Supplementary Data

**Article title:** Unique bacterial assembly, composition, and interactions in a parasitic plant and its host.

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**Fig. S2** Principle coordinate analyses and corresponding scree plots associated with different measures of community dissimilarity.
**Fig. S3** Shared ASVs among leaf and root communities.
**Fig. S4** The proportion of bacterial taxa affected by plant species and *Hedera* infection status.
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**Table S9** Results from the leave-one-out Procrustes analysis comparing *Orobanche* and *Hedera* root communities.
Figure S1 Measures of (A) ASV richness, (B) Inverse Simpson’s, (C) evenness, and (D) phylogenetic diversity across leaves and roots from *Hedera* and *Orobanche* and soil samples. Evenness was calculated as inverse Simpson’s diversity/ASV richness and phylogenetic diversity was calculated as the sum of the total phylogenetic branch length for a given sample. For results from statistical analyses see Table S2.
**Figure S2** Principle coordinate analyses and corresponding scree plots using (A and C) weighted UniFrac dissimilarity and (B and D) Bray-Curtis dissimilarity. Results were qualitatively similar between measures of dissimilarity.
Figure S3 Venn diagrams displaying the number of shared ASVs among (A) leaf communities, (B) root communities, and (C) leaf and root communities.
Figure S4 The proportion of bacterial taxa exhibiting significant differential abundance between Orobanche and Hedera (A: roots; and B: leaves), or Hedera infection status (C, D, E and F) using either DESeq2 or ALDEx2 (see Materials and Methods).
Figure S5 Root bacterial networks of Orobanche and Hedera inferred using SparCC. We inferred the bacterial network of (A) infected roots of infected Hedera, (B) uninfected roots of infected Hedera, (C) roots of uninfected Hedera, and (D) Orobanche. Node colour and size represent bacterial phylum classification and abundance (centered log-ratio transformed), respectively. Edge colour and width represent sign (green = positive association, red = negative association), and strength of co-association, respectively. At the whole network-level, we found large differences in the edge density and betweenness centrality between Hedera and Orobanche, but not across infected and uninfected Hedera roots, as reflected in the (E) degree distribution (number of associations per node) between community types. (F) At the level of individual nodes we found large significant differences in mean betweenness centrality between taxa within the root bacterial networks of Hedera and Orobanche, as well as infected and uninfected Hedera roots. We tested significance using a series of Kolmogorov-Smirnov tests on the distributions of mean node-level betweeness centrality estimated from 10,000 samples with replacement of 50 nodes (see Materials and Methods).
Figure S6 Leaf bacterial networks of *Orobanche* and *Hedera* inferred using SPIEC-EASI (qualitatively similar results obtained using SparCC for network inference). We inferred the bacterial network of (A) leaves of infected *Hedera*, (B) leaves of uninfected *Hedera*, and (C) leaves of *Orobanche*. Node colour and size represent bacterial phylum classification and abundance (centered log-ratio transformed), respectively. Nodes are labelled with an arbitrary number assigned to individual ASVs. Edge colour and width represent sign (dark shade = positive association, light shade = negative association), and strength of co-association, respectively.
Figure S7 Procrustes residuals (A-C) and dendrograms (D-F) of select bacterial community comparisons for two pairs of communities that exhibit significant congruence (PR vs. IIR [A, D]; IUR vs. IIR [B, E]), and one pair that exhibits non-significant congruence (PL vs. IL [C, F]). Colours represent the infected host/parasite sample (three per site) from a given site (site 1 – purple; site 2 – red; site 3 – blue; site 4 – green). The Procrustes residuals represent the level of discordance between corresponding observations occurring within two bacterial communities. For example, the discordance between the bacterial community occurring within (A) Orobanche roots versus infected Hedera roots was low in infected host/parasite pair 3 from site 1 but comparatively high in infected host/parasite pair 2 from site 2. Lower residual values between corresponding bacterial communities lead to higher values of the overall Procrustes correlation-like statistic ($t_0$). Hierarchical clustering of individual samples within community types reflects the results obtained from the Procrustes analysis. Community types that exhibit higher Procrustes congruence (A, B) also display greater dendrogram concordance (D, E). Hierarchical clustering was performed using the weighted UniFrac distance between all samples within a community type followed by clustering by the unweighted pair group method with arithmetic mean (UPGMA). Dendrograms were created using the 'dendextend' R package version 1.9.0 (Galili, 2015).
Figure S8 Our leave-one-out approach (see Materials and Methods: Procrustes tests), revealed that a subset of bacterial taxa at the level of (A) phylum or (B) order contributed strongly to the congruence or discordance between *Orobanche* and *Hedera* root communities.
Figure S9 The relative abundance of the (A) Burkholderiales, a bacterial order that contributes to the congruence between *Orobanche* and *Hedera* root communities (Fig. S8), is highly correlated between host and parasite roots. Note this relationship is still significant even after removal of the point in the top right corner. Conversely, the relative abundance of the (B) Actinomycetales, a bacterial order that contributes to the discordance between *Orobanche* and *Hedera* root communities, is uncorrelated between host and parasite roots.
Figure S10 Our leave-one-out approach (see Materials and Methods: Procrustes tests), revealed that a subset of bacterial taxa at the level of (A) phylum or (B) order contributed strongly to the congruence or discordance between Orobanche leaf and Hedera root communities.
Figure S11 Principle coordinate analysis of weighted UniFrac dissimilarity among soil bacterial communities. We found no consistent effects of either infection (P=0.18) or site (P=0.32; results from PERMANOVA).
**Table S1** Genome sizes and sampling locations for each *Hedera* individual collected in the experiment. Genome size (measured using flow cytometry) and species identifications were determined by Alan Whittemore (U.S. National Arboretum). Vouchers deposited at or distributed by the United States National Arboretum Herbarium (NA). Vouchers are labeled “Schneider & Fitzpatrick” followed by the collection number indicated.

| Individual | Genome size (pg) | Inferred ploidy | Species               | Latitude    | Longitude    | Voucher collection number b |
|------------|------------------|-----------------|-----------------------|-------------|--------------|-----------------------------|
| 1.I.1      | 5.95             | 4x              | *H. algeriensis*      | 37.871500   | -122.265189 | --                          |
| 1.I.2      | 5.89             | 4x              | *H. algeriensis*      | 37.871500   | -122.265189 | 1046                        |
| 1.I.3      | 5.84             | 4x              | *H. algeriensis*      | 37.871572   | -122.264768 | 1047                        |
| 1.U.1      | 6.00             | 4x              | *H. algeriensis*      | 37.871572   | -122.264768 | --                          |
| 1.U.2      | 5.88             | 4x              | *H. algeriensis*      | 37.871572   | -122.264768 | 1055                        |
| 1.U.3      | 5.86             | 4x              | *H. algeriensis*      | 37.871572   | -122.264768 | --                          |
| 2.I.1      | 3.01             | 2x              | *H. helix*            | 37.873610   | -122.264592 | --                          |
| 2.I.2      | 5.91             | 4x              | *H. algeriensis*      | 37.879736   | -122.264634 | --                          |
| 2.I.3      | 3.08             | 2x              | *H. helix*            | 37.873748   | -122.264630 | 1048                        |
| 2.U.1      | 5.86             | 4x              | *H. algeriensis*      | 37.873713   | -122.264289 | --                          |
| 2.U.2      | 5.82             | 4x              | *H. algeriensis*      | 37.873713   | -122.264289 | 1056                        |
| 2.U.3      | 6.12             | 4x              | *H. algeriensis*      | 37.873713   | -122.264289 | 1057                        |
| 3.I.1      | 5.77             | 4x              | *H. algeriensis*      | 37.872382   | -122.265023 | 1049                        |
| 3.I.2      | 5.95             | 4x              | *H. algeriensis*      | 37.872382   | -122.265023 | 1050                        |
| 3.I.3      | 5.96             | 4x              | *H. algeriensis*      | 37.872382   | -122.265023 | 1051                        |
| 3.U.1      | 5.65             | 4x              | *H. algeriensis*      | 37.872399   | -122.264800 | 1058                        |
| 3.U.2      | 5.96             | 4x              | *H. algeriensis*      | 37.872399   | -122.264800 | 1059                        |
| 3.U.3      | 6.07             | 4x              | *H. algeriensis*      | 37.872399   | -122.264800 | 1060                        |
| 4.I.1      | 5.89             | 4x              | *H. algeriensis*      | 37.869984   | -122.261662 | 1052                        |
| 4.I.2      | 5.86             | 4x              | *H. algeriensis*      | 37.869984   | -122.261662 | 1053                        |
| 4.I.3      | 5.65             | 4x              | *H. algeriensis*      | 37.869984   | -122.261662 | 1054                        |
| 4.U.1      | 5.96             | 4x              | *H. algeriensis*      | 37.869973   | -122.261492 | --                          |
| 4.U.2      | 6.03             | 4x              | *H. algeriensis*      | 37.869973   | -122.261492 | 1061                        |
| 4.U.3      | 6.07             | 4x              | *H. algeriensis*      | 37.869973   | -122.261492 | --                          |

a Possibly introgressed with *H. hibernica*

b Some specimens had too little material after DNA extraction to voucher
**Table S2** Linear mixed effect model results for the analysis of α-diversity. Evenness was calculated as inverse Simpson’s diversity/ASV richness and phylogenetic diversity was calculated as the sum of the total phylogenetic branch length for a given sample. The top table presents the effects of plant species, organ type, and site on α-diversity measures across all communities. The bottom tables present the effects of *Hedera* infection status and site on leaf and root communities separately.

**Hedera spp. & Orobanche hederae**

|                     | log(Observed ASV richness) | log(Simpson's diversity⁻¹) | Evenness | Phylogenetic diversity |
|---------------------|---------------------------|----------------------------|----------|------------------------|
|                     | F/X²                       | P                          | F/X²     | P                      | F/X²                       | P                        |
| Species (S)         | 0.01                       | 0.91                       | 1.15     | 0.31                   | 1.92                       | 0.19                     | 1.62                       | 0.23                     |
| Organ (O)           | 92.20                      | <0.001                     | 17.16    | <0.001                 | 0.46                       | 0.51                     | 153.5                      | <0.001                   |
| S × O               | 13.40                      | 0.01                       | 5.46     | 0.06                   | 0.67                       | 0.45                     | 18.07                      | 0.007                    |
| log(UsableReads)    | 243.69                     | <0.001                     | 11.15    | 0.001                  | 35.42                      | <0.001                   | 128.36                     | <0.001                   |
| Site (Si)           | 0.00                       | 1.00                       | 0.00     | 1.000                  | 0.00                       | 1.00                     | 0.00                       | 1.00                     |
| S × Si              | 0.00                       | 1.00                       | 0.65     | 0.42                   | 0.22                       | 0.64                     | 0.00                       | 1.00                     |
| O × Si              | 0.00                       | 1.00                       | 0.00     | 1.00                   | 0.00                       | 1.00                     | 0.00                       | 1.00                     |
| S × O × Si          | 0.00                       | 1.00                       | 2.56     | 0.11                   | 0.01                       | 0.92                     | 0.00                       | 1.00                     |

**Hedera spp. leaf microbiome**

|                     | log(Observed ASV richness) | log(Simpson's diversity⁻¹) | Evenness | Phylogenetic diversity |
|---------------------|---------------------------|----------------------------|----------|------------------------|
|                     | F/X²                       | P                          | F/X²     | P                      | F/X²                       | P                        |
| Infection           | 0.14                       | 0.73                       | 0.62     | 0.49                   | 0.82                       | 0.43                     | 0.81                       | 0.43                     |
| log(UsableReads)    | 488.18                     | <0.001                     | 66.17    | <0.001                 | 25.32                      | <0.001                   | 218.56                     | <0.001                   |
| Site                | 0.00                       | 1.00                       | 0.00     | 1.00                   | 0.01                       | 0.91                     | 0.00                       | 1.00                     |
| Infection × site    | 0.00                       | 1.00                       | 2.56     | 0.11                   | 0.99                       | 0.32                     | 0.00                       | 1.00                     |

**Hedera spp. root microbiome**

|                     | log(Observed ASV richness) | log(Simpson's diversity⁻¹) | Evenness | Phylogenetic diversity |
|---------------------|---------------------------|----------------------------|----------|------------------------|
|                     | F/X²                       | P                          | F/X²     | P                      | F/X²                       | P                        |
| Infection           | 0.62                       | 0.48                       | 1.00     | 0.36                   | 0.71                       | 0.44                     | 0.04                       | 0.85                     |
| log(UsableReads)    | 35.80                      | <0.001                     | 0.26     | 0.61                   | 3.81                       | 0.07                     | 23.58                      | <0.001                   |
| Site                | 0.00                       | 1.00                       | 0.00     | 1.00                   | 0.00                       | 1.00                     | 0.02                       | 0.88                     |
| Infection × site    | 2.48                       | 0.12                       | 0.00     | 1.00                   | 0.00                       | 1.00                     | 4.66                       | 0.03                     |
Table S3: Linear mixed effect model results for the analysis of β-diversity. UniFrac PCoA refers to sample scores along PCoA axes using weighted UniFrac dissimilarity among samples. Bray-Curtis PCoA refers to sample scores along PCoA axes using Bray-Curtis dissimilarity among samples. The top table presents the effects of plant species, organ type, and site on β-diversity measures across all communities. The bottom tables present the effects of *Hedera* infection status and site on leaf and root communities separately.

### Hedera spp. & Orobanche hederae

|                | UniFrac PCoA 1 | UniFrac PCoA 2 | UniFrac PCoA 3 | Bray-Curtis PCoA 1 | Bray-Curtis PCoA 2 | Bray-Curtis PCoA 3 |
|----------------|----------------|----------------|----------------|-------------------|-------------------|-------------------|
| **F/X²**       | **P**          | **F/X²**       | **P**          | **F/X²**          | **P**             | **F/X²**          | **P**             |
| Species (S)    | 51.32          | 14.85          | 7.82           | 49.39             | 61.58             | 6.28              | 0.03              |
|                | **<0.001**     | **0.002**      | **0.02**       | **<0.001**        | **<0.001**        | **0.001**         | **0.001**         |
| Organ (O)      | 64.04          | 3.07           | 4.21           | 308.75            | 0.02              | 0.46              | 0.52              |
|                | **<0.001**     | 0.10           | **0.05**       | **<0.001**        | 0.89              | 0.02              | 1.00              |
| S x O          | 65.50          | 0.09           | 11.54          | 70.96             | 12.75             | 42.43             | **0.003**         |
|                | **<0.001**     | 0.77           | **0.02**       | **<0.001**        | **0.01**          | 0.00              | 1.00              |
| log(UsableReads) | 4.93           | 0.40           | 2.78           | 9.22              | 0.23              | 0.03              | 0.86              |
|                | **0.03**       | 0.53           | 0.10           | **0.003**         | **0.89**          | **0.99**          | **0.99**          |
| Site (Si)      | 0.00           | 1.00           | 0.59           | 0.00              | 0.00              | 0.00              | 0.96              |
|                | 1.00           | 0.00           | 0.81           | 1.00              | 1.00              | 1.00              | 0.00              |
| S x Si         | 0.00           | 1.00           | 0.00           | 0.00              | 0.00              | 0.00              | 1.00              |
| O x Si         | 0.00           | 1.00           | 2.89           | 0.00              | 0.00              | 2.30              | 0.13              |
| S x O x Si     | 0.00           | 1.00           | 0.00           | 1.00              | 0.00              | 0.07              | 0.80              |

### Hedera spp. leaf microbiome

|                | UniFrac PCoA 1 | UniFrac PCoA 2 | UniFrac PCoA 3 | Bray-Curtis PCoA 1 | Bray-Curtis PCoA 2 | Bray-Curtis PCoA 3 |
|----------------|----------------|----------------|----------------|-------------------|-------------------|-------------------|
| **F/X²**       | **P**          | **F/X²**       | **P**          | **F/X²**          | **P**             | **F/X²**          | **P**             |
| Infection      | 0.89           | 0.41           | 1.59           | 0.75              | 0.79              | 0.58              | 0.50              |
|                | 0.09           | 0.79           | 0.29           | 0.45              | 0.44              | 0.07              | 0.80              |
| log(UsableReads) | 1.07           | 0.31           | 3.97           | 11.63             | 12.0              | 0.04              | 0.83              |
| Site           | 0.00           | 1.00           | 0.00           | 1.00              | 0.00              | 0.04              | 0.83              |
| Infection x site | 0.40           | 0.53           | 0.00           | 1.00              | 0.00              | 0.00              | 1.00              |

### Hedera spp. root microbiome

|                | UniFrac PCoA 1 | UniFrac PCoA 2 | UniFrac PCoA 3 | Bray-Curtis PCoA 1 | Bray-Curtis PCoA 2 | Bray-Curtis PCoA 3 |
|----------------|----------------|----------------|----------------|-------------------|-------------------|-------------------|
| **F/X²**       | **P**          | **F/X²**       | **P**          | **F/X²**          | **P**             | **F/X²**          | **P**             |
| Infection      | 0.52           | 3.43           | 0.16           | 0.96              | 1.05              | 0.74              | 0.45              |
|                | 0.51           | 0.15           | 0.71           | 0.39              | 0.37              | 2.07              | 0.16              |
| log(UsableReads) | 1.13           | 3.59           | 1.98           | 0.30              | 0.93              | 0.05              | 0.83              |
| Site           | 0.39           | 0.07           | 0.81           | 0.30              | 0.01              | 0.05              | 0.83              |
| Infection x site | 2.03           | 9.12           | 3.07           | 6.75              | 13.24             | 14.59             | **<0.001**        |
Table S4 Bacterial ASVs unique to host tissues. We list the full ASV sequence as well as the prevalence in the given tissue type (see supplemental excel sheet).

Table S5 Full differential abundance. For each taxonomic rank (different coloured rows), we report the differential abundance results for each taxon across each of the six contrasts. Positive values of differential abundance indicate that a bacterial taxon was found at higher abundance in samples corresponding to the first term in the listed contrast. Differential abundance is estimated as the log₂-fold change in read count (DESeq2: LFC) or as the relative difference in read count between experimental factors versus within experimental factors (ALDEx2: Effect). Both DESeq2 and ALDEx2 yielded qualitatively similar results. All P values were corrected using the False Discovery Rate. We also list the average relative abundance of each taxon in leaf and root tissues across both host plant species (see supplemental excel sheet).

Table S6 Network attributes of bacterial communities in Orobanche and Hedera leaves and roots using two methods, SPIEC-EASI or SparCC. Edge density is the observed proportion of the total possible associations within a network of a given size. Network centrality is the network-level measure of betweenness centrality normalized to the theoretical maximum based on network size (see Materials and Methods).

| Community | SPIEC-EASI Edge density | SPIEC-EASI Network centrality | SparCC Edge density | SparCC Network centrality |
|-----------|-------------------------|------------------------------|---------------------|----------------------------|
| IIR       | 0.020                   | 0.035                        | 0.016               | 0.093                      |
| IUR       | 0.022                   | 0.025                        | 0.014               | 0.050                      |
| UR        | 0.021                   | 0.019                        | 0.017               | 0.058                      |
| PR        | 0.009                   | 0.004                        | 0.006               | 0.004                      |
| IL        | 0.000                   | 0.000                        | 0.073               | 0.067                      |
| UL        | 0.000                   | 0.000                        | 0.111               | 0.198                      |
| PL        | 0.008                   | 0.000                        | 0.004               | 0.000                      |
Table S7 Results from a series of Procrustes analyses, in which individual sample scores along the first two principle coordinate axes of separate ordinations were matched between different bacterial communities. For example, in the first row of the following table the sample scores from a PCoA of IIR and a PCoA of IUR were matched with a Procrustes analysis. The fit between two sets of scores is given by the Procrustes correlation-like statistic ($t_0$), which ranges from 0 (no fit) to 1 (perfect fit). Numerous permutations of PCoA scores among individual samples followed by recalculation of $t_0$ provides a test of the statistical significance of the observed fit between two sets of PCoA scores. We also include three tests to serve as a ‘sanity check’, which we expect to exhibit non-significant congruence (e.g. Orobanche root microbiota should not exhibit any congruence with those of uninfected Hedera).

| Ordination 1 | Ordination 2 | Procrustes correlation ($t_0$) | P       |
|--------------|--------------|--------------------------------|---------|
| IIR          | IUR          | 0.74                           | 0.002   |
| IIR          | PL           | 0.62                           | 0.02    |
| IUR          | PL           | 0.61                           | 0.02    |
| IIR          | PR           | 0.56                           | 0.03    |
| IUR          | PR           | 0.56                           | 0.03    |
| IIR          | IS           | 0.91                           | 0.04    |
| IUR          | IS           | 0.91                           | 0.04    |
| PR           | IS           | 0.95                           | 0.08    |
| PL           | PR           | 0.50                           | 0.11    |
| IL           | IUR          | 0.46                           | 0.14    |
| IL           | PR           | 0.48                           | 0.15    |
| UR           | UL           | 0.37                           | 0.32    |
| UR           | US           | 0.83                           | 0.33    |
| PL           | IS           | 0.66                           | 0.38    |
| IIR          | IL           | 0.33                           | 0.53    |
| IL           | IS           | 0.66                           | 0.58    |
| UL           | US           | 0.72                           | 0.58    |
| IL           | PL           | 0.27                           | 0.66    |

Sanity check

| Ordination 1 | Ordination 2 | P       |
|--------------|--------------|---------|
| IIR          | UR           | 0.31    |
| PR           | UR           | 0.26    |
| PL           | UR           | 0.27    |
Table S8 Results from our leave-one-out approach at the level of bacterial phylum for both parasite root and leaf microbial communities. For parasite root and leaf communities separately, we removed all bacterial ASVs from the parasite dataset classified to a given bacterial phyla, re-calculated weighted UniFrac distances among all samples, obtained sample scores from a new PCoA, and re-calculated $t_0$ with the original *Hedera* infected root PCoA. The effect of excluding a particular bacterial phylum on the fit between host and parasite microbiota is given by $\Delta t = (t_{\text{excluded}} - t_0)$.

| Goodness of fit ($t_0$) | Number of ASVs excluded | Phylum                | $\Delta t_0$ | Organ |
|-------------------------|--------------------------|-----------------------|--------------|-------|
| 0.519                   | 129                      | Bacteroidetes         | -0.038       | root  |
| 0.533                   | 498                      | Proteobacteria        | -0.025       | root  |
| 0.549                   | 6                        | Armatimonadetes       | -0.008       | root  |
| 0.556                   | 42                       | Verrucomicrobia       | -0.001       | root  |
| 0.557                   | 5                        | Can. Div. WPS-1       | 0.000        | root  |
| 0.557                   | 1                        | Nitrospira            | 0.000        | root  |
| 0.557                   | 1                        | Chlamydiae            | 0.000        | root  |
| 0.557                   | 10                       | Chloroflexi           | 0.000        | root  |
| 0.557                   | 3                        | Firmicutes            | 0.000        | root  |
| 0.557                   | 3                        | Gemmatimonadetes      | 0.000        | root  |
| 0.563                   | 98                       | Acidobacteria         | 0.005        | root  |
| 0.564                   | 67                       | Planctomycetes        | 0.007        | root  |
| 0.614                   | 284                      | Actinobacteria        | 0.057        | root  |
| 0.605                   | 166                      | Proteobacteria        | -0.020       | leaf  |
| 0.625                   | 4                        | Verrucomicrobia       | 0.000        | leaf  |
| 0.625                   | 1                        | Chloroflexi           | 0.000        | leaf  |
| 0.625                   | 2                        | Firmicutes            | 0.000        | leaf  |
| 0.626                   | 12                       | Acidobacteria         | 0.001        | leaf  |
| 0.626                   | 6                        | Planctomycetes        | 0.001        | leaf  |
| 0.632                   | 62                       | Actinobacteria        | 0.007        | leaf  |
| 0.652                   | 31                       | Bacteroidetes         | 0.027        | leaf  |
Table S9 Results from our leave-one-out approach at the level of bacterial order for both parasite root and leaf microbial communities. For parasite root and leaf communities separately, we removed all bacterial ASVs from the parasite dataset classified to a given bacterial order, re-calculated weighted UniFrac distances among all samples, obtained sample scores from a new PCoA, and re-calculated \( t_0 \) with the original *Hedera* infected root PCoA. The effect of excluding a particular bacterial phylum on the fit between host and parasite microbiota is given by \( \Delta t = (t_{\text{excluded}} - t_0) \).

| Goodness of fit \( (t_0) \) | Number of ASVs | Order            | Phylum       | \( \Delta t_0 \) | Organ |
|-----------------------------|----------------|------------------|--------------|-----------------|-------|
| 0.424                       | 0.22           | 55               | Burkholderiales | Proteobacteria | -0.133 | root |
| 0.538                       | 0.06           | 34               | Sphingomonadales | Proteobacteria | -0.019 | root |
| 0.543                       | 0.06           | 46               | Cytophagales      | Bacteroidetes | -0.014 | root |
| 0.543                       | 0.06           | 140              | Rhizobiales       | Proteobacteria | -0.014 | root |
| 0.549                       | 0.06           | 12               | Pseudomonadales   | Proteobacteria | -0.008 | root |
| 0.549                       | 0.05           | 4                | Methylophilales   | Proteobacteria | -0.008 | root |
| 0.557                       | 0.05           | 1                | Bacteroidales     | Bacteroidetes | -0.001 | root |
| 0.557                       | 0.04           | 41               | Myxococcales      | Proteobacteria | -0.001 | root |
| 0.557                       | 0.04           | 1                | Neisseriales      | Proteobacteria | 0.000  | root |
| 0.557                       | 0.05           | 5                | Gp17             | Acidobacteria | 0.000  | root |
| 0.557                       | 0.06           | 3                | Edaphobacter      | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 2                | Terriglobus       | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 5                | Rhizocyclales     | Proteobacteria | 0.000  | root |
| 0.557                       | 0.05           | 1                | Aeromonadales     | Proteobacteria | 0.000  | root |
| 0.557                       | 0.05           | 3                | Bdellovibrionales | Proteobacteria | 0.000  | root |
| 0.557                       | 0.06           | 2                | Gp10             | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 1                | Rubrobacterales   | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 1                | Candidatus_Brocadiales | Planctomycetes | 0.000  | root |
| 0.557                       | 0.04           | 1                | Gp5              | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 2                | Gp2              | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 1                | Chthonomonadales  | Armatimonadetes | 0.000  | root |
| 0.557                       | 0.05           | 1                | Paludibaculum     | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 3                | Gp7              | Acidobacteria | 0.000  | root |
| 0.557                       | 0.04           | 1                | Armatimonadales   | Armatimonadetes | 0.000  | root |
| 0.557                       | 0.05           | 1                | Gp11             | Acidobacteria | 0.000  | root |
| 0.557                       | 0.04           | 1                | Blastocellata     | Acidobacteria | 0.000  | root |
| 0.557                       | 0.06           | 1                | Nitrosomonadales  | Proteobacteria | 0.000  | root |
| 0.557                       | 0.05           | 2                | Syntrophobacterales | Proteobacteria | 0.000  | root |
| 0.557                       | 0.03           | 14               | Gp16             | Acidobacteria | 0.000  | root |
| 0.557                       | 0.04           | 2                | Gp1              | Acidobacteria | 0.000  | root |
| 0.557                       | 0.04           | 2                | Legionellales     | Proteobacteria | 0.000  | root |
| 0.557                       | 0.05           | 2                | Gp3              | Acidobacteria | 0.000  | root |
| 0.557                       | 0.05           | 5                | Candidatus_Solibacter | Acidobacteria | 0.000  | root |
| 0.558                       | 0.05           | 5                | Rhodobacterales   | Proteobacteria | 0.000  | root |
| 0.558                       | 0.05           | 3                | Enterobacteriales | Proteobacteria | 0.000  | root |
| 0.558                       | 0.05           | 3                | Chromatiales      | Proteobacteria | 0.000  | root |
| 0.558                       | 0.06           | 9                | Alphaproteobacteria | Proteobacteria | 0.000  | root |
| 0.558                       | 0.05           | 5                | Aridibacter       | Acidobacteria | 0.000  | root |
| 0.558                       | 0.06           | 2                | Granulicella      | Acidobacteria | 0.000  | root |
Table S9 continued

| Goodness of fit ($t_0$) | P   | Number of ASVs excluded | Order           | Phylum          | $\Delta t_0$ | Organ |
|--------------------------|-----|--------------------------|-----------------|-----------------|-------------|-------|
| 0.558                    | 0.04| 3                        | Thermoleophiles | Actinobacteria  | 0.000       | root  |
| 0.558                    | 0.06| 3                        | Sneathiellales  | Proteobacteria  | 0.000       | root  |
| 0.558                    | 0.05| 4                        | Gp4             | Acidobacteria   | 0.001       | root  |
| 0.559                    | 0.05| 51                       | Rhodospirillales| Proteobacteria  | 0.002       | root  |
| 0.561                    | 0.04| 19                       | Gaiellales      | Actinobacteria  | 0.003       | root  |
| 0.561                    | 0.04| 40                       | Gp6             | Acidobacteria   | 0.004       | root  |
| 0.562                    | 0.04| 40                       | Acidimicrobiales| Actinobacteria  | 0.005       | root  |
| 0.563                    | 0.04| 37                       | Solirubrobacteria| Actinobacteria | 0.005       | root  |
| 0.564                    | 0.04| 65                       | Planctomycetes  | Planctomycetes  | 0.007       | root  |
| 0.565                    | 0.05| 53                       | Xanthomonadale  | Proteobacteria  | 0.008       | root  |
| 0.566                    | 0.04| 14                       | Caulobacterales | Proteobacteria  | 0.009       | root  |
| 0.568                    | 0.04| 58                       | Sphingobacteria | Bacteroidetes   | 0.011       | root  |
| 0.589                    | 0.03| 21                       | Flavobacteria   | Bacteroidetes   | 0.032       | root  |
| 0.600                    | 0.03| 161                      | Actinomycetes   | Actinobacteria  | 0.043       | root  |
| 0.513                    | 0.09| 12                       | Pseudomonadale  | Proteobacteria  | -0.112      | leaf  |
| 0.613                    | 0.02| 51                       | Rhizobiales     | Proteobacteria  | -0.012      | leaf  |
| 0.616                    | 0.03| 6                        | Caulobacterales | Proteobacteria  | -0.009      | leaf  |
| 0.625                    | 0.02| 11                       | Myxococcales    | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.03| 1                        | Rhodocyclales   | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.02| 1                        | Neisseriales    | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.02| 1                        | Methylophilales | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.02| 1                        | Legionellales   | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.02| 1                        | Sneathiellales  | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.01| 1                        | Rubrobacteria   | Actinobacteria  | 0.000       | leaf  |
| 0.625                    | 0.02| 2                        | Alphaproteobacteria| Proteobacteria | 0.000       | leaf  |
| 0.625                    | 0.02| 1                        | Bdellovibrionales| Proteobacteria | 0.000       | leaf  |
| 0.625                    | 0.02| 1                        | Chromatiales    | Proteobacteria  | 0.000       | leaf  |
| 0.625                    | 0.01| 3                        | Gaiellales      | Actinobacteria  | 0.000       | leaf  |
| 0.626                    | 0.01| 10                       | Rhodospirillales| Proteobacteria  | 0.001       | leaf  |
| 0.626                    | 0.01| 4                        | Acidimicrobiales| Actinobacteria  | 0.001       | leaf  |
| 0.627                    | 0.02| 6                        | Solirubrobacteria| Actinobacteria | 0.002       | leaf  |
| 0.628                    | 0.02| 6                        | Flavobacteria   | Bacteroidetes   | 0.003       | leaf  |
| 0.632                    | 0.02| 12                       | Cytophagales    | Bacteroidetes   | 0.007       | leaf  |
| 0.634                    | 0.02| 18                       | Burkholderiales | Proteobacteria  | 0.009       | leaf  |
| 0.637                    | 0.01| 14                       | Xanthomonadale  | Proteobacteria  | 0.012       | leaf  |
| 0.639                    | 0.01| 46                       | Actinomycetes   | Actinobacteria  | 0.014       | leaf  |
| 0.644                    | 0.02| 13                       | Sphingobacteria | Bacteroidetes   | 0.019       | leaf  |
| 0.655                    | 0.01| 23                       | Sphingomonadale | Proteobacteria  | 0.030       | leaf  |
| 0.657                    | 0.01| 5                        | Enterobacterials| Proteobacteria  | 0.032       | leaf  |