Manuscript title: Microbial diversity associated with the pollen stores of captive-bred bumble bee colonies

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Table 1. Unique OTUs, taxonomy, and sequence read number. Each row is a unique OTU, and each column is a pollen provision library.

| OTU   | Taxonomy                                                                 | A1 | A2 | A3 | A4 | A5 | A6 |
|-------|--------------------------------------------------------------------------|----|----|----|----|----|----|
| Otu0001 | Candida magnoliae; Candida magnoliae | 2140 | 2921 | 167 | 23948 | 41070 | 17571 | 68106 |
| Otu0002 | Candida magnoliae; Candida magnoliae | 13 | 2 | 0 | 2295 | 1097 | 647 | 11569 |
| Otu0003 | Candida magnoliae; Candida magnoliae | 391 | 798 | 27 | 6399 | 3012 | 2468 | 2500 |
| Otu0005 | Ascosphaera apis; Ascosphaera apis | 291 | 184 | 899 | 12 | 4 | 9 | 293 |
| Otu0008 | Zygosaccharomyces; Zygosaccharomyces | 16 | 16 | 2 | 32 | 30 | 572 | 120 |
| Otu0010 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 71 | 274 | 121 | 14 |
| Otu0014 | Aspergillus terreus; Aspergillus terreus | 123 | 0 | 0 | 0 | 0 | 0 | 0 |
| Otu0017 | Zygosaccharomyces rouxii; Zygosaccharomyces rouxii | 0 | 0 | 0 | 0 | 0 | 7 | 29 |
| Otu0021 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 4 | 7 | 3 | 12 |
| Otu0022 | Chaetomium strumarium; Chaetomium strumarium | 26 | 0 | 0 | 0 | 0 | 0 | 0 |
| Otu0025 | Kodamaea ohmeri; Kodamaea ohmeri | 13 | 8 | 0 | 0 | 0 | 0 | 0 |
| Otu0027 | Candida magnoliae; Candida magnoliae | 2 | 14 | 0 | 0 | 1 | 0 | 0 |
| Otu0028 | Aspergillus terreus; Aspergillus terreus | 0 | 0 | 0 | 0 | 0 | 0 | 14 |
| Otu0033 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 2 | 1 | 0 | 8 |
| Otu0048 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 5 | 0 | 0 | 0 |
| Otu0050 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 1 | 3 | 0 | 0 |
| Otu0052 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| Otu0053 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| Otu0056 | Fusarium brachygibbosum; Fusarium brachygibbosum | 2 | 0 | 1 | 0 | 0 | 0 | 0 |
| Otu0057 | Dioszegia sp; Dioszegia sp | 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| Otu0060 | Candida magnoliae; Candida magnoliae | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| Otu0064 | Candida magnoliae; Candida magnoliae | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Otu0067 | Candida magnoliae; Candida magnoliae | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| Otu0068 | Ascosphaera apis; Ascosphaera apis | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Otu0070 | Trichosphaeriales; Trichosphaeriales | 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| Otu0072 | Dothioraceae; Dothioraceae | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Otu0068 | Candida magnoliae; Candida magnoliae | 0 | 2 | 0 | 0 | 0 | 0 | 0 |

**Insects** 2020, 11, 250; doi:10.3390/insects11040250

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Bacterial_OTU_0.03.

Insects 2020, 11, 250; doi:10.3390/insects11040250   www.mdpi.com/journal/insects
| OTU ID | Phylum        | Class               | Order               | Family              | Genus                | Count | Percentage | Abundance | Count | Percentage | Abundance |
|-------|---------------|---------------------|---------------------|---------------------|----------------------|-------|------------|-----------|-------|------------|-----------|
| OTU0074 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcales_unclassified | 3 0 0 0 62 0 0     |
| OTU0076 | Bacteria      | Actinobacteria      | Micrococcales       | Microbacteriaceae    | Agromyces            | 0 0 0 0 60 0 0     |
| OTU0078 | Bacteria      | Proteobacteria      | Gammaproteobacteria | Orbaceae             | Gilliamella          | 0 2 0 6 12 26 19   |
| OTU0080 | Bacteria      | Firmicutes          | Bacilli             | Paenibacillaceae     | Paenibacillus        | 0 0 0 2 12 27 0     |
| OTU0081 | Bacteria      | Firmicutes          | Clostridia          | Peptostreptococcaceae | Peptoclostridium     | 0 0 0 2 12 31 0     |
| OTU0082 | Bacteria      | Firmicutes          | Bacilli             | Paenibacillaceae     | Paenibacillus        | 0 0 0 22 0 20 0     |
| OTU0083 | Bacteria      | Proteobacteria      | Alphaproteobacteria | Rhizobiales          | Hyphomicrobiaceae    | 0 0 0 0 26 0 0     |
| OTU0085 | Bacteria      | Proteobacteria      | Alphaproteobacteria | Caulobacterales       | Caulobacteraceae     | 0 5 0 0 28 0 0     |
| OTU0087 | Bacteria      | Bacteroidetes       | Flavobacteriia      | Flavobacteriales      | Flavobacterium       | 0 0 0 0 27 0 0     |
| OTU0088 | Bacteria      | Firmicutes          | Bacilli             | Bacillales            | Lactobacillus       | 0 0 0 0 21 0 0     |
| OTU0089 | Bacteria      | Proteobacteria      | Alphaproteobacteria | Rhizobiales          | Phenylobacterium     | 0 0 0 0 26 0 0     |
| OTU0100 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 15 0 0 0 0 0 0     |
| OTU0103 | Bacteria      | Actinobacteria      | Micrococcales       | Microbacteriaceae    | Agromyces            | 0 0 0 0 60 0 0     |
| OTU0104 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0105 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0106 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0107 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0109 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0110 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0111 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0112 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0114 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0115 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0116 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0117 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0118 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0120 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0121 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0123 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0124 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0125 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0126 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0127 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0128 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0129 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0130 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0131 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0132 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0133 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0134 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0135 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0136 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |
| OTU0137 | Bacteria      | Actinobacteria      | Micrococcales       | Micrococcaceae       | Actinoplanes         | 0 0 0 0 60 0 0     |

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| OTU   | Class            | Order       | Family                   | Genus               | Species                | Relative Abundance |
|-------|------------------|-------------|--------------------------|---------------------|------------------------|-------------------|
| Otu0150 | Bacteria         | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | Sphingomonas            | 0.00              |
| Otu0151 | Bacteria         | Actinobacteria | Propionibacteria | Nocardioidaceae | Nocardioides           | 0.00              |
| Otu0153 | Bacteria         | Actinobacteria | Streptosporangiales | Nocardiopsaceae | Nocardiopsis           | 0.00              |
| Otu0154 | Bacteria         | Chloroflexi   | Thermomicrobia | JG30-KF-CM45_fa | JG30-KF-CM45_ge       | 0.00              |
| Otu0155 | Bacteria         | Firmicutes    | Bacillales              | Planococcaceae | Planomicrobium         | 0.00              |
| Otu0156 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Geminicoccus | Geminicoccus          | 0.00              |
| Otu0157 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0158 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Rhodospirillales_Incertae_Sedis | Geminicoccus | 0.00              |
| Otu0159 | Bacteria         | Actinobacteria | Micrococcales | Microbacteriaceae | Agromyces              | 0.00              |
| Otu0160 | Bacteria         | Actinobacteria | Micrococcales | Micrococcaceae | 0.00                  |
| Otu0161 | Bacteria         | Actinobacteria | Micrococcales | Micrococcaceae | Rathsayibacter        | 0.00              |
| Otu0162 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0163 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Rhodospirillales | 0.00                  |
| Otu0164 | Bacteria         | Alphaproteobacteria | Micrococcales | Micrococcaceae | 0.00                  |
| Otu0165 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0166 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | 0.00                  |
| Otu0167 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | 0.00                  |
| Otu0168 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0169 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | 0.00                  |
| Otu0170 | Bacteria         | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | 0.00                  |
| Otu0171 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0172 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0173 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0174 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0175 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0176 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0177 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0178 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0179 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0180 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0181 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0182 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0183 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0184 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0185 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0186 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0187 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0188 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0189 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0190 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0191 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0192 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0193 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0194 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0195 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0196 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0197 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0198 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0199 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0200 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0201 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0202 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0203 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0204 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0205 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0206 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0207 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0208 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0209 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0210 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0211 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0212 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0213 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0214 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0215 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0216 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0217 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0218 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0219 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0220 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0221 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0222 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |
| Otu0223 | Bacteria         | Cyanobacteria | Chloroplast             | Chloroplast_fa | Chloroplast_ge        | 0.00              |

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| OTU      | Kingdom   | Phylum            | Class               | Order                  | Family               | Genus                | Cells   |
|----------|-----------|-------------------|---------------------|------------------------|----------------------|----------------------|---------|
| OTU0226  | Bacteria   | Chlorobacteria     | Chlorobacteriales    | Chororhabdus            | Chororhabdaceae      | Chororhabdus         | 0       |
| OTU0227  | Bacteria   | Firmicutes         | Clostridales        | Clostridaceae           | Clostridium_sensu_stricto_13 | Clostridium         | 3       |
| OTU0228  | Bacteria   | Proteobacteria     | Betaproteobacteria  | Burkholderiales         | Comamonadaceae       | Burkholderia        | 0       |
| OTU0229  | Bacteria   | Actinobacteria     | Micrococcales       | Microbacteriaceae       | Agromyces            | Agromyces           | 0       |
| OTU0230  | Bacteria   | Proteobacteria     | Alphaproteobacteria | Rickettesiales          | Anaplasmataceae      | Wolbachia           | 0       |
| OTU0232  | Bacteria   | Actinobacteria     | Propionibacteriales | Propionibacteriaceae    | Microlunatus         | Microlunatus        | 0       |
| OTU0235  | Bacteria   | Cyanobacteria      | Chloroplast         | Chloroplast_or          | Chloroplast          | Chloroplast         | 3       |
| OTU0236  | Bacteria   | Firmicutes         | Bacilli             | Paenibacillales         | Paenibacillaceae     | Paenibacillus       | 0       |
| OTU0237  | Bacteria   | Proteobacteria     | Alphaproteobacteria | Rhizobiales             | Rhizobiaceae         | Rhizobium           | 0       |
| OTU0239  | Bacteria   | Proteobacteria     | Gammaproteobacteria | Oceanospirillales        | Halomonadaceae       | Zymobacter          | 0       |
| OTU0240  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0242  | Bacteria   | Actinobacteria     | Actinobacteria      | Propionibacteriales     | Nocardioidaceae      | Nocardioides        | 0       |
| OTU0243  | Bacteria   | Actinobacteria     | Thermoleophilia     | Solirubrobacterales     | Solirubrobacteraceae | Solirubrobacter     | 0       |
| OTU0244  | Bacteria   | Actinobacteria     | Micrococcales       | Microbacteriaceae       | Planomicrobium       | Planomicrobium      | 0       |
| OTU0247  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0249  | Bacteria   | Actinobacteria     | Micrococcales       | Microbacteriaceae       | Actinomadura         | Actinomadura        | 2       |
| OTU0251  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0252  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0253  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0254  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0257  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0259  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0261  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0264  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0266  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0269  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0270  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0271  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0272  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0273  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0274  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0277  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0278  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0279  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0280  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0281  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0282  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0283  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0284  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0285  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0286  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0287  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |
| OTU0288  | Bacteria   | Firmicutes         | Bacilli             | Lactobacillales         | Lactobacillaceae     | Lactobacillus       | 0       |

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| Otu   | Bacteria Family                   | Genus                        | Species                  | Strain/Type       | Replicates | Abundance | Species Abundance | OTU Abundance | OTU Proportion |
|-------|-----------------------------------|------------------------------|--------------------------|-------------------|------------|-----------|------------------|--------------|----------------|
| Otu0302 | Bacteria; Verrucomicrobia; Verrucomicrobiaceae; Verrucomicrobiiales |                                |                          |                   |            | 0         | 0                | 0            | 2              | 0              | 0              |
| Otu0303 | Bacteria; Flavobacteria; Flavobacteriaceae; Flavobacteriales |                                |                          |                   |            | 0         | 0                | 0            | 2              | 0              | 0              |
| Otu0304 | Bacteria; Alphaproteobacteria; Alphaproteobacteriales; Alphaproteobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 0              | 0              | 0              |
| Otu0305 | Bacteria; Betaproteobacteria; Betaproteobacteriales; Betaproteobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 0              | 0              | 0              |
| Otu0306 | Bacteria; Gammaproteobacteria; Gammaproteobacteriales; Gammaproteobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 0              | 0              | 0              |
| Otu0307 | Bacteria; Actinobacteria; Actinobacteriales; Actinobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 2              | 0              | 0              |
| Otu0308 | Bacteria; Gammaproteobacteria; Gammaproteobacteriales; Gammaproteobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 0              | 0              | 0              |
| Otu0309 | Bacteria; Actinobacteria; Actinobacteriales; Actinobacteriaceae; Actinobacteriales; Actinobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 0              | 0              | 0              |
| Otu0310 | Bacteria; Firmicutes; Firmicutes |                                |                          |                   |            | 2         | 0                | 0            | 2              | 0              | 0              |
| Otu0311 | Bacteria; Gammaproteobacteria; Gammaproteobacteriales; Gammaproteobacteriaceae |                                |                          |                   |            | 2         | 0                | 0            | 2              | 0              | 0              |
| Otu0312 | Bacteria; Chloroplast; Chloroplast |                                |                          |                   |            | 2         | 0                | 0            | 0              | 0              | 0              |

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**Table S2.** Shannon’s diversity (H’) and Pielou’s evenness (J’) of bacterial and fungal community isolated from Source K (N = 3) and Source B (N = 4)

|       | K1  | K2  | K3  | Mean | SE  | B1  | B2  | B3  | B4  | Mean | SE  | P   |
|-------|-----|-----|-----|------|-----|-----|-----|-----|-----|------|-----|-----|
| Bacterial H’ | 1.49 | 0.49 | 0.75 | 0.91 | 0.3 | 2.53 | 2.38 | 2.64 | 2.58 | 2.53 | 0.06 | 0.01 |
| Bacterial J’ | 0.32 | 0.11 | 0.18 | 0.2  | 0.06 | 0.58 | 0.5  | 0.62 | 0.59 | 0.57 | 0.02 | < 0.01 |
| Fungal H’  | 1.55 | 1.24 | 0.93 | 1.24 | 0.18 | 0.85 | 0.88 | 0.69 | 0.64 | 0.77 | 0.06 | 0.04 |
| Fungal J’  | 0.44 | 0.34 | 0.3  | 0.36 | 0.04 | 0.28 | 0.27 | 0.24 | 0.19 | 0.24 | 0.02 | 0.04 |
Table S3. Distribution of sequencing reads of bacterial and fungal taxa at the family and order rank respectively. Source K $N = 3$; Source B $N = 4$.

| Bacteria community | Source K | Source B |
|---------------------|----------|----------|
|                     | Family   |          |          |
|                     | Mean     | SE       | Mean     | SE       |
| Planococcaceae      | 0.04%    | 0.03     | 4.01%    | 1.03     |
| Lactobacillaceae    | 77.11%   | 19.16    | 10.79%   | 4.42     |
| Enterococcaceae     | 0.00%    | 0.00     | 2.18%    | 1.07     |
| Acetobacteraceae    | 0.03%    | 0.01     | 1.94%    | 1.38     |
| Brucellaceae        | 0.00%    | 0.00     | 3.31%    | 1.08     |
| Comamonadaceae      | 0.05%    | 0.01     | 33.97%   | 3.39     |
| Xanthomonadaceae    | 0.04%    | 0.04     | 9.41%    | 1.93     |
| Pseudomonadaceae    | 0.66%    | 0.59     | 10.28%   | 2.47     |
| Flavobacteriaceae   | 0.01%    | 0.01     | 8.59%    | 3.34     |
| Sphingobacteriaceae | 0.01%    | 0.00     | 9.28%    | 2.69     |
| Streptomycetaceae   | 16.25%   | 16.24    | 0.01%    | 0.01     |
| Bifidobacteriaceae  | 4.72%    | 1.83     | 1.14%    | 0.55     |
| Other bacteria      | 1.08%    | 0.51     | 5.08%    | 0.89     |

| Fungal community | Source K | Source B |
|------------------|----------|----------|
|                  | Order    | Mean     | SE       | Mean     | SE       |
| Saccharomycetales| 56.14%   | 19.74    | 99.80%   | 0.09     |
| Ascosphaerales   | 35.64%   | 21.67    | 0.11%    | 0.08     |
| Eurotiales       | 1.42%    | 1.42     | 0.09%    | 0.04     |
| Sordariales      | 2.95%    | 2.95     | 0.00%    | 0.00     |
| Pleosporales     | 2.57%    | 1.45     | 0.00%    | 0.00     |
| Other fungi      | 1.27%    | 0.44     | 0.00%    | 0.00     |
Table S4. Colony demography and mother queen weights of hives from Source K (N = 3) and Source B (N = 4)

|                                | Source K |          | Source B |          |
|--------------------------------|----------|----------|----------|----------|
|                                | Mean     | SE       | Mean     | SE       |
| Initial number of workers      | 28.00    | 3.06     | 51.50    | 8.61     |
| Final number of workers        | 67.67    | 4.26     | 180.25   | 28.51    |
| Percent change in number of workers | 147.51  | 29.50     | 255.08  | 18.56     |
| Initial weight of mother queen (g) | 0.77     | 0.05     | 0.80    | 0.09     |
| Final weight of mother queen (g) | 0.76     | 0.02     | 0.81    | 0.07     |
| Percent change in weight of mother queen (g) | -1.45    | 5.68     | 2.44    | 3.48     |
Table S5. Top blast hit (Mothur) of genus *Ascosphaera* isolated in this study

| Description         | %ID  | Accession     | E-value   |
|---------------------|------|---------------|-----------|
| *Ascosphaera apis*  | 96%  | GQ867785.1    | 5e-166    |
| *Ascosphaera pollenicola* | 96%  | GQ867791.1    | 9e-163    |
| *Ascosphaera major* | 96%  | GQ867789.1    | 9e-163    |
| *Ascosphaera larvis*| 96%  | JX268535.1    | 9e-163    |
| *Ascosphaera variegata* | 96%  | JX268538.1    | 3e-162    |
| *Ascosphaera aggregata* | 94%  | GQ867784.1    | 3e-162    |
| *Ascosphaera flav* | 96%  | GQ867788.1    | 1e-161    |
| *Ascosphaera proliperda* | 95%  | GQ867792.1    | 4e-162    |
| *Ascosphaera osmophila* | 94%  | GQ867790.1    | 5e-160    |