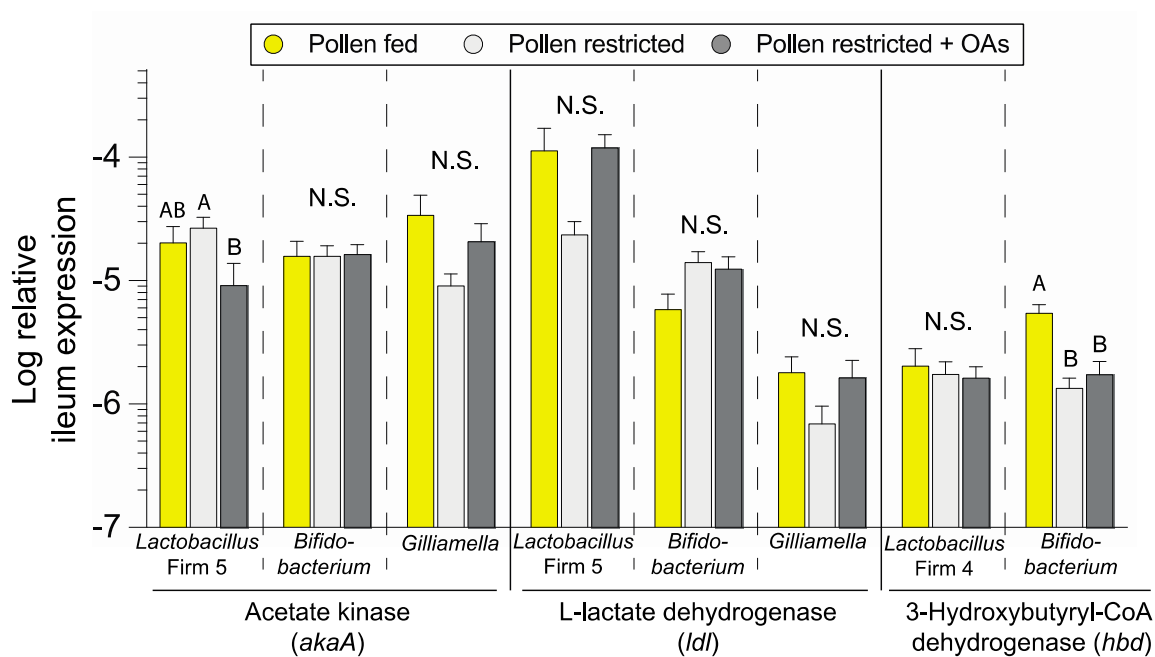


Figure S2. Expression of bacterial fermentative enzyme gene transcripts in the ileum of honey bees subjected to different feeding treatments ($n = 16$ – 19 cages). Error bars represent standard error (SE). Different letters indicate Tukey HSD $P < 0.05$.

