S1 Table. Primers used in the study

Targeted group	Primer pairs and sequences (5'→3')	Reference
Primers amplifying SSU fragments for QPCR analyses		
Bacteria	341F CCTACGGGAGGCAGCAG 534R ATTACCGCGGCTGCTGGCA	Bru D, Martin-Laurent F, Philippot L. Quantification of the detrimental effect of a single primer-template mismatch by real-time PCR using the 16S rRNA gene as an example. Appl Environ Microbiol. 2008;74: 1660-1663
Bacteria	BAC338F ACTCCTACGGGAGGCAG BAC805R GACTACCAGGGTATCTAATCC	Yu Y, Lee C, Kim J, Hwang S. Group-specific primer and probe sets to detect methanogenic communities using quantitative real-time polymerase chain reaction. Biotechnol Bioeng. 2005;89: 670-679
Bifidobacterium spp.	Bifi-F2 TCGCGTCYGGTGTGAAAG Bifi-R2 CCACATCCAGCRTCCAC	Rinttilä T, Kassinen A, Malinen E, Krogius L, Palva A. Development of an extensive set of 16S rDNA-targeted primers for quantification of pathogenic and indigenous bacteria in faecal samples by real-time PCR. J Appl Microbiol. 2004;97: 1166-1177
Lactobacillus Firm-5	Lact-F TAACGCATTAAGCACTCC Lact-R GCTGGCAACTAATAATAAGG	Li J, Qin H, Wu J, Sadd BM, Wang X, Evans JD, Peng W, Chen Y. The prevalence of parasites and pathogens in Asian honeybees *Apis cerana* in China. PLoS One. 2012;7: e47955
Lactobacillus spp.	Lact-F2 AGCAGTAGGGAATCTTCCA Lact-R2 CACCGCTACACATGGAG	Rinttilä T, Kassinen A, Malinen E, Krogius L, Palva A. Development of an extensive set of 16S rDNA-targeted primers for quantification of pathogenic and indigenous bacteria in faecal samples by real-time PCR. J Appl Microbiol. 2004;97: 1166-1177
α-proteobacteria	a682F CDAGTGTAGAGGTGAAATT 908aR CCCCGTCAATTCCTTTGAGTT	Bacchetti de Gregoris T, Aldred N, Clare AS, Burgess JG. Improvement of phylum- and class-specific primers for real-time PCR quantification of bacterial taxa. J Microbiol Methods. 2011;86: 351-356
Snodgrassella alvi	Neiss-F AAGCGGTGGATGATGTGG Neiss-R TGATGGCAACTAATGACAAGG	Li J, Qin H, Wu J, Sadd BM, Wang X, Evans JD, Peng W, Chen Y. The prevalence of parasites and pathogens in Asian honeybees *Apis cerana* in China. PLoS One. 2012;7: e47955
Snodgrassella alvi	Beta-1009-qtF CTTAGAGATAGGAGAGTG Beta-1115-qtR AATGATGGCAACTAATGACAA	Martinson VG, Moy J, Moran NA. Establishment of characteristic gut bacteria during development of the honeybee worker. Appl Environ Microbiol. 2012;78: 2830-2840
Gilliamella apicola	G1-459-qtF GTATCTAATAGGTGCATCAATT G1-648-qtR TCCTCTACAATACTCTAGTT	Martinson VG, Moy J, Moran NA. Establishment of characteristic gut bacteria during development of the honeybee worker. Appl Environ Microbiol. 2012;78: 2830-2840
Gilliamella apicola	Gill-F CCTTTGTTGCCATCGATTAGG Gill-R GACATTCTGATTCACGATTACTAGC	Xu LL, Wu J, Guo J, Li JL. Dynamic variation of symbionts in Bumblebees during hosts growth and development. *Sci. Agric. Sinica*. 2014;47: 2030–2037
Primers amplifying the SSU for sequencing		
Bacteria	27f-YM AGAGTTTGATYMTGGCTCAG 27f-Bif AGGGTTCGATTCTGGCTCAG 1492r TACCTTGTTAYGACTT	Frank JA, Reich CI, Sharma S, Weisbaum JS, Wilson BA, Olsen GJ. Critical evaluation of two primers commonly used for amplification of bacterial 16S rRNA genes. Appl Environ Microbiol. 2008;74: 2461-2470