

## Supplementary information

# Impact of Nesting Mode, Diet, and Taxonomy in Structuring the Associated Microbial Communities of Amazonian Ants

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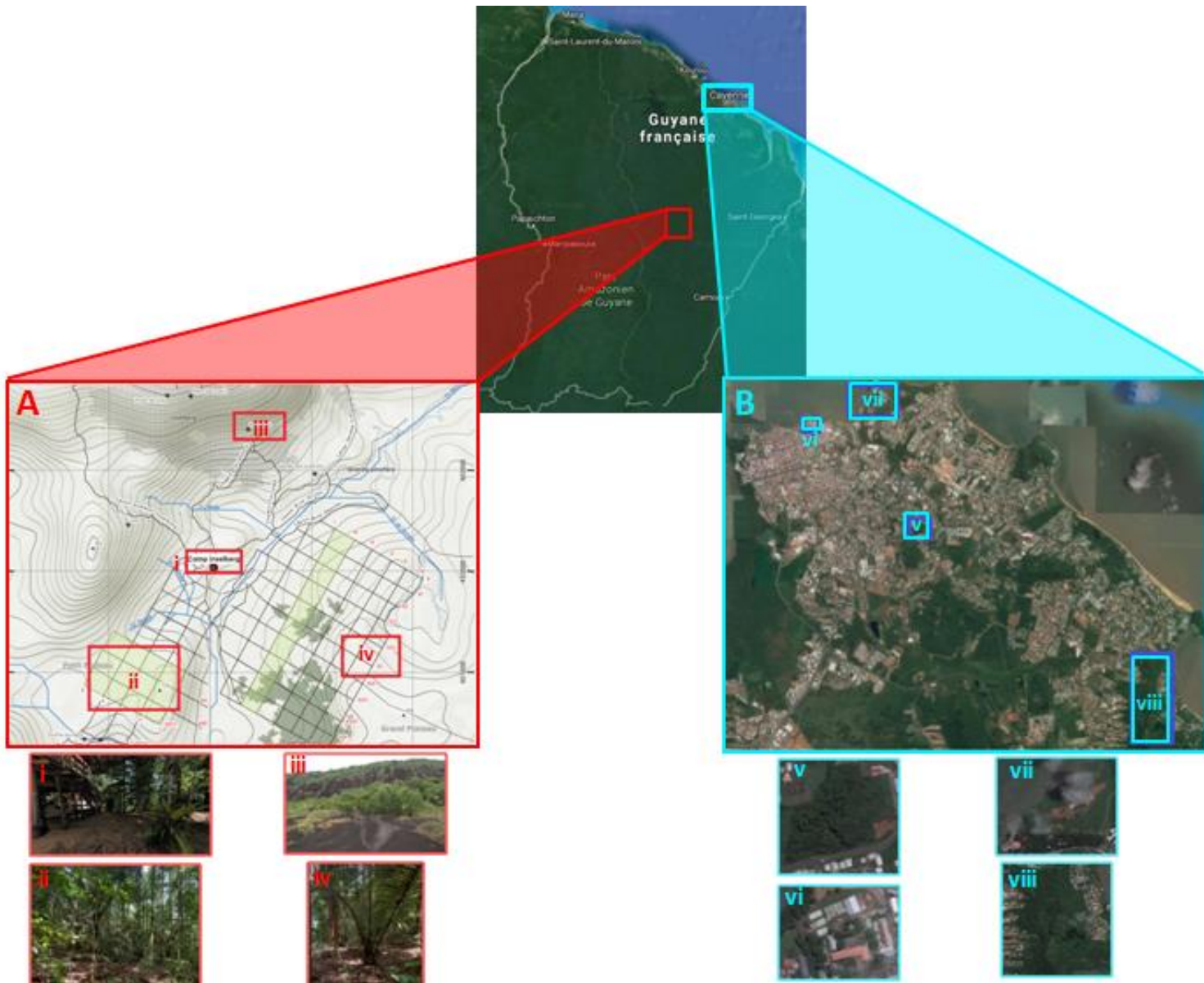
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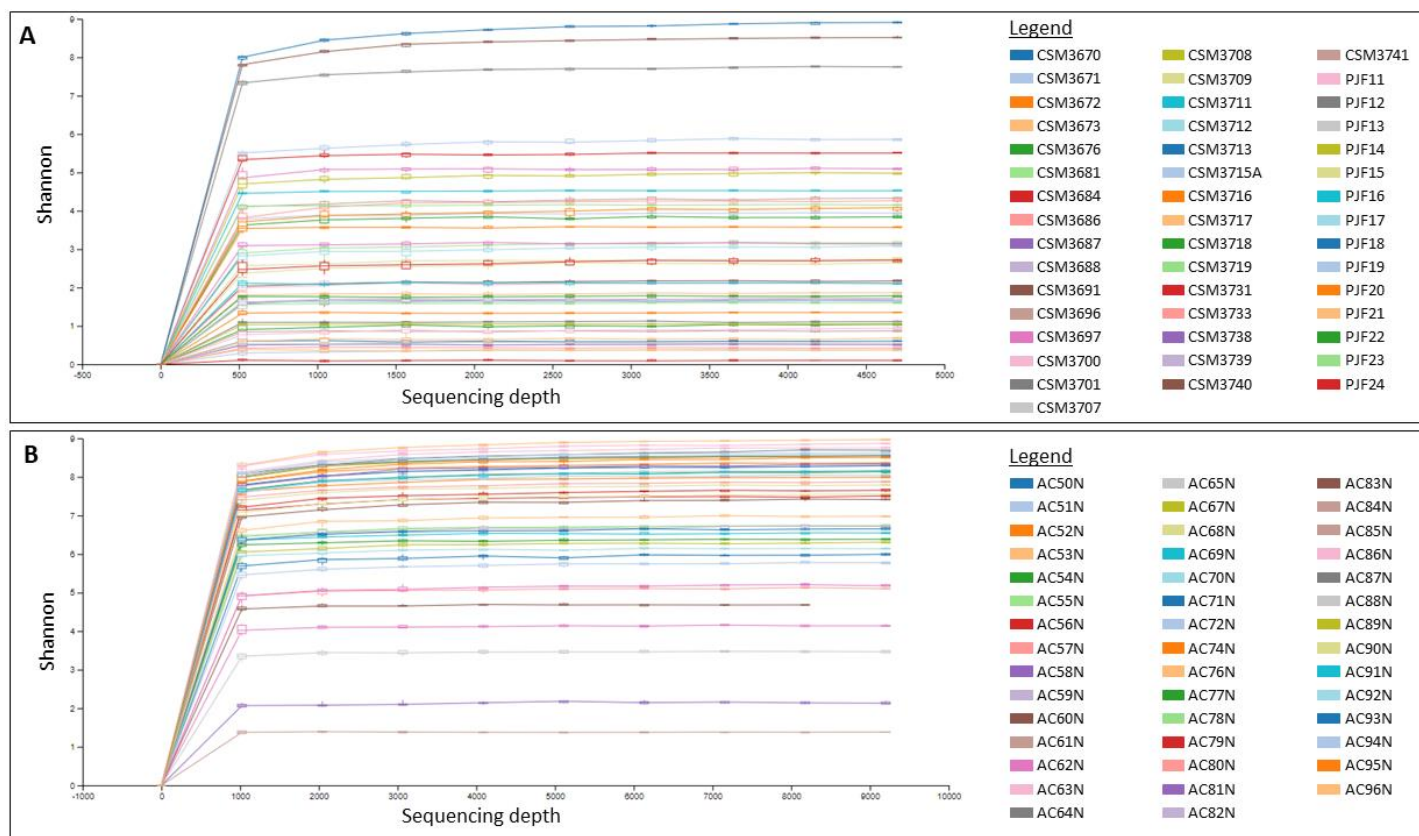
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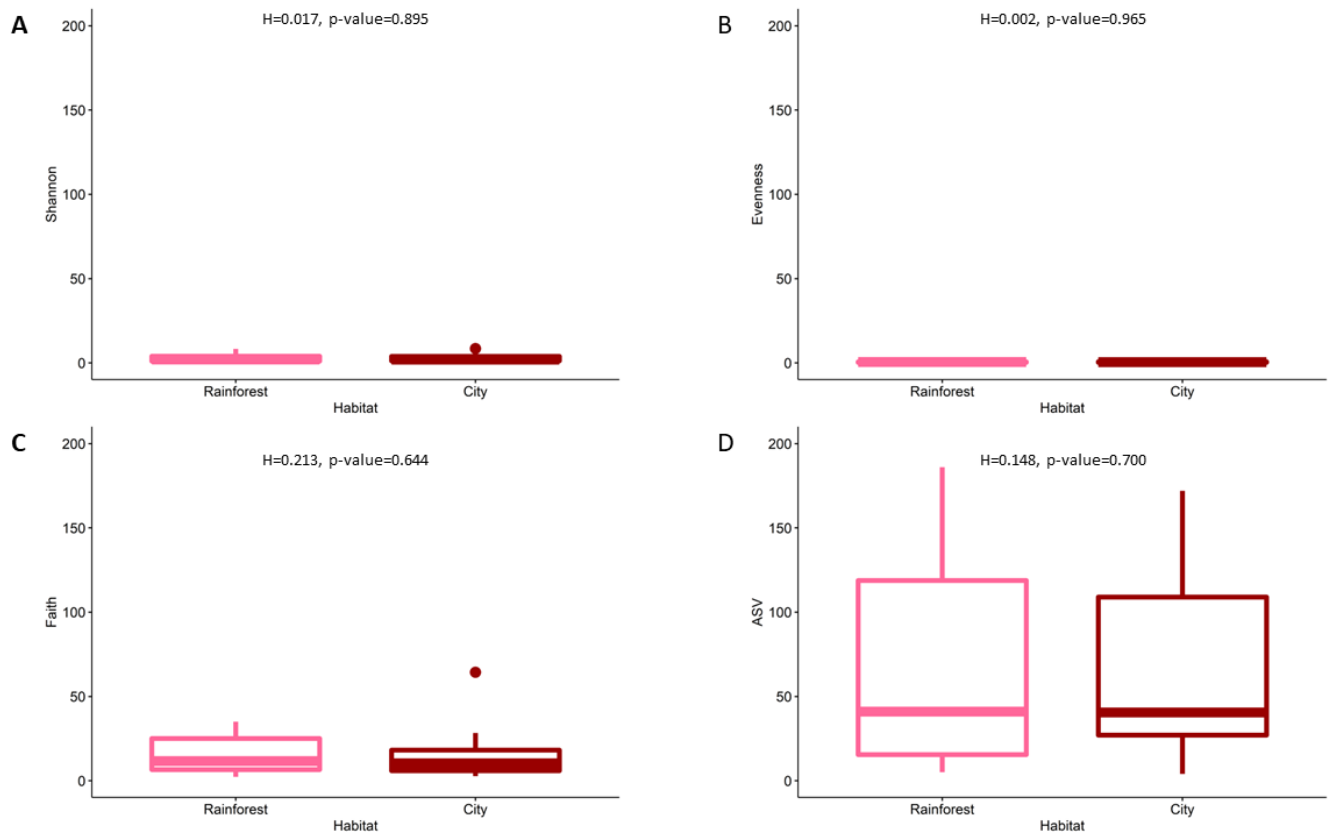


**Figure S1. Sampling Map. (A) Different sampling places in primary forest (Nouragues Field Station)** (i) Inselberg camp, Inselberg little plateau (ii), Inselberg terrace (iii), Inselberg big plateau (iv). (B) Different sampling places in urban area (Cayenne): (v) Baduel hill, (vi) Pasteur Institute, (vii) Montabo trail, (viii) Loyola trail. *(Figure made with the help of Peter Flynn, satellites images are from Google Map).*



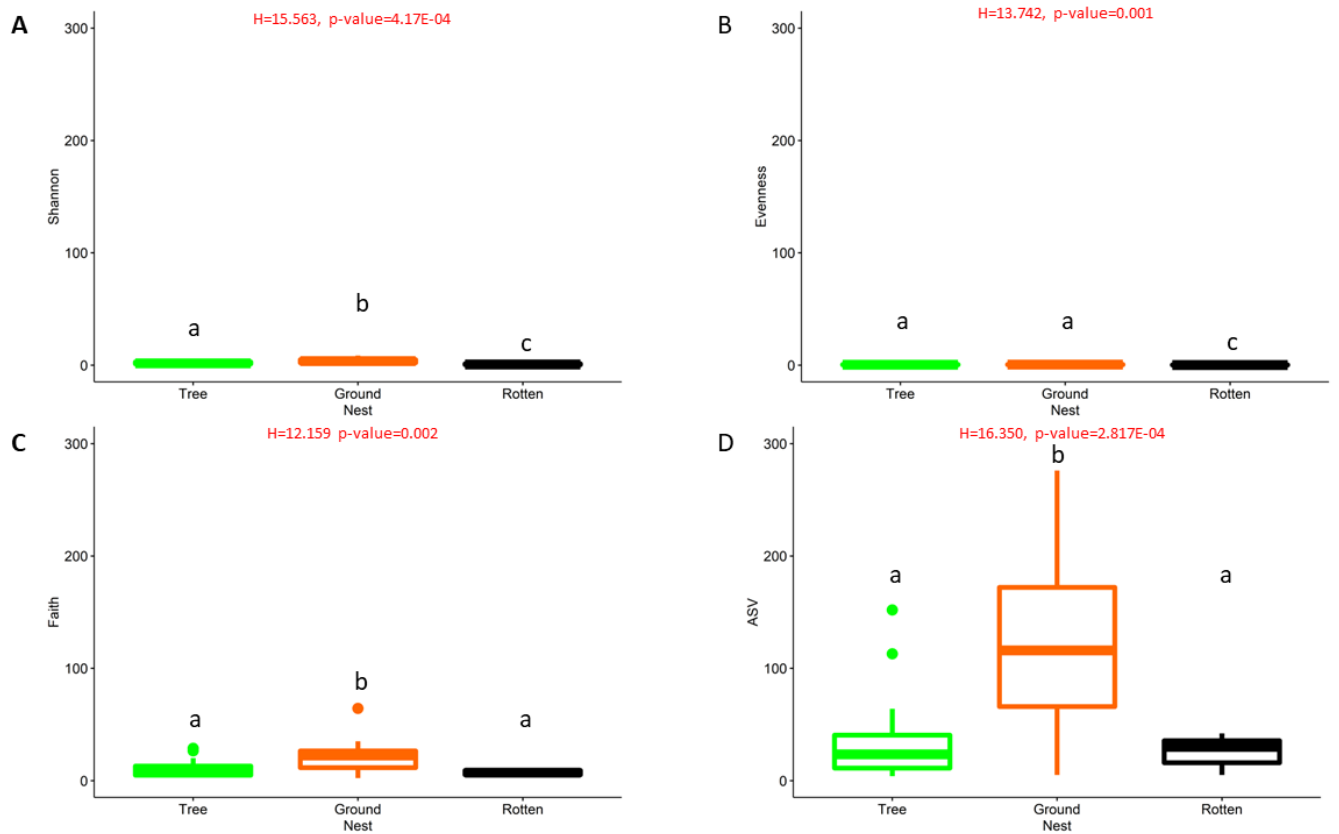
**Figure S2. Rarefaction curves used to estimate bacterial richness with the Shannon index for the ant dataset (A) and the nest dataset (B).**

The vertical axis shows the bacterial ASVs observed and the number of sequences per sample is shown on the horizontal axis. Our sequencing covers thousands of Illumina reads and samples have reached the plateau, indicating that the majority of the bacterial diversity has been recovered.



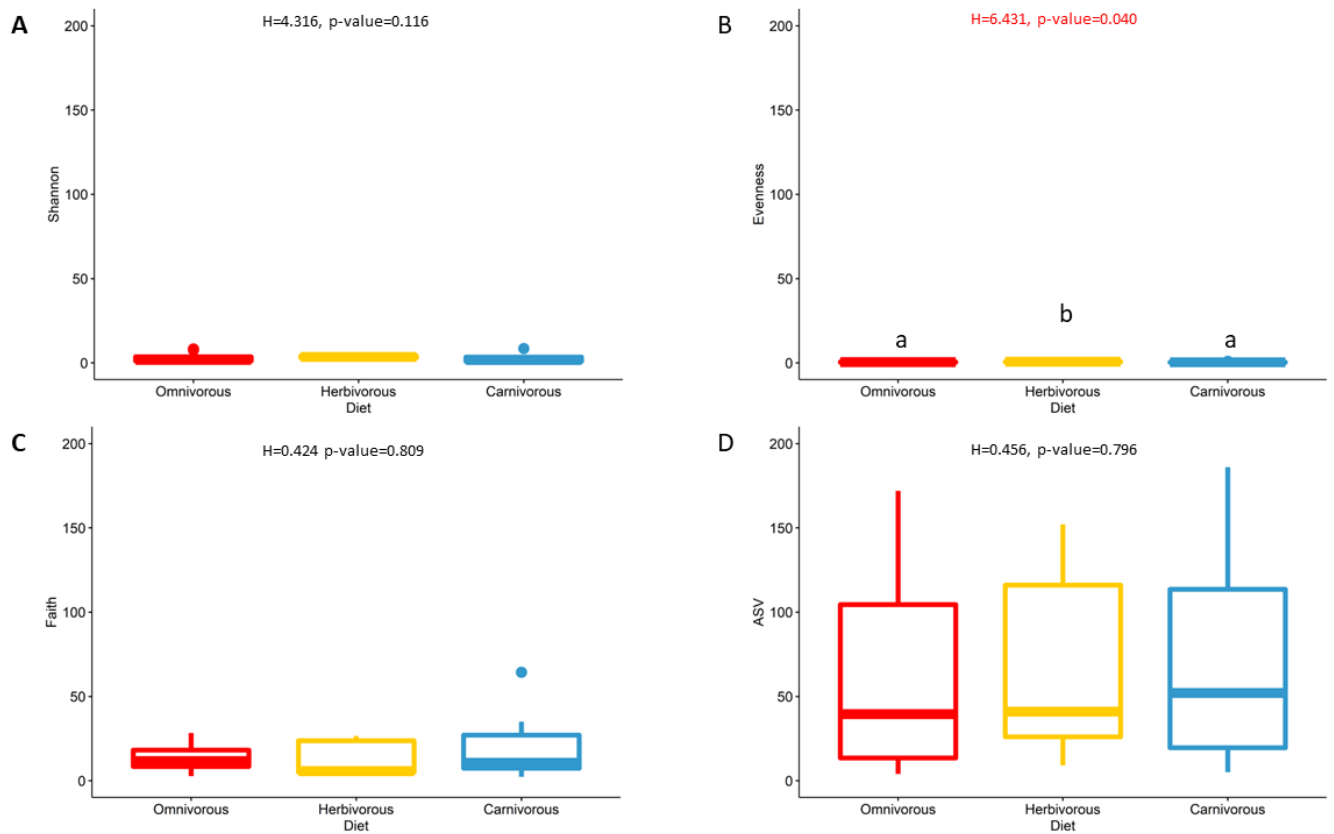
**Figure S3. Differences in bacterial alpha diversity by ant habitat.**

(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. The statistical p-values were obtained with pairwise Kruskal-Wallis.



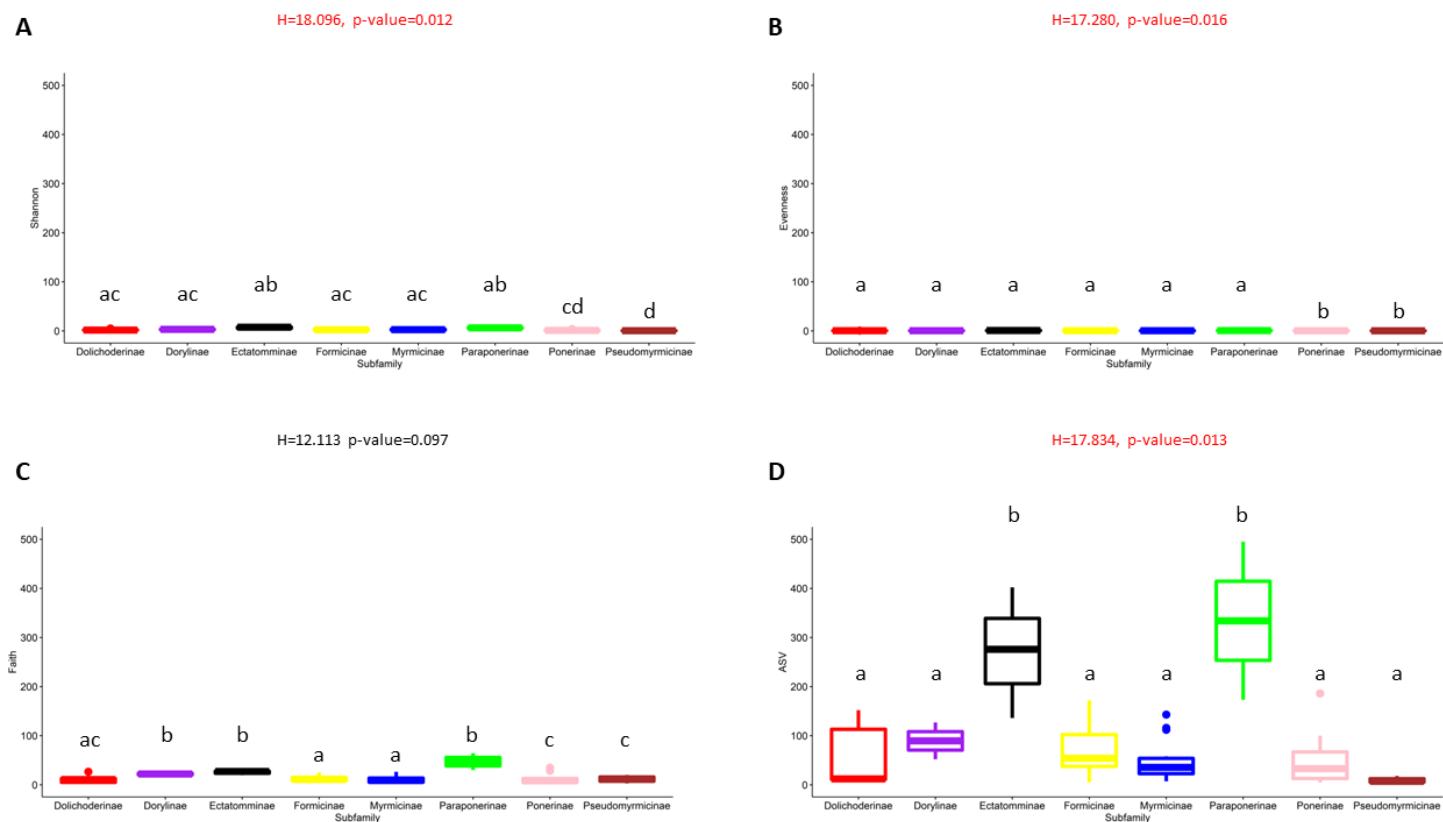
**Figure S4. Differences in bacterial alpha diversity by ant nesting mode.**

(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. Different letters at the top of the figure illustrate nesting modes with significant differences ( $P < 0.05$ ) in this alpha diversity metric. The statistical p-values were obtained with pairwise Kruskal-Wallis.



**Figure S5. Differences in bacterial alpha diversity by ant diet.**

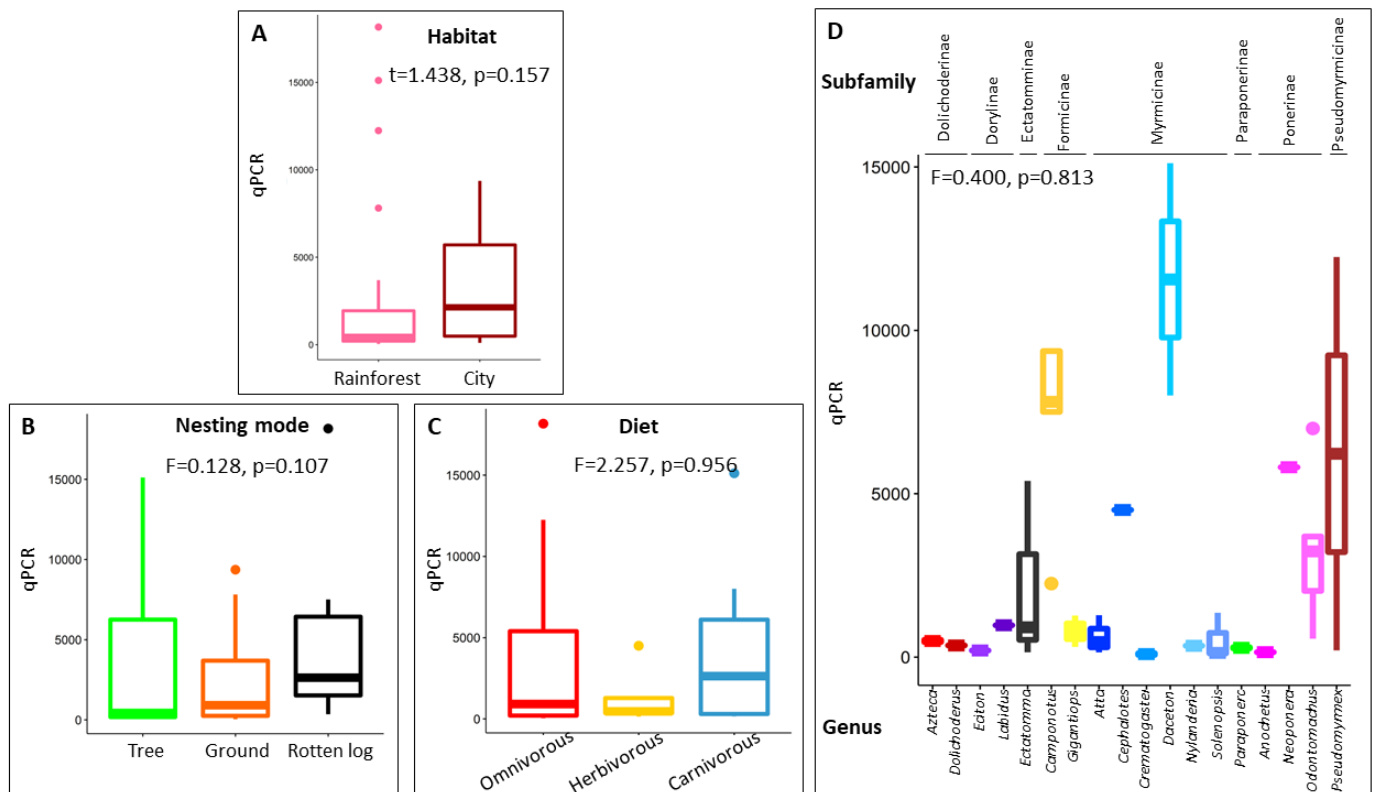
(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. Different letters at the top of the figure illustrate diets with significant differences ( $P < 0.05$ ) in this alpha diversity metric. The statistical p-values were obtained with pairwise Kruskal-Wallis.



**Figure S6. Differences in bacterial alpha diversity by ant subfamily.**

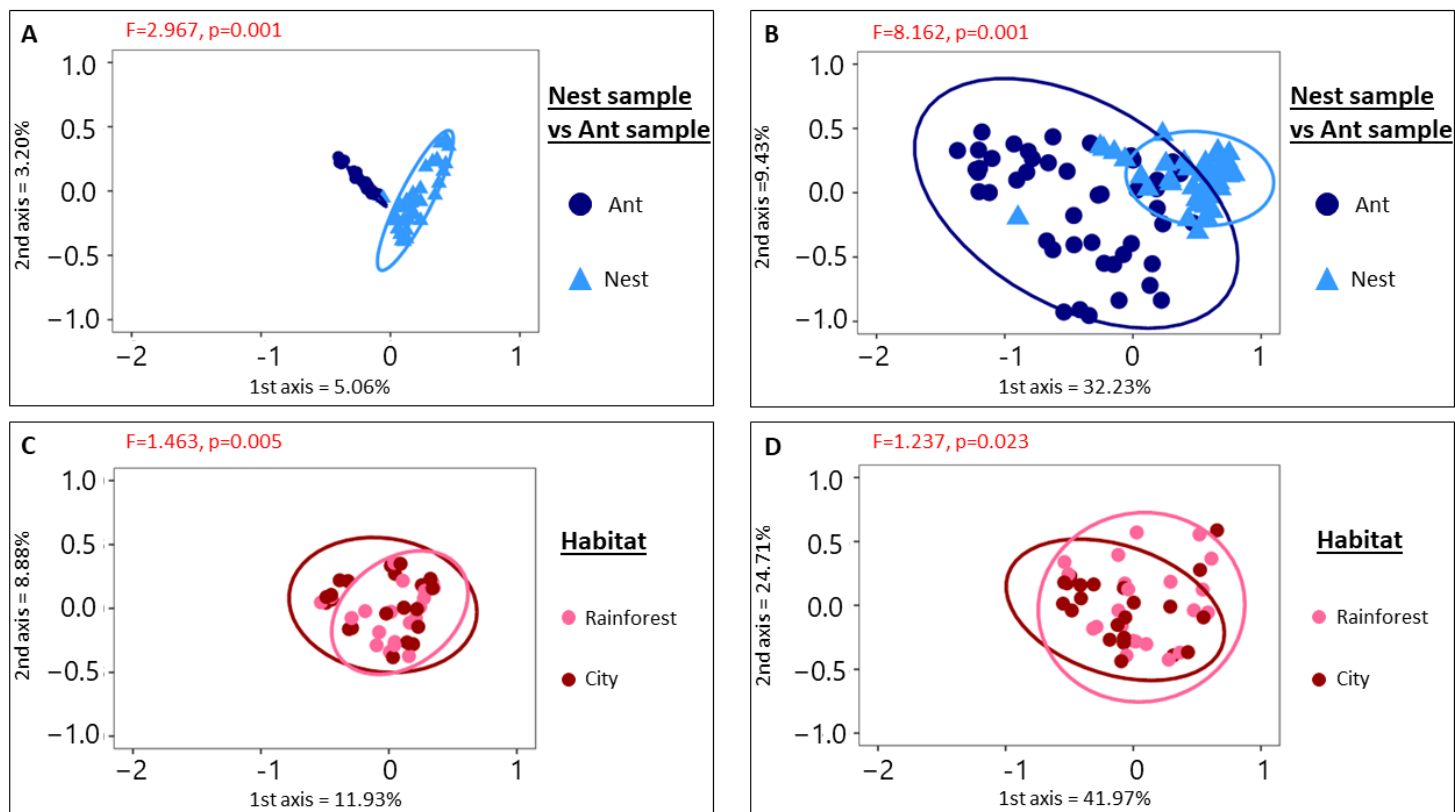
(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. Different letters at the top of the figure illustrate subfamilies with significant differences ( $P < 0.05$ ) in this alpha diversity metric. The statistical p-values were obtained with pairwise Kruskal-Wallis





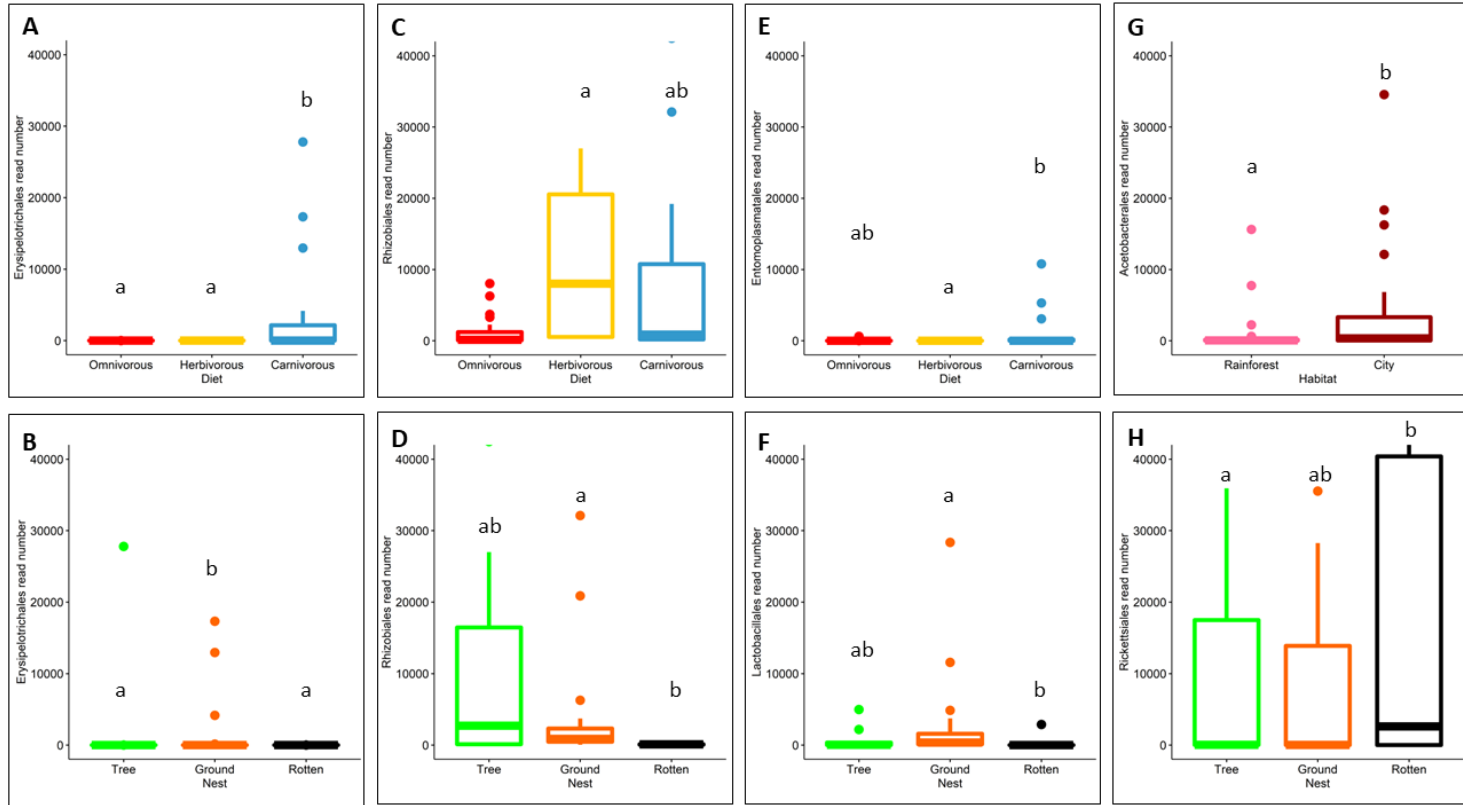
**Figure S7. Differences in bacterial communities between ants and their nest.**

(A and B) Differences in bacterial communities between ants and their nest, using the Jaccard (A) or the unUniFrac distance (B). (C and D) Differences in bacterial communities associated with rainforest nests or city nests, using the Jaccard (C) or the unUniFrac distances (D). The statistical p-values were obtained with pairwise PERMANOVAs. The circles represent a confidence interval of 0.95.



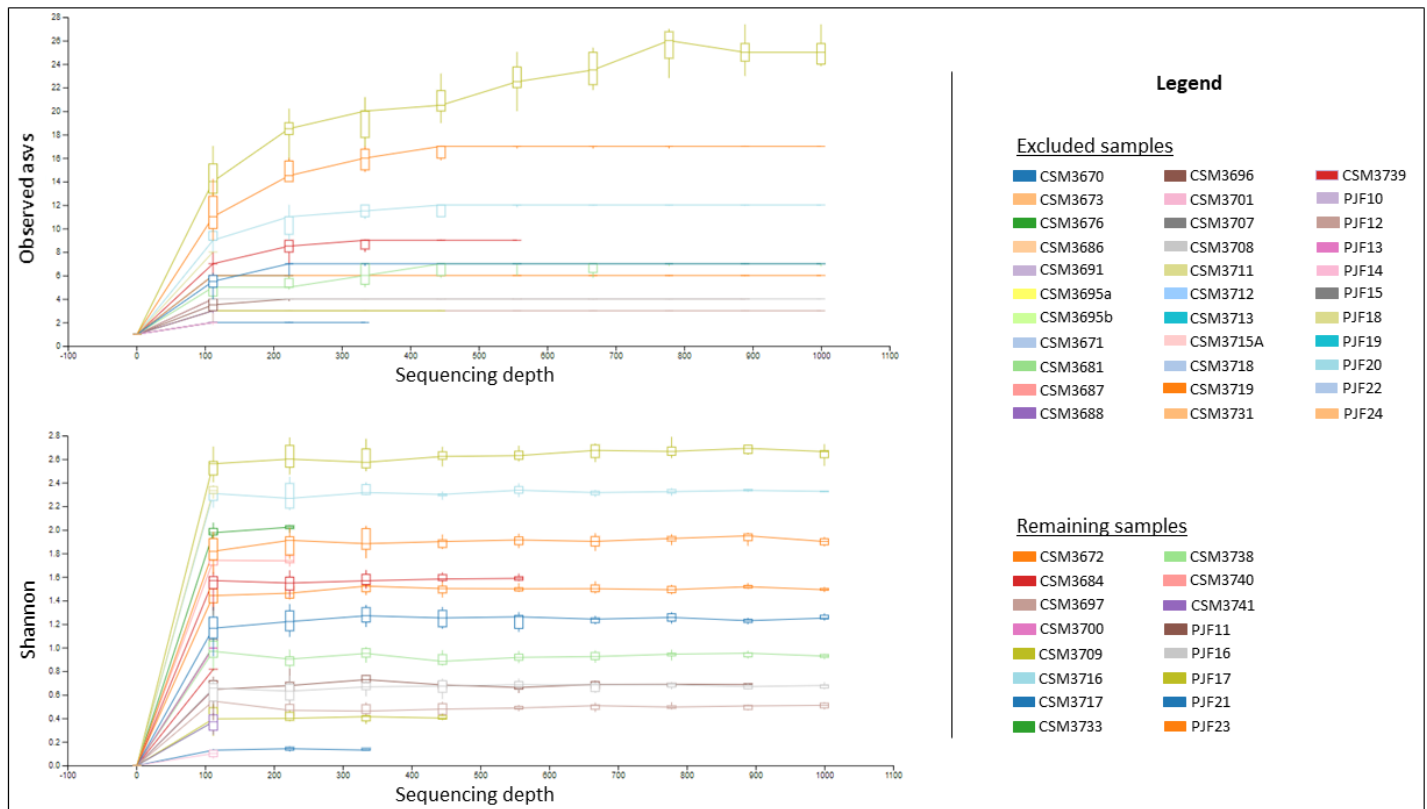
**Figure S8. Differences in mean qPCR values across subfamily and habitat (A), diet (B), nesting mode (C) and taxonomy (D).**

The statistical analyses were performed using t-test (A) and ANOVAs (B, C and D).

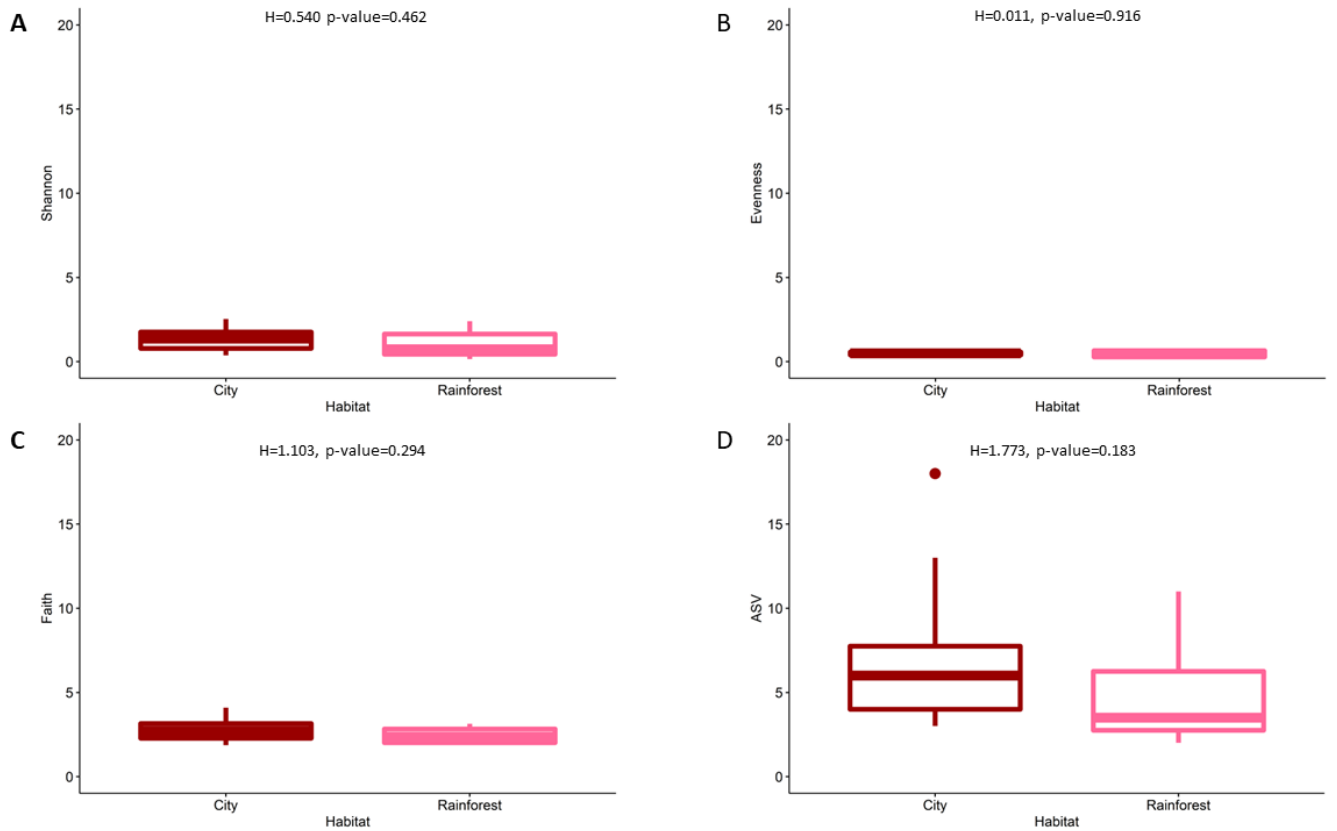


**Figure S9. SIMPER analysis using ASV abundance of different bacterial orders.**

(A and B) Mean ( $\pm$ standard error) Erysipelotrichales read number by ant diet (A) and nesting mode (B). (C and D) Mean ( $\pm$ standard error) Rhizobiales read number by ant diet (C) and nesting mode (D). (E) Mean ( $\pm$ standard error) Entomoplasmatales read number by ant diet. (F) Mean ( $\pm$ standard error) Lactobacillales read number by ant nesting mode. (G) Mean ( $\pm$ standard error) Acetobacteriales read number by ant habitat. (H) Mean ( $\pm$ standard error) Rickettsiales read number by ant nesting mode. Different letters at the top of the figure illustrate significant differences ( $P < 0.05$ ) determined by Kruskal-Wallis. P-values for this figure are found in Supplementary File 6.

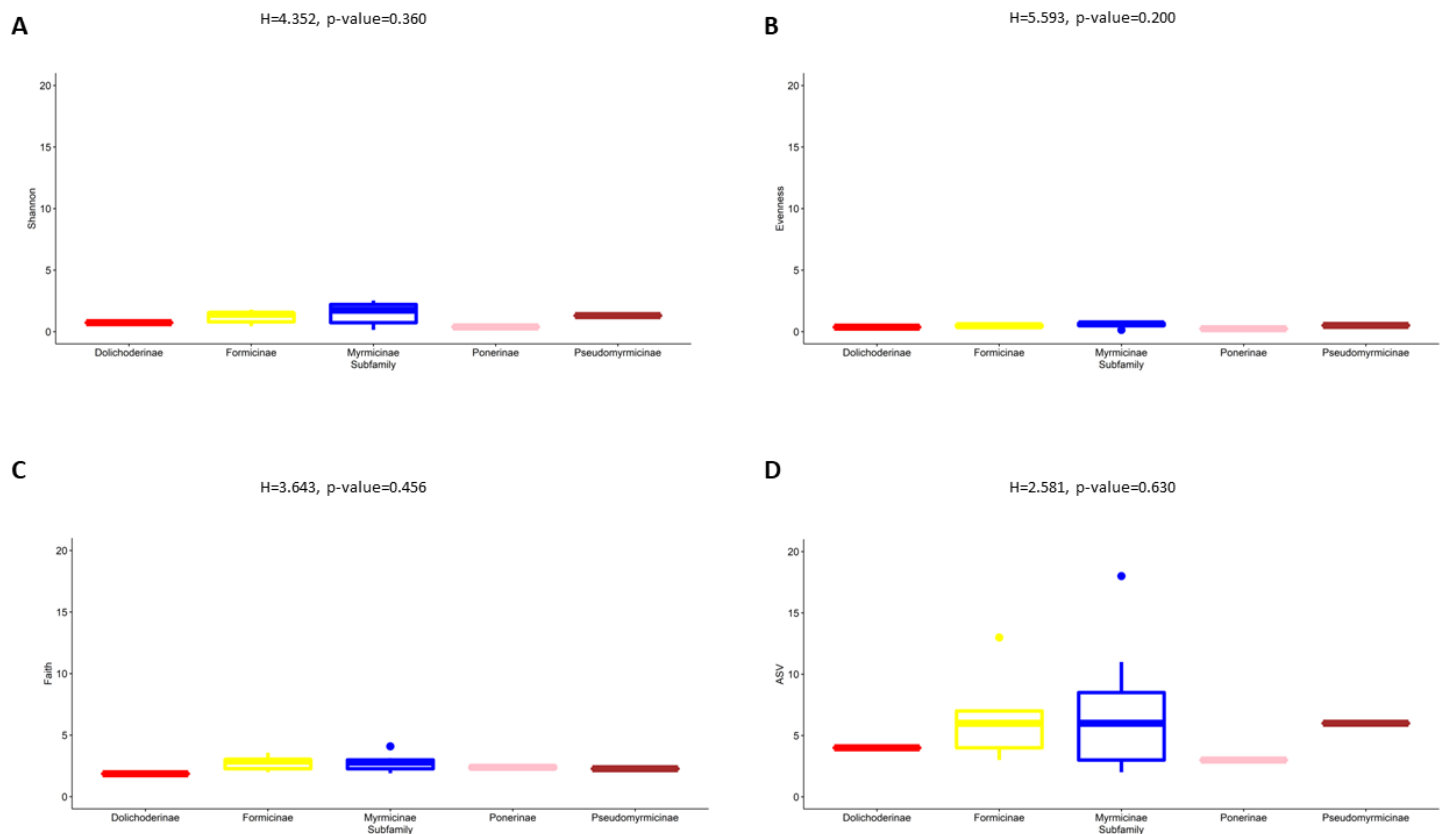


**Figure S10. Rarefaction curves used to estimate number of observed ASVs and richness in the Shannon index.** The vertical axis shows the bacterial ASVs observed (A) or the Shannon index (B) and the number of sequences per sample is shown on the horizontal axis. At our chosen rarefaction threshold (199), all the remaining samples have reached a plateau for the Shannon index (B) and the number of observed ASVs does not increase a lot after the chosen threshold in most of the remaining samples (A), indicating that we seem to have recover the majority of the eukaryote diversity.



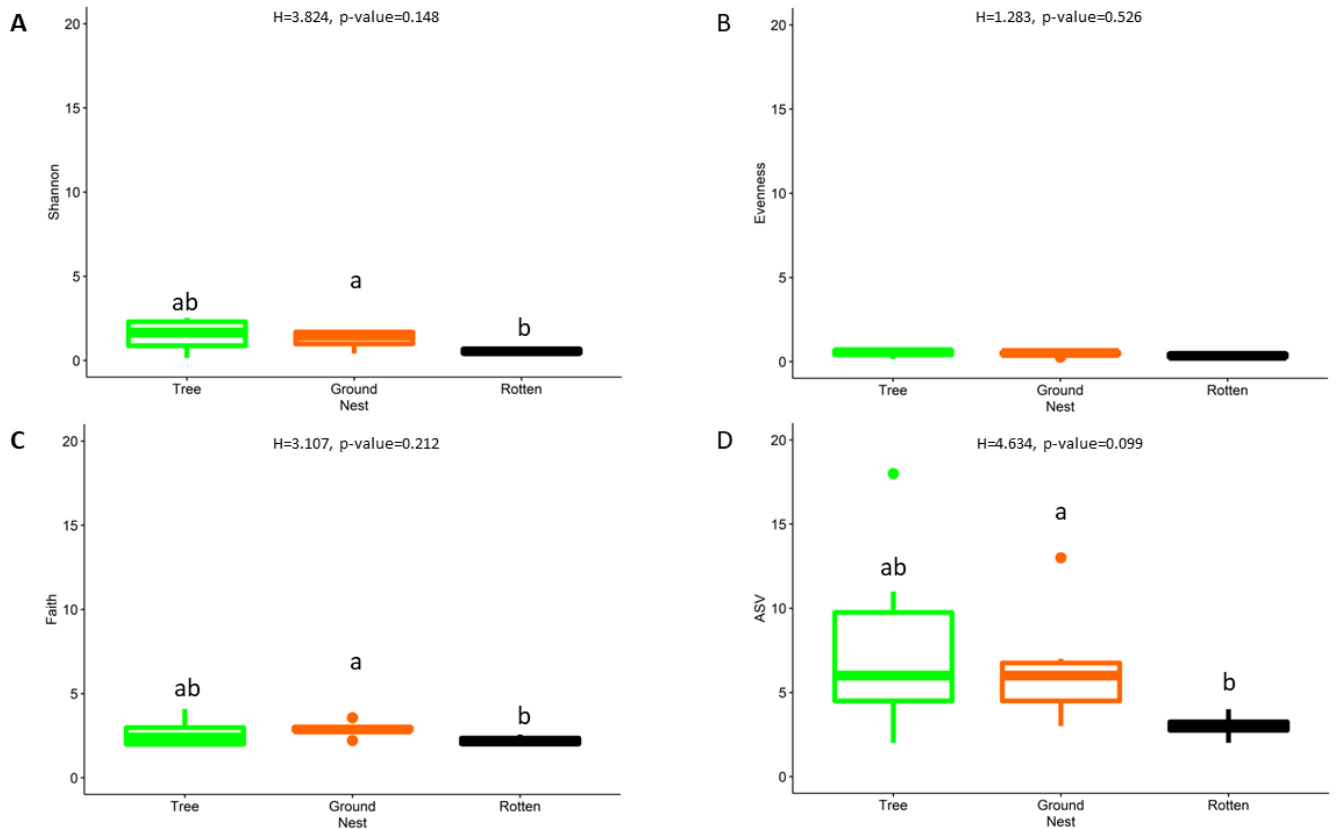
**Figure S11. Differences in eukaryote alpha diversity by ant habitat.**

(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. The statistical p-values were obtained with pairwise Kruskal-Wallis.



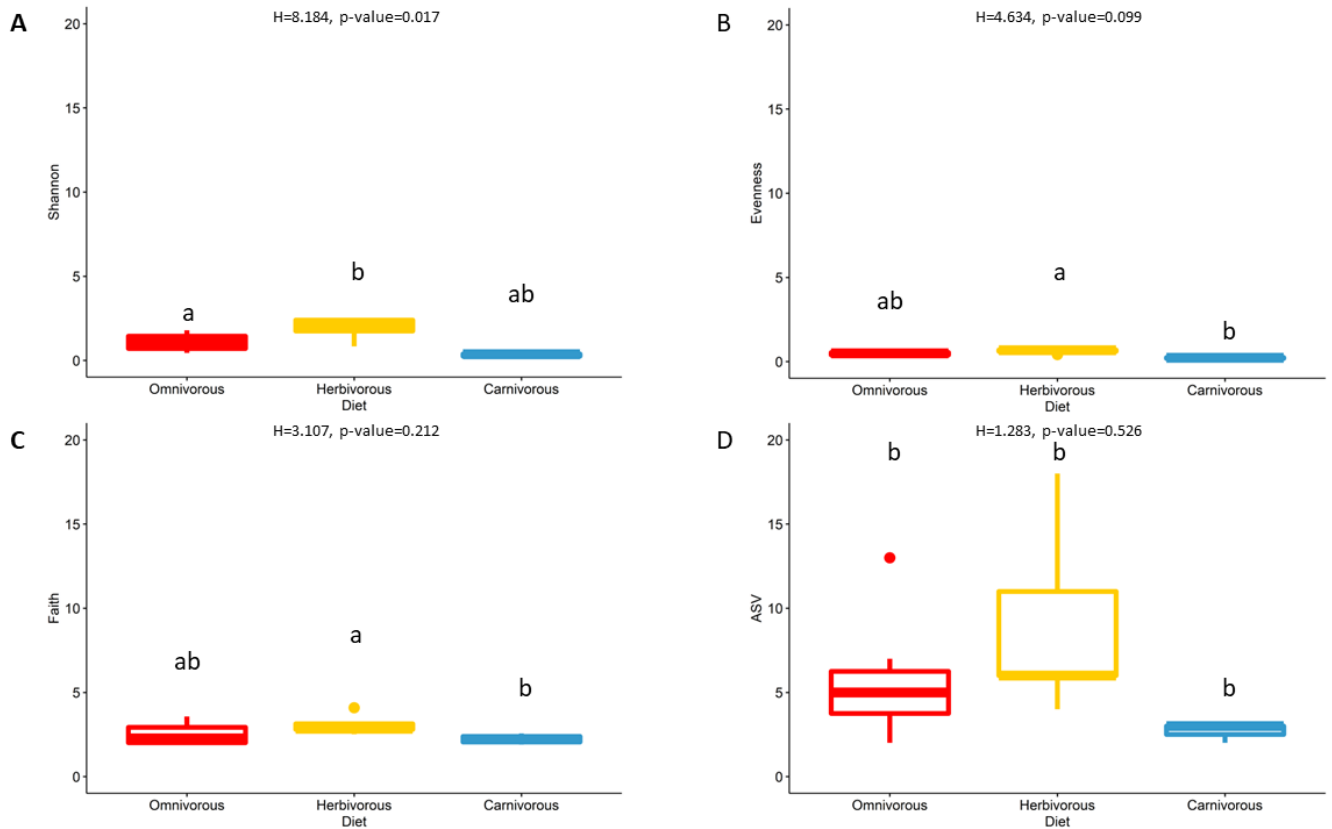
**Figure S12. Differences in eukaryote alpha diversity by ant subfamily.**

(A) Mean (±standard error) Shannon diversity. (B) Mean (±standard error) Pielou's evenness. (C) Mean (±standard error) Faith's phylogenetic diversity. (D) Mean (±standard error) ASV count. The statistical p-values were obtained with pairwise Kruskal-Wallis.



**Figure S13. Differences in eukaryote alpha diversity by ant nesting mode.**

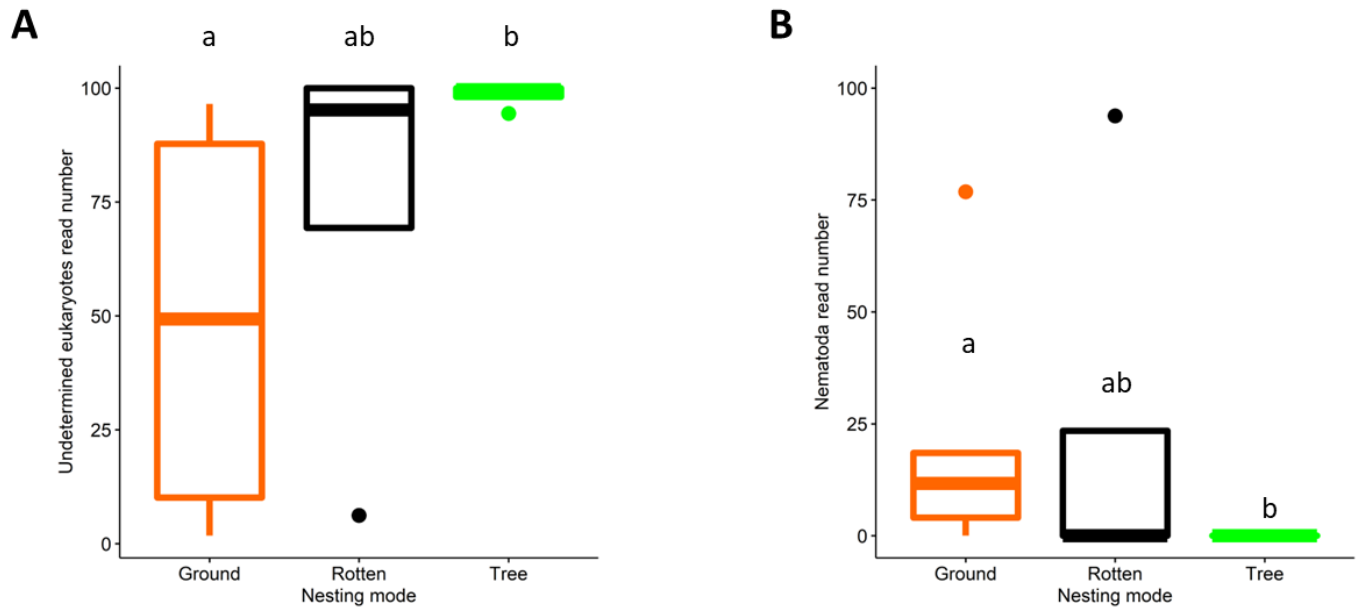
(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. Different letters at the top of the figure illustrate nesting modes with significant differences ( $P < 0.05$ ) in this alpha diversity metric. The statistical p-values were obtained with pairwise Kruskal-Wallis.



**Figure S14. Differences in eukaryote alpha diversity by ant diet.**

(A) Mean ( $\pm$ standard error) Shannon diversity. (B) Mean ( $\pm$ standard error) Pielou's evenness. (C) Mean ( $\pm$ standard error) Faith's phylogenetic diversity. (D) Mean ( $\pm$ standard error) ASV count. Different letters at the top of the figure illustrate diets with significant differences ( $P < 0.05$ ) in this alpha diversity metric. The statistical p-values were obtained with pairwise Kruskal-Wallis.





**Figure S15. SIMPER analysis using ASV abundance of different eukaryote phyla by nesting mode.**

(A) Mean ( $\pm$ standard error) undetermined eukaryotes read number. (B) Mean ( $\pm$ standard error) Nematoda read number. Different letters at the top of the figure illustrate significant differences ( $P < 0.05$ ) determined by Kruskal-Wallis. P-values for this figure are found in Supplementary File 10.

**Supplementary File S1. List of all collected samples.**

| Dataset | Ant ecology    |              |              |              |             |              | 16S rRNA analysis |             |               | 18S rRNA analysis |               | Sample ID | Corresponding Nest ID | Corresponding Ant ID |
|---------|----------------|--------------|--------------|--------------|-------------|--------------|-------------------|-------------|---------------|-------------------|---------------|-----------|-----------------------|----------------------|
|         | Subfamily      | Genus        | Species      | Habitat mode | Diet        | Nesting mode | Barcode sequence  | qPCR        | Qubit 1ng/1uL | Barcode sequence  | Qubit 1ng/1uL |           |                       |                      |
| Ant     | Dolichoderinae | Azteca       | sp           | Rainforest   | Omnivorous  | Tree         | CGATCGAACACT      | 559.36      | 0.100         | CGATCGAACACT      | 0.1           | CSM3696   | AC62N                 |                      |
| Ant     | Dolichoderinae | Azteca       | chartifex    | Rainforest   | Omnivorous  | Tree         | CATAATCTTGCT      | 427.27      | 0.082         | CATAATCTTGCT      | 0.0815        | CSM3731   | AC77N                 |                      |
| Ant     | Dolichoderinae | Azteca       | chartifex    | City         | Omnivorous  | Tree         | AATTGAATTTAC      | 32067.93    | 0.100         | AATTGAATTTAC      | 0.1           | PJF11     | AC84N                 |                      |
| Ant     | Dolichoderinae | Dolichoderus | bispinosus   | Rainforest   | Herbivorous | Tree         | TTGGGTACACGT      | 356.37      | 0.588         | TTGGGTACACGT      | 0.588         | CSM3688   | AC59N                 |                      |
| Ant     | Dolichoderinae | Dolichoderus | attelaboides | Rainforest   | Herbivorous | Tree         | GATATCGATGAA      | 36888.05    | 1.533         | GATATCGATGAA      | 1.5329        | CSM3691   | AC60N                 |                      |
| Ant     | Dorylinae      | Eciton       | rapax        | Rainforest   | Carnivorous | Ground       | CAGGTAATAATG      | 203.33      | 0.160         | CAGGTAATAATG      | 0.1599        | CSM3707   |                       |                      |
| Ant     | Dorylinae      | Labidus      | coecus       | Rainforest   | Carnivorous | Ground       | CATGACGCCTCC      | 972.71      | 0.294         | CATGACGCCTCC      | 0.2935        | CSM3718   |                       |                      |
| Ant     | Ectatomminae   | Ectatomma    | brunneum     | City         | Omnivorous  | Ground       | AGCCGACTCTGT      | 909.98      | 1.320         | AGCCGACTCTGT      | 1.32          | CSM3676   | AC54N                 |                      |
| Ant     | Ectatomminae   | Ectatomma    | tuberculatum | Rainforest   | Omnivorous  | Ground       | GCTGTGATTCGA      | 146.02      | 1.384         | GCTGTGATTCGA      | 1.3842        | CSM3686   | AC57N                 |                      |
| Ant     | Ectatomminae   | Ectatomma    | tuberculatum | City         | Omnivorous  | Ground       | GTCCCTATTATC      | 5391.95     | 0.124         | GTCCCTATTATC      | 0.1235        | PJF20     | AC92N                 |                      |
| Ant     | Formicinae     | Camponotus   | sp1          | City         | Omnivorous  | Ground       | TAAGATGCAGTC      | 2247.18     | 1.411         | TAAGATGCAGTC      | 1.4113        | CSM3672   | AC52N                 |                      |
| Ant     | Formicinae     | Camponotus   | rapax        | Rainforest   | Omnivorous  | Ground       | CTCGAGCGTACT      | 7810.37     | 1.524         | CTCGAGCGTACT      | 1.5243        | CSM3684   | AC56N                 |                      |
| Ant     | Formicinae     | Camponotus   | femoratus    | Rainforest   | Omnivorous  | Tree         | AACGCGAAATTC      | 28058.12    | 3.700         | AACGCGAAATTC      | 3.7           | CSM3695a  | AC61N                 |                      |
| Ant     | Formicinae     | Camponotus   | atriceps     | Rainforest   | Omnivorous  | Rotten       | TTCGCTAACCTT      | 18168.36    | 2.110         | TTCGCTAACCTT      | 2.1096        | CSM3697   | AC63N                 |                      |
| Ant     | Formicinae     | Camponotus   | atriceps     | City         | Omnivorous  | Rotten       | ATGGCTGTCAGT      | 7503.38     | 1.333         | ATGGCTGTCAGT      | 1.3325        | PJF13     | AC86N                 |                      |
| Ant     | Formicinae     | Camponotus   | sp2          | City         | Omnivorous  | Rotten       | AGTAAGTCGATA      | 27158159.79 | 5.099         | AGTAAGTCGATA      | 5.0985        | PJF16     | AC89N                 |                      |
| Ant     | Formicinae     | Camponotus   | blandus      | City         | Omnivorous  | Ground       | ATGGTTCACCCG      | 9367.56     | 28.000        | ATGGTTCACCCG      | 28            | PJF23     | AC95N                 |                      |
| Ant     | Formicinae     | Gigantiops   | destructor   | Rainforest   | Omnivorous  | Ground       | CCGTCAAGATGT      | NA          | 0.100         | CCGTCAAGATGT      | 0.1           | CSM3715A  | AC72N                 |                      |
| Ant     | Formicinae     | Gigantiops   | destructor   | City         | Omnivorous  | Ground       | TCTATCTGGCTT      | 1268.32     | 1.161         | TCTATCTGGCTT      | 1.1611        | PJF18     |                       |                      |
| Ant     | Myrmicinae     | Atta         | cephalotes   | Rainforest   | Herbivorous | Ground       | ACTATATTAGCT      | 460.75      | 0.730         | ACTATATTAGCT      | 0.73          | CSM3738   | AC79N                 |                      |

|     |               |               |             |            |             |        |               |            |       |               |        |          |       |  |
|-----|---------------|---------------|-------------|------------|-------------|--------|---------------|------------|-------|---------------|--------|----------|-------|--|
| Ant | Myrmicinae    | Atta          | cephalotes  | City       | Herbivorous | Ground | TCCAGGGCTATA  | 1282.31    | 1.816 | TCCAGGGCTATA  | 1.8164 | CSM3740  | AC81N |  |
| Ant | Myrmicinae    | Atta          | sexdens     | City       | Herbivorous | Ground | AGGAAAGCCAGA  | 138.85     | 0.481 | AGGAAAGCCAGA  | 0.4812 | PJF12    | AC85N |  |
| Ant | Myrmicinae    | Cephalotes    | minutus     | City       | Herbivorous | Tree   | CGATAGGCCTTA  | 4502.36    | 0.173 | CGATAGGCCTTA  | 0.1729 | CSM3671  | AC51N |  |
| Ant | Myrmicinae    | Cephalotes    | atratus     | Rainforest | Herbivorous | Tree   | GGTGACTAGTTC  | 55993.14   | 1.306 | GGTGACTAGTTC  | 1.3056 | CSM3716  |       |  |
| Ant | Myrmicinae    | Cephalotes    | pavonii     | Rainforest | Herbivorous | Tree   | TGCGTGGGTGGA  | 130878.47  | 0.336 | TGCGTGGGTGGA  | 0.3362 | CSM3733  | AC78N |  |
| Ant | Myrmicinae    | Cephalotes    | atratus     | City       | Herbivorous | Tree   | TTGGGCCACATA  | 9772831.73 | 4.112 | TTGGGCCACATA  | 4.1124 | PJF17    | AC90N |  |
| Ant | Myrmicinae    | Crematogaster | levior      | Rainforest | Omnivorous  | Tree   | GTGAGCACGCAG  | 147.91     | 2.100 | GTGAGCACGCAG  | 2.1    | CSM3695b | AC61N |  |
| Ant | Myrmicinae    | Crematogaster | limata      | Rainforest | Omnivorous  | Ground | TAGAGGCGTAGG  | 38.01      | 0.100 | TAGAGGCGTAGG  | 0.1    | CSM3701  | AC65N |  |
| Ant | Myrmicinae    | Crematogaster | sp2         | City       | Omnivorous  | Tree   | GCGACGCGGCAT  | NA         | 0.100 | GCGACGCGGCAT  | 0.1    | PJF24    | AC96N |  |
| Ant | Myrmicinae    | Daceton       | armigerum   | Rainforest | Omnivorous  | Tree   | GGAGTGCCCGAA  | 15113.49   | 0.834 | GGAGTGCCCGAA  | 0.8339 | CSM3717  | AC74N |  |
| Ant | Myrmicinae    | Daceton       | armigerum   | City       | Omnivorous  | Tree   | TTCTGGTCTTGT  | 8008.35    | 0.707 | TTCTGGTCTTGT  | 0.7073 | CSM3739  | AC80N |  |
| Ant | Myrmicinae    | Nylanderia    | sp          | City       | Omnivorous  | Rotten | GAGGGTTGTCGG  | 345.53     | 0.100 | GAGGGTTGTCGG  | 0.1    | PJF14    | AC87N |  |
| Ant | Myrmicinae    | Solenopsis    | virulens    | Rainforest | Omnivorous  | Rotten | GCAGGGTCGAAC  | 1350.93    | 0.216 | GCAGGGTCGAAC  | 0.2161 | CSM3700  | AC64N |  |
| Ant | Myrmicinae    | Solenopsis    | geminata    | City       | Omnivorous  | Ground | CTATCATCCTCA  | 105.03     | 0.100 | CTATCATCCTCA  | 0.1    | PJF10    | AC83N |  |
| Ant | Myrmicinae    | Solenopsis    | sp          | City       | Omnivorous  | Tree   | ATACCTAAATAT  | 127.12     | 0.887 | ATACCTAAATAT  | 0.887  | PJF22    | AC94N |  |
| Ant | Paraponerinae | Paraponera    | clavata     | City       | Carnivorous | Ground | TCCGCAACCTGA  | 314.83     | 8.792 | TCCGCAACCTGA  | 8.7923 | CSM3673  | AC53N |  |
| Ant | Paraponerinae | Paraponera    | clavata     | Rainforest | Carnivorous | Ground | GCCGAACGCCGA  | 252.79     | 1.407 | GCCGAACGCCGA  | 1.407  | CSM3708  | AC67N |  |
| Ant | Ponerinae     | Anochetus     | emarginatus | Rainforest | Carnivorous | Tree   | CCGCTGATGTCA  | 148.26     | 1.066 | CCGCTGATGTCA  | 1.0661 | CSM3712  | AC70N |  |
| Ant | Ponerinae     | Neoponera     | commutata   | Rainforest | Carnivorous | Ground | GTCTAGTATTTTC | 3996045.20 | 3.906 | GTCTAGTATTTTC | 3.9063 | CSM3709  | AC68N |  |
| Ant | Ponerinae     | Neoponera     | commutata   | City       | Carnivorous | Ground | CCGTGGACCAGG  | 5810.32    | 2.859 | CCGTGGACCAGG  | 2.8585 | PJF19    | AC91N |  |
| Ant | Ponerinae     | Odontomachus  | haematodus  | City       | Carnivorous | Rotten | AAGGCTGGGCAC  | 2027.91    | 1.111 | AAGGCTGGGCAC  | 1.1113 | CSM3670  | AC50N |  |
| Ant | Ponerinae     | Odontomachus  | hastatus    | Rainforest | Carnivorous | Tree   | GTGTTCCCAGAA  | 109427.44  | 2.287 | GTGTTCCCAGAA  | 2.2866 | CSM3681  | AC55N |  |
| Ant | Ponerinae     | Odontomachus  | scalptus    | Rainforest | Carnivorous | Ground | CTGCCCTCGATG  | 558.45     | 1.795 | CTGCCCTCGATG  | 1.7947 | CSM3687  | AC58N |  |
| Ant | Ponerinae     | Odontomachus  | haematodus  | Rainforest | Carnivorous | Ground | GTATTATGACTT  | 3691.90    | 1.599 | GTATTATGACTT  | 1.5994 | CSM3719  | AC76N |  |

|      |                  |              |              |            |             |         |              |            |        |              |        |           |       |          |
|------|------------------|--------------|--------------|------------|-------------|---------|--------------|------------|--------|--------------|--------|-----------|-------|----------|
| Ant  | Ponerinae        | Odontomachus | haematodus   | City       | Carnivorous | Rotten  | GACTATAATGGC | 3235.66    | 2.192  | GACTATAATGGC | 2.1916 | CSM3741   | AC82N |          |
| Ant  | Ponerinae        | Odontomachus | bori         | City       | Carnivorous | Ground  | CCACGTACGTAA | 6998.29    | 0.929  | CCACGTACGTAA | 0.9291 | PJF15     | AC88N |          |
| Ant  | Pseudomyrmicinae | Pseudomyrmex | sp1          | Rainforest | Omnivorous  | Tree    | AAGCATTGAGAT | 202.28     | 0.022  | AAGCATTGAGAT | 0.0219 | CSM3711   | AC69N |          |
| Ant  | Pseudomyrmicinae | Pseudomyrmex | gracilis     | Rainforest | Omnivorous  | Tree    | ACCCTCAGCCCA | 12245.70   | 2.355  | ACCCTCAGCCCA | 2.355  | CSM3713   | AC71N |          |
| Ant  | Pseudomyrmicinae | Pseudomyrmex | sp2          | City       | Omnivorous  | Tree    | GCCTGCAGTACT | NA         | 4.710  | GCCTGCAGTACT | 4.71   | PJF21     | AC93N |          |
| Ant  | Control          | Control      | Control      | Control    | Control     | Control | CAGAGCTAATTG | 931712.85  | 0.101  | CAGAGCTAATTG | 0.101  | negative1 |       |          |
| Ant  | Control          | Control      | Control      | Control    | Control     | Control | ATATATAGTATC | 303571.13  | 0.102  | ATATATAGTATC | 0.1017 | negative2 |       |          |
| Nest | Dolichoderinae   | Azteca       | sp           | Rainforest | Omnivorous  | Tree    | CTACTAGCGGTA | 146182.38  | 28.100 |              |        | AC62N     |       | CSM3696  |
| Nest | Dolichoderinae   | Azteca       | chartifex    | Rainforest | Omnivorous  | Tree    | ATGAAGCACTGT | 54321.97   | 6.210  |              |        | AC77N     |       | CSM3731  |
| Nest | Dolichoderinae   | Azteca       | chartifex    | City       | Omnivorous  | Tree    | TGACAACCGAAT | 164.38     | 0.309  |              |        | AC84N     |       | PJF11    |
| Nest | Dolichoderinae   | Dolichoderus | bispinosus   | Rainforest | Herbivorous | Tree    | CCTGTAGGTTGC | 777166.81  | 45.100 |              |        | AC59N     |       | CSM3688  |
| Nest | Dolichoderinae   | Dolichoderus | attelaboides | Rainforest | Herbivorous | Tree    | TACGTCGTTATT | 15488.15   | 1.560  |              |        | AC60N     |       | CSM3691  |
| Nest | Ectatomminae     | Ectatomma    | brunneum     | City       | Omnivorous  | Ground  | ACCATTACCATT | 39084.65   | 8.650  |              |        | AC54N     |       | CSM3676  |
| Nest | Ectatomminae     | Ectatomma    | tuberculatum | Rainforest | Omnivorous  | Ground  | ATTGAGATGGCA | 27546.76   | 3.270  |              |        | AC57N     |       | CSM3686  |
| Nest | Ectatomminae     | Ectatomma    | tuberculatum | City       | Omnivorous  | Ground  | TCTGAATGGTAG | 91209.69   | 7.020  |              |        | AC92N     |       | PJF20    |
| Nest | Formicinae       | Camponotus   | sp1          | City       | Omnivorous  | Ground  | CATACCGTGAGT | 1392.04    | 0.337  |              |        | AC52N     |       | CSM3672  |
| Nest | Formicinae       | Camponotus   | rapax        | Rainforest | Omnivorous  | Ground  | CCAGCCTTCAGA | 43114.00   | 10.100 |              |        | AC56N     |       | CSM3684  |
| Nest | Formicinae       | Camponotus   | femoratus    | Rainforest | Omnivorous  | Tree    | GAGTAGGGCACC | 410.25     | 0.199  |              |        | AC61N     |       | CSM3695a |
| Nest | Formicinae       | Camponotus   | atriceps     | Rainforest | Omnivorous  | Rotten  | CGATTTAGGCCA | 991.21     | 0.758  |              |        | AC63N     |       | CSM3697  |
| Nest | Formicinae       | Camponotus   | atriceps     | City       | Omnivorous  | Rotten  | CGTTAAGTCAGC | 200753.90  | 7.210  |              |        | AC86N     |       | PJF13    |
| Nest | Formicinae       | Camponotus   | sp2          | City       | Omnivorous  | Rotten  | CGGACTCGTTAC | 1548645.00 | 18.000 |              |        | AC89N     |       | PJF16    |
| Nest | Formicinae       | Camponotus   | blandus      | City       | Omnivorous  | Ground  | TTCGCAGATACG | 280176.57  | 5.920  |              |        | AC95N     |       | PJF23    |
| Nest | Formicinae       | Gigantiops   | destructor   | Rainforest | Omnivorous  | Ground  | CACGTCGCGGAG | 3011.89    | 3.440  |              |        | AC72N     |       | CSM3715A |
| Nest | Myrmicinae       | Atta         | cephalotes   | Rainforest | Herbivorous | Ground  | CGTCGATTGCAC | 330662.52  | 21.300 |              |        | AC79N     |       | CSM3738  |

|      |               |               |             |            |             |        |              |           |        |  |  |       |  |          |
|------|---------------|---------------|-------------|------------|-------------|--------|--------------|-----------|--------|--|--|-------|--|----------|
| Nest | Myrmicinae    | Atta          | cephalotes  | City       | Herbivorous | Ground | GCCGACGTGCCG | 28851.52  | 4.610  |  |  | AC81N |  | CSM3740  |
| Nest | Myrmicinae    | Atta          | sexdens     | City       | Herbivorous | Ground | GCCGGTACTCTA | 18689.52  | 1.380  |  |  | AC85N |  | PJF12    |
| Nest | Myrmicinae    | Cephalotes    | minutus     | City       | Herbivorous | Tree   | CAACACATGCTG | 495.71    | 0.449  |  |  | AC51N |  | CSM3671  |
| Nest | Myrmicinae    | Cephalotes    | pavonii     | Rainforest | Herbivorous | Tree   | TCGTTCAGGACC | 3362.22   | 0.538  |  |  | AC78N |  | CSM3733  |
| Nest | Myrmicinae    | Cephalotes    | atratus     | City       | Herbivorous | Tree   | CAGACGAGGAAC | 201516.64 | 5.610  |  |  | AC90N |  | PJF17    |
| Nest | Myrmicinae    | Crematogaster | levior      | Rainforest | Omnivorous  | Tree   | GAGTAGGGCACC | 410.25    | 0.199  |  |  | AC61N |  | CSM3695b |
| Nest | Myrmicinae    | Crematogaster | limata      | Rainforest | Omnivorous  | Ground | AGGCGCTCTCCT | 4921.04   | 0.954  |  |  | AC65N |  | CSM3701  |
| Nest | Myrmicinae    | Crematogaster | sp2         | City       | Omnivorous  | Tree   | AACACATGGGTT | 29890.24  | 2.980  |  |  | AC96N |  | PJF24    |
| Nest | Myrmicinae    | Daceton       | armigerum   | Rainforest | Omnivorous  | Tree   | CGTTACCGGACT | 62417.44  | 3.260  |  |  | AC74N |  | CSM3717  |
| Nest | Myrmicinae    | Daceton       | armigerum   | City       | Omnivorous  | Tree   | CGAACAGAGCGC | 168836.52 | 9.190  |  |  | AC80N |  | CSM3739  |
| Nest | Myrmicinae    | Nylanderia    | sp          | City       | Omnivorous  | Rotten | TTATAGATCTCC | 141260.50 | 4.760  |  |  | AC87N |  | PJF14    |
| Nest | Myrmicinae    | Solenopsis    | virulens    | Rainforest | Omnivorous  | Rotten | GCTTGGTAGGTT | 335.11    | 0.531  |  |  | AC64N |  | CSM3700  |
| Nest | Myrmicinae    | Solenopsis    | geminata    | City       | Omnivorous  | Ground | TACGCAGCACTA | 303625.83 | 12.500 |  |  | AC83N |  | PJF10    |
| Nest | Myrmicinae    | Solenopsis    | sp          | City       | Omnivorous  | Tree   | GGACTATCGTTG | 113402.27 | 4.140  |  |  | AC94N |  | PJF22    |
| Nest | Paraponerinae | Paraponera    | clavata     | City       | Carnivorous | Ground | GTCCATGGTTCG | 55219.30  | 11.800 |  |  | AC53N |  | CSM3673  |
| Nest | Paraponerinae | Paraponera    | clavata     | Rainforest | Carnivorous | Ground | ACCTGATCCGCA | 5980.62   | 2.550  |  |  | AC67N |  | CSM3708  |
| Nest | Ponerinae     | Anochetus     | emarginatus | Rainforest | Carnivorous | Tree   | ATTCTGCCGAAG | 34987.56  | 7.200  |  |  | AC70N |  | CSM3712  |
| Nest | Ponerinae     | Neoponera     | commutata   | Rainforest | Carnivorous | Ground | GAGATTTAAGCA | 6150.59   | 2.550  |  |  | AC68N |  | CSM3709  |
| Nest | Ponerinae     | Neoponera     | commutata   | City       | Carnivorous | Ground | CTCGATGTAAGC | 14781.64  | 0.797  |  |  | AC91N |  | PJF19    |
| Nest | Ponerinae     | Odontomachus  | haematodus  | City       | Carnivorous | Rotten | GTCCGCAAGTTA | 42933.28  | 4.670  |  |  | AC50N |  | CSM3670  |
| Nest | Ponerinae     | Odontomachus  | hastatus    | Rainforest | Carnivorous | Tree   | TGGTAAGAGTCT | 16722.33  | 4.880  |  |  | AC55N |  | CSM3681  |
| Nest | Ponerinae     | Odontomachus  | scalptus    | Rainforest | Carnivorous | Ground | GTATAGTCCGTG | 76439.16  | 14.300 |  |  | AC58N |  | CSM3687  |
| Nest | Ponerinae     | Odontomachus  | haematodus  | Rainforest | Carnivorous | Ground | GGACTCAACTAA | 26203.48  | 3.860  |  |  | AC76N |  | CSM3719  |
| Nest | Ponerinae     | Odontomachus  | haematodus  | City       | Carnivorous | Rotten | GTGCTGCGCTTA | 542018.66 | 29.200 |  |  | AC82N |  | CSM3741  |

|      |                  |              |          |            |             |         |              |           |       |  |  |        |  |         |
|------|------------------|--------------|----------|------------|-------------|---------|--------------|-----------|-------|--|--|--------|--|---------|
| Nest | Ponerinae        | Odontomachus | bori     | City       | Carnivorous | Ground  | GGTAGCGACGCC | 160027.60 | 7.130 |  |  | AC88N  |  | PJF15   |
| Nest | Pseudomyrmicinae | Pseudomyrmex | sp1      | Rainforest | Omnivorous  | Tree    | TGGGTCCCACAT | 1474.96   | 0.525 |  |  | AC69N  |  | CSM3711 |
| Nest | Pseudomyrmicinae | Pseudomyrmex | gracilis | Rainforest | Omnivorous  | Tree    | CATTACTTATGC | 32014.97  | 3.420 |  |  | AC71N  |  | CSM3713 |
| Nest | Pseudomyrmicinae | Pseudomyrmex | sp2      | City       | Omnivorous  | Tree    | CAGGGAGGATCC | 84747.32  | 4.380 |  |  | AC93N  |  | PJF21   |
| Nest | Control          | Control      | Control  | Control    | Control     | Control | CACGAGCTACTC | 27.31     | 0.211 |  |  | T-Kit1 |  |         |
| Nest | Control          | Control      | Control  | Control    | Control     | Control | ATGAGATGATAC | 27.04     | 0.134 |  |  | T-Kit2 |  |         |

The rows in yellow represent ant samples of the same species collected both in the rainforest and in the city. The linker primer sequences used were the following: GTGTGYCAGCMGCCGCGGTAA (for 16S) and CGGTACACACCGCCCGTC (for 18S).

Supplementary File S2. Statistic calculations of 16S rRNA alpha diversity metrics for each factor.

The four tested alpha diversity metrics are Shannon diversity, Pielou's evenness, Faith's PD and ASV richness. Each metric is calculated for the whole dataset and the forest/city dataset. The cells colored in red in each table represent p-values < 0.05. The statistical p-values were obtained with pairwise Kruskal-Wallis.

Shannon diversity habitat whole dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=24) | City (n=22) | 0.017 | 0.895   | 0.895   |

Shannon diversity habitat filtered dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=10) | City (n=11) | 0.045 | 0.833   | 0.833   |

Shannon diversity nesting mode whole dataset

| Group 1       | Group 2      | H      | p-value   | q-value |
|---------------|--------------|--------|-----------|---------|
| Overall       |              | 15.563 | 4.173E-04 | NA      |
| Ground (n=21) | Rotten (n=7) | 11.711 | 0.001     | 0.002   |
|               | Tree (n=18)  | 7.013  | 0.008     | 0.012   |
| Rotten (n=7)  | Tree (n=18)  | 4.487  | 0.034     | 0.034   |

Shannon diversity nesting mode filtered dataset

| Group 1       | Group 2      | H     | p-value | q-value |
|---------------|--------------|-------|---------|---------|
| Overall       |              | 5.834 | 0.045   | NA      |
| Ground (n=11) | Rotten (n=4) | 4.926 | 0.026   | 0.080   |
|               | Tree (n=6)   | 1.455 | 0.228   | 0.228   |
| Rotten (n=4)  | Tree (n=6)   | 2.227 | 0.136   | 0.203   |

Shannon diversity diet whole dataset

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 4.316 | 0.116   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 4.232 | 0.040   | 0.119   |
|                    | Omnivorous (n=24) | 0.138 | 0.710   | 0.710   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 2.880 | 0.090   | 0.134   |

Shannon diversity diet filtered dataset

| Group 1           | Group 2           | H     | p-value | q-value |
|-------------------|-------------------|-------|---------|---------|
| Overall           |                   | 4.701 | 0.095   | NA      |
| Carnivorous (n=7) | Herbivorous (n=4) | 2.381 | 0.123   | 0.184   |
|                   | Omnivorous (n=10) | 3.704 | 0.054   | 0.163   |
| Herbivorous (n=4) | Omnivorous (n=10) | 0.462 | 0.497   | 0.497   |

Shannon diversity subfamily whole dataset

| Group 1              | Group 2                | H      | p-value | q-value |
|----------------------|------------------------|--------|---------|---------|
| Overall              |                        | 18.096 | 0.012   | NA      |
| Dolichoderinae (n=5) | Dorylinae (n=2)        | 0.600  | 0.439   | 0.559   |
|                      | Ectatomminae (n=3)     | 3.756  | 0.053   | 0.167   |
|                      | Formicinae (n=8)       | 0.536  | 0.464   | 0.565   |
|                      | Myrmicinae (n=14)      | 0.214  | 0.643   | 0.630   |
|                      | Paraponerinae (n=2)    | 2.400  | 0.121   | 0.184   |
|                      | Ponerinae (n=9)        | 2.351  | 0.125   | 0.184   |
|                      | Pseudomyrmicinae (n=3) | 5.000  | 0.025   | 0.167   |

Shannon diversity subfamily filtered dataset

| Group 1              | Group 2             | H      | p-value | q-value |
|----------------------|---------------------|--------|---------|---------|
| Overall              |                     | 12.620 | 0.027   | NA      |
| Dolichoderinae (n=2) | Ectatomminae (n=2)  | 2.400  | 0.121   | 0.202   |
|                      | Formicinae (n=4)    | 0.214  | 0.643   | 0.742   |
|                      | Myrmicinae (n=6)    | 0.111  | 0.739   | 0.792   |
|                      | Paraponerinae (n=2) | 0.600  | 0.439   | 0.598   |
|                      | Ponerinae (n=5)     | 2.400  | 0.121   | 0.202   |
|                      | Formicinae (n=4)    | 3.429  | 0.064   | 0.137   |
| Ectatomminae (n=2)   | Myrmicinae (n=6)    | 4.000  | 0.046   | 0.132   |

|                     |                        |       |       |       |
|---------------------|------------------------|-------|-------|-------|
| Dorylinae (n=2)     | Ectatomminae (n=3)     | 1.333 | 0.248 | 0.347 |
|                     | Formicinae (n=8)       | 0.068 | 0.794 | 0.794 |
|                     | Myrmicinae (n=14)      | 0.403 | 0.525 | 0.613 |
|                     | Paraponerinae (n=2)    | 0.600 | 0.439 | 0.559 |
|                     | Ponerinae (n=9)        | 2.722 | 0.099 | 0.178 |
|                     | Pseudomyrmicinae (n=3) | 3.000 | 0.083 | 0.167 |
| Ectatomminae (n=3)  | Formicinae (n=8)       | 3.375 | 0.066 | 0.167 |
|                     | Myrmicinae (n=14)      | 3.111 | 0.078 | 0.078 |
|                     | Paraponerinae (n=2)    | 0.333 | 0.564 | 0.564 |
|                     | Ponerinae (n=9)        | 5.342 | 0.021 | 0.021 |
|                     | Pseudomyrmicinae (n=3) | 3.857 | 0.049 | 0.049 |
| Formicinae (n=8)    | Myrmicinae (n=14)      | 0.116 | 0.733 | 0.733 |
|                     | Paraponerinae (n=2)    | 2.455 | 0.117 | 0.117 |
|                     | Ponerinae (n=9)        | 2.676 | 0.102 | 0.102 |
|                     | Pseudomyrmicinae (n=3) | 4.167 | 0.042 | 0.167 |
| Myrmicinae (n=14)   | Paraponerinae (n=2)    | 3.050 | 0.081 | 0.167 |
|                     | Ponerinae (n=9)        | 3.571 | 0.059 | 0.167 |
|                     | Pseudomyrmicinae (n=3) | 5.143 | 0.023 | 0.167 |
| Paraponerinae (n=2) | Ponerinae (n=9)        | 4.500 | 0.034 | 0.167 |
|                     | Pseudomyrmicinae (n=3) | 3.000 | 0.083 | 0.167 |
| Ponerinae (n=9)     | Pseudomyrmicinae (n=3) | 3.769 | 0.052 | 0.167 |

|                     |                     |       |       |       |
|---------------------|---------------------|-------|-------|-------|
|                     | Paraponerinae (n=2) | 0.000 | 1.000 | 1.000 |
|                     | Ponerinae (n=5)     | 3.750 | 0.052 | 0.132 |
| Formicinae (n=4)    | Myrmicinae (n=6)    | 0.409 | 0.522 | 0.653 |
|                     | Paraponerinae (n=2) | 0.857 | 0.355 | 0.532 |
|                     | Ponerinae (n=5)     | 3.840 | 0.050 | 0.132 |
| Myrmicinae (n=6)    | Paraponerinae (n=2) | 4.000 | 0.046 | 0.132 |
|                     | Ponerinae (n=5)     | 4.800 | 0.028 | 0.132 |
| Paraponerinae (n=2) | Ponerinae (n=5)     | 3.750 | 0.053 | 0.132 |

Pielou's evenness habitat whole dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=24) | City (n=22) | 0.002 | 0.965   | 0.965   |

Pielou's evenness habitat filtered dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=10) | City (n=11) | 0.005 | 0.944   | 0.944   |

Pielou's evenness nesting mode whole dataset

| Group 1       | Group 2      | H      | p-value | q-value |
|---------------|--------------|--------|---------|---------|
| Overall       |              | 13.742 | 0.001   | NA      |
| Ground (n=21) | Rotten (n=7) | 12.077 | 0.001   | 0.002   |
|               | Tree (n=18)  | 3.051  | 0.081   | 0.081   |
| Rotten (n=7)  | Tree (n=18)  | 6.773  | 0.009   | 0.014   |

Pielou's evenness nesting mode filtered dataset

| Group 1       | Group 2      | H     | p-value | q-value |
|---------------|--------------|-------|---------|---------|
| Overall       |              | 6.390 | 0.041   | NA      |
| Ground (n=11) | Rotten (n=4) | 5.523 | 0.019   | 0.049   |
|               | Tree (n=6)   | 0.162 | 0.688   | 0.688   |
| Rotten (n=4)  | Tree (n=6)   | 4.545 | 0.033   | 0.049   |

Pielou's evenness diet whole dataset

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 6.431 | 0.040   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 6.124 | 0.013   | 0.040   |
|                    | Omnivorous (n=24) | 0.551 | 0.458   | 0.458   |

Pielou's evenness diet filtered dataset

| Group 1           | Group 2           | H     | p-value | q-value |
|-------------------|-------------------|-------|---------|---------|
| Overall           |                   | 3.964 | 0.138   | NA      |
| Carnivorous (n=7) | Herbivorous (n=4) | 2.381 | 0.123   | 0.184   |
|                   | Omnivorous (n=10) | 3.000 | 0.083   | 0.184   |



|                   |                   |       |       |       |
|-------------------|-------------------|-------|-------|-------|
| Herbivorous (n=9) | Omnivorous (n=24) | 4.008 | 0.045 | 0.068 |
|-------------------|-------------------|-------|-------|-------|

Pielou's evenness subfamily whole dataset

| Group 1              | Group 2                | H      | p-value | q-value |
|----------------------|------------------------|--------|---------|---------|
| Overall              |                        | 17.280 | 0.016   | NA      |
| Dolichoderinae (n=5) | Dorylinae (n=2)        | 0.000  | 1.000   | 1.000   |
|                      | Ectatomminae (n=3)     | 1.800  | 0.180   | 0.296   |
|                      | Formicinae (n=8)       | 0.086  | 0.770   | 0.897   |
|                      | Myrmicinae (n=14)      | 0.000  | 1.000   | 1.000   |
|                      | Paraponerinae (n=2)    | 2.400  | 0.121   | 0.226   |
|                      | Ponerinae (n=9)        | 4.271  | 0.039   | 0.153   |
|                      | Pseudomyrmicinae (n=3) | 5.000  | 0.025   | 0.153   |
| Dorylinae (n=2)      | Ectatomminae (n=3)     | 1.333  | 0.248   | 0.347   |
|                      | Formicinae (n=8)       | 0.000  | 1.000   | 1.000   |
|                      | Myrmicinae (n=14)      | 0.000  | 1.000   | 1.000   |
|                      | Paraponerinae (n=2)    | 0.600  | 0.439   | 0.585   |
|                      | Ponerinae (n=9)        | 2.722  | 0.099   | 0.205   |
|                      | Pseudomyrmicinae (n=3) | 3.000  | 0.083   | 0.205   |
| Ectatomminae (n=3)   | Formicinae (n=8)       | 2.667  | 0.102   | 0.205   |
|                      | Myrmicinae (n=14)      | 2.683  | 0.101   | 0.205   |
|                      | Paraponerinae (n=2)    | 0.333  | 0.564   | 0.717   |
|                      | Ponerinae (n=9)        | 5.342  | 0.021   | 0.153   |
|                      | Pseudomyrmicinae (n=3) | 3.857  | 0.049   | 0.154   |
| Formicinae (n=8)     | Myrmicinae (n=14)      | 0.117  | 0.733   | 0.892   |
|                      | Paraponerinae (n=2)    | 1.705  | 0.192   | 0.298   |
|                      | Ponerinae (n=9)        | 4.481  | 0.034   | 0.153   |
|                      | Pseudomyrmicinae (n=3) | 5.042  | 0.025   | 0.153   |
| Myrmicinae (n=14)    | Paraponerinae (n=2)    | 1.613  | 0.204   | 0.300   |
|                      | Ponerinae (n=9)        | 4.063  | 0.044   | 0.153   |
|                      | Pseudomyrmicinae (n=3) | 4.063  | 0.044   | 0.153   |
| Paraponerinae (n=2)  | Ponerinae (n=9)        | 4.500  | 0.034   | 0.153   |
|                      | Pseudomyrmicinae (n=3) | 3.000  | 0.083   | 0.205   |
| Ponerinae (n=9)      | Pseudomyrmicinae (n=3) | 1.923  | 0.166   | 0.290   |

Faith's PD habitat whole dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=24) | City (n=22) | 0.213 | 0.644   | 0.644   |

|                   |                   |       |       |       |
|-------------------|-------------------|-------|-------|-------|
| Herbivorous (n=4) | Omnivorous (n=10) | 0.000 | 1.000 | 1.000 |
|-------------------|-------------------|-------|-------|-------|

Pielou's evenness subfamily filtered dataset

| Group 1              | Group 2             | H      | p-value | q-value |
|----------------------|---------------------|--------|---------|---------|
| Overall              |                     | 11.378 | 0.044   | NA      |
| Dolichoderinae (n=2) | Ectatomminae (n=2)  | 2.400  | 0.121   | 0.228   |
|                      | Formicinae (n=4)    | 0.214  | 0.643   | 0.804   |
|                      | Myrmicinae (n=6)    | 0.000  | 1.000   | 1.000   |
|                      | Paraponerinae (n=2) | 0.600  | 0.439   | 0.598   |
|                      | Ponerinae (n=5)     | 2.400  | 0.121   | 0.228   |
|                      |                     |        |         |         |
| Ectatomminae (n=2)   | Formicinae (n=4)    | 3.429  | 0.064   | 0.192   |
|                      | Myrmicinae (n=6)    | 4.000  | 0.046   | 0.192   |
|                      | Paraponerinae (n=2) | 0.000  | 1.000   | 1.000   |
| Formicinae (n=4)     | Ponerinae (n=5)     | 3.750  | 0.053   | 0.192   |
|                      | Myrmicinae (n=6)    | 0.045  | 0.831   | 0.959   |
|                      | Paraponerinae (n=2) | 0.857  | 0.355   | 0.532   |
|                      | Ponerinae (n=5)     | 2.940  | 0.086   | 0.216   |
| Myrmicinae (n=6)     | Paraponerinae (n=2) | 1.778  | 0.182   | 0.304   |
|                      | Ponerinae (n=5)     | 4.800  | 0.028   | 0.192   |
| Paraponerinae (n=2)  | Ponerinae (n=5)     | 3.750  | 0.053   | 0.192   |

Faith's PD habitat filtered dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=10) | City (n=11) | 0.079 | 0.778   | 0.778   |

Faith's PD nesting mode whole dataset

| Group 1       | Group 2      | H      | p-value | q-value |
|---------------|--------------|--------|---------|---------|
| Overall       |              | 12.159 | 0.002   | NA      |
| Ground (n=21) | Rotten (n=7) | 9.307  | 0.002   | 0.006   |
|               | Tree (n=18)  | 1.013  | 0.008   | 0.012   |
| Rotten (n=7)  | Tree (n=18)  | 0.824  | 0.364   | 0.386   |

Faith's PD diet whole dataset

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 0.424 | 0.809   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 0.320 | 0.571   | 0.857   |
|                    | Omnivorous (n=24) | 0.001 | 0.975   | 0.975   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 0.371 | 0.542   | 0.857   |

Faith's PD subfamily whole dataset

| Group 1              | Group 2                | H      | p-value | q-value |
|----------------------|------------------------|--------|---------|---------|
| Overall              |                        | 12.113 | 0.097   | NA      |
| Dolichoderinae (n=5) | Dorylinae (n=2)        | 1.350  | 0.245   | 0.386   |
|                      | Ectatomminae (n=3)     | 3.756  | 0.053   | 0.237   |
|                      | Formicinae (n=8)       | 0.000  | 1.000   | 1.000   |
|                      | Myrmicinae (n=14)      | 1.137  | 0.711   | 0.948   |
|                      | Paraponerinae (n=2)    | 3.750  | 0.053   | 0.237   |
|                      | Ponerinae (n=9)        | 0.040  | 0.841   | 0.961   |
|                      | Pseudomyrmicinae (n=3) | 0.022  | 0.881   | 0.961   |
| Dorylinae (n=2)      | Ectatomminae (n=3)     | 1.333  | 0.248   | 0.386   |
|                      | Formicinae (n=8)       | 2.455  | 0.117   | 0.273   |
|                      | Myrmicinae (n=14)      | 2.521  | 0.112   | 0.273   |
|                      | Paraponerinae (n=2)    | 2.400  | 0.121   | 0.273   |
|                      | Ponerinae (n=9)        | 1.389  | 0.239   | 0.386   |
|                      | Pseudomyrmicinae (n=3) | 1.333  | 0.248   | 0.386   |
| Ectatomminae (n=3)   | Formicinae (n=8)       | 4.167  | 0.041   | 0.237   |
|                      | Myrmicinae (n=14)      | 5.143  | 0.023   | 0.237   |
|                      | Paraponerinae (n=2)    | 3.000  | 0.083   | 0.259   |
|                      | Ponerinae (n=9)        | 1.923  | 0.166   | 0.331   |
|                      | Pseudomyrmicinae (n=3) | 2.333  | 0.127   | 0.273   |
| Formicinae (n=8)     | Myrmicinae (n=14)      | 0.377  | 0.539   | 0.789   |
|                      | Paraponerinae (n=2)    | 4.364  | 0.037   | 0.237   |

Faith's PD nesting mode filtered dataset

| Group 1       | Group 2      | H      | p-value | q-value |
|---------------|--------------|--------|---------|---------|
| Overall       |              | 10.139 | 0.007   | NA      |
| Ground (n=11) | Rotten (n=4) | 5.523  | 0.019   | 0.028   |
|               | Tree (n=6)   | 7.364  | 0.007   | 0.020   |
| Rotten (n=4)  | Tree (n=6)   | 0.409  | 0.522   | 0.522   |

Faith's PD diet filtered dataset

| Group 1           | Group 2           | H     | p-value | q-value |
|-------------------|-------------------|-------|---------|---------|
| Overall           |                   | 1.019 | 0.601   | NA      |
| Carnivorous (n=7) | Herbivorous (n=4) | 0.095 | 0.758   | 0.758   |
|                   | Omnivorous (n=10) | 0.231 | 0.630   | 0.758   |
| Herbivorous (n=4) | Omnivorous (n=10) | 1.413 | 0.234   | 0.703   |

Faith's PD subfamily filtered dataset

| Group 1              | Group 2             | H      | p-value | q-value |
|----------------------|---------------------|--------|---------|---------|
| Overall              |                     | 10.655 | 0.059   | NA      |
| Dolichoderinae (n=2) | Ectatomminae (n=2)  | 2.400  | 0.121   | 0.228   |
|                      | Formicinae (n=4)    | 0.929  | 0.165   | 0.275   |
|                      | Myrmicinae (n=6)    | 0.111  | 0.739   | 0.739   |
|                      | Paraponerinae (n=2) | 2.400  | 0.121   | 0.228   |
|                      | Ponerinae (n=5)     | 0.150  | 0.699   | 0.739   |
|                      | Formicinae (n=4)    | 0.857  | 0.355   | 0.443   |
| Ectatomminae (n=2)   | Myrmicinae (n=6)    | 4.000  | 0.046   | 0.192   |
|                      | Paraponerinae (n=2) | 2.400  | 0.121   | 0.228   |
|                      | Ponerinae (n=5)     | 3.750  | 0.053   | 0.192   |
| Formicinae (n=4)     | Myrmicinae (n=6)    | 1.636  | 0.201   | 0.301   |
|                      | Paraponerinae (n=2) | 3.429  | 0.064   | 0.192   |
|                      | Ponerinae (n=5)     | 1.500  | 0.221   | 0.301   |
| Myrmicinae (n=6)     | Paraponerinae (n=2) | 4.000  | 0.046   | 0.192   |
|                      | Ponerinae (n=5)     | 0.133  | 0.715   | 0.739   |
| Paraponerinae (n=2)  | Ponerinae (n=5)     | 3.750  | 0.053   | 0.192   |

|                     |                        |       |       |       |
|---------------------|------------------------|-------|-------|-------|
| Myrmicinae (n=14)   | Ponerinae (n=9)        | 0.333 | 0.564 | 0.789 |
|                     | Pseudomyrmicinae (n=3) | 0.042 | 0.838 | 0.961 |
|                     | Paraponerinae (n=2)    | 4.941 | 0.026 | 0.237 |
|                     | Ponerinae (n=9)        | 0.016 | 0.900 | 0.961 |
|                     | Pseudomyrmicinae (n=3) | 0.016 | 0.900 | 0.961 |
| Paraponerinae (n=2) | Ponerinae (n=9)        | 3.556 | 0.059 | 0.237 |
|                     | Pseudomyrmicinae (n=3) | 3.000 | 0.083 | 0.259 |
| Ponerinae (n=9)     | Pseudomyrmicinae (n=3) | 0.009 | 0.926 | 0.961 |

ASV richness habitat whole dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=24) | City (n=22) | 0.148 | 0.700   | 0.700   |

ASV richness habitat filtered dataset

| Group 1           | Group 2     | H     | p-value | q-value |
|-------------------|-------------|-------|---------|---------|
| Rainforest (n=10) | City (n=11) | 0.011 | 0.916   | 0.916   |

ASV richness nesting mode whole dataset

| Group 1       | Group 2      | H      | p-value   | q-value |
|---------------|--------------|--------|-----------|---------|
| Overall       |              | 16.350 | 2.817E-04 | NA      |
| Ground (n=21) | Rotten (n=7) | 8.832  | 0.003     | 0.004   |
|               | Tree (n=18)  | 12.802 | 0.006     | 0.001   |
| Rotten (n=7)  | Tree (n=18)  | 0.023  | 0.880     | 0.880   |

ASV richness nesting mode filtered dataset

| Group 1       | Group 2      | H     | p-value | q-value |
|---------------|--------------|-------|---------|---------|
| Overall       |              | 8.350 | 0.015   | NA      |
| Ground (n=11) | Rotten (n=4) | 5.523 | 0.019   | 0.031   |
|               | Tree (n=6)   | 5.343 | 0.021   | 0.031   |
| Rotten (n=4)  | Tree (n=6)   | 0.286 | 0.593   | 0.593   |

ASV richness diet whole dataset

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 0.456 | 0.796   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 0.356 | 0.551   | 0.826   |
|                    | Omnivorous (n=24) | 0.024 | 0.877   | 0.877   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 0.372 | 0.542   | 0.826   |

ASV richness diet filtered dataset

| Group 1           | Group 2           | H     | p-value | q-value |
|-------------------|-------------------|-------|---------|---------|
| Overall           |                   | 2.072 | 0.355   | NA      |
| Carnivorous (n=7) | Herbivorous (n=4) | 0.722 | 0.395   | 0.395   |
|                   | Omnivorous (n=10) | 1.333 | 0.248   | 0.372   |
| Herbivorous (n=4) | Omnivorous (n=10) | 1.413 | 0.234   | 0.372   |

ASV richness subfamilies whole dataset

| Group 1              | Group 2            | H      | p-value | q-value |
|----------------------|--------------------|--------|---------|---------|
| Overall              |                    | 17.834 | 0.013   | NA      |
| Dolichoderinae (n=5) | Dorylinae (n=2)    | 0.600  | 0.439   | 0.572   |
|                      | Ectatomminae (n=3) | 3.756  | 0.053   | 0.148   |
|                      | Formicinae (n=8)   | 0.537  | 0.464   | 0.572   |

ASV richness subfamilies filtered dataset

| Group 1              | Group 2            | H      | p-value | q-value |
|----------------------|--------------------|--------|---------|---------|
| Overall              |                    | 11.380 | 0.044   | NA      |
| Dolichoderinae (n=2) | Ectatomminae (n=2) | 2.400  | 0.121   | 0.213   |
|                      | Formicinae (n=4)   | 0.857  | 0.355   | 0.483   |
|                      | Myrmicinae (n=6)   | 0.000  | 1.000   | 1.000   |

|                     |                        |       |       |       |
|---------------------|------------------------|-------|-------|-------|
|                     | Myrmicinae (n=14)      | 0.309 | 0.579 | 0.647 |
|                     | Paraponerinae (n=2)    | 3.750 | 0.053 | 0.148 |
|                     | Ponerinae (n=9)        | 0.004 | 0.947 | 0.947 |
|                     | Pseudomyrmicinae (n=3) | 1.800 | 0.180 | 0.280 |
| Dorylinae (n=2)     | Ectatomminae (n=3)     | 3.000 | 0.083 | 0.155 |
|                     | Formicinae (n=8)       | 0.274 | 0.600 | 0.647 |
|                     | Myrmicinae (n=14)      | 2.042 | 0.153 | 0.252 |
|                     | Paraponerinae (n=2)    | 2.400 | 0.121 | 0.212 |
|                     | Ponerinae (n=9)        | 0.889 | 0.346 | 0.484 |
|                     | Pseudomyrmicinae (n=3) | 3.000 | 0.083 | 0.155 |
| Ectatomminae (n=3)  | Formicinae (n=8)       | 4.186 | 0.041 | 0.148 |
|                     | Myrmicinae (n=14)      | 6.349 | 0.012 | 0.148 |
|                     | Paraponerinae (n=2)    | 0.333 | 0.564 | 0.647 |
|                     | Ponerinae (n=9)        | 5.342 | 0.021 | 0.148 |
|                     | Pseudomyrmicinae (n=3) | 3.857 | 0.049 | 0.148 |
| Formicinae (n=8)    | Myrmicinae (n=14)      | 1.683 | 0.195 | 0.287 |
|                     | Paraponerinae (n=2)    | 4.390 | 0.036 | 0.148 |
|                     | Ponerinae (n=9)        | 0.522 | 0.470 | 0.572 |
|                     | Pseudomyrmicinae (n=3) | 4.186 | 0.041 | 0.148 |
| Myrmicinae (n=14)   | Paraponerinae (n=2)    | 4.941 | 0.026 | 0.148 |
|                     | Ponerinae (n=9)        | 0.036 | 0.850 | 0.882 |
|                     | Pseudomyrmicinae (n=3) | 5.439 | 0.020 | 0.148 |
| Paraponerinae (n=2) | Ponerinae (n=9)        | 3.555 | 0.059 | 0.151 |
|                     | Pseudomyrmicinae (n=3) | 3.000 | 0.083 | 0.155 |
| Ponerinae (n=9)     | Pseudomyrmicinae (n=3) | 3.085 | 0.079 | 0.155 |

|                     |                     |       |       |       |
|---------------------|---------------------|-------|-------|-------|
|                     | Paraponerinae (n=2) | 2.400 | 0.121 | 0.213 |
|                     | Ponerinae (n=5)     | 0.150 | 0.699 | 0.806 |
| Ectatomminae (n=2)  | Formicinae (n=4)    | 0.429 | 0.064 | 0.160 |
|                     | Myrmicinae (n=6)    | 4.000 | 0.046 | 0.160 |
|                     | Paraponerinae (n=2) | 0.000 | 1.000 | 1.000 |
|                     | Ponerinae (n=5)     | 3.750 | 0.053 | 0.160 |
| Formicinae (n=4)    | Myrmicinae (n=6)    | 2.227 | 0.136 | 0.212 |
|                     | Paraponerinae (n=2) | 3.429 | 0.064 | 0.160 |
|                     | Ponerinae (n=5)     | 2.160 | 0.142 | 0.212 |
| Myrmicinae (n=6)    | Paraponerinae (n=2) | 4.000 | 0.046 | 0.160 |
|                     | Ponerinae (n=5)     | 0.410 | 0.522 | 0.652 |
| Paraponerinae (n=2) | Ponerinae (n=5)     | 3.750 | 0.053 | 0.160 |

**Supplementary File S3. Bacteria relative abundance of the 15 most abundant bacterial order for each factor.**

| <b>Factors</b>   |                        | Rickettsiales | Rhizobiales | Acetobacterales | Enterobacteriales | Lactobacillales | Burkholderiales | Xanthomonadales | Erysipelotrichales | Flavobacteriales | Pseudomonadales | Corynebacteriales | Entomoplasmatales | Opitutales | Sphingomonadales | Micrococcales |
|------------------|------------------------|---------------|-------------|-----------------|-------------------|-----------------|-----------------|-----------------|--------------------|------------------|-----------------|-------------------|-------------------|------------|------------------|---------------|
| <b>Subfamily</b> | Dolichoderinae (n=6)   | 39.33         | 15.36       | 8.96            | 0.14              | 14.41           | 0.66            | 0.55            | 0.00               | 0.10             | 0.73            | 6.98              | 0.00              | 0.02       | 0.24             | 4.55          |
|                  | Dorylinae (n=1)        | 0.05          | 1.83        | 0.26            | 1.87              | 3.68            | 5.11            | 1.39            | 48.64              | 10.69            | 4.13            | 0.20              | 10.08             | 0.00       | 0.52             | 0.71          |
|                  | Ectatomminae (n=3)     | 0.08          | 9.62        | 1.04            | 0.85              | 25.04           | 5.94            | 3.62            | 0.03               | 0.53             | 2.73            | 2.28              | 0.00              | 0.19       | 3.81             | 0.25          |
|                  | Formicinae (n=6)       | 13.21         | 2.88        | 19.50           | 33.98             | 3.27            | 1.85            | 1.18            | 0.01               | 0.18             | 0.41            | 3.81              | 0.00              | 0.03       | 2.83             | 0.20          |
|                  | Myrmicinae (n=14)      | 23.04         | 20.49       | 8.59            | 0.46              | 3.74            | 7.72            | 6.78            | 0.01               | 1.22             | 2.52            | 2.05              | 1.76              | 2.34       | 0.72             | 0.32          |
|                  | Paraponerinae (n=2)    | 0.05          | 5.03        | 0.70            | 0.55              | 1.17            | 4.10            | 6.03            | 0.05               | 0.10             | 20.60           | 0.84              | 0.00              | 0.06       | 0.37             | 0.43          |
|                  | Ponerinae (n=9)        | 48.58         | 18.00       | 0.22            | 0.11              | 1.54            | 0.66            | 0.79            | 5.71               | 7.86             | 0.29            | 0.16              | 0.00              | 0.10       | 0.12             | 0.11          |
|                  | Pseudomyrmicinae (n=3) | 0.00          | 0.07        | 3.40            | 0.00              | 0.10            | 0.15            | 0.00            | 0.00               | 0.03             | 0.03            | 0.00              | 0.55              | 0.00       | 0.00             | 0.03          |
| <b>Genus</b>     | Crematogaster (n=2)    | 78.58         | 10.85       | 0.07            | 0.00              | 4.74            | 0.71            | 0.04            | 0.00               | 0.49             | 0.31            | 0.27              | 0.00              | 0.06       | 0.17             | 0.17          |
|                  | Daceton (n=2)          | 0.10          | 72.49       | 11.31           | 0.05              | 0.05            | 0.05            | 0.86            | 0.00               | 0.01             | 0.27            | 0.00              | 13.20             | 0.00       | 0.00             | 0.00          |
|                  | Dolichoderus (n=2)     | 49.05         | 38.06       | 0.31            | 0.29              | 0.56            | 0.41            | 0.19            | 0.00               | 0.13             | 0.05            | 0.79              | 0.00              | 0.00       | 0.45             | 0.38          |
|                  | Eciton (n=1)           | 0.00          | 3.29        | 0.00            | 3.73              | 1.61            | 8.83            | 2.67            | 34.47              | 21.37            | 4.68            | 0.29              | 0.93              | 0.00       | 0.87             | 0.00          |
|                  | Ectatomma (n=3)        | 0.08          | 9.62        | 1.04            | 0.85              | 25.04           | 5.94            | 3.62            | 0.03               | 0.53             | 2.73            | 2.28              | 0.00              | 0.22       | 3.81             | 0.71          |
|                  | Gigantiops (n=2)       | 0.05          | 10.46       | 22.59           | 0.32              | 0.38            | 6.61            | 3.33            | 0.00               | 0.22             | 1.87            | 11.28             | 0.00              | 0.00       | 11.04            | 0.71          |
|                  | Labidus (n=1)          | 0.00          | 0.37        | 0.09            | 0.00              | 5.75            | 1.40            | 0.00            | 62.80              | 0.00             | 3.75            | 0.17              | 19.24             | 0.00       | 0.18             | 0.00          |
|                  | Neoponera (n=2)        | 0.08          | 45.07       | 0.08            | 0.00              | 1.77            | 2.05            | 3.10            | 5.70               | 35.31            | 0.39            | 0.25              | 0.02              | 0.10       | 0.31             | 0.27          |
|                  | Nylanderia (n=1)       | 0.00          | 0.77        | 89.50           | 0.27              | 0.10            | 0.35            | 0.10            | 0.10               | 0.84             | 0.92            | 0.56              | 0.00              | 0.00       | 0.17             | 0.20          |
|                  | Odontomachus (n=6)     | 72.87         | 11.60       | 0.10            | 0.17              | 1.66            | 0.21            | 0.12            | 6.66               | 0.03             | 0.29            | 0.06              | 0.00              | 0.02       | 0.02             | 0.06          |
|                  | Paraponera (n=2)       | 0.05          | 5.03        | 0.70            | 0.55              | 1.17            | 4.10            | 6.03            | 0.05               | 0.20             | 20.60           | 0.84              | 0.00              | 0.06       | 0.36             | 0.43          |
|                  | Pseudomyrmex (n=3)     | 62.61         | 0.07        | 3.40            | 0.00              | 0.10            | 0.15            | 0.00            | 0.00               | 0.03             | 0.03            | 0.00              | 0.55              | 0.00       | 0.00             | 0.02          |
|                  | Solenopsis (n=2)       | 59.59         | 1.38        | 0.04            | 1.62              | 3.94            | 5.21            | 0.38            | 0.03               | 0.03             | 3.76            | 0.08              | 0.00              | 0.00       | 0.00             | 0.00          |
| <b>Diet</b>      | Carnivorous (n=13)     | 29.14         | 21.38       | 1.73            | 0.38              | 1.57            | 1.65            | 1.57            | 9.92               | 6.16             | 3.49            | 0.23              | 3.10              | 0.03       | 0.18             | 0.12          |
|                  | Herbivorous (n=9)      | 11.90         | 23.63       | 1.90            | 0.51              | 4.40            | 11.00           | 10.98           | 0.00               | 1.86             | 2.72            | 3.45              | 0.00              | 3.89       | 1.25             | 0.58          |
|                  | Omnivorous (n=24)      | 33.08         | 3.57        | 13.76           | 12.71             | 8.61            | 2.40            | 1.08            | 0.02               | 0.22             | 2.23            | 3.27              | 0.08              | 0.04       | 1.59             | 1.21          |
| <b>Nest</b>      | Ground (n=21)          | 19.90         | 10.25       | 4.36            | 3.90              | 7.65            | 3.51            | 1.99            | 4.98               | 4.44             | 5.42            | 3.13              | 0.92              | 0.07       | 2.13             | 0.34          |
|                  | Rotten (n=7)           | 41.62         | 0.28        | 24.53           | 28.69             | 0.82            | 0.16            | 0.10            | 0.01               | 0.16             | 0.21            | 0.24              | 0.00              | 0.01       | 0.07             | 0.07          |
|                  | Tree (n=18)            | 30.24         | 21.36       | 4.40            | 0.06              | 4.40            | 5.45            | 5.77            | 2.20               | 0.88             | 0.31            | 1.99              | 1.56              | 1.95       | 0.07             | 1.43          |
| <b>Habitat</b>   | City (n=22)            | 23.60         | 8.98        | 10.93           | 8.39              | 8.52            | 4.45            | 3.34            | 0.00               | 3.81             | 1.78            | 3.33              | 0.44              | 1.03       | 1.85             | 0.28          |
|                  | Rainforest (n=24)      | 30.39         | 16.87       | 3.95            | 3.94              | 2.34            | 3.09            | 2.97            | 6.19               | 1.08             | 3.55            | 2.13              | 1.59              | 0.50       | 0.25             | 1.13          |

The cells colored in red in each table bacterial abundance higher than 10%.

**Supplementary File S4. Statistic calculations of 16S rRNA beta diversity metrics for each factor.**

The two tested beta diversity metrics are Bray-Curtis and Weighted unifrac. Each metric is calculated for the whole dataset and the forest/city dataset. The cells colored in red in each table represent p-values < 0.05. The statistical p-values were obtained with PERMANOVAs.

Bray-Curtis habitat whole dataset

| Group 1           | Group 2     | pseudo-F | p-value | q-value |
|-------------------|-------------|----------|---------|---------|
| Rainforest (n=24) | City (n=22) | 0.920    | 0.619   | 0.619   |

Bray-Curtis habitat filtered dataset

| Group 1           | Group 2     | pseudo-F | p-value | q-value |
|-------------------|-------------|----------|---------|---------|
| Rainforest (n=10) | City (n=11) | 0.645    | 0.987   | 0.987   |

Bray-Curtis nesting mode whole dataset

| Group 1       | Group 2      | pseudo-F | p-value | q-value |
|---------------|--------------|----------|---------|---------|
| Overall       |              | 1.473    | 0.005   | NA      |
| Ground (n=21) | Rotten (n=7) | 1.659    | 0.016   | 0.042   |
|               | Tree (n=18)  | 1.268    | 0.049   | 0.049   |
| Rotten (n=7)  | Tree (n=18)  | 1.601    | 0.028   | 0.042   |

Bray-Curtis nesting mode filtered dataset

| Group 1       | Group 2      | pseudo-F | p-value | q-value |
|---------------|--------------|----------|---------|---------|
| Overall       |              | 1.688    | 0.004   | NA      |
| Ground (n=11) | Rotten (n=4) | 1.669    | 0.027   | 0.027   |
|               | Tree (n=6)   | 1.458    | 0.001   | 0.003   |
| Rotten (n=4)  | Tree (n=6)   | 2.192    | 0.006   | 0.009   |

Bray-Curtis diet whole dataset

| Group 1            | Group 2           | pseudo-F | p-value | q-value |
|--------------------|-------------------|----------|---------|---------|
| Overall            |                   | 1.361    | 0.018   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 1.618    | 0.012   | 0.018   |
|                    | Omnivorous (n=24) | 1.096    | 0.255   | 0.255   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 1.482    | 0.007   | 0.018   |

Bray-Curtis diet filtered dataset

| Group 1           | Group 2           | pseudo-F | p-value | q-value |
|-------------------|-------------------|----------|---------|---------|
| Overall           |                   | 1.578    | 0.008   | NA      |
| Carnivorous (n=7) | Herbivorous (n=4) | 1.636    | 0.041   | 0.062   |
|                   | Omnivorous (n=10) | 1.694    | 0.082   | 0.062   |
| Herbivorous (n=4) | Omnivorous (n=10) | 1.357    | 0.039   | 0.093   |

Bray-Curtis subfamily whole dataset

| Group 1              | Group 2                | pseudo-F | p-value | q-value |
|----------------------|------------------------|----------|---------|---------|
| Overall              |                        | 1.368    | 0.018   | NA      |
| Dolichoderinae (n=5) | Dorylinae (n=2)        | 1.694    | 0.045   | 0.165   |
|                      | Ectatomminae (n=3)     | 1.149    | 0.106   | 0.165   |
|                      | Formicinae (n=8)       | 1.471    | 0.037   | 0.165   |
|                      | Myrmicinae (n=14)      | 1.117    | 0.230   | 0.293   |
|                      | Paraponerinae (n=2)    | 1.164    | 0.097   | 0.165   |
|                      | Ponerinae (n=9)        | 1.021    | 0.287   | 0.349   |
|                      | Pseudomyrmicinae (n=3) | 0.833    | 0.726   | 0.726   |
| Dorylinae (n=2)      | Ectatomminae (n=3)     | 1.692    | 0.088   | 0.165   |
|                      | Formicinae (n=8)       | 1.832    | 0.071   | 0.165   |
|                      | Myrmicinae (n=14)      | 1.675    | 0.030   | 0.165   |
|                      | Paraponerinae (n=2)    | 1.948    | 0.368   | 0.429   |
|                      | Ponerinae (n=9)        | 1.981    | 0.023   | 0.165   |
|                      | Pseudomyrmicinae (n=3) | 1.650    | 0.123   | 0.172   |
| Ectatomminae (n=3)   | Formicinae (n=8)       | 1.295    | 0.145   | 0.193   |

Bray-Curtis subfamily filtered dataset

| Group 1              | Group 2             | pseudo-F | p-value | q-value |
|----------------------|---------------------|----------|---------|---------|
| Overall              |                     | 1.605    | 0.002   | NA      |
| Dolichoderinae (n=2) | Ectatomminae (n=2)  | 1.111    | 0.366   | 0.392   |
|                      | Formicinae (n=4)    | 1.379    | 0.112   | 0.202   |
|                      | Myrmicinae (n=6)    | 1.249    | 0.148   | 0.202   |
|                      | Paraponerinae (n=2) | 1.125    | 0.325   | 0.375   |
|                      | Ponerinae (n=5)     | 1.828    | 0.049   | 0.140   |
|                      | Formicinae (n=4)    | 1.380    | 0.142   | 0.202   |
| Ectatomminae (n=2)   | Myrmicinae (n=6)    | 1.250    | 0.193   | 0.241   |
|                      | Paraponerinae (n=2) | 0.971    | 0.664   | 0.664   |
|                      | Ponerinae (n=5)     | 1.868    | 0.056   | 0.140   |
| Formicinae (n=4)     | Myrmicinae (n=6)    | 1.704    | 0.019   | 0.140   |
|                      | Paraponerinae (n=2) | 1.398    | 0.148   | 0.202   |
|                      | Ponerinae (n=5)     | 2.402    | 0.035   | 0.140   |
| Myrmicinae (n=6)     | Paraponerinae (n=2) | 1.282    | 0.111   | 0.202   |
|                      | Ponerinae (n=5)     | 2.301    | 0.009   | 0.135   |

|                     |                        |       |       |       |
|---------------------|------------------------|-------|-------|-------|
|                     | Myrmicinae (n=14)      | 1.183 | 0.105 | 0.165 |
|                     | Paraponerinae (n=2)    | 0.978 | 0.633 | 0.656 |
|                     | Ponerinae (n=9)        | 1.424 | 0.076 | 0.165 |
|                     | Pseudomyrmicinae (n=3) | 1.079 | 0.093 | 0.165 |
| Formicinae (n=8)    | Myrmicinae (n=14)      | 1.712 | 0.001 | 0.028 |
|                     | Paraponerinae (n=2)    | 1.315 | 0.084 | 0.165 |
|                     | Ponerinae (n=9)        | 2.068 | 0.006 | 0.084 |
|                     | Pseudomyrmicinae (n=3) | 1.282 | 0.117 | 0.172 |
| Myrmicinae (n=14)   | Paraponerinae (n=2)    | 1.196 | 0.047 | 0.165 |
|                     | Ponerinae (n=9)        | 1.421 | 0.079 | 0.165 |
|                     | Pseudomyrmicinae (n=3) | 0.966 | 0.526 | 0.589 |
| Paraponerinae (n=2) | Ponerinae (n=9)        | 1.396 | 0.068 | 0.165 |
|                     | Pseudomyrmicinae (n=3) | 1.089 | 0.103 | 0.165 |
| Ponerinae (n=9)     | Pseudomyrmicinae (n=3) | 0.756 | 0.577 | 0.621 |

|                     |                 |       |       |       |
|---------------------|-----------------|-------|-------|-------|
| Paraponerinae (n=2) | Ponerinae (n=5) | 1.855 | 0.051 | 0.140 |
|---------------------|-----------------|-------|-------|-------|

Weighted UniFrac habitat whole dataset

| Group 1           | Group 2     | pseudo-F | p-value | q-value |
|-------------------|-------------|----------|---------|---------|
| Rainforest (n=24) | City (n=22) | 0.945    | 0.502   | 0.502   |

Weighted UniFrac habitat filtered dataset

| Group 1           | Group 2     | pseudo-F | p-value | q-value |
|-------------------|-------------|----------|---------|---------|
| Rainforest (n=10) | City (n=11) | 0.515    | 0.965   | 0.965   |

Weighted UniFrac nesting mode whole dataset

| Group 1       | Group 2      | pseudo-F | p-value | q-value |
|---------------|--------------|----------|---------|---------|
| Overall       |              | 2.217    | 0.002   | NA      |
| Ground (n=21) | Rotten (n=7) | 2.533    | 0.006   | 0.018   |
|               | Tree (n=18)  | 2.122    | 0.026   | 0.036   |
| Rotten (n=7)  | Tree (n=18)  | 1.996    | 0.057   | 0.057   |

Weighted UniFrac nesting mode filtered dataset

| Group 1       | Group 2      | pseudo-F | p-value | q-value |
|---------------|--------------|----------|---------|---------|
| Overall       |              | 1.641    | 0.021   | NA      |
| Ground (n=11) | Rotten (n=4) | 1.906    | 0.052   | 0.092   |
|               | Tree (n=6)   | 1.347    | 0.155   | 0.155   |
| Rotten (n=4)  | Tree (n=6)   | 1.875    | 0.061   | 0.092   |

Weighted UniFrac diet whole dataset

| Group 1            | Group 2           | pseudo-F | p-value | q-value |
|--------------------|-------------------|----------|---------|---------|
| Overall            |                   | 1.675    | 0.029   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 1.418    | 0.046   | 0.157   |
|                    | Omnivorous (n=24) | 1.751    | 0.062   | 0.093   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 1.797    | 0.059   | 0.093   |

Weighted UniFrac diet filtered dataset

| Group 1           | Group 2           | pseudo-F | p-value | q-value |
|-------------------|-------------------|----------|---------|---------|
| Overall           |                   | 1.300    | 0.145   | NA      |
| Carnivorous (n=7) | Herbivorous (n=4) | 1.049    | 0.360   | 0.519   |
|                   | Omnivorous (n=10) | 1.691    | 0.050   | 0.150   |
| Herbivorous (n=4) | Omnivorous (n=10) | 0.935    | 0.519   | 0.519   |

Weighted UniFrac subfamily whole dataset

| Group 1              | Group 2            | pseudo-F | p-value | q-value |
|----------------------|--------------------|----------|---------|---------|
| Overall              |                    | 1.715    | 0.025   | NA      |
| Dolichoderinae (n=5) | Dorylinae (n=2)    | 3.169    | 0.043   | 0.100   |
|                      | Ectatomminae (n=3) | 1.332    | 0.152   | 0.193   |
|                      | Formicinae (n=8)   | 1.865    | 0.063   | 0.126   |
|                      | Myrmicinae (n=14)  | 0.933    | 0.465   | 0.482   |

Weighted UniFrac subfamily filtered dataset

| Group 1              | Group 2             | pseudo-F | p-value | q-value |
|----------------------|---------------------|----------|---------|---------|
| Overall              |                     | 2.144    | 0.001   | NA      |
| Dolichoderinae (n=2) | Ectatomminae (n=2)  | 1.418    | 0.332   | 0.385   |
|                      | Formicinae (n=4)    | 1.291    | 0.382   | 0.409   |
|                      | Myrmicinae (n=6)    | 1.728    | 0.105   | 0.225   |
|                      | Paraponerinae (n=2) | 2.300    | 0.334   | 0.385   |

|                     |                        |       |       |       |
|---------------------|------------------------|-------|-------|-------|
|                     | Paraponerinae (n=2)    | 2.987 | 0.051 | 0.110 |
|                     | Ponerinae (n=9)        | 0.331 | 0.964 | 0.964 |
|                     | Pseudomyrmicinae (n=3) | 1.083 | 0.285 | 0.333 |
| Dorylinae (n=2)     | Ectatomminae (n=3)     | 3.643 | 0.106 | 0.156 |
|                     | Formicinae (n=8)       | 3.814 | 0.025 | 0.095 |
|                     | Myrmicinae (n=14)      | 5.631 | 0.013 | 0.073 |
|                     | Paraponerinae (n=2)    | 3.102 | 0.335 | 0.375 |
|                     | Ponerinae (n=9)        | 3.043 | 0.027 | 0.095 |
|                     | Pseudomyrmicinae (n=3) | 3.447 | 0.099 | 0.156 |
|                     | Formicinae (n=8)       | 2.068 | 0.112 | 0.156 |
| Ectatomminae (n=3)  | Myrmicinae (n=14)      | 2.021 | 0.042 | 0.100 |
|                     | Paraponerinae (n=2)    | 1.925 | 0.106 | 0.156 |
|                     | Ponerinae (n=9)        | 1.659 | 0.117 | 0.156 |
|                     | Pseudomyrmicinae (n=3) | 3.033 | 0.105 | 0.156 |
|                     | Myrmicinae (n=14)      | 3.119 | 0.001 | 0.028 |
| Formicinae (n=8)    | Paraponerinae (n=2)    | 2.837 | 0.040 | 0.100 |
|                     | Ponerinae (n=9)        | 2.954 | 0.002 | 0.028 |
|                     | Pseudomyrmicinae (n=3) | 2.833 | 0.013 | 0.073 |
|                     | Paraponerinae (n=2)    | 5.045 | 0.004 | 0.037 |
| Myrmicinae (n=14)   | Ponerinae (n=9)        | 1.387 | 0.174 | 0.212 |
|                     | Pseudomyrmicinae (n=3) | 2.679 | 0.026 | 0.095 |
|                     | Paraponerinae (n=2)    | 3.184 | 0.031 | 0.096 |
| Paraponerinae (n=2) | Pseudomyrmicinae (n=3) | 2.743 | 0.105 | 0.156 |
|                     | Ponerinae (n=9)        | 1.057 | 0.459 | 0.482 |

|                     |                     |       |       |       |
|---------------------|---------------------|-------|-------|-------|
| Ectatomminae (n=2)  | Ponerinae (n=5)     | 1.734 | 0.140 | 0.250 |
|                     | Formicinae (n=4)    | 1.174 | 0.529 | 0.529 |
|                     | Myrmicinae (n=6)    | 1.374 | 0.244 | 0.366 |
|                     | Paraponerinae (n=2) | 1.507 | 0.323 | 0.385 |
|                     | Ponerinae (n=5)     | 2.098 | 0.150 | 0.250 |
| Formicinae (n=4)    | Myrmicinae (n=6)    | 2.034 | 0.035 | 0.153 |
|                     | Paraponerinae (n=2) | 2.164 | 0.051 | 0.153 |
|                     | Ponerinae (n=5)     | 2.507 | 0.009 | 0.350 |
| Myrmicinae (n=6)    | Paraponerinae (n=2) | 4.061 | 0.040 | 0.153 |
|                     | Ponerinae (n=5)     | 1.769 | 0.094 | 0.225 |
| Paraponerinae (n=2) | Ponerinae (n=5)     | 4.152 | 0.042 | 0.153 |



Supplementary File S5. 16S rRNA SIMPER statistics for each factor in the whole dataset and the forest/city dataset.

SIMPER statistics according to the ant subfamily for the whole dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |           |              |            |            |               |           |                  |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|-----------|--------------|------------|------------|---------------|-----------|------------------|
|                                      |                       |                                |                | Dolichoderinae             | Dorylinae | Ectatomminae | Formicinae | Myrmicinae | Paraponerinae | Ponerinae | Pseudomyrmicinae |
| Rickettsiales                        | 25.01                 | 28.98                          | 28.98          | 1.97E+04                   | 6.5       | 25.3         | 7.65E+03   | 8.66E+03   | 3             | 2.46E+04  | 1.91E+04         |
| Rhizobiales                          | 12.19                 | 14.13                          | 43.12          | 4.22E+03                   | 669       | 3.33E+03     | 992        | 1.02E+04   | 1.53E+03      | 8.73E+03  | 15.7             |
| Acetobacterales                      | 7.158                 | 8.295                          | 51.41          | 6.96E+03                   | 92        | 363          | 7.14E+03   | 1.79E+03   | 216           | 4.56E+01  | 1.32E+03         |
| Enterobacterales                     | 6.956                 | 8.062                          | 59.47          | 40                         | 701       | 323          | 1.47E+04   | 42.3       | 197           | 56.3      | 0                |
| Lactobacillales                      | 5.900                 | 6.838                          | 66.31          | 9.87E+03                   | 1.10E+03  | 9.57+03      | 1.11E+03   | 1.21E+03   | 3.97E+02      | 629       | 17               |
| Erysipelotrichales                   | 3.907                 | 4.528                          | 70.84          | 0                          | 1.51E+04  | 3.33         | 1          | 0.6        | 4.5           | 3.56E+03  | 0                |
| Burkholderiales                      | 3.535                 | 4.097                          | 74.94          | 199                        | 1.85E+03  | 2.15+03      | 620        | 3.68E+03   | 1.31E+03      | 283       | 24               |
| Xanthomonadales                      | 3.225                 | 3.738                          | 78.67          | 171                        | 508       | 1.32+03      | 358        | 3.58E+03   | 2.10E+03      | 336       | 0                |
| Flavobacteriales                     | 2.888                 | 3.348                          | 82.02          | 31.8                       | 4.01E+03  | 186          | 49         | 619        | 65            | 3.60E+03  | 1.67             |
| Pseudomonadales                      | 2.602                 | 3.016                          | 85.04          | 244                        | 1.37E+03  | 1.02E+03     | 812        | 324        | 7.41E+03      | 113       | 1                |
| Corynebacterales                     | 2.088                 | 2.420                          | 87.46          | 2.30E+03                   | 78        | 838          | 1.34E+03   | 358        | 263           | 50.7      | 2.33             |
| Entomoplasmatales                    | 1.088                 | 1.261                          | 88.72          | 3                          | 2.83E+03  | 0            | 0          | 926        | 1             | 3         | 208              |
| Sphingomonadales                     | 0.990                 | 1.148                          | 89.87          | 73                         | 187       | 1.41E+03     | 872        | 98.5       | 142           | 43.4      | 3.67             |
| Opitutales                           | 0.863                 | 1.000                          | 90.87          | 9.2                        | 4.5       | 71           | 3.63       | 1.28E+03   | 24            | 13.1      | 0                |
| Micrococcales                        | 0.781                 | 0.905                          | 91.77          | 1.47E+03                   | 5         | 255          | 92.9       | 145        | 142           | 45.3      | 9                |

SIMPER statistics according to the ant subfamily for the forest/city dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |              |            |            |               |           |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|--------------|------------|------------|---------------|-----------|
|                                      |                       |                                |                | Dolichoderinae             | Ectatomminae | Formicinae | Myrmicinae | Paraponerinae | Ponerinae |
| Rhizobiales                          | 16.09                 | 19.02                          | 19.02          | 2.29E+03                   | 5.71E+03     | 1.41E+03   | 1.69E+04   | 1.53E+03      | 1.08E+04  |
| Rickettsiales                        | 14.92                 | 17.64                          | 36.66          | 19                         | 25           | 1.19E+04   | 23.2       | 3             | 2.15E+04  |
| Acetobacterales                      | 8.182                 | 9.673                          | 46.34          | 664                        | 325          | 5.94E+03   | 7.30E+03   | 216           | 2.58E+03  |
| Lactobacillales                      | 5.737                 | 6.782                          | 53.12          | 890                        | 311          | 789        | 8.19E+03   | 397           | 2.33E+03  |
| Flavobacteriales                     | 5.481                 | 6.480                          | 59.60          | 1.62E+04                   | 4.12E+03     | 115        | 134        | 65            | 16        |
| Burkholderiales                      | 4.410                 | 5.214                          | 64.81          | 2.18E+03                   | 5.81E+03     | 1.74E+03   | 3.33E+03   | 1.31E+03      | 163       |
| Enterobacterales                     | 4.088                 | 4.833                          | 69.65          | 75.5                       | 0            | 2.77E+03   | 37.8       | 197           | 3.21E+03  |
| Pseudomonadales                      | 3.513                 | 4.153                          | 73.80          | 633                        | 21.5         | 771        | 680        | 7.41E+03      | 110       |
| Corynebacterales                     | 3.058                 | 3.615                          | 77.41          | 3.31E+03                   | 275          | 273        | 2.27E+03   | 263           | 176       |
| Xanthomonadales                      | 3.045                 | 3.600                          | 81.01          | 2.23E+03                   | 5.73E+03     | 917        | 907        | 2.10E+03      | 141       |
| Sphingomonadales                     | 1.720                 | 2.033                          | 83.05          | 3.33E+03                   | 115          | 1.06E+03   | 71.3       | 142           | 76.8      |
| Opitutales                           | 1.452                 | 1.716                          | 84.76          | 11.5                       | 5.14E+03     | 53         | 181        | 24            | 16        |
| Entomoplasmatales                    | 1.344                 | 1.588                          | 86.35          | 0                          | 0            | 0          | 2.31E+03   | 1             | 3.8       |
| Micrococcales                        | 1.254                 | 1.483                          | 87.33          | 190                        | 562          | 202        | 1.34E+03   | 142           | 59.4      |
| Erysipelotrichales                   | 0.547                 | 0.647                          | 87.98          | 4                          | 0            | 0          | 0          | 4.5           | 831       |

SIMPER statistics according to the ant diet for the whole dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |            |             |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|------------|-------------|
|                                      |                       |                                |                | Carnivorous                | Omnivorous | Herbivorous |
| Rickettsiales                        | 24.27                 | 27.91                          | 27.91          | 1.48E+04                   | 1.19E+04   | 8.19E+03    |
| Rhizobiales                          | 15.02                 | 17.28                          | 45.19          | 1.04E+04                   | 1.18E+03   | 1.01E+04    |
| Acetobacterales                      | 6.201                 | 7.132                          | 52.32          | 527                        | 4.92E+03   | 420         |
| Enterobacteriales                    | 5.333                 | 6.135                          | 58.46          | 124                        | 5.15E+03   | 77.3        |
| Lactobacillales                      | 4.978                 | 5.726                          | 64.18          | 577                        | 3.90E+03   | 1.71E+03    |
| Burkholderiales                      | 4.611                 | 5.304                          | 69.49          | 600                        | 574        | 6.05E+03    |
| Xanthomonadales                      | 4.384                 | 5.042                          | 74.53          | 587                        | 335        | 5.91E+03    |
| Erysipelotrichales                   | 4.009                 | 4.611                          | 79.14          | 4.32E+06                   | 1.17       | 0           |
| Flavobacteriales                     | 3.259                 | 3.749                          | 82.89          | 2.71E+03                   | 69.6       | 975         |
| Pseudomonadales                      | 2.519                 | 2.897                          | 85.78          | 1.25E+03                   | 492        | 455         |
| Corynebacteriales                    | 1.916                 | 2.204                          | 87.99          | 76.5                       | 1.06E+03   | 637         |
| Opitutales                           | 1.344                 | 1.546                          | 89.53          | 13.1                       | 14.7       | 2.19E+03    |
| Entomoplasmatales                    | 1.271                 | 1.462                          | 91.00          | 1.30E+03                   | 27.6       | 2           |
| Sphingomonadales                     | 0.844                 | 0.970                          | 91.97          | 71.3                       | 499        | 172         |
| Micrococcales                        | 0.633                 | 0.728                          | 92.70          | 48                         | 385        | 244         |

SIMPER statistics according to the ant diet for the forest/city dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |            |             |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|------------|-------------|
|                                      |                       |                                |                | Carnivorous                | Omnivorous | Herbivorous |
| Rhizobiales                          | 16.84                 | 19.96                          | 19.96          | 1.24E+04                   | 2.71E+03   | 1.16E+04    |
| Rickettsiales                        | 13.57                 | 16.09                          | 36.05          | 1.20E+04                   | 5.97E+03   | 15.3        |
| Acetobacterales                      | 8.946                 | 10.61                          | 46.65          | 1.73E+03                   | 3.22E+03   | 1.04E+04    |
| Lactobacillales                      | 7.148                 | 8.474                          | 55.13          | 1.42E+03                   | 695        | 1.22E+04    |
| Burkholderiales                      | 4.935                 | 5.851                          | 60.98          | 515                        | 2.86E+03   | 4.70E+03    |
| Flavobacteriales                     | 4.748                 | 5.629                          | 66.61          | 89.2                       | 5.13E+03   | 53.3        |
| Enterobacteriales                    | 3.71                  | 4.398                          | 71.01          | 1.85E+03                   | 1.40E+03   | 11          |
| Corynebacteriales                    | 3.359                 | 3.982                          | 74.99          | 470                        | 1.03E+03   | 2.70E+03    |
| Pseudomonadales                      | 2.98                  | 3.532                          | 78.52          | 2.02E+03                   | 548        | 325         |
| Xanthomonadales                      | 2.839                 | 3.366                          | 81.89          | 563                        | 2.45E+03   | 1.32E+03    |
| Micrococcales                        | 1.678                 | 1.989                          | 83.88          | 76.4                       | 289        | 1.98E+03    |
| Sphingomonadales                     | 1.600                 | 1.730                          | 85.77          | 107                        | 1.39E+03   | 33.5        |
| Entomoplasmatales                    | 1.459                 | 1.530                          | 89.03          | 1.20E+03                   | 0          | 774         |
| Opitutales                           | 1.291                 | 0.877                          | 89.91          | 16.6                       | 1.31E+03   | 266         |
| Erysipelotrichales                   | 0.494                 | 0.586                          | 90.50          | 463                        | 1          | 0           |

SIMPER statistics according to the ant nesting mode for the whole dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |          |          |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|----------|----------|
|                                      |                       |                                |                | Ground                     | Rotten   | Tree     |
| Rickettsiales                        | 25.68                 | 29.68                          | 29.68          | 1.03E+04                   | 2.08E+04 | 1.08E+04 |
| Rhizobiales                          | 12.76                 | 14.74                          | 44.42          | 3.64E+03                   | 85.1     | 1.08E+04 |
| Enterobacteriales                    | 8.057                 | 9.311                          | 53.73          | 1.37E+03                   | 1.30E+04 | 18.9     |
| Acetobacterales                      | 7.861                 | 9.085                          | 62.81          | 1.88E+03                   | 5.37E+03 | 2.55E+03 |
| Lactobacillales                      | 5.164                 | 5.967                          | 68.78          | 2.66E+03                   | 413      | 2.90E+03 |
| Burkholderiales                      | 3.838                 | 4.435                          | 73.22          | 990                        | 56.4     | 3.02E+03 |
| Xanthomonadales                      | 3.547                 | 4.099                          | 77.31          | 716                        | 22.1     | 2.99E+03 |
| Erysipelotrichales                   | 3.113                 | 3.598                          | 80.91          | 1.57E+03                   | 1        | 1.54+03  |
| Flavobacteriales                     | 2.488                 | 2.875                          | 83.79          | 1.92E+03                   | 27.9     | 480      |
| Pseudomonadales                      | 2.219                 | 2.564                          | 86.35          | 1.46E+03                   | 54       | 98.4     |
| Corynebacteriales                    | 1.951                 | 2.254                          | 88.61          | 868                        | 57       | 655      |
| Entomoplasmatales                    | 1.062                 | 1.227                          | 89.83          | 258                        | 0        | 807      |
| Opitutales                           | 1.053                 | 1.217                          | 91.05          | 18.5                       | 3.71     | 1.07E+03 |
| Sphingomonadales                     | 0.854                 | 0.988                          | 92.04          | 613                        | 21.4     | 25.8     |
| Micrococcales                        | 0.732                 | 0.846                          | 92.88          | 114                        | 18.7     | 508      |

SIMPER statistics according to the ant nesting mode for the forest/city dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |          |          |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|----------|----------|
|                                      |                       |                                |                | Ground                     | Rotten   | Tree     |
| Rickettsiales                        | 16.83                 | 19.81                          | 19.81          | 6.79E+03                   | 2.02E+04 | 24.3     |
| Rhizobiales                          | 16.71                 | 19.67                          | 39.48          | 6.58E+03                   | 5.27E+03 | 1.44E+04 |
| Acetobacterales                      | 8.265                 | 9.731                          | 49.21          | 3.29E+03                   | 2.12E+03 | 6.37E+03 |
| Lactobacillales                      | 7.172                 | 8.444                          | 57.66          | 616                        | 3.61E+03 | 7.66E+03 |
| Flavobacteriales                     | 5.416                 | 6.377                          | 64.03          | 816                        | 8.75     | 5.51E+03 |
| Burkholderiales                      | 4.438                 | 5.225                          | 69.26          | 2.03E+03                   | 113      | 3.92E+03 |
| Enterobacteriales                    | 4.095                 | 4.822                          | 74.08          | 1.49E+03                   | 2.78E+03 | 55.7     |
| Corynebacteriales                    | 2.968                 | 3.494                          | 77.57          | 1.20E+03                   | 176      | 1.57E+03 |
| Pseudomonadales                      | 2.77                  | 3.262                          | 80.84          | 1.78E+03                   | 41.3     | 691      |
| Xanthomonadales                      | 2.591                 | 3.050                          | 83.89          | 1.88E+03                   | 150      | 1.45E+03 |
| Sphingomonadales                     | 1.638                 | 1.929                          | 85.82          | 453                        | 61.5     | 1.16E+03 |
| Entomoplasmatales                    | 1.522                 | 1.792                          | 87.61          | 281                        | 0        | 1.80E+03 |
| Micrococcales                        | 1.070                 | 1.260                          | 88.87          | 859                        | 51.8     | 211      |
| Opitutales                           | 1.035                 | 1.218                          | 90.09          | 965                        | 4.25     | 181      |
| Erysipelotrichales                   | 0.422                 | 0.497                          | 90.59          | 379                        | 0        | 1.33     |

SIMPER statistics according to the ant habitat for the whole dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |          |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|----------|
|                                      |                       |                                |                | Rainforest                 | City     |
| Rickettsiales                        | 24.64                 | 28.92                          | 28.92          | 1.41E+04                   | 9.94E+03 |
| Rhizobiales                          | 12.82                 | 15.05                          | 43.97          | 8.26E+03                   | 3.21E+03 |
| Acetobacterales                      | 7.124                 | 8.363                          | 52.33          | 1.15E+03                   | 4.23E+03 |
| Enterobacterales                     | 6.424                 | 7.541                          | 59.87          | 904                        | 4.33E+03 |
| Lactobacillales                      | 5.658                 | 6.642                          | 66.51          | 706                        | 4.21E+03 |
| Burkholderiales                      | 3.747                 | 4.398                          | 70.91          | 1.62E+03                   | 1.65E+03 |
| Erysipelotrichales                   | 3.564                 | 4.184                          | 75.09          | 2.60E+03                   | 1.17     |
| Xanthomonadales                      | 3.498                 | 4.106                          | 79.20          | 1.46E+03                   | 1.51E+03 |
| Flavobacteriales                     | 2.863                 | 3.361                          | 82.56          | 401                        | 1.80E+03 |
| Pseudomonadales                      | 2.450                 | 2.876                          | 85.44          | 1.14E+03                   | 295      |
| Corynebacteriales                    | 2.019                 | 2.370                          | 87.81          | 679                        | 652      |
| Entomoplasmatales                    | 1.115                 | 1.308                          | 89.12          | 713                        | 135      |
| Opitutales                           | 1.004                 | 1.178                          | 90.29          | 282                        | 562      |
| Sphingomonadales                     | 0.964                 | 1.132                          | 91.43          | 84.3                       | 525      |
| Micrococcales                        | 0.721                 | 0.847                          | 92.27          | 385                        | 111      |

SIMPER statistics according to the ant habitat for the forest/city dataset

| 15 most influential bacterial orders | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |          |
|--------------------------------------|-----------------------|--------------------------------|----------------|----------------------------|----------|
|                                      |                       |                                |                | Rainforest                 | City     |
| Rhizobiales                          | 16.65                 | 19.99                          | 19.99          | 1.25E+04                   | 4.99E+03 |
| Rickettsiales                        | 14.90                 | 17.89                          | 37.89          | 7.47E+03                   | 7.35E+03 |
| Acetobacterales                      | 8.168                 | 9.806                          | 47.69          | 2.66E+03                   | 5.11E+03 |
| Lactobacillales                      | 6.059                 | 7.274                          | 54.97          | 623                        | 5.54E+03 |
| Flavobacteriales                     | 4.841                 | 5.812                          | 60.78          | 127                        | 3.71E+03 |
| Burkholderiales                      | 4.323                 | 5.19                           | 65.97          | 2.48E+03                   | 1.96E+03 |
| Enterobacterales                     | 3.970                 | 4.766                          | 70.73          | 1.12E+03                   | 1.52E+03 |
| Pseudomonadales                      | 3.331                 | 3.999                          | 74.73          | 1.92E+03                   | 422      |
| Corynebacteriales                    | 3.011                 | 3.614                          | 78.35          | 1.51E+03                   | 750      |
| Xanthomonadales                      | 2.790                 | 3.350                          | 81.70          | 964                        | 1.84E+03 |
| Sphingomonadales                     | 1.636                 | 1.964                          | 83.66          | 128                        | 994      |
| Entomoplasmatales                    | 1.444                 | 1.734                          | 85.40          | 1.08E+03                   | 281      |
| Micrococcales                        | 1.338                 | 1.606                          | 87.00          | 881                        | 192      |
| Opitutales                           | 1.278                 | 1.534                          | 88.54          | 116                        | 960      |
| Erysipelotrichales                   | 0.571                 | 0.685                          | 89.23          | 416                        | 0.727    |

**Supplementary File S6. 16S rRNA SIMPER pairwise comparisons for each factor.**

| Factor  | Comparison              | SIMPER | Bacterial order    | p-value | fdr_correction | Left.mean.abund | Left.stdev | Right.mean.abund | Right.stdev |
|---------|-------------------------|--------|--------------------|---------|----------------|-----------------|------------|------------------|-------------|
| Diet    | Carnivorous_Herbivorous | 0.053  | Erysipelotrichales | 0.011   | 0.157          | 0.099           | 0.195      | 0.000            | 0.000       |
|         | Carnivorous_Omnivorous  | 0.059  | Erysipelotrichales | 0.002   | 0.094          | 0.099           | 0.195      | 5.35E-05         | 1.18E-04    |
|         | Herbivorous_Omnivorous  | 0.157  | Rhizobiales        | 0.007   | 0.157          | 0.236           | 0.332      | 0.036            | 0.061       |
|         | Carnivorous_Herbivorous | 0.015  | Entomoplasmatales  | 0.014   | 0.157          | 0.031           | 0.065      | 0.000            | 0.000       |
| Nest    | Rotten_Ground           | 0.075  | Lactobacillales    | 0.033   | 0.297          | 0.008           | 0.021      | 0.077            | 0.168       |
|         | Rotten_Ground           | 0.031  | Erysipelotrichales | 0.044   | 0.297          | 5.50E-05        | 1.46E-04   | 0.052            | 0.153       |
|         | Tree_Ground             | 0.041  | Erysipelotrichales | 0.015   | 0.242          | 0.022           | 0.093      | 0.052            | 0.153       |
|         | Rotten_Ground           | 0.131  | Rhizobiales        | 0.016   | 0.242          | 0.003           | 0.003      | 0.107            | 0.212       |
|         | Tree_Rotten             | 0.249  | Rickettsiales      | 0.049   | 0.297          | 0.302           | 0.433      | 0.208            | 0.355       |
| Habitat | City_Rainforest         | 0.061  | Acetobacterales    | 0.016   | 0.265          | 0.114           | 0.207      | 0.000            | 0.000       |

Only the comparisons in which the bacterial relative abundance were statistically different (p-value < 0.05) are shown here. The statistical p-values were obtained with pairwise Kruskal-Wallis.

Supplementary File S7. Statistic calculations of 18S rRNA alpha diversity metrics for each factor.

The four tested alpha diversity metrics are Shannon diversity, Pielou's evenness, Faith's PD and ASV richness. The cells colored in red in each table represent p-values < 0.05. The statistical p-values were obtained with pairwise Kruskal-Wallis.

Shannon diversity habitat

| Group 1          | Group 2    | H     | p-value | q-value |
|------------------|------------|-------|---------|---------|
| Rainforest (n=8) | City (n=8) | 0.540 | 0.462   | 0.462   |

Shannon diversity nesting mode

| Group 1      | Group 2      | H     | p-value | q-value |
|--------------|--------------|-------|---------|---------|
| Overall      |              | 3.824 | 0.148   | NA      |
| Ground (n=6) | Rotten (n=4) | 3.682 | 0.045   | 0.165   |
|              | Tree (n=6)   | 0.231 | 0.631   | 0.631   |
| Rotten (n=4) | Tree (n=6)   | 2.227 | 0.136   | 0.203   |

Shannon diversity diet

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 8.184 | 0.017   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 3.750 | 0.053   | 0.079   |
|                    | Omnivorous (n=24) | 2.722 | 0.099   | 0.099   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 5.444 | 0.020   | 0.059   |

Shannon diversity subfamily

| Group 1              | Group 2                | H     | p-value | q-value |
|----------------------|------------------------|-------|---------|---------|
| Overall              |                        | 4.352 | 0.36    | NA      |
| Dolichoderinae (n=1) | Formicinae (n=5)       | 0.771 | 0.380   | 0.633   |
|                      | Myrmicinae (n=7)       | 0.429 | 0.513   | 0.641   |
|                      | Ponerinae (n=2)        | 1.500 | 0.221   | 0.552   |
|                      | Pseudomyrmicinae (n=1) | 1.000 | 0.317   | 0.633   |
| Formicinae (n=5)     | Myrmicinae (n=7)       | 0.534 | 0.465   | 0.641   |
|                      | Ponerinae (n=2)        | 3.750 | 0.053   | 0.528   |
|                      | Pseudomyrmicinae (n=1) | 0.086 | 0.770   | 0.827   |
| Myrmicinae (n=7)     | Ponerinae (n=2)        | 2.143 | 0.143   | 0.552   |
|                      | Pseudomyrmicinae (n=1) | 0.048 | 0.827   | 0.827   |
| Ponerinae (n=2)      | Pseudomyrmicinae (n=1) | 1.500 | 0.221   | 0.552   |

Pielou's evenness habitat

| Group 1          | Group 2    | H     | p-value | q-value |
|------------------|------------|-------|---------|---------|
| Rainforest (n=8) | City (n=8) | 0.011 | 0.916   | 0.916   |

Pielou's evenness nesting mode

| Group 1      | Group 2      | H     | p-value | q-value |
|--------------|--------------|-------|---------|---------|
| Overall      |              | 4.634 | 0.099   | NA      |
| Ground (n=6) | Rotten (n=4) | 1.136 | 0.286   | 0.591   |
|              | Tree (n=6)   | 0.231 | 0.631   | 0.631   |
| Rotten (n=4) | Tree (n=6)   | 0.727 | 0.394   | 0.591   |

Pielou's evenness diet

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 7.698 | 0.021   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 3.750 | 0.053   | 0.079   |
|                    | Omnivorous (n=24) | 2.722 | 0.099   | 0.099   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 4.840 | 0.028   | 0.028   |

Pielou's evenness subfamilies

| Group 1              | Group 2                | H     | p-value | q-value |
|----------------------|------------------------|-------|---------|---------|
| Overall              |                        | 2.581 | 0.630   | NA      |
| Dolichoderinae (n=1) | Formicinae (n=5)       | 0.771 | 0.380   | 0.475   |
|                      | Myrmicinae (n=7)       | 1.190 | 0.275   | 0.453   |
|                      | Ponerinae (n=2)        | 1.500 | 0.221   | 0.441   |
|                      | Pseudomyrmicinae (n=1) | 1.000 | 0.317   | 0.453   |
| Formicinae (n=5)     | Myrmicinae (n=7)       | 2.380 | 0.123   | 0.441   |
|                      | Ponerinae (n=2)        | 3.750 | 0.053   | 0.441   |
|                      | Pseudomyrmicinae (n=1) | 0.086 | 0.770   | 0.770   |
| Myrmicinae (n=7)     | Ponerinae (n=2)        | 2.143 | 0.143   | 0.441   |
|                      | Pseudomyrmicinae (n=1) | 0.429 | 0.513   | 0.570   |
| Ponerinae (n=2)      | Pseudomyrmicinae (n=1) | 1.500 | 0.221   | 0.441   |

Faith's PD habitat whole dataset

| Group 1          | Group 2    | H     | p-value | q-value |
|------------------|------------|-------|---------|---------|
| Rainforest (n=8) | City (n=8) | 1.103 | 0.294   | 0.294   |

Faith's PD nesting mode

| Group 1      | Group 2      | H     | p-value | q-value |
|--------------|--------------|-------|---------|---------|
| Overall      |              | 3.107 | 0.212   | NA      |
| Ground (n=6) | Rotten (n=4) | 4.545 | 0.033   | 0.099   |
|              | Tree (n=6)   | 0.641 | 0.423   | 0.635   |
| Rotten (n=4) | Tree (n=6)   | 0.045 | 0.831   | 0.831   |

Faith's PD diet

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 3.494 | 0.174   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 2.400 | 0.121   | 0.182   |
|                    | Omnivorous (n=24) | 0.056 | 0.814   | 0.814   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 2.778 | 0.096   | 0.182   |

Faith's PD subfamilies

| Group 1              | Group 2                | H     | p-value | q-value |
|----------------------|------------------------|-------|---------|---------|
| Overall              |                        | 3.643 | 0.456   | NA      |
| Dolichoderinae (n=1) | Formicinae (n=5)       | 2.143 | 0.143   | 0.698   |
|                      | Myrmicinae (n=7)       | 2.333 | 0.127   | 0.698   |
|                      | Ponerinae (n=2)        | 1.500 | 0.221   | 0.698   |
|                      | Pseudomyrmicinae (n=1) | 1.000 | 0.317   | 0.698   |
| Formicinae (n=5)     | Myrmicinae (n=7)       | 0.059 | 0.808   | 0.897   |
|                      | Ponerinae (n=2)        | 0.600 | 0.439   | 0.698   |
|                      | Pseudomyrmicinae (n=1) | 0.770 | 0.380   | 0.698   |
| Myrmicinae (n=7)     | Ponerinae (n=2)        | 0.343 | 0.558   | 0.698   |
|                      | Pseudomyrmicinae (n=1) | 0.429 | 0.513   | 0.698   |
| Ponerinae (n=2)      | Pseudomyrmicinae (n=1) | 0.000 | 1.000   | 1.000   |

ASV richness habitat whole dataset

| Group 1          | Group 2    | H     | p-value | q-value |
|------------------|------------|-------|---------|---------|
| Rainforest (n=8) | City (n=8) | 1.773 | 0.183   | 0.183   |

ASV richness nesting mode

| Group 1      | Group 2      | H     | p-value | q-value |
|--------------|--------------|-------|---------|---------|
| Overall      |              | 1.283 | 0.526   | NA      |
| Ground (n=6) | Rotten (n=4) | 4.257 | 0.039   | 0.002   |
|              | Tree (n=6)   | 0.007 | 0.935   | 0.410   |
| Rotten (n=4) | Tree (n=6)   | 2.981 | 0.084   | 0.039   |

ASV richness diet

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 4.232 | 0.121   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 3.889 | 0.049   | 0.146   |
|                    | Omnivorous (n=24) | 0.918 | 0.338   | 0.338   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 2.027 | 0.155   | 0.232   |

ASV richness subfamilies

| Group 1              | Group 2                | H     | p-value | q-value |
|----------------------|------------------------|-------|---------|---------|
| Overall              |                        | 5.993 | 0.200   | NA      |
| Dolichoderinae (n=1) | Formicinae (n=5)       | 0.353 | 0.552   | 0.913   |
|                      | Myrmicinae (n=7)       | 0.198 | 0.657   | 0.913   |
|                      | Ponerinae (n=2)        | 2.000 | 0.157   | 0.524   |
|                      | Pseudomyrmicinae (n=1) | 1.000 | 0.317   | 0.747   |
| Formicinae (n=5)     | Myrmicinae (n=7)       | 0.108 | 0.743   | 0.913   |
|                      | Ponerinae (n=2)        | 2.585 | 0.108   | 0.524   |
|                      | Pseudomyrmicinae (n=1) | 0.000 | 1.000   | 1.000   |
| Myrmicinae (n=7)     | Ponerinae (n=2)        | 0.791 | 0.374   | 0.747   |
|                      | Pseudomyrmicinae (n=1) | 0.051 | 0.822   | 0.913   |
| Ponerinae (n=2)      | Pseudomyrmicinae (n=1) | 2.000 | 0.157   | 0.524   |

Supplementary File S8. Statistic calculations of 18S rRNA beta diversity metrics for each factor.

The two tested beta diversity metrics are Bray-Curtis and Weighted unifrac. The cells colored in red in each table represent p-values < 0.05. The statistical p-values were obtained with PERMANOVAs.

Bray-Curtis habitat

| Group 1          | Group 2    | H     | p-value | q-value |
|------------------|------------|-------|---------|---------|
| Rainforest (n=8) | City (n=8) | 1.042 | 0.340   | 0.340   |

Bray-Curtis nesting mode

| Group 1      | Group 2      | H     | p-value | q-value |
|--------------|--------------|-------|---------|---------|
| Overall      |              | 0.988 | 0.042   | NA      |
| Ground (n=6) | Rotten (n=4) | 0.814 | 0.809   | 1.000   |
|              | Tree (n=6)   | 1.121 | 0.048   | 0.252   |
| Rotten (n=4) | Tree (n=6)   | 1.000 | 1.000   | 1.000   |

Bray-Curtis diet

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 1.041 | 0.281   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 0.764 | 0.718   | 0.718   |
|                    | Omnivorous (n=24) | 1.104 | 0.049   | 0.074   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 1.128 | 0.033   | 0.074   |

Bray-Curtis subfamily

| Group 1          | Group 2          | H     | p-value | q-value |
|------------------|------------------|-------|---------|---------|
| Overall          |                  | 1.043 | 0.245   | NA      |
| Formicinae (n=5) | Myrmicinae (n=7) | 1.135 | 0.067   | 0.402   |
|                  | NA (n=2)         | 1.061 | 0.209   | 0.418   |
|                  | Ponerinae (n=2)  | 1.146 | 0.153   | 0.418   |
| Myrmicinae (n=7) | NA (n=2)         | 1.035 | 0.599   | 0.719   |
|                  | Ponerinae (n=2)  | 0.823 | 0.727   | 0.727   |
| NA (n=2)         | Ponerinae (n=2)  | 1.092 | 0.317   | 0.476   |

Weighted UniFrac habitat

| Group 1          | Group 2    | H     | p-value | q-value |
|------------------|------------|-------|---------|---------|
| Rainforest (n=8) | City (n=8) | 1.295 | 0.194   | 0.194   |

Weighted UniFrac nesting mode

| Group 1      | Group 2      | H     | p-value | q-value |
|--------------|--------------|-------|---------|---------|
| Overall      |              | 2.311 | 0.043   | NA      |
| Ground (n=6) | Rotten (n=4) | 0.800 | 0.446   | 0.446   |
|              | Tree (n=6)   | 3.143 | 0.029   | 0.087   |
| Rotten (n=4) | Tree (n=6)   | 1.164 | 0.347   | 0.446   |

Weighted UniFrac diet

| Group 1            | Group 2           | H     | p-value | q-value |
|--------------------|-------------------|-------|---------|---------|
| Overall            |                   | 1.113 | 0.313   | NA      |
| Carnivorous (n=13) | Herbivorous (n=9) | 0.339 | 0.627   | 0.627   |
|                    | Omnivorous (n=24) | 1.591 | 0.236   | 0.416   |
| Herbivorous (n=9)  | Omnivorous (n=24) | 1.282 | 0.277   | 0.416   |

Weighted UniFrac subfamily

| Group 1          | Group 2          | H     | p-value | q-value |
|------------------|------------------|-------|---------|---------|
| Overall          |                  | 1.121 | 0.103   | NA      |
| Formicinae (n=5) | Myrmicinae (n=7) | 0.691 | 0.607   | 0.705   |
|                  | NA (n=2)         | 0.606 | 0.458   | 0.705   |
|                  | Ponerinae (n=2)  | 0.996 | 0.421   | 0.705   |
| Myrmicinae (n=7) | NA (n=2)         | 0.578 | 0.705   | 0.705   |
|                  | Ponerinae (n=2)  | 0.535 | 0.677   | 0.705   |
| NA (n=2)         | Ponerinae (n=2)  | 1.300 | 0.334   | 0.705   |



## Supplementary File S9. 18S rRNA SIMPER statistics for each factor with all ASVs and after removing the undetermined eukaryote ASVs.

### SIMPER statistics according to the ant subfamily with all ASVs

| 11 most influential subphyla | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |            |            |           |                  |
|------------------------------|-----------------------|--------------------------------|----------------|----------------------------|------------|------------|-----------|------------------|
|                              |                       |                                |                | Dolichoderinae             | Formicinae | Myrmicinae | Ponerinae | Pseudomyrmicinae |
| Undetermined                 | 18.46                 | 44                             | 44.00          | 100.00                     | 72.70      | 73.90      | 51.40     | 99.30            |
| Nematoda                     | 12.05                 | 28.71                          | 72.70          | 0.000                      | 4.920      | 13.50      | 48.60     | 0.000            |
| Eugrargarinorida             | 6.205                 | 14.79                          | 87.49          | 0.000                      | 19.60      | 0.493      | 0.000     | 0.000            |
| Chytridiomycota              | 4.045                 | 9.368                          | 97.13          | 0.000                      | 0.000      | 11.30      | 0.000     | 0.000            |
| Mortierellomycotina          | 0.301                 | 0.717                          | 97.84          | 0.000                      | 0.962      | 0.000      | 0.000     | 0.000            |
| Saccharomycotina             | 0.168                 | 0.401                          | 98.24          | 0.000                      | 0.323      | 0.094      | 0.000     | 0.655            |
| Ustilaginomycotina           | 0.158                 | 0.376                          | 98.62          | 0.000                      | 0.455      | 0.056      | 0.000     | 0.000            |
| Pezizomycotina               | 0.084                 | 0.201                          | 98.82          | 0.000                      | 0.000      | 0.235      | 0.000     | 0.000            |
| Mucoromycotina               | 0.070                 | 0.168                          | 98.99          | 0.000                      | 0.225      | 0.000      | 0.000     | 0.000            |
| Basidiobolomycetes           | 0.069                 | 0.164                          | 99.15          | 0.000                      | 0.000      | 0.193      | 0.000     | 0.000            |
| Arthropoda                   | 0.041                 | 0.097                          | 99.25          | 0.000                      | 0.000      | 0.113      | 0.000     | 0.000            |

### SIMPER statistics according to the ant subfamily without undetermined eukaryote ASVs

| Most influential phyla |                |                | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |            |           |                  |
|------------------------|----------------|----------------|-----------------------|--------------------------------|----------------|----------------------------|------------|-----------|------------------|
| Subphylum              | Infrakingdom   | Phylum         |                       |                                |                | Formicinae                 | Myrmicinae | Ponerinae | Pseudomyrmicinae |
| Nematoda               | Holozoa        | Metazoa        | 30.47                 | 35.53                          | 35.53          | 63.00                      | 115.00     | 108.00    | 0.00             |
| Gregarinasina          | Alveolata      | Apicomplexa    | 28.77                 | 33.55                          | 69.08          | 342.00                     | 60.80      | 0.000     | 0.000            |
| Chytridiomycota        | Nuclemycea     | Fungi          | 11.73                 | 13.68                          | 82.76          | 0.000                      | 293.00     | 0.000     | 0.000            |
| Pezizomycotina         | Nuclemycea     | Fungi          | 3.140                 | 3.661                          | 86.42          | 0.000                      | 22.30      | 0.000     | 0.000            |
| Saccharomycotina       | Nuclemycea     | Fungi          | 2.879                 | 3.358                          | 89.78          | 5.750                      | 2.750      | 0.000     | 9.000            |
| Mortierellomycotina    | Nuclemycea     | Fungi          | 2.145                 | 2.502                          | 92.28          | 13.50                      | 0.000      | 0.000     | 0.000            |
| Ustilaginomycotina     | Nuclemycea     | Fungi          | 1.757                 | 2.049                          | 94.33          | 0.000                      | 15.50      | 0.000     | 0.000            |
| Arthropoda             | Holozoa        | Metazoa        | 1.729                 | 2.017                          | 96.35          | 6.500                      | 1.000      | 0.000     | 0.000            |
| Dinophyceae            | Alveolata      | Dinoflagellata | 1.320                 | 1.539                          | 97.89          | 0.000                      | 2.750      | 0.000     | 0.000            |
| Phyllopharyngea        | Alveolata      | Ciliophora     | 0.453                 | 0.529                          | 98.42          | 0.000                      | 4.000      | 0.000     | 0.000            |
| Colpodea               | Alveolata      | Ciliophora     | 0.340                 | 0.397                          | 98.81          | 0.000                      | 3.000      | 0.000     | 0.000            |
| Basidiobolomycetes     | Nuclemycea     | Fungi          | 0.200                 | 0.233                          | 99.05          | 0.000                      | 5.000      | 0.000     | 0.000            |
| Rhizaspididae          | Rhizaria       | Cercozoa       | 0.198                 | 0.231                          | 99.28          | 0.000                      | 1.750      | 0.000     | 0.000            |
| Oligohymenophorea      | Alveolata      | Ciliophora     | 0.171                 | 0.200                          | 99.48          | 4.000                      | 0.000      | 0.000     | 0.000            |
| Mucoromycotina         | Nuclemycea     | Fungi          | 0.170                 | 0.198                          | 99.68          | 0.000                      | 1.500      | 0.000     | 0.000            |
| Chrysophyceae          | Stremenophiles | Ochrophyta     | 0.118                 | 0.138                          | 99.81          | 2.750                      | 0.000      | 0.000     | 0.000            |
| Annelida               | Holozoa        | Metazoa        | 0.096                 | 0.113                          | 99.93          | 2.250                      | 0.000      | 0.000     | 0.000            |
| Puccinimycotina        | Nuclemycea     | Fungi          | 0.064                 | 0.075                          | 100.00         | 1.500                      | 0.000      | 0.000     | 0.000            |

# SIMPER statistics according to the ant nesting mode with all ASVs

| 11 most influential subphyla | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |        |       |
|------------------------------|-----------------------|--------------------------------|----------------|----------------------------|--------|-------|
|                              |                       |                                |                | Ground                     | Rotten | Tree  |
| Undetermined                 | 21.11                 | 46.42                          | 46.42          | 49.10                      | 74.20  | 98.60 |
| Nematoda                     | 12.53                 | 27.56                          | 73.98          | 20.40                      | 23.40  | 0.000 |
| Eugregarinorida              | 5.925                 | 13.03                          | 87.01          | 14.70                      | 2.400  | 0.576 |
| Chytridiomycota              | 4.708                 | 10.35                          | 97.36          | 13.20                      | 0.000  | 0.000 |
| Mortierellomycotina          | 0.286                 | 0.630                          | 97.99          | 0.802                      | 0.000  | 0.000 |
| Saccharomycotina             | 0.159                 | 0.349                          | 98.34          | 0.270                      | 0.000  | 0.219 |
| Ustilaginomycotina           | 0.154                 | 0.339                          | 98.68          | 0.379                      | 0.000  | 0.066 |
| Pezizomycotina               | 0.093                 | 0.205                          | 98.88          | 0.034                      | 0.000  | 0.241 |
| Mucoromycotina               | 0.08                  | 0.177                          | 99.06          | 0.225                      | 0.000  | 0.000 |
| Basidiobolomycetes           | 0.067                 | 0.147                          | 99.21          | 0.188                      | 0.000  | 0.000 |
| Arthropoda                   | 0.047                 | 0.104                          | 99.31          | 0.000                      | 0.000  | 0.132 |

# SIMPER statistics according to the ant nesting mode without undetermined eukaryote ASVs

| Most influential phyla |                |                | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |        |       |
|------------------------|----------------|----------------|-----------------------|--------------------------------|----------------|----------------------------|--------|-------|
| Subphylum              | Infrakingdom   | Phylum         |                       |                                |                | Ground                     | Rotten | Tree  |
| Nematoda               | Holozoa        | Metazoa        | 34.13                 | 38.14                          | 38.14          | 122.00                     | 98.00  | 0.00  |
| Gregarinasina          | Alveolata      | Apicomplexa    | 30.21                 | 33.77                          | 71.91          | 209.00                     | 57.50  | 81.00 |
| Chytridiomycota        | Nucleotmycea   | Fungi          | 10.190                | 11.39                          | 83.30          | 196.00                     | 0.000  | 0.000 |
| Saccharomycotina       | Nucleotmycea   | Fungi          | 3.321                 | 3.711                          | 87.01          | 0.500                      | 0.000  | 28.70 |
| Pezizomycotina         | Nucleotmycea   | Fungi          | 3.129                 | 3.497                          | 90.51          | 3.830                      | 0.000  | 6.670 |
| Arthropoda             | Holozoa        | Metazoa        | 2.024                 | 2.262                          | 92.77          | 0.000                      | 0.000  | 20.70 |
| Mortierellomycotina    | Nucleotmycea   | Fungi          | 1.952                 | 2.182                          | 94.95          | 9.000                      | 0.000  | 0.000 |
| Ustilaginomycotina     | Nucleotmycea   | Fungi          | 1.487                 | 1.662                          | 96.61          | 4.330                      | 0.000  | 1.330 |
| Dinophyceae            | Alveolata      | Dinoflagellata | 1.119                 | 1.251                          | 97.86          | 0.000                      | 0.000  | 3.670 |
| Phyllopharyngea        | Alveolata      | Ciliophora     | 0.522                 | 0.584                          | 98.45          | 0.000                      | 0.000  | 5.330 |
| Colpodea               | Alveolata      | Ciliophora     | 0.392                 | 0.438                          | 98.88          | 0.000                      | 0.000  | 4.000 |
| Rhizaspidae            | Rhizaria       | Cercozoa       | 0.229                 | 0.255                          | 99.14          | 0.000                      | 0.000  | 2.330 |
| Oligohymenophorea      | Alveolata      | Ciliophora     | 0.196                 | 0.219                          | 99.36          | 0.000                      | 0.000  | 2.000 |
| Basidiobolomycetes     | Nucleotmycea   | Fungi          | 0.174                 | 0.194                          | 99.55          | 3.330                      | 0.000  | 0.000 |
| Mucoromycotina         | Nucleotmycea   | Fungi          | 0.153                 | 0.17                           | 99.72          | 2.670                      | 0.000  | 0.000 |
| Chrysophyceae          | Stremenophiles | Ochrophyta     | 0.105                 | 0.117                          | 99.84          | 1.830                      | 0.000  | 0.000 |
| Annelida               | Holozoa        | Metazoa        | 0.086                 | 0.096                          | 99.94          | 1.500                      | 0.000  | 0.000 |
| Puccinimycotina        | Nucleotmycea   | Fungi          | 0.057                 | 0.064                          | 100.00         | 1.000                      | 0.000  | 0.000 |

### SIMPER statistics according to the ant habitat with all ASVs

| 11 most influential subphyla | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |            |
|------------------------------|-----------------------|--------------------------------|----------------|----------------------------|------------|
|                              |                       |                                |                | City                       | Rainforest |
| Undetermined                 | 20.02                 | 44.76                          | 44.76          | 61.90                      | 86.00      |
| Nematoda                     | 12.26                 | 27.41                          | 72.17          | 23.70                      | 3.360      |
| Eugregarinorida              | 6.270                 | 14.02                          | 86.19          | 12.50                      | 0.186      |
| Chytridiomycota              | 4.944                 | 11.05                          | 97.25          | 0.000                      | 9.890      |
| Mortierellomycotina          | 0.281                 | 0.629                          | 97.88          | 0.523                      | 0.078      |
| Saccharomycotina             | 0.164                 | 0.366                          | 98.24          | 0.292                      | 0.074      |
| Ustilaginomycotina           | 0.161                 | 0.359                          | 98.60          | 0.284                      | 0.049      |
| Pezizomycotina               | 0.094                 | 0.209                          | 98.81          | 0.131                      | 0.075      |
| Basidiobolomycetes           | 0.070                 | 0.157                          | 99.16          | 0.141                      | 0.000      |
| Mucoromycotina               | 0.084                 | 0.189                          | 99.00          | 0.000                      | 0.169      |
| Arthropoda                   | 0.050                 | 0.111                          | 99.27          | 0.099                      | 0.000      |

### SIMPER statistics according to the ant habitat without undetermined eukaryote ASVs

| Most influential phyla |               |                | Average dissimilarity | Contribution to difference (%) | Cumulative (%) | Mean read number per group |            |
|------------------------|---------------|----------------|-----------------------|--------------------------------|----------------|----------------------------|------------|
| Subphylum              | Infrakingdom  | Phylum         |                       |                                |                | City                       | Rainforest |
| Nematoda               | Holozoa       | Metazoa        | 32.52                 | 36.11                          | 36.11          | 87.10                      | 79.30      |
| Gregarinasina          | Alveolata     | Apicomplexa    | 27.35                 | 30.37                          | 66.48          | 228.00                     | 3.750      |
| Chytridiomycota        | Nucleomyces   | Fungi          | 16.72                 | 18.57                          | 85.06          | 0.000                      | 293.00     |
| Pezizomycotina         | Nucleomyces   | Fungi          | 2.766                 | 3.072                          | 88.13          | 11.70                      | 1.750      |
| Saccharomycotina       | Nucleomyces   | Fungi          | 2.729                 | 3.031                          | 91.16          | 5.290                      | 1.500      |
| Mortierellomycotina    | Nucleomyces   | Fungi          | 1.935                 | 2.149                          | 93.31          | 7.140                      | 1.000      |
| Ustilaginomycotina     | Nucleomyces   | Fungi          | 1.609                 | 1.786                          | 95.10          | 3.710                      | 1.000      |
| Arthropoda             | Holozoa       | Metazoa        | 1.545                 | 1.716                          | 96.81          | 8.860                      | 0.000      |
| Dinophyceae            | Alveolata     | Dinoflagellata | 1.177                 | 1.307                          | 98.12          | 0.714                      | 1.500      |
| Phyllopharyngea        | Alveolata     | Ciliophora     | 0.399                 | 0.443                          | 98.56          | 2.290                      | 0.000      |
| Colpodea               | Alveolata     | Ciliophora     | 0.299                 | 0.332                          | 98.89          | 1.710                      | 0.000      |
| Basidiobolomycetes     | Nucleomyces   | Fungi          | 0.285                 | 0.317                          | 99.21          | 0.000                      | 5.000      |
| Rhizaspidae            | Rhizaria      | Cercozoa       | 0.174                 | 0.194                          | 99.40          | 1.000                      | 0.000      |
| Oligohymenophorea      | Alveolata     | Ciliophora     | 0.150                 | 0.166                          | 99.57          | 0.857                      | 0.000      |
| Mucoromycotina         | Nucleomyces   | Fungi          | 0.148                 | 0.164                          | 99.73          | 2.290                      | 0.000      |
| Chrysophyceae          | Stromatolites | Ochrophyta     | 0.102                 | 0.113                          | 99.85          | 1.570                      | 0.000      |
| Annelida               | Holozoa       | Metazoa        | 0.083                 | 0.092                          | 99.94          | 1.290                      | 0.000      |
| Puccinimycotina        | Nucleomyces   | Fungi          | 0.055                 | 0.062                          | 100.00         | 0.857                      | 0.000      |

### Tables color legend

Holozoa
  Alveolates
  Nucleomyces
  Rhizaria
  Stromatolites

The color of the cells in the tables without undetermined eukaryote ASVs correspond to the eukaryote infrakingdom.

**Supplementary File S10. 18S rRNA SIMPER pairwise comparisons for each factor.**

| Factor | Comparison  | SIMPER | Subphylum    | p-value | fdr_correction | Left.mean.abund | Left.stdev | Right.mean.abund | Right.stdev |
|--------|-------------|--------|--------------|---------|----------------|-----------------|------------|------------------|-------------|
| Nest   | Ground_Tree | 0.201  | Nematoda     | 0.007   | 0.041          | 0.204           | 0.287      | 0.000            | 0.000       |
|        | Ground_Tree | 0.489  | Undetermined | 0.006   | 0.041          | 0.491           | 0.437      | 0.986            | 0.022       |

Only the comparisons in which the bacterial relative abundance were statistically different (p-value < 0.05) are shown here. The statistical p-values were obtained with pairwise Kruskal-Wallis.

**Supplementary File S11. Description of the eukaryote subphyla identified in our samples.**

| Eukaryote subphyla  | Description  | Genus examples  |
|---------------------|--|---|
| Nematoda            | Diverse subphylum containing a large number of parasitic species, some of them being entomopathogenic        | <i>Heterorhabditis</i> ;<br><i>Steinernema</i>        |
| Gregarinasina       | A subphylum of alveolates inhabiting the intestines of many invertebrates                                    | <i>Exoschizon</i> ;<br><b><i>Gregarina</i></b>        |
| Saccharomycotina    | A subphylum containing most of the ascomycete yeasts, with some of its members being associated with insects | <i>Saccharomyces</i> ;<br><b><i>Starmerella</i></b>   |
| Chytridiomycota     | Zoosporic fungi with some members found on scale of insects  | <i>Batrachochytrium</i> ;<br><i>Myiophagus</i>        |
| Pezizomycotina      | Filamentous and lichenized fungi with some members closely associated with insects                           | <i>Ascobolus</i> ;<br><i>Urceolaria</i>               |
| Dinophyceae         | Dinoflagellates living in marine environment, with some members being parasitic of marine organisms          | <i>Ceratocorys</i> ;<br><i>Ostreopsis</i>             |
| Ustilaginomycotina  | A subphylum of fungi, composed of mostly parasites of vascular plants and associated with insects            | <b><i>Malassezia</i></b> ;<br><i>Ustilago</i>         |
| Arthropoda          | Invertebrate animals   | <b><i>Achipteria</i></b> ;<br><b><i>Sarcoptes</i></b> |
| Mortierellomycotina | Subphylum composed of soil fungi, with some members being weak insect parasites                              | <b><i>Mortierella</i></b>                             |
| Phyllopharyngea     | Ciliates living in marine environments, with some members being ectosymbionts of crustaceans                 | <b><i>Chilodonella</i></b> ;<br><i>Vasichona</i>      |
| Colpodea            | Ciliates common in freshwater and soil habitats  | <b><i>Colpoda</i></b> ; <i>Kreyella</i>               |
| Rhizaspididae       | Protists living in marine environments   | <i>Capsellina</i> ;<br><b><i>Rhogostoma</i></b>       |
| Oligohymenophorea   | Ciliates living in marine environments, with some members being parasites of aquatic organisms               | <i>Cothurnia</i> ;<br><i>Trichodina</i>               |
| Basidiobolomycetes  | Fungi found in the intestines of cold-blooded vertebrates and on decaying fruits and soil                    | <b><i>Basidiobolus</i></b> ;<br><i>Schizangiella</i>  |
| Mucoromycotina      | Fungi which can be insect parasitic  | <i>Endogone</i> ; <b><i>Mucor</i></b>                 |
| Chrysophyceae       | Algae found mostly in freshwater   | <i>Hydrurus</i> ;<br><i>Stichogloea</i>               |
| Annelida            | Segmented worms living in aquatic or terrestrial moist environments  | <i>Haplotaxis</i> ; <i>Palola</i>                     |
| Pucciniomycotina    | Subphylum of entomopathogenic fungi  | <i>Agaricostibum</i> ;<br><i>Puccinia</i>             |

The genera in bold are genera which were found in associations with our Amazonian ant samples.