**Supplementary Materials**



**Figure S1.** **Left panel:** **Distribution of node degree.** Node degree is the number of links that a node shares with others. DBF: the deciduous broad-leaved forest. MBF: the mixed deciduous-evergreen broad-leaved forest. EBF: the evergreen broad-leaved forest. For the network of MBF, node degree is limited to a maximum of 20, whereas for the network of DBF, more than 20 nodes have the degree > 20. **Right panel: Plots of the within-module connectivity (Zi) and the among-module connectivity (Pi).** Keystone taxa were selected based on the values of Zi and Pi: network hubs (Zi > 2.5, Pi > 0.62), module hubs (Zi > 2.5, Pi ≤ 0.62), connectors (Zi ≤ 2.5, Pi > 0.62) and peripherals (Zi < 2.5, Pi < 0.62). Each dot indicates a node. Different colors indicate different bacterial phyla.

**Table S1.** Summary of canopy tree species (those trees with diameter at breast height > 5 cm) and their growth habit (deciduous or evergreen) in the three subtropical broad-leaved forests.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Canopy Tree Species | Growth Habit | Canopy Tree Species | Growth Habit | Canopy Tree Species | Growth Habit | Canopy Tree Species | Growth Habit |
| *Acer amplum* | Deciduous | *Cerasus pseudocerasus* | Deciduous | *Hamamelis mollis* | Deciduous | *Quercus engleriana* | Evergreen |
| *Acer davidii* | Deciduous | *Cercis glabra* | Deciduous | *Idesia polycarpa* | Deciduous | *Quercus serrata* | Deciduous |
| *Acer henryi* | Deciduous | *Choerospondias axillaris* | Deciduous | *Lindera glauca* | Deciduous | *Quercus variabilis* | Deciduous |
| *Acer oliverianum* | Deciduous | *Cinnamomum porrectum* | Evergreen | *Lindera megaphylla* | Evergreen | *Rhamnella franguloides* | Deciduous |
| *Acer sinense* | Deciduous | *Cinnamomum wilsonii* | Evergreen | *Lindera obtusiloba* | Deciduous | *Rhododendron fortunei* | Evergreen |
| *Acer tenellum* | Deciduous | *Clethra fargesii* | Deciduous | *Litsea pedunculata* | Evergreen | *Rhododendron latoucheae* | Evergreen |
| *Acer wilsonii* | Deciduous | *Clethra faberi* | Evergreen | *Litsea coreana* | Evergreen | *Rhododendron mariesii* | Deciduous |
| *Alangium chinense* | Deciduous | *Cyclobalanopsis glauca* | Evergreen | *Litsea pungens* | Deciduous | *Salix mictotricha* | Deciduous |
| *Albizia kalkora* | Deciduous | *Cyclobalanopsis gracilis* | Evergreen | *Machilus ichangensis* | Evergreen | *Sorbus folgneri* | Deciduous |
| *Betula insignis* | Deciduous | *Cyclobalanopsis multinervis* | Evergreen | *Morus alba* | Deciduous | *Sorbus wilsoniana* | Deciduous |
| *Bothrocaryum controversum* | Deciduous | *Cyclobalanopsis oxyodon* | Evergreen | *Neolitsea aurata* | Evergreen | *Sycopsis sinensis* | Evergreen |
| *Camellia caudata* | Evergreen | *Daphniphyllum macropodum* | Evergreen | *Neolitsea levinei* | Evergreen | *Symplocos hunanensis* | Deciduous |
| *Camellia fraterna* | Evergreen | *Dendrobenthamia angustata* | Evergreen | *Padus buergeriana* | Deciduous | *Symplocos anomala* | Evergreen |
| *Carpinus chuniana* | Deciduous | *Dendrobenthamia japonica* | Deciduous | *Padus racemosa* | Deciduous | *Symplocos botryantha* | Evergreen |
| *Carpinus cordata* | Deciduous | *Diospyros glaucifolia* | Deciduous | *Philadelphus incanus* | Deciduous | *Symplocos laurina* | Evergreen |
| *Carpinus fargesiana* | Deciduous | *Diospyros lotus* | Deciduous | *Phoebe faberi* | Evergreen | *Symplocos paniculata* | Deciduous |
| *Carpinus pubescens* | Deciduous | *Enkianthus quinqueflorus* | Deciduous | *Photinia beauverdiana* | Deciduous | *Symplocos phyllocalyx* | Evergreen |
| *Carpinus turczaninowii* | Deciduous | *Euonymus myrianthus* | Evergreen | *Picrasma chinensis* | Deciduous | *Symplocos setchuensis* | Evergreen |
| *Carpinus viminea* | Deciduous | *Eurya groffii* | Evergreen | *Pinus armandii* | Evergreen | *Tetracentron sinense* | Deciduous |
| *Carrierea calycina* | Deciduous | *Euscaphis japonica* | Deciduous | *Platycarya strobilacea* | Deciduous | *Toona ciliata* | Deciduous |
| *Celtis sinensis* | Deciduous | *Ficus heteromorpha* | Deciduous | *Pteroceltis tatarinowii* | Deciduous | *Zelkova serrata* | Deciduous |

**Table S2.** Dissimilarity of soil bacterial communities among vegetation types. Bold values indicate *P* < 0.01.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Distance  Method | MRPP\* | | Adonis\* | | | ANOSIM\* | | |
| δ | *P* | | F | *P* | | R | *P* |
| DBF vs. MBF | Bray-Curtis  Euclidean  Horn | 0.38  1648.00  0.29 | **0.001†**  **0.001**  **0.001** | | 10.54  10.54  10.54 | **0.001**  **0.001**  **0.001** | | 0.89  0.42  0.53 | **0.001**  **0.001**  **0.001** |
| DBF vs. EBF | Bray-Curtis  Euclidean  Horn | 0.43  2132.00  0.32 | **0.001**  **0.001**  **0.001** | | 22.52  22.52  22.52 | **0.001**  **0.001**  **0.001** | | 0.99  0.70  1.00 | **0.001**  **0.001**  **0.001** |
| MBF vs. EBF | Bray-Curtis  Euclidean  Horn | 0.40  2460.00  0.35 | **0.001**  **0.001**  **0.001** | | 30.96  30.96  30.96 | **0.001**  **0.001**  **0.001** | | 1.00  0.58  0.90 | **0.001**  **0.001**  **0.001** |

\*Three nonparametric statistical tests: the multi-response permutation procedure (MRPP), the non-parametric multivariate analysis of variance (Adonis), and the analysis of similarity (ANOSIM).

† Bold values indicate significance at the *P* < 0.01 level.

**Table S3.** Comparisons of relative abundances of the most abundant bacterial genera (relative abundance > 0.50%) among vegetation types.

|  |  |  |  |
| --- | --- | --- | --- |
| Genus | DBF (%) | MBF (%) | EBF (%) |
| *Burkholderia* | 5.45±3.56 a\* | 5.24±1.19 a | 0.04±0.03 b |
| *Massilia* | 0.30±0.31 b | 5.54±6.47 a | 5.47±3.56 a |
| *Arthrobacter* | 0.30±0.34 b | 1.83±1.13 b | 8.08±3.33 a |
| *Bradyrhizobium* | 3.32±1.14 a | 1.97±0.82 b | 0.53±0.24 c |
| *Sporosarcina* | 0.01±0.01 b | < 0.01 b | 3.23±3.87 a |
| *Rhodoplanes* | 0.68±0.16 b | 1.72±0.50 a | 0.57±0.30 b |
| *Rhizomicrobium* | 1.62±0.25 a | 0.90±0.22 b | 0.40±0.10 c |
| *Kitasatospora* | 0.69±0.40 b | 2.04±0.67 a | 0.01±0.01 c |
| *Steroidobacter* | 1.32±0.41 a | 0.74±0.33 b | 0.72±0.30 b |
| *Pseudomonas* | 0.14±0.09 a | 0.13±0.08 a | 2.36±4.10 a |
| *Actinoallomurus* | 0.73±0.38 b | 1.63±0.47 a | 0.03±0.02 c |
| *Pseudolabrys* | 0.80±0.33 a | 0.28±0.18 a | 0.71±0.86 a |
| *Granulicella* | 0.91±0.51 a | 0.79±0.30 a | 0.01±0.01 b |
| *Phenylobacterium* | 0.90±0.25 a | 0.74±0.19 a | 0.06±0.02 b |
| *Gemmatimonas* | 0.74±0.23 a | 0.59±0.23 ab | 0.37±0.16 b |
| *Sphingomonas* | 0.72±0.28 a | 0.05±0.05 b | 0.91±0.64 a |

**\***Different letters next to values (mean±standard deviation, n = 9) indicate significant differences (*P* < 0.05, one-way ANOVA, Tukey HSD).

**Table S4.** Bacterial indicator genera of the three vegetation types, based on the threshold that specificity > 0.8 and fidelity = 1.0.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Forest | Genus | Relative abundance (%) | Specificity | Fidelity |
| DBF | *Rathayibacter* | 0.09 | 0.89 | 1.00 |
| *Luteibacter* | 0.01 | 0.89 | 1.00 |
| *Thermomonas* | 0.03 | 0.88 | 1.00 |
| *Dokdonella* | 0.07 | 0.86 | 1.00 |
| *Thermomonospora* | 0.04 | 0.84 | 1.00 |
| MBF | *Zoogloea* | 0.02 | 0.93 | 1.00 |
| *Rhodocista* | 0.07 | 0.92 | 1.00 |
| *Rhodanobacter* | 0.07 | 0.90 | 1.00 |
| *Ktedonobacter* | 0.27 | 0.81 | 1.00 |
| EBF | *Desulfomonile* | < 0.01 | 1.00 | 1.00 |
| *Levilinea* | 0.01 | 1.00 | 1.00 |
| *Sporosarcina* | 1.08 | 1.00 | 1.00 |
| *Cryobacterium* | 0.16 | 0.99 | 1.00 |
| *Adhaeribacter* | 0.07 | 0.96 | 1.00 |
| *Microvirga* | 0.01 | 0.96 | 1.00 |
| *Geminicoccus* | 0.03 | 0.95 | 1.00 |
| *Brevundimonas* | 0.02 | 0.95 | 1.00 |
| *Geobacter* | 0.03 | 0.94 | 1.00 |
| *Flavobacterium* | 0.19 | 0.92 | 1.00 |
| *Lysobacter* | 0.14 | 0.92 | 1.00 |
| *Longilinea* | < 0.01 | 0.91 | 1.00 |
| *Bosea* | 0.02 | 0.91 | 1.00 |
| *Pseudomonas* | < 0.01 | 0.90 | 1.00 |
| *Pedobacter* | 0.11 | 0.90 | 1.00 |
| *Afifella* | 0.01 | 0.89 | 1.00 |
| *Anderseniella* | 0.06 | 0.89 | 1.00 |
| *Luteimonas* | 0.03 | 0.88 | 1.00 |
| *Solitalea* | 0.07 | 0.87 | 1.00 |
| *Janthinobacterium* | 0.45 | 0.84 | 1.00 |
| *Haliea* | 0.02 | 0.83 | 1.00 |
| *Phaselicystis* | 0.06 | 0.83 | 1.00 |
| *Frondihabitans* | 0.02 | 0.82 | 1.00 |

**Table S5.** Topological properties of the meta-network and three vegetation type-specific networks and their corresponding random networks.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Network topological properties | Meta-network | DBF | MBF | EBF |
| Total nodes | 294 | 868 | 511 | 623 |
| Total links | 968 | 1942 | 674 | 1128 |
| R2 of power-law | 0.81 | 0.95 | 0.92 | 0.90 |
| Average degree | 6.59 | 4.48 | 2.64 | 3.62 |
| Average clustering coefficient | 0.36 | 0.16 | 0.11 | 0.17 |
| Average path distance | 5.50 | 5.29 | 7.17 | 5.69 |
| Modularity | 0.67 | 0.66 | 0.82 | 0.71 |
| Total modules | 17 | 52 | 62 | 55 |
| Maximal node degree | 30 | 47 | 20 | 43 |
| Percentage of positive links (%) | 96.39 | 87.95 | 87.39 | 84.31 |
| Total keystone taxa | 3 | 56 | 13 | 36 |
| Clustering coefficient of random networks | 0.02±0.01 | 0.02±0.01 | 0.01±0.01 | 0.01±0.01 |
| Path distance of random networks | 4.08±0.10 | 4.07±0.03 | 5.14±0.08 | 4.46±0.04 |
| Modularity of random networks | 0.54±0.01 | 0.47±0.01 | 0.69±0.01 | 0.55±0.01 |

**Table S6.** Taxonomy of bacterial keystone taxa of the deciduous broad-leaved forest (DBF).

| OTU | Keystone role\* | Taxonomy | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Phylum | Class | Order | Family | Genus |
| OTU\_10245 | Connector | *Proteobacteria* | *δ-Proteobacteria* | *Myxococcales* | Unclassified | Unclassified |
| OTU\_1052 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_121 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_12213 | Connector | *Planctomycetes* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_12225 | Module hub | *Proteobacteria* | *γ-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_1252 | Connector | *Actinobacteria* | *Actinobacteria* | *Actinomycetales* | *Actinospicaceae* | *Actinospica* |
| OTU\_1408 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_14103 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_1414 | Module hub | *Proteobacteria* | *δ-Proteobacteria* | *Myxococcales* | Unclassified | Unclassified |
| OTU\_1452 | Module hub | *Proteobacteria* | *δ-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_14737 | Module hub | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | *Chitinophagaceae* | *Flavisolibacter* |
| OTU\_1568 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_159 | Module hub | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | *Chitinophagaceae* | *Terrimonas* |
| OTU\_15902 | Module hub | *Proteobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_16449 | Module hub | *Proteobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_16494 | Connector | *Proteobacteria* | *α-Proteobacteria* | *Rhodospirillales* | Unclassified | Unclassified |
| OTU\_18718 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_18826 | Connector | *Proteobacteria* | *γ-Proteobacteria* | *Xanthomonadales* | *Sinobacteraceae* | *Steroidobacter* |
| OTU\_1918 | Module hub | *Proteobacteria* | *δ-Proteobacteria* | *Bdellovibrionales* | *Bdellovibrionaceae* | *Vampirovibrio* |
| OTU\_1958 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_2016 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_2032 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_2077 | Connector | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | *Chitinophagaceae* | Unclassified |
| OTU\_21124 | Connector | *Verrucomicrobia* | *Spartobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_22403 | Connector | *Proteobacteria* | *α-Proteobacteria* | *Rhodospirillales* | Unclassified | Unclassified |
| OTU\_2263 | Module hub | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | *Chitinophagaceae* | Unclassified |
| OTU\_233 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_23439 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_25302 | Module hub | *Proteobacteria* | *δ-Proteobacteria* | *Myxococcales* | *Polyangiaceae* | *Chondromyces* |
| OTU\_25619 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Terriglobus |
| OTU\_2611 | Connector | *Planctomycetes* | *Planctomycetacia* | *Planctomycetales* | *Planctomycetaceae* | *Blastopirellula* |
| OTU\_27047 | Module hub | *Proteobacteria* | *α-Proteobacteria* | *Rhizobiales* | *Rhodobiaceae* | Unclassified |
| OTU\_27088 | Connector | *Proteobacteria* | *α-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_3002 | Module hub | *Proteobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3035 | Module hub | *Chloroflexi* | *Ktedonobacteria* | *Ktedonobacterales* | *Ktedonobacteraceae* | *Ktedonobacter* |
| OTU\_3042 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3284 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3475 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3725 | Module hub | *Chlamydiae* | *Chlamydiae* | *Chlamydiales* | *Simkaniaceae* | *Simkania* |
| OTU\_409 | Connector | *Actinobacteria* | *Actinobacteria* | *Actinomycetales* | *Pseudonocardiaceae* | *Pseudonocardia* |
| OTU\_4248 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_432 | Module hub | *Proteobacteria* | *β-Proteobacteria* | *Burkholderiales* | *Burkholderiaceae* | *Pandoraea* |
| OTU\_441 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_4663 | Connector | *Actinobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_506 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_5616 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_659 | Connector | *Bacteroidetes* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_6949 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_7122 | Connector | *Chloroflexi* | *Ktedonobacteria* | *Ktedonobacterales* | *Ktedonobacteraceae* | *Ktedonobacter* |
| OTU\_740 | Connector | *Verrucomicrobia* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_79 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_837 | Connector | *Planctomycetes* | Unclassified | Unclassified | Unclassified | Unclassified |

\*Keystone roles were characterized based on the values of within-module connectivity (Zi) and among-module connectivity (Pi): network hubs (Zi > 2.5, Pi > 0.62), module hubs (Zi > 2.5, Pi ≤ 0.62), connectors (Zi ≤ 2.5, Pi > 0.62) and peripherals (Zi < 2.5, Pi < 0.62).

**Table S7.** Taxonomy of bacterial keystone taxa of the mixed deciduous-evergreen broad-leaved forest (MBF).

| OTU | Keystone role | Taxonomy | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Phylum | Class | Order | Family | Genus |
| OTU\_10618 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_11740 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_1375 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_14201 | Module hub | *Actinobacteria* | *Actinobacteria* | *Actinomycetales* | *Thermomonosporaceae* | *Actinoallomurus* |
| OTU\_1811 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_18427 | Connector | *Proteobacteria* | *γ-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_1914 | Module hub | *Actinobacteria* | *Actinobacteria* | *Solirubrobacterales* | *Solirubrobacteraceae* | *Solirubrobacter* |
| OTU\_2325 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_24419 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_27136 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3196 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_4609 | Module hub | *Proteobacteria* | *γ-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_6614 | Connector | *Planctomycetes* | *Planctomycetacia* | *Planctomycetales* | *Planctomycetaceae* | *Gemmata* |

**Table S8.** Taxonomy of bacterial keystone taxa of the evergreen broad-leaved forest (EBF).

| OTU | Keystone role | Taxonomy | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Phylum | Class | Order | Family | Genus |
| OTU\_10484 | Connector | *Verrucomicrobia* | *Spartobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_11484 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_11977 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_1296 | Connector | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | Unclassified | Unclassified |
| OTU\_13199 | Module hub | Acidobacteria | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_13209 | Connector | *Proteobacteria* | *δ-Proteobacteria* | *Syntrophobacterales* | *Syntrophaceae* | *Desulfomonile* |
| OTU\_13255 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_133 | Connector | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | *Chitinophagaceae* | *Ferruginibacter* |
| OTU\_1704 | Module hub | *Proteobacteria* | *δ-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_1753 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_181 | Module hub | *Proteobacteria* | *α-Proteobacteria* | *Sphingomonadales* | *Sphingomonadaceae* | *Sphingomonas* |
| OTU\_1862 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_1880 | Connector | *Planctomycetes* | *Planctomycetacia* | *Planctomycetales* | *Planctomycetaceae* | *Zavarzinella* |
| OTU\_19 | Connector | *Actinobacteria* | *Actinobacteria* | *Actinomycetales* | *Thermomonosporaceae* | *Actinoallomurus* |
| OTU\_19484 | Connector | *Proteobacteria* | *β-Proteobacteria* | *Burkholderiales* | Unclassified | Unclassified |
| OTU\_19823 | Connector | *Chloroflexi* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_2068 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_21201 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_245 | Module hub | *Proteobacteria* | *γ-Proteobacteria* | *Xanthomonadales* | *Xanthomonadaceae* | *Lysobacter* |
| OTU\_2485 | Connector | *Actinobacteria* | *Actinobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_2738 | Connector | *Actinobacteria* | *Actinobacteria* | *Acidimicrobiales* | *Acidimicrobiaceae* | *Ferrimicrobium* |
| OTU\_274 | Connector | *Proteobacteria* | *α-Proteobacteria* | *Rhizobiales* | *Methylobacteriaceae* | *Microvirga* |
| OTU\_3504 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3627 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_3791 | Connector | *Proteobacteria* | *δ-Proteobacteria* | Unclassified | Unclassified | Unclassified |
| OTU\_4056 | Connector | *Proteobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_5394 | Module hub | *Planctomycetes* | *Planctomycetacia* | *Planctomycetales* | *Planctomycetaceae* | Unclassified |
| OTU\_5852 | Module hub | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_6441 | Module hub | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_662 | Module hub | *Proteobacteria* | *α-Proteobacteria* | *Caulobacterales* | *Caulobacteraceae* | *Brevundimonas* |
| OTU\_719 | Connector | *Gemmatimonadetes* | *Gemmatimonadetes* | *Gemmatimonadales* | *Gemmatimonadaceae* | *Gemmatimonas* |
| OTU\_7201 | Connector | *Chloroflexi* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_851 | Connector | *Acidobacteria* | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_8749 | Connector | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| OTU\_9297 | Module hub | *Planctomycetes* | *Planctomycetacia* | *Planctomycetales* | *Planctomycetaceae* | *Gemmata* |
| OTU\_980 | Connector | *Bacteroidetes* | *Sphingobacteria* | *Sphingobacteriales* | *Chitinophagaceae* | *Terrimonas* |