Diversity and evolutionary patterns in the bacterial gut microbiota of termites and cockroaches

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(*In Vorbereitung*)

Weiterhin ist in Kooperation folgende Publikation entstanden, die nicht im Fokus dieser Arbeit stand:

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(*Eingereicht*)

[…]
But you will be always dear to my heart
I close my eyes, I reminisce ... about you

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1 Introduction

Dictyopteran phylogeny – "Death of an order"

Termites (Isoptera) and cockroaches (Blattodea) belong to the superorder *Dictyoptera*. The termites evolved 150 million years ago (Grimaldi and Engel, 2005) and comprise seven families: Mastotermitidae, Kalotermitidae, Hodotermitidae, Termopsidae, Rhinotermitidae, Serritermitidae, and Termitidae (Abe *et al.*, 2000; Engel and Krishna, 2004). The latter includes all more derived higher termites that differentiate from the other lower termite families by the absence of flagellates in the guts. The cockroaches consist of the families Blaberidae, Blattidae, Blattellidae, Nocticolidae, Polyphagidae, and Cryptocercidae.

For a long time the phylogenetic relationship of termites and cockroaches was debated. With the use of molecular tools by investigating multiple phylogenetic and functional marker genes, first hints for termite evolution from wood-feeding cockroaches were revealed (Lo *et al.*, 2000).

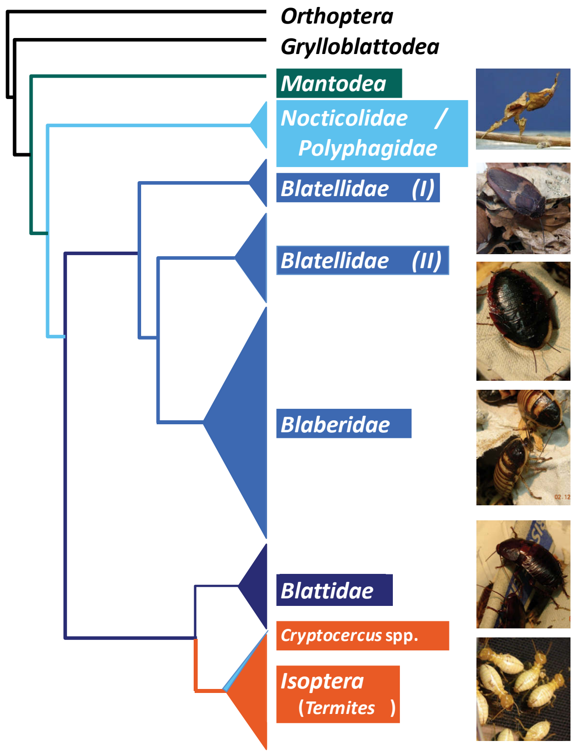


Figure 1: Phylogenetic tree of the superorder *Dictyoptera*.

Termites are eusocial cockroaches that share a common ancestor with other dictyopteran lineages. Figure was adapted from Inward *et al.*, 2007.

Following molecular studies included even more phylogenetic marker genes and dictyopteran species and could reveal termites as monophyletic group falling within the cockroaches as sister group to the Blattidae family (Inward et al., 2007; Legendre et al., 2008; Fig. 1). In the course of these studies, the phylogenetic position of the special wood-feeding cockroach Cryptocercus punctulatus to cockroaches and termites was consistently recovered as a termite–Cryptocercus clade. The presence of unique genera of parabasalid and oxymonad flagellates that only occurs in lower termites suggests the genus Cryptocercus more to be a termite than a cockroach (Cleveland et al., 1934; Inoue et al., 2000; Ohkuma et al., 2009).

A third group and the smallest order of the *Dictyoptera* is the Mantodea (praying mantises). They have a predatory lifestyle and are only distantly related to cockroaches and termites. They are not part of this study.

Feeding traits of termites and cockroaches

The diet of termites and cockroaches differ significantly. The latter have an omnivorous lifestyle and thrive on a wide variety of substances like fruits, fungi, dung, and decaying wood or litter (Grimaldi and Engel, 2005). Cockroaches of the genus *Cryptocercus* and some genera in the family Blaberidae are exceptions. Both developed the ability to digest cellulose independently (Klass *et al.*, 2008).

Termites exhibit a very specific feeding. While the lower termites are restricted to wood-feeding, many lineages within the higher termites show specializations to recalcitrant diets that can include soil (e.g., *Cubitermes* spp.), grass (e.g., *Trinervitermes* spp.), and wood (e.g., *Nasutitermes* spp.) (Donovan *et al.*, 2001). Another special case is fungus cultivation in higher termite species (e.g., *Macrotermes* spp.). They digest both the cellulose and the cultivated fungus.

Digestive tracts of termites and cockroaches

Termites and cockroaches have similar digestive systems (Fig. 2). In general, they comprise mouth, esophagus, salivary glands, foregut, midgut, and hindgut. However, in detail the cockroaches exhibit distinctively large foreguts (including crop; Watanabe and Tokuda, 2010). The hindgut of higher termites shows a more complex structure compared to the cockroaches, i.e., compartmentation in P1 to P5, Noirot, 1995; Noirot, 2001).

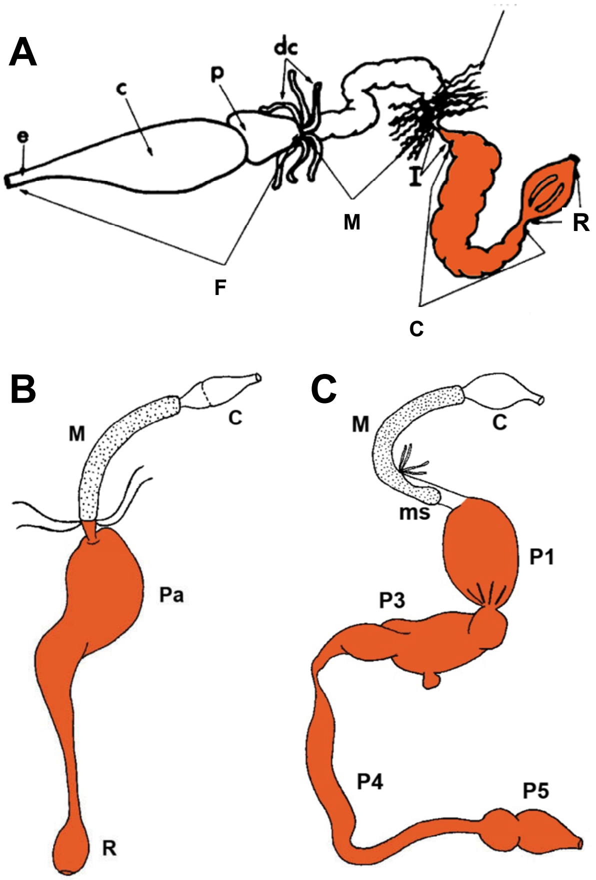


Figure 2: Gut morphology of individual groups within the *Dictyoptera*.

A. Gut of a cockroach with foregut (F), midgut (M), colon (C), and rectum (R).

B. Gut of a lower termite with crop (C), midgut (M), paunch (Pa), and rectum (R).

C. Gut of a higher termite with crop (C), midgut (M), mixed segment (ms), and the proctodeal hindgut compartments (P1–P5).

Hindguts are orange-colored. A was taken from Bracke *et al.*, 1979. B and C were taken from Brune, 2006.

Physicochemical parameters of the guts

The compartmentation of the termite gut leads to different axially and radially physicochemical states along the gut. While in the lower termites the paunch exhibits anoxia and high hydrogen accumulations (Ebert and Brune, 1997) at a circumneutral pH (Brune *et al.*, 1995), the higher soil-feeding termites have extremely alkaline hindguts (Brune and Kühl, 1996) which favors the extraction of organic matter from the soil. Higher wood-feeding *Nasutitermes* species also have slightly elevated pH values in their hindguts (Brune *et al.*, 1995). Despite the bulk of literature about microsensor studies in termites, hydrogen partial pressures never have been measured in higher wood-feeding termites. The information about physicochemical parameters in cockroaches is very scarce. So-far pH was measured in some cockroach species (Bignell, 1977; Vinokurov *et al.*, 2007).

Microbiology of termites and cockroaches

Microbial diversity has been investigated for representatives of all the major families and feeding traits of the termites (e.g., Hongoh *et al.*, 2003; Schmitt-Wagner *et al.*, 2003; Shinzato *et al.*, 2007; Warnecke *et al.*, 2007). The termite hindgut is physiologically and spatially heterogeneous and has numerous microhabitats that house well-adapted and niche-specialized symbionts. In the lower termites, one encounters different levels of obligate symbioses which involve mutualistic interactions between host, symbiotic protists, and their endosymbionts (Brune and Ohkuma, 2011). For cockroaches the current knowledge about their gut microbiota is lacking detailed information. Mostly the pest species *Periplaneta americana* and *Blatta orientalis* were investigated and these studies were only isolation-based (Cruden and Markovetz, 1987).

Digestive mutualism in the Dictyoptera evolved with different stages of coprophagy in omnivorous cockroaches up to highly eusocial proctodeal trophallaxis in termites (Nalepa *et al.*, 2001).

A novel lineage of uncultured Deltaproteobacteria

Previous studies (see above) have identified numerous bacterial lineages that seem to occur exclusively in termite guts. However, despite the less information about cockroach gut microbiota, some of the termite-specific clusters are currently also affiliated with sequences originating from cockroaches.

In order to strengthen the hypothesis that there is the existence of autochthonous bacterial groups explicitly within the *Dictyoptera* lineage, we further investigated as an example the class Deltaproteobacteria. In lower and higher termites there are two distinct clusters of Deltaproteobacteria; first the *Desulfovibrio*-like species including also isolates from termite guts (Fröhlich *et al.*, 1999) and second a group of uncultured Deltaproteobacteria. We designed a specific primer for the uncultured Deltaproteobacteria group using known sequences from public databases and unpublished data from our laboratory. Sampling higher and lower termite species as well as several cockroach species, we were able to achieve sequences exclusively from the Blaberidae family of cockroaches (Fig. 3). This shows another hint for relations of bacterial groups within the *Dictyoptera*.

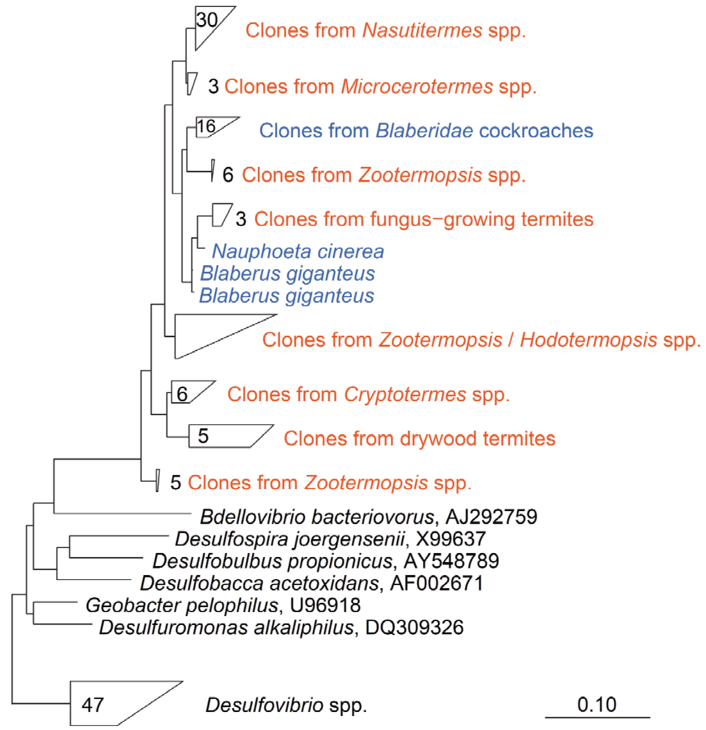


Figure 3: Maximum-likelihood tree of bacterial 16S rRNA genes from a novel lineage of uncultured Deltaproteobacteria (unpublished results from Ikeda-Ohtsubo et al.).

This cluster consists exclusively of sequences obtained from termites or other dictyopteran species.

Pyrosequencing

Although the procedure of pyrosequencing is known since the mid nineties (Ronaghi *et al.*, 1996; for procedure explanations, see Margulies *et al.*, 2005) pyrotag sequencing was first used in microbial ecology in a study about deep see microbial communities (Sogin, 2006). With less effort an enormous amount of sequence information is achieved and samples can be handled in parallel at a time. The application of this high-throughput sequencing method to microbial ecology opened a new dimension of detecting even very low-abundant, so-far undetected groups (Sogin, 2006). Presently pyrotag sequencing is widely deployed.

As in all microbial ecology studies, for covering the whole diversity of habitats like gut samples a universal primer set is necessary. The commonly used universal primer set 27F–1492R cannot be used as the generated PCR product is too long and cannot bind to the DNA capture beads due to steric problems. As pyrotag sequencing provides sequence information of about 400 nucleotides it is necessary to cover a variable region to get enough phylogenetic information. Previously molecular ecology studies used the V6 region (Sogin, 2006) but currently the V3 and V4 regions are commonly used for pyrosequencing (Huse *et al.*, 2008).

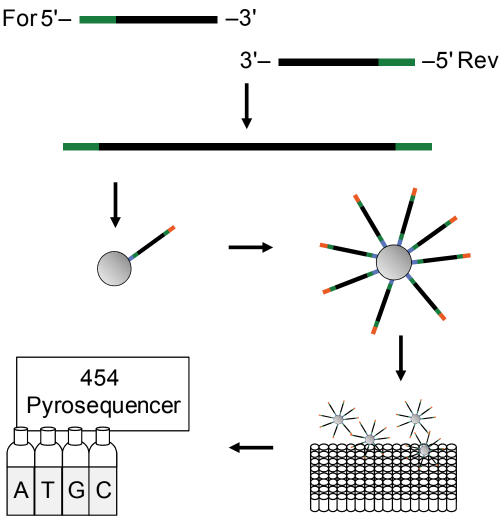


Figure 4: Schematic view of the pyrotag sequencing procedure.

Important steps: PCR using universal primers with a unique 6-bp tag (green) at the 5' ends. Ligation of pyrotag sequencing adaptors (blue and orange) to the PCR products. Binding of the DNA molecules to beads (gray). Oil emulsion PCR to amplify these molecules on the beads. Loading in well-containing fibre-optic slides. Pyrosequencing reactions and detection.

Modified after Margulies *et al.*, 2005.

Aims of this study

The aims of this work were first to establish the pyrotag sequencing method for insect gut systems with the main focus on the classification procedure (Chapter 2). The often used *Naïve Bayesian Classifier* of the Ribosomal Database Project (RDP) online platform (Wang *et al.*, 2007) resulted in large fractions of unclassified sequences already at the phylum level of termite gut samples. Classification therefore was improved by using a manually extended and refined database. To test the established pyrotag sequencing pipeline, all gut compartments of the wood-feeding higher termite *Nasutitermes corniger* were sampled in order to investigate the diversity therein. Additionally, physicochemical parameters were recorded to try to link the microbial community to functions.

After establishing pyrotag sequencing for insect guts, a comprehensive survey of specimen covering all families and subfamilies of cockroaches and lower and higher termites including all known feeding habits was conducted (Chapter 3). By exhaustively sampling dictyopteran species, the hypothesis was tested whether the gut microbiota is influenced by diet or by the phylogeny of the dictyopteran host.

The data collected in Chapter 3 was deeper analyzed in order to investigate the persistence and development of bacterial lineages in dictyopteran gut systems. The question of specific niche exploitation in phylogenetic or dietary groups of host guts was tried to answer in Chapter 4.

References

Abe, T., Bignell, D.E., Higashi, M. (eds.) (2000) Termites: Evolution, Sociality, Symbiosis, Ecology. Kluwer Academic Publishers, Dordrecht.

Bignell, D.E. (1977) Some observations on the distribution of gut flora in the American cockroach. J. Invert. Pathol. 29, 338-343**.**

Bracke, J.W., Cruden, D.L., Markovetz, A.J. (1979) Intestinal microbial flora of the of the American cockroach, *Periplaneta americana* L.. Appl. Environ. Microbiol. 38, 945-955.

Brune, A. (2006) Symbiotic associations between termites and prokaryotes. In: The Prokaryotes, 3rd ed., Volume 1: Symbiotic associations, Biotechnology, Applied Microbiology, Vol. 1 (Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, K-H., Stackebrandt, E. (eds.), Eds.), pp. 439-474. Springer, New York.

Brune, A., Emerson, D., Breznak, J.A. (1995) The termite gut microflora as an oxygen sink: microelectrode determination of oxygen and pH gradients in guts of lower and higher termites. Appl. Environ. Microbiol. 61, 2681-2687.

Brune, A., Kühl, M. (1996) pH profiles of the extremely alkaline hindguts of soil-feeding termites (Isoptera: Termitidae) determined with microelectrodes. J. Insect Physiol. 42, 1121-1127.

Brune, A., Ohkuma, M. (2011) Role of the termite gut microbiota in symbiotic digestion. In: Biology of Termites: A Modern Synthesis, Vol. (D.E. Bignell, Y. Roisin, N. Lo, eds, Eds.), pp. 439-475. Springer, Dordrecht.

Cleveland, L.R., Hall, S.R., Sanders, E.P., Collier, J. (1934) The wood-feeding roach Cryptocercus, its protozoa and the symbiosis between protozoa and roach. Mem. Am. Acad. Arts Sci. 17, 185-342.

Cruden, D.L., Markovetz, A.J. (1987) Microbial ecology of the cockroach gut. Annu. Rev. Microbiol. 41, 617-643.

Donovan, S.E; Eggleton, P., Bignell, D.E. (2001) Gut content analysis and a new feeding group classification of termites. Ecol. Entomol. 26, 356-366.

Ebert, A., Brune, A. (1997) Hydrogen concentration profiles at the oxic-anoxic interface: a microsensor study of the hindgut of the wood-feeding lower termite *Reticulitermes flavipes* (Kollar). Appl. Environ. Microbiol. 63, 4039-4046.

Engel, S. E., Krishna, K. (2004) Family-group names for termites (Isoptera). Am. Mus. Nov., 1-9.

Fröhlich, J., Sass, H., Babenzien, H.-D., Kuhnigk, T., Varma, A., Saxena, S., Nalepa, C., Pfeiffer, P., König, H. (1999) Isolation of *Desulfovibrio intestinalis* sp. nov. from the hindgut of the lower termite *Mastotermes darwiniensis*. Can. J. Microbiol. 45, 145-152.

Grimaldi, D., Engel, M.S. (2005) Evolution of the Insects. Cambridge Univ. Press, New York.

Hongoh, Y., Ohkuma, M., Kudo, T. (2003) Molecular analysis of bacterial microbiota in the gut of the termite *Reticulitermes speratus* (Isoptera; Rhinotermitidae). FEMS Microbiol. Ecol. 44, 231-242.

Huse, S.M., Dethlefsen, L., Huber, J.A., Mark Welch, D., Relman, D.A., Sogin, M.L. (2008) Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. PLoS Gen. 4, e1000255.

Inoue, T., Kitade, O., Yoshimura, T., Yamaoka, I. (2000) Symbiotic associations with protists. In: Termites: Evolution, Sociality, Symbiosis, Ecology, Vol. (Abe, T., Bignell, D.E., Higashi, M., Eds.), pp. 275-288. Kluwer Academic Publishers, Dordrecht.

Inward, D., Beccaloni, G., Eggleton, P. (2007) Death of an order: a comprehensive molecular phylogenetic study confirms that termites are eusocial cockroaches. Biol. Lett. 3, 331-335.

Inward, D.J.G., Vogler, A.P., Eggleton, P. (2007) A comprehensive phylogenetic analysis of termites (Isoptera) illuminates key aspects of their evolutionary biology. Mol. Phylogenet. Evol. 44, 953-967.

Klass, K-D., Nalepa, C., Lo, N. (2008) Wood-feeding cockroaches as models for termite evolution (Insecta: Dictyoptera): Cryptocercus vs. Parasphaeria boleiriana. Mol. Phylogenet. Evol. 46, 809-817.

Legendre F, Whiting MF; Bordereau C; Cancello EM; Evans TA; Grandcolas P (2008) The phylogeny of termites (Dictyoptera: Isoptera) based on mitochondrial and nuclear markers: implications for the evolution of the worker and pseudergate castes, and foraging behaviors. Mol. Phylogenet. Evol. 48, 615-627.

Lo, N., Tokuda, G., Watanabe, H., Rose, H., Slaytor, M., Maekawa, K., Bandi, C., Noda, H. (2000) Evidence from multiple gene sequences indicates that termites evolved from wood-feeding cockroaches. Curr. Biol. 10, 801-804.

Margulies, M., Egholm, M., Altman, W.E., Attiya, S., Bader, J.S., Bemben, L. A., Berka, J., Braverman, M. S. ; Chen Y.J., Chen, Z. et al. (2005) Genome sequencing in microfabricated high-density picolitre reactors. Nature 437.

Nalepa, C.A., Bignell, D.E., Bandi, C. (2001) Detritivory, coprophagy, and the evolution of digestive mutualisms in Dictyoptera. Insect. Soc. 48, 194-201.

Noirot, C. (1995) The gut of termites (isoptera). Comparative anatomy, systematics, phylogeny. I. Lower termites. Ann. Soc. Entomol. Fr. (N.S.) 31, 197-226.

Noirot, C. (2001) The gut of termites (isoptera). Comparative anatomy, systematics, phylogeny. II. Higher termites (termitidae). Ann. Soc. Entomol. Fr. (N.S.) 37, 431-471.

Ohkuma M; Noda S; Hongoh Y; Nalepa CA; Inoue T (2009) Inheritance and diversification of symbiotic trichonymphid flagellates from a common ancestor of termites and the cockroach *Cryptocercus*. Proc. R. Soc. B 276, 239-245.

Ronaghi, M., Karamohamed, S., Pettersson, B., Uhlén, M., Nyrén, P. (1996) Real-Time DNA sequencing using detection of pyrophosphate release. Anal. Biochem. 242, 84-89.

Schmitt-Wagner, D., Friedrich, M.W., Wagner, B., Brune, A. (2003) Phylogenetic diversity, abundance, and axial distribution of bacteria in the intestinal tract of two soil-feeding termites (*Cubitermes* spp.). Appl. Environ. Microbiol. 69, 6007-6017.

Shinzato, N; Muramatsu, M; Matsui, T; Watanabe, Y (2007) Phylogenetic analysis of the gut bacterial microflora of the fungus-growing termite *Odontotermes formosanus*. Biosci. Biotechnol. Biochem. 71, 906-912.

Sogin ML, Morrison HG, Huber JA, Welch DM, Huse SM, Neal PR, Arrieta JM, Herndl GJ. (2006) Microbial diversity in the deep sea and the underexplored "rare biosphere". Proc. Natl. Acad. Sci. USA 103, 12115-12120.

Vinokurov, K., Taranushenko, Y., Krishnan, N., Sehnal, F. (2007) Proteinase, amylase, and proteinase-inhibitor activities in the gut of six cockroach species . J. Insect Physiol. 53, 794-802.

Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R. (2007) Naive Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. Appl. Environ. Microbiol. 73, 5261-5267.

Warnecke F., Luginbühl, P., Ivanova, N., ***et al.*** **Hugenholtz P; Leadbetter JR** (2007) Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature 450, 560-565.

Watanabe, H., Tokuda, G. (2010) Cellulolytic systems in insects. Annu. Rev. Entomol. 55, 609-632.

2 Physicochemical gradients and deep sequencing of the bacterial microbiota indicate functional compartmentation in the gut of the higher termite *Nasutitermes corniger*

Tim Köhler, Carsten Dietrich, Rudolph H. Scheffrahn, and Andreas Brune

Summary

Higher termites are characterized by a purely prokaryotic gut microbiota and an increasing compartmentation of their intestinal tract. Preliminary studies on soil-feeding species have shown that each compartment is characterized by different physicochemical conditions and is colonized by a specific microbial community. Although a lot of information, including cellulase activities and metagenomic data, has been reported for wood-feeding species of the genus *Nasutitermes*, a comprehensive study linking physicochemical gut conditions with the structure of the microbial communities in the different gut compartments are lacking. In this study, we measured high-resolution profiles of hydrogen, oxygen, pH, and redox potential in the gut of *Nasutitermes corniger*, determined the fermentation products accumulating in the individual gut compartments, and conducted a detailed analysis of the bacterial communities by pyrotag sequencing of the V3–V4 region of the 16S rRNA genes. The dilated hindgut paunch (P3) was the only anoxic gut region, showed the highest density of bacteria and accumulated hydrogen to high partial pressures (up to 12 kPa), which is apparently produced by the dense community of Spirochaetes and Fibrobacteres dominating also the gut of other *Nasutitermes* species. All other compartments such as the alkaline P1 (average pH 10.0) showed high redox potentials and comprised small but distinct populations characteristic for each gut region. In the case of the tubular P4, the community was even more diverse than in the paunch. Similarities in the communities of posterior hindgut and crop suggested that proctodeal trophallaxis or coprophagy is present also in higher termites.

Introduction

Termites contribute substantially to the turnover of carbon and nitrogen in tropical ecosystems (Jouquet *et al.*, 2011). Their diet consists exclusively of lignocellulose in various stages of decomposition, ranging from sound wood to humus. The digestion of this recalcitrant diet relies on the metabolic activities of a dense and diverse intestinal microbiota (Brune and Ohkuma, 2011). While the hydrolysis of wood and the fermentation of the resulting monomers in the evolutionary lower termites are carried out by flagellate protists, higher termites lack these cellulolytic symbionts (Brune and Ohkuma, 2011 and references therein). Although there is a tendency towards an enhanced secretion of endoglucanases by the midgut tissue (Watanabe and Tokuda, 2010), the cellulolytic activities in the hindgut seem to be of bacterial origin (Tokuda and Watanabe, 2007).

In many higher termites, there is a trend towards an increased compartmentation of the hindgut (Noirot, 2001), forming several consecutive microbial bioreactors, and a strong alkalinity of the anterior hindgut (Bignell and Eggleton, 1995). Preliminary studies of soil-feeding *Cubitermes* spp. indicated that the individual gut compartments are colonized by different communities of bacteria and archaea (Schmitt-Wagner *et al.*, 2003, Friedrich *et al.*, 2001). Little is known about the microorganisms colonizing the different hindgut sections of wood-feeding species and the functional role of the different populations in the breakdown of lignocellulose.

The gut microbiota of wood-feeding *Microcerotermes* and *Nasutitermes* spp. has been characterized in some detail. It is dominated by Spirochaetes, Fibrobacteres, and members of the candidate phylum TG3 (Hongoh *et al.*, 2005; Hongoh *et al.*, 2006). A metagenomic analysis of the microbiota in the luminal P3 implicated members of Spirochaetes and Fibrobacteres in the hydrolysis of wood (Warnecke *et al.*, 2007). Although the presence of hydrogenase genes indicates the capacity of the gut microbiota to form or consume hydrogen, the presence of hydrogen in the paunch or other sections of *Nasutitermes* spp. remains to be elucidated, particularly because other parameters, e.g., oxygen status and pH, differ among the different gut regions (Brune *et al.*, 1995).

In this study, we combine microsensor measurements of physicochemical conditions (O_2 and H_2 partial pressure, redox potential, and pH) with high-resolution profiles of the bacterial microbiota in the different gut compartments of *Nasutitermes corniger*. In addition, we determined the density of the microbial communities and their fermentation products in each section.

Materials and Methods

Sample preparation

Nasutitermes corniger were from a laboratory-reared colony (Scheffrahn lab, University of Florida). *Nasutitermes takasagoensis* were collected on Iriomote Island, Japan by Gaku Tokuda (University of the Ryukyus, Okinawa). Only worker caste termites were used for the experiments. After dissecting the termites with sterile, fine-tipped forceps, we used intact guts (Fig. 1) for microsensor studies of the individual compartments. For metabolic profiles and pyrotag sequencing, the guts were separated into six major sections, comprising the crop, the midgut, and the major hindgut compartments using a stereomicroscope, and homogenized with sterile Micropistill sticks (Eppendorf). For technical reasons, the mixed segment (ms) was always included with the P1. To increase sensitivity of detection and to account for intraspecific variations, we always pooled a certain number of individual gut sections (see below).

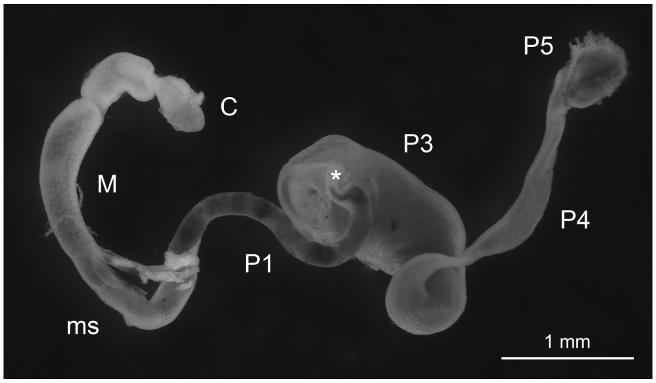


Figure 1: The intestinal tract of *Nasutitermes corniger*.

The gut includes crop (C), midgut (M), mixed segment (ms), and several hindgut segments (P1–P5); asterisk marks the position of the P2 (enteric valve).

Microsensor measurements

All microsensors had tip diameters of 10 µm and were purchased from Unisense (Aarhus, Denmark). Oxygen and hydrogen microsensors had detection limits of ca. 0.023 kPa and 0.04 kPa, respectively, and were calibrated as previously described (Brune *et al.*, 1995; Ebert and Brune, 1997). pH and redox microsensors were used together with an Ag–AgCl reference electrode and a high-impedance voltmeter. pH microsensors were calibrated using standard curves obtained with commercial standard solutions of pH 4, 7, 9, and 11 as previously described (Brune and Kühl, 1996). Redox microsensors were calibrated using saturated quinhydrone solutions in pH standard at pH 4 and 7 (Zimmer and Brune, 2005). All measurements were done in glass-faced microchambers (Brune *et al.*, 1995). Freshly dissected guts of *N. corniger* were placed flat on a 4-mm thick layer of 2% (w/v) agarose in Ringer's solution (Brune *et al.*, 1995), covered with 0.5% (w/v) agarose in Ringer's solution, and allowed to equilibrate for 10 min prior to the measurement. Microsensors were positioned using a manual micromanipulator, and tip position was visually controlled with a horizontally mounted stereomicroscope.

Metabolite pools

At least 40 sections each of *N. corniger* were homogenized in 80 µl NaOH (10 mM), and the clarified supernatants were subject to metabolite analysis using a combination of gas chromatography and high performance liquid chromatography, as previously described in detail (Tholen and Brune, 2000; Pester and Brune, 2007).

Microbial cell counts

Twenty gut sections each of *N. corniger* were homogenized in 0.5 ml 1× phosphate-buffered saline (PBS; Pernthaler *et al.*, 2004) and fixed with 4% (v/v) formaldehyde at 4°C for 13 h, Microbial cells were counted using the procedure of Pernthaler *et al.* (2001) but excluding the sonication step. Samples were washed with PBS, appropriate dilutions were filtered onto polycarbonate filters (0.2 µm; GTTP; Millipore), and stored at –20°C. For analysis, filters were stained with 4′,6′-diamidino-2-phenylindole (DAPI), washed first with sterile water and then with 70% (v/v) ethanol, and embedded in Citifluor AF1 (Citifluor). Microbial cells were counted at 1000-fold magnification using a Zeiss Axiophot epifluorescence microscope equipped as previously described (Schmitt-Wagner *et al.*, 2003).

Primer design

Commonly used primers targeting the V3–V4 region of the bacterial 16S rRNA gene (based on the "classical" primers of Muyzer *et al.*, 1993 [341f] and Hugenholtz and Goebel, 2001 [787R]) were further improved using the SILVA 100 database of 345,212 high-quality sequences > 1,200 bp (Pruesse *et al.*, 2007), focusing on an optimal coverage of the taxa known to prevail in termite guts. Modifications were tested using the probe match function of the ARB software (version 5.1; Ludwig *et al.*, 2004). The resulting primer set 343Fmod (TACGGGWGGCWGCA) and 784Rmod (GGGTMTCTAATCCBKTT) showed perfect matches to 87% of the sequences in the database (90.5% allowing one mismatch), and coverage was even higher in the phyla relevant to termite gut environment (Fig. 2).

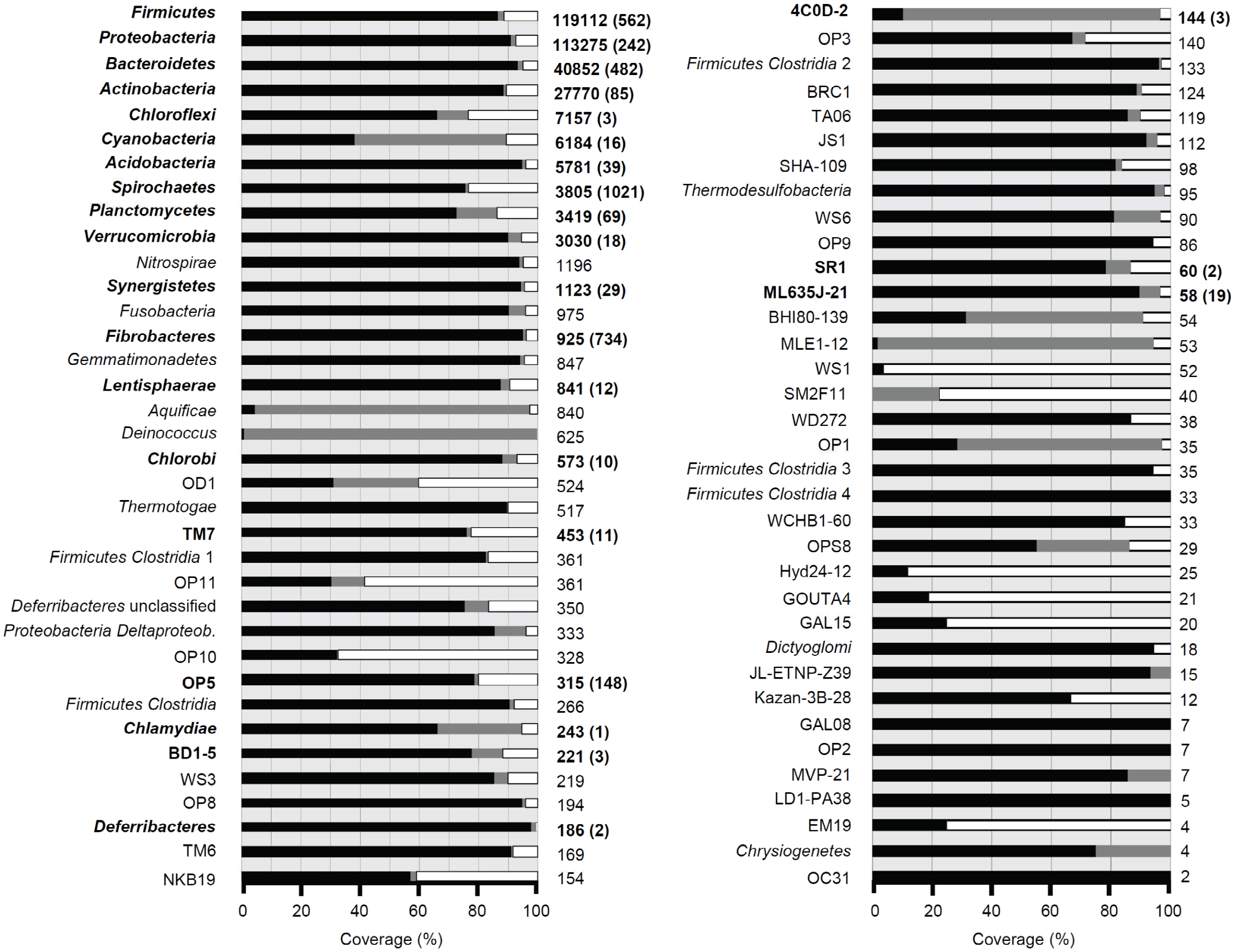


Figure 2: Phylum-level coverage of the improved primer set used for 454 sequencing of the V3–V4 region based on all bacterial sequences > 1200 bp in the SILVA 100 database.

Phyla containing clones from dictyopteran guts are marked in bold and numbers of sequences are shown in parentheses. The bars indicate the proportion of sequences without (black), with one (grey), and with two or more mismatches (white) and are followed by the total number of sequences in the dataset.

Pyrotag sequencing

Twenty sections of each gut compartment of *N. corniger*, 10 complete hindguts (P1–P5) of both *N. corniger* and *N. takasagoensis*, and 10 whole guts of *N. corniger* were homogenized in PBS. DNA was extracted with phenol–chloroform using the bead-beating protocol of Henckel *et al.* (1999), precipitated with two volumes of polyethylene glycol, and amplified with the newly designed primers using a high-fidelity polymerase (Herculase II Fusion Enzyme with dNTPs Combo Kit, Agilent). The PCR conditions were: initial denaturation (3 min at 95°C), 26 cycles of amplification (20 s at 95°C, 20 s at 48°C, and 30 s at 72°C), terminal extension (3 min at 72°C). Both forward and reverse primer each had an additional, sample-specific 6-bp barcode at the 5' end, which differed by at least 2 bp between samples and contained no homopolymers. The amplicons were quantified photometrically (NanoDrop, Thermo Fisher Scientific) and mixed in equimolar amounts before further analysis. Adaptor ligation, subsequent amplification, and pyrosequencing (454 GS FLX with Titanium technology, Roche) were done by a commercial service (GATC Biotech, Konstanz, Germany).

Pyrotag processing and classification

Pyrotag data was pre-processed using the *mothur* software suite (version 1.15.0; Schloss *et al.*, 2009) and the strategy described by (Kunin *et al.*, 2010) with slight modifications. In the first step, sequences were sorted by sample according their unique barcodes. Sequences shorter than 200 bp and all sequences that contained ambiguous bases, had errors in the primer sequence, or showed homopolymer regions of more than 10 nucleotides were removed from the dataset. The remaining sequences were aligned against the SILVA 102 non-redundant database (Pruesse *et al.*, 2007) using a stand-alone version of the SINA aligner (http://www.arb-silva.de). The latter led to the removal of additional non-16S sequences.

The taxonomy of the pyrotags was assigned with the *Naïve Bayesian Classifier* implemented in the *mothur* software, setting the confidence threshold to 60%, and using a manually curated reference database. The latter was based on the SILVA 102 non-redundant database and included numerous unpublished sequences from our lab. The existing classification of the SILVA database was extended and refined down to the genus level by introducing additional, termite-specific groups and renaming redundant or uninformative taxa. In order to allow processing in the *mothur* software environment and to improve the speed of the classifier, we removed from the database many uninformative sequences from those taxa that contained no gut-related sequences. The resulting reference database (82,400 sequences) contained all bacterial isolates, all uncultivated bacteria from intestinal environments, and at least 3 representative sequences from every other lowest-level group in the SILVA database.

Results

Physicochemical conditions

Axial profiles showed strong dynamics of oxygen concentration along the gut of *N. corniger* (Fig. 3A). Complete anoxia is only achieved in the dilated hindgut compartment P3, suggesting that oxygen concentration is related to the diameter of the respective gut region (Fig. 1). Radial profiles of the P3 compartment showed that oxygen is removed within 200–300 μm below the gut wall, indicating the presence of an oxygen sink in the gut periphery. Sometimes the posterior part of the P3 compartment showed traces of oxygen, independent of the depth at which the guts were embedded. Radial profiles showed that inflowing oxygen was not completely removed before it reached the gut center, probably because of the relatively small diameter of the posterior part of the P3. The depth of embedding had an effect on the profiles. If the layer of agarose above the P3 compartment was < 2 mm, hydrogen concentrations decreased and occasionally the whole compartment became oxic down to its center.

The oxygen status of the gut corresponded to the redox conditions in the respective compartments (Fig. 3C). Axial profiles of the redox potential showed negative values only in the anoxic P3 compartment. This also correlates with the distribution of hydrogen, which accumulated only in the P3 compartment, with maximal values in the anterior region (Fig. 3B). Radial profiles of the anterior P3 revealed steep hydrogen profiles from the gut center towards the gut wall (Fig. 4). However, hydrogen partial pressures in the P3 varied over a wide range (from 0.02 to 12 kPa). Since the values were sensitive to the depth of embedding, we determined hydrogen concentrations also *in situ*. When the dorsal cuticle of living termites was penetrated with the microsensor, hydrogen concentrations measured in the abdomen were between 0.1 and 2.4 kPa. However, these values have to be regarded with caution because the intransparency of the cuticle did not allow to determine the exact location of the microsensor tip or to assess any damage possibly caused by the sensor.

Also the intestinal pH was found to be highly dynamic along the gut axis. The pH in the crop was slightgly acidic, circumneutral in the midgut, and increased sharply in the mixed segment. The most alkaline values (pH 9.3–10.9) were found in the anterior P1. The pH decreased again in the P3 compartment and remained neutral in most of the posterior hindgut, with slightly acidic values in the P5 (Fig. 3D).

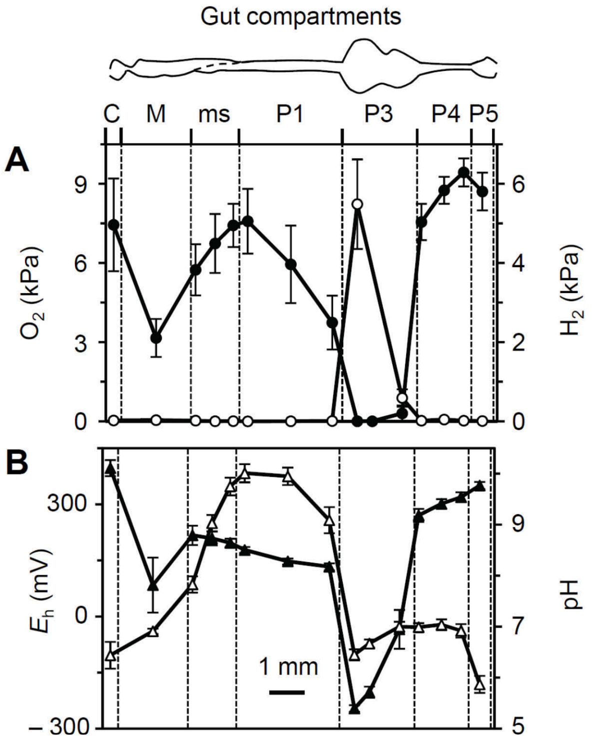


Figure 3: Axial profiles of oxygen (filled circles) and hydrogen (open circles) partial pressure (A), and redox potential (filled triangles) and pH (open triangles) (B) along the gut of Nasutitermes corniger, measured at the gut center.

Values are means ± standard errors obtained with 8–12 termites (except for the crop, which was lost in about half of the preparations). For abbreviations of gut compartments, see Fig. 1.

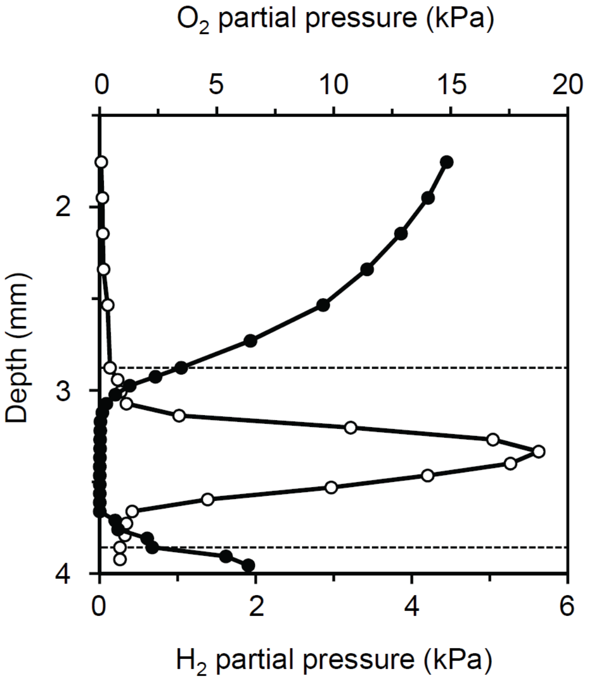


Figure 4: Radial profile of oxygen (●) and hydrogen (○) partial pressures in the agarose-embedded anterior P3 compartment of Nasutitermes corniger, relative to the agarose surface.

The dotted lines indicate the position of the proximal and distal gut wall. The profile was selected as typical among six similar profiles obtained with different termites.

Metabolite pools

Metabolite pools in the different gut sections of *N. corniger* were determined by means of high performance liquid and gas chromatography (Table 1). Acetate was the predominant metabolite in all gut sections—except for the midgut, where succinate was more abundant. Highest concentrations of acetate were present in the P3 section, which also contained the largest metabolite pool of all compartments. Lactate was detected only in the posterior gut, with highest concentration in the P5 section. Similar results have been previously reported for other *Nasutitermes* spp., except that the pool sizes of propionate, butyrate and formate were lower (Tholen and Brune, 2000).

Bacterial diversity

Gut homogenates of sections of *N. corniger* showed large differences in the number of bacteria (Table 1). The highest numbers were always observed in the P3 compartment (1.5×10^7 cells), surpassing those in the other gut regions by more than two orders of magnitude. The microbiota of the crop consisted mostly of cocci, whereas the midgut microbiota was dominated by short rods; cells with spirochetal shape were rare in either compartment. In the P1 compartment, we observed mostly longer rods; cocci were less abundant, and the density of cells with spirochetal shape began to increase. The highest density of spirochetes was present in the P3 compartment, but decreased again in the posterior sections, whose microbiota was dominated by coccoid cells.

The V3–V4 region of the bacterial 16S rRNA genes in the DNA extracted from different gut sections of *N. corniger* and total hindguts of *N. corniger* and *N. takasagoensis* was amplified by PCR. Trimming and quality control removed between 10–20% of the sequences from each dataset, resulting in sequence libraries of 3,200–26,000 reads per sample (for details, see Supplementary Table 4). Preliminary analysis using the classifier of the Ribosomal Database Project (RDP) online platform (Release 10; Wang *et al.*, 2007) resulted in large fractions of unclassified sequences already at the phylum level, ranging from 4% in the midgut to 22% in the P3 sample (details not shown). Since most of the unclassified sequences represented termite-specific bacterial groups that were not or only poorly classified in the training set sequences of RDP, we prepared a manually curated reference database (see Methods). Reclassification of the samples using the *mothur* software suite (version 1.15.0; Schloss *et al.*, 2009) resulted in a significantly improved classification, leaving only 0.6–2.4% unclassified sequences at the phylum level.

Table 1: Pool sizes of major metabolites, fresh weight, and microbial cell counts for different gut sections of *Nasutitermes corniger*. Values are means ± range determined in two independent experiments**.**

Section	**Amount (nmol section^{-1})**						**Fresh wt. (mg)**	**Prokaryotes (10^5 cells section^{-1})**
	Acetate	**Propionate**	**Butyrate**	**Succinate**	**Lactate**	**Formate**		
N. corniger								
Crop	0.7 ± 0.1	0.2 ± 0.2	—[a]	0.4 ± 0.1	—	0.3 ± 0.1	0.7 ± 0.2	1.55 ± 0.32
Midgut	0.9 ± 0.0	0.2 ± 0.2	—	2.0 ± 1.0	—	0.1 ± 0.1	0.6 ± 0.1	0.77 ± 0.15
P1 (incl. ms)	1.4 ± 0.2	0.1 ± 0.1	—	1.1 ± 0.7	—	0.7 ± 0.1	0.8 ± 0.2	0.97 ± 0.35
P3	8.6 ± 1.8	0.7 ± 0.4	0.1 ± 0.1	1.0 ± 0.8	0.1 ± 0.1	0.5 ± 0.1	1.4 ± 0.3	152 ± 31
P4	2.1 ± 1.0	0.6 ± 0.2	0.1 ± 0.1	0.3 ± 0.1	0.1 ± 0.1	0.7 ± 0.1	0.4 ± 0.2	0.81 ± 0.10
P5	1.9 ± 1.2	0.4 ± 0.2	—	0.3 ± 0.2	0.7 ± 0.7	0.6 ± 0.2	0.6 ± 0.5	0.36 ± 0.13
Total gut[b]	15.6 ± 2.4	2.2 ± 0.5	0.2 ± 0.2	5.1 ± 1.5	0.9 ± 0.7	2.9 ± 0.3	4.5 ± 0.7	156 ± 31

[a]…Detection limit ca. 0.02 nmol per section
[b]…Calculated from the amount in each compartment

The effect was even stronger at lower taxonomic ranks, where sequences classified at the family level increased from 17–88% to 79–96% in the respective compartments (details not shown). Closer inspection of the 36 sequences without phylum-level classification from the *N. corniger* hindgut sample revealed that half of them were putative chimerae and the other half were not coding for 16S rRNA.

Table 2: Diversity and evenness of the bacterial communities in the different gut sections of *Nasutitermes corniger*.

Gut section	Number of genera[a]	Estimated coverage[b] (%)	Diversity[c]	Evenness[d]
Crop	298	73.9	3.72	0.62
Midgut	217	63.4	1.70	0.29
P1	187	67.5	3.32	0.59
P3	264	80.7	3.15	0.54
P4	307	72.0	4.00	0.66
P5	173	69.2	3.84	0.70

[a]…Lowest-level of the reference database
[b]…Based on Chao1 (Chao, 1984)
[c]…Non-parametric Shannon index (since the coverage was less than 100%; Chao and Shen, 2003)
[d]…Evenness (Legendre and Legendre, 1998)

Sequences of each gut sections of *N. corniger* fell into 200–300 different classes (genus-level), with higher numbers in the crop, P3, and P4. Based on Chao1 as predictor of the total diversity in the different compartments, the estimated diversity coverage was between 63% and 81% (genus level; Table 2). Diversity (1.70) and evenness (0.29) of the bacterial community were lowest in the midgut compartment, which harbored a few very abundant groups. Diversity in the posterior hindgut compartments (P4 and P5) was much higher and community structure was more balanced (evenness of 0.66 and 0.70, respectively). Despite more than 26,000 reads from the P4 compartment, the estimated coverage was only 72%, reflecting the high diversity of the community. The composition of the communities in the respective compartments differed substantially. There were moderate similarities (Bray-Curtis similarities 0.43–0.63) between the crop and all hindgut compartments (P1–P5; Table 3), whereas the midgut had only low similarity to all other gut compartments.

Table 3: Bray-Curtis similarities between the different gut sections.

Section	Similarity[a]					
	Crop	**Midgut**	**P1**	**P3**	**P4**	**P5**
Crop	1.00					
Midgut	0.30	1.00				
P1 (incl. ms)	0.49	0.29	1.00			
P3	0.43	0.19	0.38	1.00		
P4	0.55	0.23	0.49	0.52	1.00	
P5	0.63	0.22	0.54	0.48	0.68	1.00

[a]...Bray–Curtis coefficient (Bray and Curtis, 1957)

Community structure in N. corniger

The major bacterial phyla consistently encountered in the different gut compartments of *N. corniger* were Spirochaetes, TG3, Firmicutes, Fibrobacteres, Bacteroidetes, Proteobacteria, and Actinobacteria (Fig. 5). The most abundant groups in the dilated P3 were the Spirochaetes and members of the TG3 phylum. These phyla were represented also in all other compartments, but with significantly decreased relative abundances. By contrast, the candidate divisions OP11, TM7, and SR1 increased in relative abundance in the posterior hindgut sections (P4 and P5). The phylum-level patterns in these compartments were similar to that of the crop, except for an increased abundance of Firmicutes, which was found in all anterior sections.

At higher taxonomic resolution, it became apparent that most phyla are represented by various lineages that are unevenly distributed among the compartments (Fig. 6; Supplementary Table 4). A prominent example are the Firmicutes: In the midgut, the sequences of this phylum (almost 80% relative abundance) are dominated by members of the *Lachnospiraceae* (order Clostridiales), consisting almost exclusively of a particular group ("uncultured 67"; Supplementary Table 4) harboring sequences from higher and lower termites as well as other diverse gut environments (feces and intestines). Although members of this group are also abundant in the other compartments, they are outnumbered by other Clostridiales (*Ruminococcaceae*, Family XIII) in the posterior hindgut (P4 compartment). In the crop, the majority of Lactobacillales are *Streptococcaceae* (about 21% relative abundance), whereas *Enterococcaceae* and other lineages (e.g., PeH08) predominate in the anterior hindgut (P1 compartment). Many family-level taxa are abundant present in all gut sections (e.g. Fibrobacteres subphylum 2 and TG3 subphylum 1). The same is true for some Bacteroidetes (e.g., the *Rikenellaceae*, represented by the genus *Alistipes* and three termite-specific clusters; see Supplementary Table 4). A similar preference is encountered in the *Ruminococcaceae* (Clostridiales), and the *Acidobacteriaceae* (Acidobacteria).

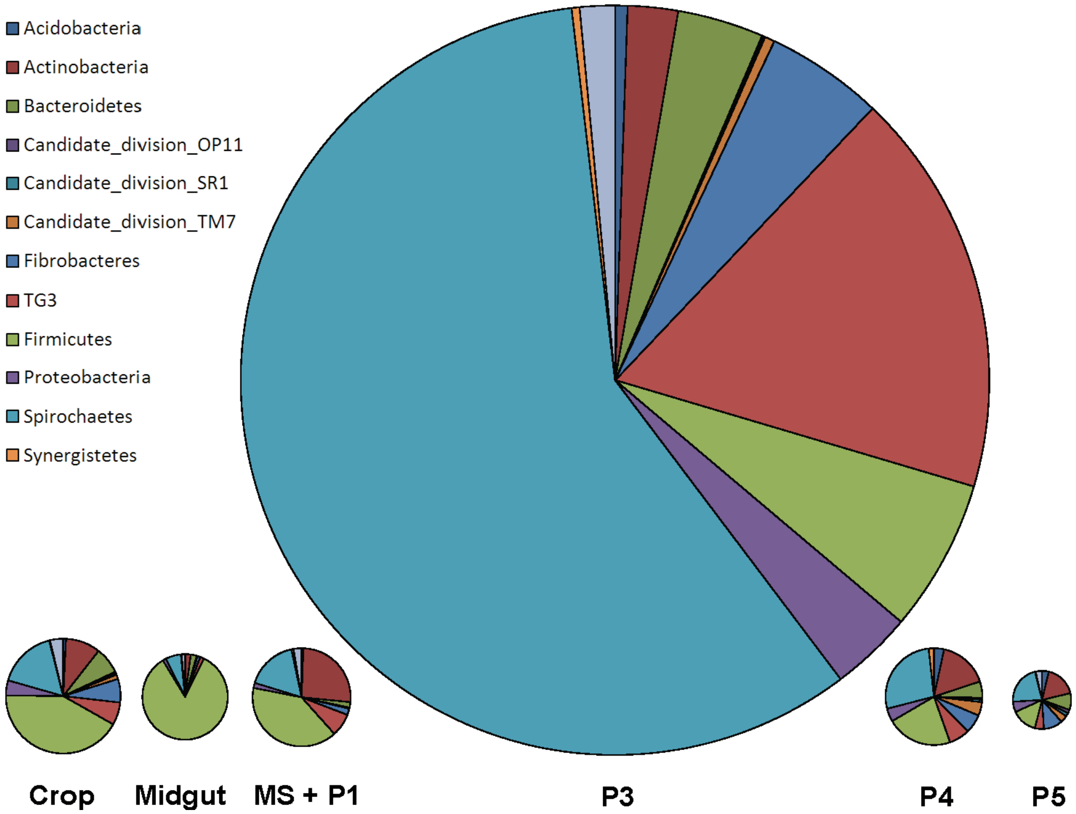


Figure 5: Relative abundance of bacterial 16S rRNA genes at phylum level.

The microbial cell counts in the respective gut sections are reflected in the area of the respective graph.

Many of the sequences obtained in this study represent termite-specific lineages that had been encountered already in clone-based inventories of the gut microbiota of *Nasutitermes* species (e.g., Tokuda *et al.*, 2000; Hongoh *et al.*, 2006; Miyata *et al.*, 2007; Warnecke *et al.*, 2007). However, the deep-sequencing approach also revealed the presence of many hitherto undetected lineages, e.g., from the phyla Lentisphaerae, Planctomycetes, Firmicutes, and candidate divisions OP11, TM7, and SR1 (Fig. 6). The high diversity of the gut microbiota in *Nasutitermes* spp. is reflected in high Shannon indices for each compartment (Table 2). Although 75% of the families detected each represent < 1% of the sequences obtained from the different sections (Supplementary Table 4), many of these groups are numerically important, either because of the high density of the community (i.e., is the P3 compartment; Fig. 5), or because of their apparent specificity for termite guts. In any case, it should be considered that especially in the P3 section, taxa that are close to the detection limit of the pyrotag analysis still form substantial populations.

Interspecific variation

The high similarities of the bacterial community profile of the P3 compartment to that of the total (hind-)gut of *N. corniger* illustrates that the bulk of the microbiota residing in the P3 dominates also the community of the total hindgut (Fig. 7). Also the community profile of the hindgut of the closely related *N. takasagoensis*, an allopatric species from Japan, shows striking similarities in the presence and abundance of family-level taxa, although there are also distinct differences between the two species (Fig. 6).

A comparison of the pyrotag datasets of *N. corniger* and *N. takasagoensis* with clone libraries obtained from these and another *Nasutitermes* species showed that each of the major family-level lineages is represented in all *Nasutitermes* species, although their relative abundance apparently differs between analyses (Fig. 6 and Fig. 7). An exception is a lineage of Bacteroidetes (Termite group M2PB4-65), which was not represented in the clone libraries. Strong differences in presence and relative abundance among the termite species are encountered in the Fibrobacteres, TG3, Firmicutes, and the Spirochaetes. A very evident difference is the virtual absence of Fibrobacteres in the hindgut sample of *N. takasagoensis* used in this study.

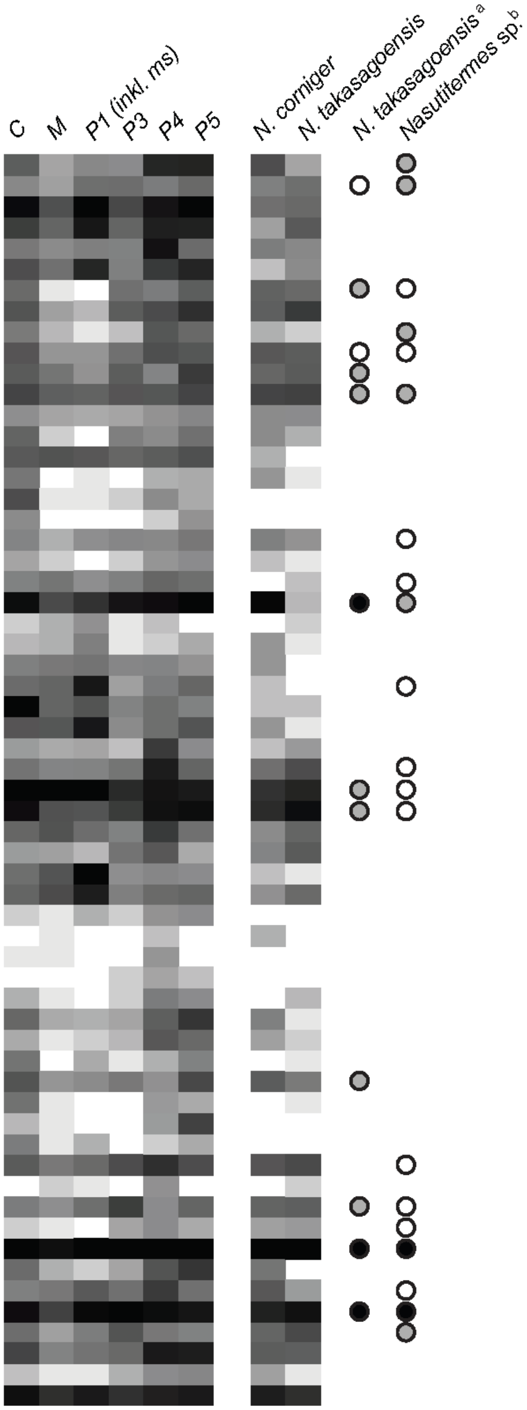
A genus-level comparison to the bacteria detected in the lumen of the P3 compartment of a *Nasutitermes* sp. (Warnecke *et al.*, 2007) revealed that 79% of the taxa in the pyrotag libraries of the P3 section of *N. corniger* were represented, indicating that the bulk of the P3 compartment gut microbiota was already detected by a clone library of 1252 sequence. However, the pyrotag library of the P3 (24029 reads) comprised 217 additional taxa. Many of them were present also in the pyrotag library of *N. takasagoensis*, indicating that they are likely to occur also in other *Nasutitermes* spp. – further *Nasutitermes* spp. have to be analyzed before a core microbiota can be identified.

An interesting aspect became apparent when the two datasets were compared in the opposite direction. Since the pyrotag dataset for *N. corniger* generated in this study was obtained from a homogenate of the complete P3 compartment and the clone library of *Nasutitermes* sp. was based only on its luminal content (Warnecke *et al.*, 2007), any major taxa present in the analysis of the total compartment but missing from the luminal sample potentially represent wall-associated bacteria. To compensate the lower sequencing depth of the luminal sample, a threshold for the larger amounts of pyrotag sequences was set by taking the noise signal (i.e., one sequence); multiplied by three (i.e., 3 sequences in the luminal dataset corresponding to 0.24% in the pyrotag dataset). Taking this threshold, we discovered 10 taxa that are strong candidates of gut–wall-associated bacteria (Supplementary Table 4; highlighted in red), including *Sanguibacter* spp. and other Actinobacteria, Bacteroidetes Cluster V (*Porphyromonadaceae* 1), *Arthromitus* spp. (*Lachnospiraceae*), and some lineages of *Spirochaetaceae* specific for termite guts. Together, they formed 10% of the sequences from the P3 compartment. By contrast, taxa that were exclusively present in the luminal sample (Supplementary Table 4; highlighted in yellow) were only a small fraction (0.6%) of the clones in the library. Moreover, two of these groups, OPB56 (Chlorobi) and Rs-H88 (Spirochaetes) were present in the total hindgut sample of *N. corniger*.

↓ **Figure 6:** Relative abundance of the major bacterial taxa in the different gut sections of *Nasutitermes corniger* and in the total hindguts of *N. corniger* and *N. takasagoensis*.

When possible, classification is shown down to the family level. To increase the sensitivity for low-abundant groups, $\log_{10}$-transformation was performed. Additionally, the relative abundance of the families obtained from published clone libraries is given in circles. Open circles, < 1%; gray-filled, 1.4–3%; black-filled, > 10%.

[a]…Data of Hongoh *et al.* (2006)
[b]…Data of Warnecke *et al.* (2007)
[c]…Batch of 39–100 phylotypes / families (for further detail, see Supplementary Table 4)

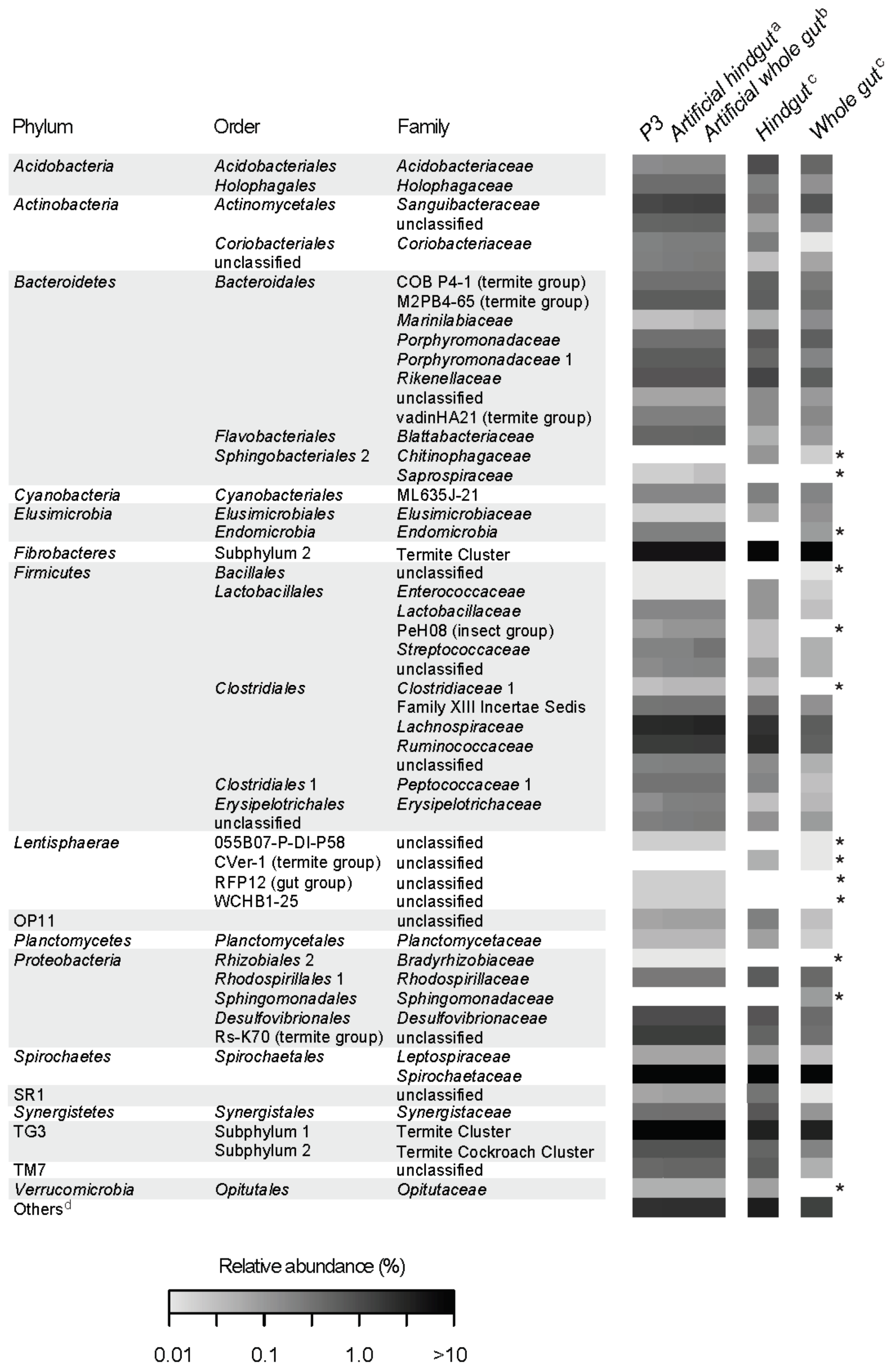


Phylum	Ordnung	Familie	*N. takasagoensis*[a]	*Nasutitermes* sp.[b]
Acidobacteria	*Acidobacteriales*	*Acidobacteriaceae*		◍
	Holophagales	*Holophagaceae*	○	◍
Actinobacteria	*Actinomycetales*	*Sanguibacteraceae*		
		unklassifiziert		
	Coriobacteriales	*Coriobacteriaceae*		
	unklassifiziert			
Bacteroidetes	*Bacteroidales*	COB P4-1 (Termitengruppe)	◍	○
		M2PB4-65 (Termitengruppe)		
		Marinilabiaceae		◍
		Porphyromonadaceae	○	○
		Porphyromonadaceae 1	◍	
		Rikenellaceae	◍	◍
		unklassifiziert		
		vadinHA21 (Termitengruppe)		
	Flavobacteriales	*Blattabacteriaceae*		
	Sphingobacteriales 2	*Chitinophagaceae*		
		Saprospiraceae		
Chloroflexi	*Anaerolineales*	*Anaerolineaceae*		
Cyanobacteria	*Cyanobacteriales*	ML635J-21		○
Elusimicrobia	*Elusimicrobiales*	*Elusimicrobiaceae*		
	Endomicrobia	*Endomicrobia*		○
Fibrobacteres	Subphylum 2	Termite Cluster	●	◍
Firmicutes	*Bacillales*	unklassifiziert		
	Lactobacillales	*Enterococcaceae*		
		Lactobacillaceae		
		PeH08 (Insektengruppe)		○
		Streptococcaceae		
		unklassifiziert		
	Clostridiales	*Clostridiaceae* 1		
		Familie XIII Incertae Sedis		○
		Lachnospiraceae	◍	○
		Ruminococcaceae	◍	○
		unklassifiziert		
	Clostridiales 1	*Peptococcaceae* 1		
	Erysipelotrichales	*Erysipelotrichaceae*		
	unklassifiziert			
Lentisphaerae	055B07-P-DI-P58	unklassifiziert		
	CVer-1 (Termitengruppe)	unklassifiziert		
	CVer-2 (Termitengruppe)	unklassifiziert		
	RFP12 (Darmgruppe)	unklassifiziert		
	WCHB1-25	unklassifiziert		
OP11		unklassifiziert		
Planctomycetes	*Planctomycetales*	*Planctomycetaceae*		
Proteobacteria	*Rhizobiales* 2	*Bradyrhizobiaceae*		
	Rhodospirillales 1	*Rhodospirillaceae*	◍	
	Sphingomonadales	*Sphingomonadaceae*		
	Burkholderiales	unklassifiziert		
	Nitrosomonadales	*Nitrosomonadaceae*		
	Desulfovibrionales	*Desulfovibrionaceae*		○
		unklassifiziert		
	Rs-K70 (Termitengruppe)	unklassifiziert	◍	○
Spirochaetes	*Spirochaetales*	*Leptospiraceae*		○
		Spirochaetaceae	●	●
SR1		unklassifiziert		
Synergistetes	*Synergistales*	*Synergistaceae*		○
TG3	Subphylum 1	Termite Cluster	●	●
	Subphylum 2	Termite Cockroach Cluster		◍
TM7		unklassifiziert		
Verrucomicrobia	*Opitutales*	*Opitutaceae*		
Andere[c]				

Relative Abundanz (%)

0,01 0,1 1,0 >10

○ <1%
◍ 1–3%
● >10



Phylum	Order	Family	
Acidobacteria	*Acidobacteriales*	*Acidobacteriaceae*	
	Holophagales	*Holophagaceae*	
Actinobacteria	*Actinomycetales*	*Sanguibacteraceae*	
		unclassified	
	Coriobacteriales	*Coriobacteriaceae*	
	unclassified		
Bacteroidetes	*Bacteroidales*	COB P4-1 (termite group)	
		M2PB4-65 (termite group)	
		Marinilabiaceae	
		Porphyromonadaceae	
		Porphyromonadaceae 1	
		Rikenellaceae	
		unclassified	
		vadinHA21 (termite group)	
	Flavobacteriales	*Blattabacteriaceae*	
	Sphingobacteriales 2	*Chitinophagaceae*	*
		Saprospiraceae	*
Cyanobacteria	*Cyanobacteriales*	ML635J-21	
Elusimicrobia	*Elusimicrobiales*	*Elusimicrobiaceae*	
	Endomicrobia	*Endomicrobia*	*
Fibrobacteres	Subphylum 2	Termite Cluster	
Firmicutes	*Bacillales*	unclassified	*
	Lactobacillales	*Enterococcaceae*	
		Lactobacillaceae	
		PeH08 (insect group)	*
		Streptococcaceae	
		unclassified	
	Clostridiales	*Clostridiaceae* 1	*
		Family XIII Incertae Sedis	
		Lachnospiraceae	
		Ruminococcaceae	
		unclassified	
	Clostridiales 1	*Peptococcaceae* 1	
	Erysipelotrichales	*Erysipelotrichaceae*	
	unclassified		
Lentisphaerae	055B07-P-DI-P58	unclassified	*
	CVer-1 (termite group)	unclassified	*
	RFP12 (gut group)	unclassified	*
	WCHB1-25	unclassified	*
OP11		unclassified	
Planctomycetes	*Planctomycetales*	*Planctomycetaceae*	
Proteobacteria	*Rhizobiales* 2	*Bradyrhizobiaceae*	*
	Rhodospirillales 1	*Rhodospirillaceae*	
	Sphingomonadales	*Sphingomonadaceae*	*
	Desulfovibrionales	*Desulfovibrionaceae*	
	Rs-K70 (termite group)	unclassified	
Spirochaetes	*Spirochaetales*	*Leptospiraceae*	
		Spirochaetaceae	
SR1		unclassified	
Synergistetes	*Synergistales*	*Synergistaceae*	
TG3	Subphylum 1	Termite Cluster	
	Subphylum 2	Termite Cockroach Cluster	
TM7		unclassified	
Verrucomicrobia	*Opitutales*	*Opitutaceae*	*
Others[d]			

↑ **Figure 7:** Comparison of the P3 compartment, hindgut, and whole gut of *Nasutitermes corniger*.

The artificial hindgut is calculated by the relative abundance of the P1 to P5 hindgut sections multiplied by the cell number of each section. All samples were from different batches of the same nest. To increase the sensitivity for low-abundant groups, log10-transformation was performed. Gut sections, hindgut and whole gut each were derived from different batches of termites. *, taxa missing in one or more samples.

[a] Calculated from all hindgut sections (P1–P5)
[b] Calculated from all gut sections
[c] Derived from different batches of termites.
[d] 39 to 100 remaining families, each representing less than 0.63(2.4)% of the respective community (for details, see Supplementary Table 4)

Discussion

This study is the first comprehensive analysis of the digestive tract of a wood-feeding higher termite, combining microsensor profiles of physicochemical gut conditions with a highly resolved analysis of the bacterial microbiota in the individual gut compartments. The results revealed that the gut is a highly structured microenvironment, with distinct differences in metabolic activities and microbial communities between the compartments. The bulk of the microbiota is located in the dilated paunch (P3), but also other compartments such as the alkaline P1 or the tubular P4 harbor microbial communities distinct from those in other gut regions. The differences in community structure are apparent already at the phylum level, but a more detailed analysis of relative abundance indicates that individual lineages preferentially colonize particular niches.

The hindgut paunch

Since higher termites lack cellulolytic flagellates, fiber degradation in the dilated hindgut paunch must be accomplished by the prokaryotic microbiota (Brune and Stingl, 2005). Metagenomic analysis of the luminal contents of the P3 compartment of a *Nasutitermes* sp. revealed the presence of numerous glycosyl hydrolases putatively involved in the degradation of (hemi-)celluloses, which were tentatively assigned to members of the phyla Fibrobacteres and Spirochaetes (Warnecke *et al.*, 2007). The hindgut microbiota of *Nasutitermes* sp. is characterized by a large abundance of spirochetes (Czolij *et al.*, 1985; Paster *et al.*, 1996), which are also highly diverse (Ohkuma *et al.*, 1999). In accordance with these reports, members of both phyla were highly represented in the pyrotag sequences of the P3 section of *N. corniger* (Fig. 5), the gut compartment that forms the main bioreactor based on its anoxic status, microbial cell count, and the highest concentrations of fermentation products.

Interestingly, the hydrogen profiles of the *N. corniger* gut identified the P3 compartment also as the only gut region exhibiting a strong accumulation of H_2. Hydrogen partial pressures were in the same range as those in the paunch of *Reticulitermes flavipes* (Ebert and Brune, 1997), where H_2 production is attributed largely to the gut flagellates. Although an emission of hydrogen has been previously observed also for several higher termites, including *Nasutitermes triodiae* (Sugimoto *et al.*, 1998), microsensor profiles were so far available only for soil-feeding *Cubitermes* spp., where the mixed segment and the P3 showed substantial accumulation of hydrogen (Schmitt-Wagner and Brune, 1999). The bacterial populations responsible for hydrogen production have not been identified, but by means of phylogenetic analyses of conserved single-copy protein-coding genes, Warnecke *et al.* (2007) could link the iron-only hydrogenases in the metagenome of *Nasutitermes* sp. to Spirochaetes. Molecular hydrogen is a major fermentation product of glucose in many species of the genus *Spirochaeta* (Leschine *et al.*, 2006). Moreover, it has been shown that *Treponema azotonutricium*, an isolate from the lower termite *Zootermopsis angusticollis*, produces hydrogen during fermentation of carbohydrates (Graber *et al.*, 2004). Further evidences for the hydrogen metabolism were recently published about [FeFe] hydrogenase in the *Dictyoptera* (Ballor and Leadbetter, 2011) and of [FeFe] hydrogenases of spirochetes in the lower termite *Zootermopsis angusticollis* (Ballor *et al.*, 2011). It is therefore likely that the spirochetes are—at least in part—responsible for hydrogen production.

The steep radial profiles of hydrogen in the P3 compartment of *N. corniger* indicate the presence of a strong hydrogen sink, consolidating the high partial pressures in the lumen with the low hydrogen emission rates of the living termite (Sugimoto *et al.*, 1998). This is in agreement with the high rates of reductive acetogenesis in the hindgut of Nasutitermes spp. (Brauman *et al.*, 1992). Analyses of functional marker genes of the acetyl-CoA pathway provided strong evidence that spirochetes are the dominant populations responsible for reductive acetogenesis from hydrogen and CO_2 in the gut of lower termites (e.g., Leadbetter *et al.*, 1999; Salmassi and Leadbetter, 2003; Pester and Brune, 2006; Ballor *et al.*, 2011; Ottesen and Leadbetter, 2011). It is not clear whether all spirochetal lineages from the *Nasutitermes* gut are involved in reductive acetogenesis – they comprise both the homoacetogenic isolate *Treponema primitia* and the non-homoacetogenic *Treponema azotonutricium* (Graber *et al.*, 2004). It is possible that also *Ruminococcus*-related bacteria contribute to reductive acetogenesis like many *Ruminococcus* isolates from other environments (Lorowitz and Bryant, 1984; Rieu-Lesme *et al.*, 1996; Leaphart and Lovell, 2001). The same could be true for the *Holophagaceae*-related bacteria (Acidobacteria) present in all gut compartments of *N. corniger* and the hindgut sample of *N. takasagoensis*, which are closely related to the homoacetogenic *Holophaga foetida* (Liesack *et al.*, 1994).

The small diameter of the gut renders the gut wall an important microhabitat. Methanogenic archaea associated with the gut wall of lower termites have been implicated as hydrogen sink, both in methanogenesis and due to their capacity for hydrogen-dependent reduction of inflowing oxygen (Tholen *et al.*, 2007). Since methanogenesis is not an important process in *Nasutitermes* spp. (see Brune, 2010 and references therein), it is unlikely a major hydrogen sink. The situation is a bit more ambiguous in the case of sulfate reduction. About 1% of the sequences in the P3 represent sulfate-reducing Deltaproteobacteria. The group *Desulfovibrio* 1 (Supplementary Table 4) comprises *Desulfovibrio intestinalis*, a hydrogenotrophic isolate from the gut of a lower termite (Fröhlich *et al.*, 1999), and *Candidatus* Desulfovibrio trichonymphae, a symbiont of cellulolytic protists that encodes and expresses a hydrogenase involved in hydrogen uptake (Sato *et al.*, 2009). Evidence for an association of *Desulfovibrio* spp. with the gut wall of *Nasutitermes* is lacking, but the extremely high rates of hydrogen-dependent oxygen reduction in all *Desulfovibrio* strains isolated from termite guts (Kuhnigk *et al.*, 1996; Fröhlich *et al.*, 1999) may contribute to the oxygen-reducing activities of the gut. Moreover, also the functional role of other bacterial populations associated with the gut wall need to be investigated.

The 454 datasets of whole gut compartments do not contain direct information concerning the radial organization of the microbiota, but the obvious absence of some bacterial groups from the purely luminal sample of the P3 gut compartment from Warnecke *et al.* (2007) allows some careful inferences regarding their localization. Among the possible gut wall colonizers are *Sanguibacter* populations (a genus comprising aerobic and facultatively anaerobic isolates; (e.g. Huang *et al.*, 2005) and possibly other unclassified Actinobacteria . Spirochetes are known to attach to the gut wall in lower and higher termites (Czolij *et al.*, 1985; Nakajima *et al.*, 2005). In the inspected data sets the *Trinervitermes* "cluster a" and several other termite-specific *Spirochaetaceae* groups (Supplementary Table 4) are also relevant candidate groups for being attached to the gut wall. Relatives of the Bacteroidales Cluster V (Hongoh *et al.*, 2005; Noda *et al.*, 2006; Noda *et al.*, 2006b) were not only found in the gut walls of many lower termites (Nakajima *et al.*, 2005; Nakajima *et al.*, 2006) but also in gut homogenates of higher termites including *Nasutitermes takasagoensis* (Hongoh *et al.*, 2006). It is possible, that these Bacteroidales bacteria are reliant on attachment sites for not getting lost through the gut passage and it is obvious that they have to have oxygen-removing mechanisms like *Bacteroides fragilis* (Baughn and Malamy, 2004).

The posterior hindgut

Although the microbial biomass in the P3 will be inevitable transported into the posterior hindgut with the flow of the digesta, there is a tremendous two order of magnitudes decrease in microbial cell numbers and the density drops more than 30 times (Table 1). Furthermore, there are distinct patterns in the community structure of the following compartments, accompanied by a further increase in bacterial diversity (Table 2). The relative abundance of

Acidobacteriaceae and *Coriobacteriaceae* in the P4 compartment is considerably higher (about 3% and 5%, respectively) than in the P3. Also specific lineages of Lentisphaerae are enhanced in numbers in the P4 compartment. Finally, the candidate divisions OP11, SR1, and TM7 are enriched in the posterior gut.

A previous analysis of bacterial diversity and community structure in different gut compartments of soil-feeding *Cubitermes* spp. based on small clone libraries and terminal restriction fragment length polymorphism profiles had indicated also a distinct increase in diversity and distinct changes in the community structure between P3 and P4 compartment (Schmitt-Wagner *et al.*, 2003; Schmitt-Wagner *et al.*, 2003b). However, *Cubitermes* spp. show distinct differences in intestinal pH between the alkaline P3 and the neutral P4 compartment (Brune and Kühl, 1996), whereas both gut regions are neutral in *Nasutitermes* spp. (Brune *et al.*, 1995; this study). It is therefore unlikely that pH alone is responsible for this shift. Rather, driving forces could be the change back to oxic conditions and hence the inhibition of strictly anaerobic metabolic processes in the P4. The slightly acidic pH of the P5 compartment was found also among several soil-feeding species (ph 5–6, Brune and Kühl, 1996).

Crop and midgut

Since sound wood is a highly nitrogen-deficient diet, termites have developed the strategy to exploit the assimilatory capacities of their gut microbiota to acquire essential amino acids and vitamins (Potrikus and Breznak, 1981). This is accomplished by digesting microbial biomass present in the wood or derived of the hindgut contents. Although little is known about the behavior of *Nasutitermes* species, numerous similarities in the community patterns of the rectum (P5) and the anterior gut (crop) suggest that fecal material is consumed again by the termites – either by coprophagy or proctodeal trophallaxis. The strong shift in the bacterial community profiles between crop and midgut and the reduced microbial density in this gut region indicates that most bacteria are digested in the midgut, which is in agreement with the presence of lysozyme and protease activities in this gut region (Fujita and Abe, 2002). The community of the midgut is dominated by Firmicutes, particularly of the "uncultured 67" group (*Lachnospiraceae*), a phylogenetic cluster of sequences from the intestinal environments, including termite guts (Fig. 6; Supplementary Table 4). The group has no cultured representatives and is only distantly related to *Butyrivibrio* and *Pseudobutyrivibrio* spp., which have high proteolytic, xylanolytic, and also cellulolytic activities (Cotta and Forster, 2006; Moon *et al.*, 2008). It is not clear whether they contribute to the digestive capacities of the midgut of *Nasutitermes* spp. (Watanabe and Tokuda, 2010) or whether they are simply transients (spores) residing in other gut regions.

Alkalinity in mixed segment and P1

The anterior hindgut of higher termites has been identified as a region of high alkalinity (Bignell and Eggleton, 1995). In soil-feeding Termitinae, the pH increase sharply in the mixed segment and reaches its maximum (pH > 12) in the P1 compartment (Brune and Kühl, 1996). The alkalinity the tubular P1 of *N. corniger* is considerably less pronounced (pH 10), and the pH returns to neutrality already in the P3, a compartment that is still strongly alkaline in the soil feeders (Brune and Kühl, 1996). Since the profiles obtained for *N. corniger* (this study) were almost identical to previous profiles of *N. nigriceps* (Brune *et al.*, 1995), it seems safe to conclude that they are typical for members of this genus.

The P1 sample of *N. corniger* contains several bacterial groups that are most abundant in this section. A most prevalent group of sequences falls into the genus *Turicibacter* (Firmicutes; Erysipelotrichaceae; 13.4% relative abundance). Representatives of this cluster have been previously detected in the putatively alkaline P1 region of the grass-feeding *Speculitermes* sp. and the soil-feeding *Pericapritermes latignathus* (Thongaram *et al.*, 2005), and also in the alkaline midgut of the humivorous larva of the scarab beetle *Pachnoda ephippiata* (Egert *et al.*, 2003). The genus *Turicibacter* showed less than 1% relative abundance in all the other compartments of *N. corniger*, which may indicate an adaptation to the high pH of the P1 environment. The occurrence of *Turicibacter* spp. in the gut of *Microcerotermes* sp. (Hongoh *et al.*, 2005), which also comprises an alkaline P1 (Brune *et al.*, 1995), is in agreement with this assumption. However, this trait is not typical for the whole genus, since the next relative, *Turicibacter sanguinis*, does not grow above pH 8 (Bosshard *et al.*, 2002), and other members of the *Turicibacter* clade have been detected in the feces of a variety of mammals (Ley *et al.*, 2008).

Other bacterial groups predominant in the P1 compartment are several lineages of Lactobacillales (Firmicutes). Sequences of cluster PeH08 (4.6% relative abundance) have been obtained from the alkaline compartments of other higher termites (Thongaram *et al.*, 2005) and beetle larvae (Egert *et al.*, 2003), but were encountered also in the following hindgut compartments of *N. corniger* (Fig. 6; Supplementary Table 4). Additionally they are also present in the luminal content of another *Nasutitermes* species (Warnecke *et al.*, 2007), albeit in low relative abundance (<1%, Supplementary Table 4). Lactobacillales seem to be virtually absent (0.04%) from in the hindgut of *N. takasagoensis*, suggesting that colonization by certain microbial groups may differ substantially among termites of the same genus. However, the absence can also be error-prone (see below) due to the very low abundance in *Nasutitermes* hindguts in general.

The P1 section also contained a small number of sequences (1.2%) from a termite-specific lineage of Lachnospiraceae that is related to the sequences NT-1 and NT-2, which have been previously assigned to rod-shaped bacteria predominantly colonizing the mixed segment of *N. takasagoensis* (Tokuda *et al.*, 2000). The presence of these bacteria in this sample is explained by the inclusion of the mixed segment in the P1 section, which was not separated for technical reasons.

Pyrotag sequencing as a method for community profiling

The diversity and community structure of the bacterial gut microbiota of termites has been addressed by numerous studies (see Ohkuma and Brune, 2011). Many of the more detailed studies combined Sanger sequencing of 16S rRNA genes with T-RFLP analyses, thus compensating for the shortcomings of the individual approaches (Sanger sequencing is notoriously undersampled and T-RFLP analyses lack phylogenetic resolution). The application of high-throughput sequencing techniques in targeting the 16S rRNA gene opened a new dimension of detecting even very low-abundant, so-far undetected microorganisms in microbial ecology studies (Sogin *et al.*, 2006).

As in all diversity studies, the choice of primer is crucial. Therefore, we improved existing primers for especially termite-specific groups. To compare the primer match *in situ* we compared the pyrotag sequencing data of the P3 compartment to the Sanger sequencing data of Warnecke *et al.* (2007) yielding a good coverage of the previously found groups and additional groups (Supplementary Table 4). The enormous difference in the abundance of Fibrobacteres sequences between the two *N. takasagoensis* samples (Hongoh *et al.*, 2006; this study) may be rooted in the different batches of termites used in the respective studies.

The RDP classifier algorithm (Wang *et al.*, 2007) and software suites like *mothur* (Schloss *et al.*, 2009) are often used for taxonomic classification of pyrotag sequences (see, e.g. Bowman *et al.*, 2011). However, the crucial aspect for a reliable sequence assignment is a comprehensive and well curated database (Werner *et al.*, 2011). Refining the classification of the SILVA database by introducing additional, termite-specific groups significantly improved the assignment of pyrotag reads. To avoid an inflation of diversity estimates due to sequencing errors (Kunin *et al.*, 2010), we restricted our analyses to a genus-level classification.

Increased sampling depths allows discovery of rare taxa and helps detecting constancy in colonization (avoids apparent absence problem). Due to this high resolution sequences related to the fat-body-colonizing *Blattabacterium* (Flavobacteria) could be detected. These bacteria were so far only found in cockroaches and the primitive termite *Mastotermes darwiniensis* (Lo *et al.*, 2003). Here we can offer a first hint, that relatives of *Blattabacterium* can be also detected in evolutionary younger termites (0.5% relative abundance). Further analyses have to be done to elucidate the true nature and source of these bacteria.

Comparing samples, especially the presence and absence of rare bacterial taxa, should be handled with care. The high sensitivity of the pyrotag sequencing technology can happen to be its own drawback. Comparison of the P3 hindgut compartment with the total hindgut, the artificially calculated hindgut (relative abundance of the P1 to P5 hindgut sections multiplied by the cell number of each section), and total gut of *N. corniger* shows some differences in the absence of particular groups (Fig. 7). This can be explained by biological errors (different batches from the same nest were used; individual variety of bacterial gut composition) but also by systematical errors and the noise at the lower end of detection.

The high resolution and fast sample treatment using pyrotag sequencing provides a perfect tool for community profiling. Additionally, the gained phylogenetic information replaces T-RFLP-based approaches. Pyrotag sequencing would help investigating common lineages shared among the gut microbiota of termites and would help understanding the evolution of the gut microbiota from a putative dictopteran ancestor.

References

Amend, A.S., Seifert, K.A., Bruns, T.D. (2010) Quantifying microbial communities with 454 pyrosequencing: does read abundance count?. Mol. Ecol.19, 5555-65.

Baker, B.J., Hugenholtz, P., Dawson, S.C., Banfield, J.F. (2003) Extremely acidophilic protists from acid mine drainage host Rickettsiales-lineage endosymbionts that have intervening sequences in their 16S rRNA genes. Appl. Environ. Microbiol. 69, 5512-5518.

Ballor, N.R., Leadbetter, J.R. (2011) Analysis of Extensive [FeFe] Hydrogenase Gene Diversity Within the Gut Microbiota of Insects Representing Five Families of Dictyoptera. Microb. Ecol.

Ballor, N.R., Paulsen, I., Leadbetter, J.R. (2011) Genomic Analysis Reveals Multiple [FeFe] Hydrogenases and Hydrogen Sensors Encoded by Treponemes from the H2-Rich Termite Gut. Microb. Ecol.

Baughn, A.D., Malamy, M.H. (2004) The strict anaerobe *Bacteroides fragilis* grows in and benefits from nanomolar concentrations of oxygen. Nature 427, 441-444.

Bignell, D.E., Anderson, J.M. (1980) Determination of pH and oxygen status in the guts of lower and higher termites. J. Insect Physiol. 26, 183-188.

Bignell, D.E., Eggleton, P. (1995) On the elevated intestinal pH of higher termites (Isoptera: Termitidae). Insect. Soc. 42, 57-69.

Bignell, D.E., Oskarsson, H., Anderson, J.M. (1980) Specialization of the hindgut wall for the attachment of symbiotic microorganisms in a termite *Procubitermes aburiensis*. Zoomorphology 96, 103-112.

Bloodgood, R.A. (1975) Ultrastructure of the attachment of *Pyrsonympha* to the hind-gut wall of *Reticulitermes tibialis*. J. Insect Physiol. 21, 391-399.

Bosshard, P.P., Zbinden, R., Altwegg, M (2002) Turicibacter sanguinis gen. nov., sp. nov., a novel anaerobic, Gram-positive bacterium. Int. J. Syst. Evol. Microbiol. 52, 1263-1266.

Bowman, J.S., Rasmussen, S., Blom, N., Deming, J.W., Rysgaard, S., Sicheritz-Ponten, T. (2011) Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. ISME J.

Brauman, A., Kane, M.D., Labat, M., Breznak, J.A. (1992) Genesis of acetate and methane by gut bacteria of nutritionally diverse termites. Science 257, 1384-1387.

Bray, J.R., Curtis, J.T. (1957) An ordination of the upland forest communities of southern Wisconsin. Ecol. Monogr. 27, 325-349.

Brune, A. (2010) Methanogenesis in the digestive tracts of insects. In: Handbook of Hydrocarbon and Lipid Microbiology, Vol. 8 (Timmis, K.N., Eds.), pp. 707-728. Springer, Heidelberg.

Brune, A., Emerson, D., Breznak, J.A. (1995) The termite gut microflora as an oxygen sink: microelectrode determination of oxygen and pH gradients in guts of lower and higher termites. Appl. Environ. Microbiol. 61, 2681-2687.

Brune, A., Kühl, M. (1996) pH profiles of the extremely alkaline hindguts of soil-feeding termites (Isoptera: Termitidae) determined with microelectrodes. J. Insect Physiol. 42, 1121-1127.

Brune, A., Ohkuma, M. (2011) Role of the termite gut microbiota in symbiotic digestion. In: Biology of Termites: A Modern Synthesis, Vol. (D.E. Bignell, Y. Roisin, N. Lo, eds, Eds.), pp. 439-475. Springer, Dordrecht.

Brune, A., Stingl, U. (2005) Prokaryotic symbionts of termite gut flagellates: phylogenetic and metabolic implications of a tripartite symbiosis. In: Molecular Basis of Symbiosis, Vol. 41 (Overmann, J., Eds.), pp. 39-60. Springer, Berlin.

Chao, A. (1984) Nonparametric estimation of the number of classes in a population . Scan. J. Stat. 11, 265-270.

Chao, A., Shen, T.-J. (2003) Nonparametric estimation of Shannon's index of diversity when there are unseen species in sample. Environ. Ecolog. Stat. 10, 429-443.

Cotta, M., Forster, R. (2006) The family Lachnospiraceae, including the genera *Butyrivibrio*, *Lachnospira* and *Roseburia*. In: The Prokaryotes, Vol 4, 3rd edn. (Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, K.H., Stackebrandt, E., Eds.), pp. 1002-1021. Springer, New York.

Cypionka, H. (2000) Oxygen respiration by Desulfovibrio species. Annu. Rev. Microbiol. 54, 827-848.

Czolij, R., Slaytor, M., O'Brien, R.W. (1985) Bacterial flora of the mixed segment and the hindgut of the higher termite *Nasutitermes exitiosus* Hill (Termitidae, Nasutitermitinae). Appl. Environ. Microbiol. 49, 1226-1236.

Drake, H. L., Küsel, K., and Matthies, C. (2006) Acetogenic Prokaryotes, Volume 2: Ecophysiology and Biochemistry. In: The Prokaryotes: An Evolving Electronic Resource for the Microbiological Community, Vol. 2 (Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, K.-H. and Stackebrandt, E., Eds.), pp. 354–420. Springer-Verlag, New York.

Dunbar, J., Ticknor, L.O., Kuske, C.R. (2001) Phylogenetic specificity and reproducibility and new method for analysis of terminal restriction fragment profiles of 16S rRNA genes from bacterial communities. Appl. Environ. Microbiol. 67, 190-197.

Ebert, A., Brune, A. (1997) Hydrogen concentration profiles at the oxic-anoxic interface: a microsensor study of the hindgut of the wood-feeding lower termite *Reticulitermes flavipes* (Kollar). Appl. Environ. Microbiol. 63, 4039-4046.

Egert, M., Wagner, B., Lemke, T., Brune, A., Friedrich, M. W. (2003) Microbial community structure in midgut and hindgut of the humus-feeding larva of *Pachnoda ephippiata* (Coleoptera: Scarabaeidae). Appl. Environ. Microbiol. 69, 6659-6668.

Friedrich, M.W., Schmitt-Wagner, D., Lueders, T., Brune, A. (2001) Axial differences in community structure of *Crenarchaeota* and *Euryarchaeota* in the highly compartmentalized gut of the soil-feeding termite *Cubitermes orthognathus*. Appl. Environ. Microbiol. 67, 4880-4890.

Fröhlich, J., Sass, H., Babenzien, H.-D., Kuhnigk, T., Varma, A., Saxena, S., Nalepa, C., Pfeiffer, P., König, H. (1999) Isolation of *Desulfovibrio intestinalis* sp. nov. from the hindgut of the lower termite *Mastotermes darwiniensis*. Can. J. Microbiol. 45, 145-152.

Fujita, A., Abe, T. (2002) Amino acid concentration and distribution of lysozyme and protease activities in the guts of higher termites. Physiol. Entomol. 27, 76-78.

Gomez-Alvarez, V., Teal, T.K., Schmidt, T.M. (2009) Systematic artifacts in metagenomes from complex microbial communities.. ISME J. 3, 1314-1317.

Graber, J.R., Breznak, J.A. (2004) Physiology and nutrition of *Treponema primitia*, an H_2/CO_2-acetogenic spirochete from termite hindguts. Appl. Environ. Microbiol. 70, 1307-1314.

Graber, J.R., Leadbetter, J.R., Breznak, J.A. (2004) Description of *Treponema azotonutricium* sp. nov. and *Treponema primitia* sp. nov., the first spirochetes isolated from termite guts. Appl. Environ. Microbiol. 70, 1315-1320.

Henckel, T., Friedrich, M., Conrad, R. (1999) Molecular analyses of the methane-oxidizing microbial community in rice field soil by targeting the genes of the 16S rRNA, particulate methane monooxygenase, and methanol dehydrogenase. Appl. Environ. Microbiol. 65, 1980-1990.

Herlemann; D.P.R., Labrenz, M., Jürgens, K., Bertilsson, S., Waniek, J.J., Andersson, A.F. (2011) Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. ISME

Herranen, M., Kariluoto, S., Edelmann, M., Piironen, V., Ahvenniemi, K., Iivonen, V., Salovaara, H., Korhola, M. (2010) Isolation and characterization of folate-producing bacteria from oat bran and rye flakes. Int. J. Food Microbiol. 142, 277-285.

Hongoh, Y., Deevong, P., Hattori, S., Inoue, T., Noda, S., Noparatnaraporn, N., Kudo, T., Ohkuma, M. (2006) Phylogenetic diversity, localization and cell morphologies of the candidate phylum TG3 and a subphylum in the phylum *Fibrobacteres*, recently found bacterial groups dominant in termite guts. Appl. Environ. Microbiol. 72, 6780-6788.

Hongoh, Y., Deevong, P., Inoue, T., Moriya, S., Trakulnaleamsai, S., Ohkuma, M., Vongkaluang, C., Noparatnaraporn, N., Kudo, T. (2005) Intra- and interspecific comparisons of bacterial diversity and community structure support coevolution of gut microbiota and termite host. Appl. Environ. Microbiol. 71, 6590-6599.

Hongoh, Y., Sato, T., Noda, S., Ui, S., Kudo, T., Ohkuma, M. (2007) *Candidatus* Symbiothrix dinenymphae: bristle-like *Bacteroidales* ectosymbionts of termite gut protists. Environ. Microbiol. 9, 2631-2635.

Hooper, S.D., Raes, J., Foerstner, K.U., Harrington, E.D., Dalevi, D., Bork, P. (2008) A Molecular Study of Microbe Transfer between Distant Environments.. PLoS ONE 3, e2607.

Huang, Y., Dai, X., He, L., Wang, Y.N., Wang, B.J., Liu, Z., Liu, S.J. (2005) *Sanguibacter marinus* sp. nov., isolated from coastal sediment. Int. J. Syst. Evol. Microbiol. 55, 1755-1758.

Hugenholtz, P., Goebel, B.M. (2001) The polymerase chain reaction as a tool to investigate microbial diversity in environmental samples. In: Environmental molecular microbiology: Protocols and applications, (Rochelle, P.A., Ed.), pp. 31-41. Horizon Press Inc., New York.

Husseneder, C., Ho, H.-Y., Blackwell, M. (2010) Comparison of the bacterial symbiont composition of the Formosan Subterranean Termite from its native and introduced range. Open Microbiol. J. 4, 53-66.

Jouquet, P., Traoré, S., Choosai, C., Hartmann, C., Bignell, D. (2011) Influence of termites on ecosystem functioning. Ecosystem services provided by termites . Eur. J. Soil Biol. 47, 215-222.

Kappler, A., Brune, A. (2002) Dynamics of redox potential and changes in redox state of iron and humic acids during gut passage in soil-feeding termites (*Cubitermes* spp.). Soil Biol. Biochem. 34, 221-227.

Khan, S.T., Harayama, S., Tamura, T., Ando, K., Takagi, M., Kazuo, S.Y. (2009) *Paraoerskovia marina* gen. nov., sp. nov., an actinobacterium isolated from marine sediment. Int. J. Syst. Evol. Microbiol. 59, 2094-2098.

Kim, M.K., Pulla, R.K., Kim, S.Y., Yi, T.H., Soung, N.K., Yang, D.C. (2008) *Sanguibacter soli* sp. nov., isolated from soil of a ginseng field. Int. J. Syst. Evol. Microbiol. 58, 538-541.

Köhler, T., Stingl, U., Meuser, K., Brune, A. (2008) Novel lineages of *Planctomycetes* densely colonize the alkaline gut of soil-feeding termites (*Cubitermes* spp.). Environ. Microbiol. 10, 1260-1270.

Kuhnigk, T., Branke, J., Krekeler, D., Cypionka, H., König, H. (1996) A feasible role of sulfate-reducing bacteria in the termite gut. System. Appl. Microbiol. 19, 139-149.

Kunin, V., Engelbrektson, A., Ochman, H., Hugenholtz, P. (2010) Wrinkles in the rare biosphere: pyrosequencing errors lead to artificial inflation of diversity estimates.. Environ. Microbiol. 12, 118-123.

Kunin, V., Hugenholtz, P. (2010) PyroTagger: A fast, accurate pipeline for analysis of rRNA amplicon pyrosequence data. The Open Journal 1, 1-8.

Lane, D.J. (1991) 16S/23S rRNA sequencing. In: Nucleic acids techniques in bacterial systematics, Vol. (Stackebrandt, E., Goodfellow, M., Eds.), pp. 115-175. John Wiley & Sons, Chichester.

Leadbetter, J.R., Schmidt, T.M., Graber, J.R., Breznak, J.A. (1999) Acetogenesis from H_2 plus CO_2 by spirochetes from termite guts. Science 283, 686-689.

Leaphart, A.B., Lovell, C.R. (2001) Recovery and analysis of formyltetrahydrofolate synthetase gene sequences from natural populations of acetogenic bacteria. Appl. Environ. Microbiol. 67, 1392-1395.

Legendre, P., Legendre, L. (1998) Numerical Ecology 2nd Edition. Elsevier Amsterdam

Leschine, S., Paster, B., Canale-Parola, E. (2006) Free-living saccharolytic spirochetes: the genus *Spirochaeta*. In: The Prokaryotes, 3rd ed., Volume 7: Proteobacteria: Delta and Epsilon Subclasses. Deeply Rooting Bacteria, Vol. 7 (Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, K-H., Stackebrandt, E. (eds.), Eds.), pp. 195-210. Springer, New York.

Ley, R.E., Hamady, M., Lozupone, C., Turnbaugh, P.J., Ramey, R.R., Bircher, J.S., Schlegel, M.L., Tucker, T.A., Schrenzel, M.D., Knight, R., Gordon J.I. (2008) Evolution of Mammals and Their Gut Microbes. Science 320, 1647-1651.

Liesack, W., Bak, F., Kreft, J.U., Stackebrandt, E. (1994) *Holophaga foetida* gen. nov., sp. nov., a new, homoacetogenic bacterium degrading methoxylated aromatic compounds.. Arch. Microbiol. 162, 85-90.

Lo N; Bandi C; Watanabe H; Nalepa C; Beninati T (2003) Evidence for co-cladogenesis between diverse dictyopteran lineages and their intracellular endosymbionts. Mol. Biol. Evol. 20, 907-913.

Lo N; Evans TA (2007) Phylogenetic diversity of the intracellular symbiont *Wolbachia* in termites. Mol. Phylogenet. Evol. 44, 461-466.

Lorowitz, W.H., Bryant, M.P. (1984) *Peptostreptococcus productus* strain that grows rapidly with CO as the energy source. Appl. Environ. Microbiol. 47, 961-964.

Lozupone, C., Hamady, M., Knight, R. (2006) UniFrac - An online tool for comparing microbial community diversity in a phylogenetic context.. BMC Bioinform. 7, .

Lozupone, C., Knight, R. (2005) UniFrac: a New Phylogenetic Method for Comparing Microbial Communities.. Appl. Environ. Microbiol. 71, 8228-8235.

Ludwig, W., Strunk, O., Westram, R., Richter, L., Meier, H. and 27 other authors (2004) ARB: a software environment for sequence data. Nucleic Acids Res. 32, 1363-1371.

McKenna, P., Hoffmann, C., Minkah, N., Aye, P.P., Lackner, A., Liu, Z., Lozupone, C.A., Hamady, M., Knight, R., Bushman, F.D. (2008) The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis.. PLoS Pathog. 4, e20.

Miyata R, Noda N, Tamaki H, Kinjyo K; Aoyagi H; Uchiyama H; Tanaka H (2007) Influence of feed components on symbiotic bacterial community structure in the gut of the wood-feeding higher termite *Nasutitermes takasagoensis*. Biosci. Biotechnol. Biochem. 71, 1244-1251.

Moon, C.D., Pacheco, D.M., Kelly, W.J., Leahy, S.C., Li, D., Kopecny, J., Attwood, G.T. (2008) Reclassification of *Clostridium proteoclasticum* as *Butyrivibrio proteoclasticus* comb. nov., a butyrate-producing ruminal bacterium. Int. J. Syst. Evol. Microbiol. 58, 2041-2045.

Morales, S.E., Cosart, T.F., Johnson, J.V., Holben, W.E. (2009) Extensive Phylogenetic Analysis of a Soil Bacterial Community Illustrates Extreme Taxon Evenness and the Effects of Amplicon Length, Degree of Coverage, and DNA Fractionation on Classification and Ecological Parameters.. Appl. Environ. Microbiol. 75, 668-675.

Muyzer, G., de Waal, E.C., Uitterlinden, A.G. (1993) Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. Appl. Environ. Microbiol. 59, 695-700.

Nakajima H; Hongoh Y; Noda S; Yoshida Y; Usami R; Kudo T; Ohkuma M (2006) Phylogenetic and morphological diversity of *Bacteroidales* members associated with the gut wall of termites. Biosci. Biotechnol. Biochem. 70, 211-218.

Nakajima, H., Hongoh, Y., Usamib, R., Kudo, T., Ohkuma, M. (2005) Spatial distribution of bacterial phylotypes in the gut of the termite *Reticulitermes speratus* and the bacterial community colonizing the gut ephitelium. FEMS Microbiol. Ecol. 54, 247-255.

Noda S; Inoue T; Hongoh Y; Nalepa CA; Vongkaluang C; Kudo T; Ohkuma M (2006) Identification and characterization of ectosymbionts of distinct lineages in *Bacteroidales* attached to flagellated protists in the gut of termites and a wood-feeding cockroach. Environ. Microbiol. 8, 11-20.

Noda, S., Kawai, M., Nakajima, H., Kudo, T., Ohkuma, M. (2006b) Identification and *in situ* detection of two lineages of *Bacteroidales* ectosymbionts associated with a termite gut protist, *Oxymonas* sp. Microb. Environ. 21, 16-22.

Noirot, C. (2001) The gut of termites (Isoptera). Comparative anatomy, systematics, phylogeny. II. Higher termites (Termitidae). Ann. Soc. Entomol. Fr. (N.S.) 37, 431-471.

Ohkuma, M., Brune, A. (2011) Diversity, structure, and evolution of the termite gut microbial community. In: Biology of Termites: A Modern Synthesis, Vol. (D.E. Bignell, Y. Roisin, N. Lo, eds, Eds.), pp. 413-438. Springer, Dordrecht.

Ohkuma, M., Iida, T., Kudo, T. (1999) Phylogenetic relationships of symbiotic spirochetes in the gut of diverse termites. FEMS Microbiol. Lett. 181, 123-129.

Oksanen, J., Blanchet, F.G., Kindt, R., Legendre, P., O'Hara, R.B., Simpson, G.L., Solymos, P., Stevens, M.H.H., Wagner, H. (2010) vegan: Community Ecology Package. R package version 1.17-4. http://CRAN.R-project.org/package=vegan.

Ottesen, E. A., Hong, J. W., Quake, S. R., Leadbetter, J. R. (2006) Microfluidic digital PCR enables multigene analysis of individual environmental bacteria. Science 314, 1464-1467.

Ottesen, E.A., Leadbetter, J.R. (2011) Formyltetrahydrofolate synthetase gene diversity in the guts of higher termites with different diets and lifestyles. Appl. Environ. Microbiol. 77, 3461-3467.

Paster, B.J., Dewhirst, F.E., Cooke, S.M., Fussing, V., Poulsen, L.K., Breznak, J.A. (1996) Phylogeny of not-yet-cultured spirochetes from termite guts. Appl. Environ. Microbiol. 62, 347-352.

Pernthaler, A., Pernthaler, J., Amann, R. (2004) Sensitive multi-color fluorescence in situ hybridization for the identification of environmental microorganisms. In: Molecular Microbial Ecology Manual, 2nd edition, Vol. 1 (Kowalchuk, G. A., de Brujin; F. J., Head, I. M., Akkermans, A. D. L., and van Elsas, J. D., Eds.), pp. 711-726. Kluwer Academic Publisher, London.

Pernthaler, J., Glöckner, F.-O., Schönhuber, W., Amann, R. (2001) Methods in Microbiology: Marine Microbiology. Academic Press, London.

Pester, M., Brune, A. (2006) Expression profiles of *fhs* (FTHFS) genes support the hypothesis that spirochaetes dominate reductive acetogenesis in the hindgut of lower termites. Environ. Microbiol. 8, 1261-1270.

Pester, M., Brune, A. (2007) Hydrogen is the central free intermediate during lignocellulose degradation by termite gut symbionts. ISME Journal 1, 551-565.

Potrikus, C.J., Breznak, J.A. (1981) Gut bacteria recycle uric acid nitrogen in termites: A strategy for nutrient conservation. Proc. Natl. Acad. Sci. USA 78, 4601-4605.

Pruesse, E., Quast, C., Knittel, K., Fuchs, B., Ludwig, W., Peplies, J., Glöckner, F.O. (2007) SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucleic Acids Res. 35, 7188-7196.

Quince, C., Lanzén, A., Curtis, T.P., Davenport, R.J., Hall, N., Head, I.M., Read, L.F., Sloan, W.T. (2009) Accurate determination of microbial diversity from 454 pyrosequencing data.. Nat. Methods 6, 639-641.

R Development Core Team (2009) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org , .

Rieu-Lesme, F., Morvan, B., Collins, M.D., Fonty, G., Willems, A. (1996) A new H_2/CO_2-using acetogenic bacterium from the rumen: Description of *Ruminococcus schinkii* sp. nov.. FEMS Microbiol. Lett. 140, 281-286.

Rosenthal, A.Z., Matson, E.G., Eldar, A., Leadbetter, J.R. (2011) RNA-seq reveals cooperative metabolic interactions between two termite-gut spirochete species in co-culture. ISME J. 5, 1133-1142.

Russel, J.B., Rychlik, J.L (2001) Factors that alter rumen microbial ecology. Science 292, 1119-1122.

Salmassi, T.M., Leadbetter, J.R. (2003) Molecular aspects of CO_2-reductive acetogenesis in cultivated spirochetes and the gut community of the termite *Zootermopsis angusticollis*. Microbiology 149, 2529-2537.

Sato T; Hongoh Y; Noda S; Hattori S; Ui S; Ohkuma M (2009) *Candidatus* Desulfovibrio trichonymphae, a novel intracellular symbiont of the flagellate *Trichonympha agilis* in termite gut. Environ. Microbiol. 11, 1007-1015.

Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., Hartmann, M., Hollister, E.B., Lesniewski, R.A., Oakley, B.B., Parks, D.H., Robinson, C.J., Sahl, J.W., Stres, B., Thallinger, G.G., Van Horn, D.J., Weber, C.F. (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities.. Appl. Environ. Microbiol. 75, 7537-7541.

Schmitt-Wagner, D., Brune, A. (1999) Hydrogen profiles and localization of methanogenic activities in the highly compartmentalized hindgut of soil-feeding higher termites (*Cubitermes* spp.). Appl. Environ. Microbiol. 65, 4490-4496.

Schmitt-Wagner, D., Friedrich, M.W., Wagner, B., Brune, A. (2003) Phylogenetic diversity, abundance, and axial distribution of bacteria in the intestinal tract of two soil-feeding termites (*Cubitermes* spp.). Appl. Environ. Microbiol. 69, 6007-6017.

Schmitt-Wagner, D., Friedrich, M.W., Wagner, B., Brune, A. (2003) Axial dynamics, stability, and interspecies similarity of bacterial community structure in the highly compartmentalized gut of soil-feeding termites (*Cubitermes* spp.). Appl. Environ. Microbiol. 69, 6018-6024.

Sogin ML, Morrison HG, Huber JA, Welch DM, Huse SM, Neal PR, Arrieta JM, Herndl GJ. (2006) Microbial diversity in the deep sea and the underexplored "rare biosphere". Proc. Natl. Acad. Sci. USA 103, 12115-12120.

Sugimoto, A., Inoue, T., Tayasu, I., Miller, L., Takeichi, S., Abe, T. (1998) Methane and hydrogen production in a termite-symbiont system. Ecol. Res. 13, 241-257.

Tholen, A., Brune, A. (2000) Impact of oxygen on metabolic fluxes and *in situ* rates of reductive acetogenesis in the hindgut of the wood-feeding termite *Reticulitermes flavipes*. Environ. Microbiol. 2, 436-449.

Tholen, A., Pester, M., Brune, A. (2007) Simultaneous methanogenesis and oxygen reduction by *Methanobrevibacter cuticularis* at low oxygen fluxes. FEMS Microbiol. Ecol. 62, 303-312.

Thongaram, T., Hongoh, Y., Kosono, S., Ohkuma, M., Trakulnaleamsai, S., Noparatnaraporn, N., Kudo, T. (2005) Comparison of bacterial communities in the alkaline gut segment among various species of higher termites. Extremophiles 9, 229-238.

Tokuda, G., Yamaoka, I., Noda, H. (2000) Localization of symbiotic clostridia in the mixed segment of the termite *Nasutitermes takasagoensis* (Shiraki). Appl. Environ. Microbiol. 66, 2199-2207.

Tokuda, G; Watanabe, H (2007) Hidden cellulases in termites: revision of an old hypothesis. Biol. Lett. 3, 336-339.

Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R. (2007) Naive Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. Appl. Environ. Microbiol. 73, 5261-5267.

Wang, Y., Stingl, U., Anton-Erxleben, F., Zimmer, M., Brune, A. (2004) '*Candidatus* Hepatincola porcellionum' gen. nov., sp. nov., a new, stalk-forming lineage of Rickettsiales colonizing the midgut glands of a terrestrial isopod. Arch. Microbiol. 181, 299-304.

Warnecke F., Luginbühl, P., Ivanova, N., et al. Hugenholtz P; Leadbetter JR (2007) Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature 450, 560-565

Watanabe, H., Tokuda, G. (2010) Cellulolytic systems in insects. Annu. Rev. Entomol. 55, 609-632.

Weisburg, W.G., Barns, S.M., Pelletier, D.A., Lane, D.J. (1991) 16S ribosomal DNA amplification for phylogenetic study. J. Bacteriol. 173, 697-703.

Werner, J.J., Koren, O., Hugenholtz, P., Desantis, T.Z., Walters, W.A., Caporaso, J.G., Angenent, L.T., Knight, R., Ley, R.E. (2011) Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. ISME J.

Yang, H., Schmitt-Wagner, D., Stingl, U., Brune, A. (2005) Niche heterogeneity determines bacterial community structure in the termite gut (*Reticulitermes santonensis*). Environ. Microbiol. 7, 916-932.

Zimmer, M., Brune, A. (2005) Physiological properties of the gut lumen of terrestrial isopods (Isopoda: Oniscidea) adaptive to digesting lignocellulose? J. Comp. Physiol. B 175, 275-283.

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3 Digesting the diversity – Evolutionary patterns in the gut microbiota of termites and cockroaches

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Summary

The phylogenetic relationship of termites and cockroaches was for a long time debated. Previous studies have identified numerous bacterial lineages that seem to occur exclusively in termite guts. However, some of these termite-specific clusters are also affiliated with sequences originating from their evolutionary ancestors, the cockroaches. We conducted a comprehensive analysis of bacterial diversity by exhaustively sampling dictyopteran species and 454 pyrotag sequencing of the bacterial 16S rRNA genes in the gut environments. Thorough statistical and community analyses revealed the cockroach gut microbiota to be more diverse and less specialized than that of the termites and both differ significantly in their composition already on phylum level. The emerging patterns document a long history of (co)evolution of the gut microbiota with their dictyopteran host species and result in a clear and distinct clustering of the hosts concerning their phylogenetic relationship and dietary demands. Furthermore, this study adds to the peculiar outstanding position of the wood-feeding cockroach *Cryptocercus punctulatus*.

Introduction

Termites (Isoptera) and cockroaches (Blattodea) are members of the superorder Dictyoptera. First hints for termite evolution from wood-feeding cockroaches were revealed by investigating multiple functional genes (Lo *et al.*, 2000). The thorough investigation of their phylogeny rectified the long-believed hypothesis that termites constitute a monophyletic group within the *Dictyoptera* but are rather eusocial cockroaches (Inward *et al.*, 2007; Legendre *et al.*, 2008). Also the appearance and phylogenetic relationship between *Blattabacterium* spp. from cockroaches and the evolutionary oldest termite *Mastotermes darwiniensis* supports their close relatedness (Lo *et al.*, 2003). Termites can be sub-divided in lower termites and the evolutionary younger higher termites. The latter comprise the majority of termite species and developed a wide range of ecological feeding traits like fungus-cultivating and soil-feeding.

Digestive mutualism in the *Dictyoptera* evolved with different stages of coprophagy in omnivorous cockroaches up to highly eusocial proctodeal trophallaxis in termites (Nalepa *et al.*, 2001). This established prerequisites for coevolution of host-specific gut symbionts like flagellates in termites and wood-feeding cockroaches of the *Cryptocercus* genus. A lot of information on the coevolution of these flagellates (Keeling *et al.*, 1998; Ohkuma *et al.*, 2009) and their bacterial symbionts (Ikeda-Ohtsubo and Brune, 2009; Noda *et al.*, 2009) has accumulated. Also the bacterial diversity of complete intestinal tracts of some termites was investigated (Schmitt-Wagner *et al.*, 2003; Hongoh *et al.*, 2003; Shinzato *et al.*, 2007) and gave first insights into possible coevolution of the gut microbiota (Hongoh *et al.*, 2005). However, in-depth molecular analysis of the gut microbiota of cockroaches is still missing.

Previous studies on the intestinal microbiota of termites have identified numerous clusters of bacteria that seem to occur exclusively in termite guts. However, evidence is increasing that some of these termite-specific clusters are also affiliated with sequences originating from cockroaches. It is not clear so far whether this exclusiveness reflects evolutionary patterns. We addressed this question using a bacterial 16S rRNA-based pyrotag sequencing approach analyzing gut samples of all families and subfamilies in cockroaches and termites.

This study is outstanding in comparison of evolutionary patterns of bacteria since it investigates confined systems in related host animals of known phylogenetic relationship.

Materials and Methods

Sample preparation

A broad range of insects were sampled covering all families and subfamilies of cockroaches and lower and higher termites including all known feeding habits. All cockroaches and the Gryllidae samples were purchased from German breeders.. The termites were bred in the lab, collected in the field, or provided by colleague scientists (for details, see Table 1). Only worker caste termites were used in the experiments.

Species affiliation of all the animals was checked by partially sequencing the cytochrome c oxidase II (COII) or 12S rRNA gene as described in (Pester and Brune, 2006; Inward *et al.*, 2007) and phylogenetic comparison with known species. The sequences were submitted to GenBank (numbers will follow).

Dissection of the animals was undergone using sterile scissors and sterile, fine-tipped forceps. For comparison of the gut microbiota between the samples, we used complete hindguts since they are anoxic and harbor the highest amounts of cells in the gut (Schauer *et al.*, 2012; Chapter 2).

Table 1: Information about all samples.

Species	(Sub)Family	Feeding guild	Section[5]	Storage / Maintenance	Sampling area / obtained from (collector)
Cryptocercus punctulatus	Cryptocercidae	Wood	Wg[1]	Freshly dissected	Heywood County, NC, USA
Mastotermes darwiniensis	Mastotermitidae	Wood	Hg	Freshly dissected	BAM[8]
Zootermopsis nevadensis	Termopsidae	Damp wood	Hg	In the laboratory 1[2]	California, USA
Hodotermopsis sjoestedti	Termopsidae	Damp wood	Hg	Freshly dissected	BAM[8]
Hodotermes mossambicus	Hodotermitidae	Grass	Wg	In the laboratory 4[10]	Pretoria, South Africa
Incisitermes marginipennis	Kalotermitidae	Dry wood	Hg	In the laboratory 3[7]	BAM[8]
Neotermes jouteli	Kalotermitidae	Dry wood	Wg	Freshly dissected	Rudolf H. Scheffrahn
Reticulitermes santonensis	Rhinotermitidae	Wood	Hg	In the laboratory 1	Forêt de la Coubre, France
Coptotermes niger	Rhinotermitidae	Wood	Hg	Freshly dissected	BAM[8]
Microtermes sp.	Macrotermitinae	Fungus[9]	Wg	Ethanol-stored	Kajiado, Kenya
Macrotermes bellicosus	Macrotermitinae	Fungus	Hg	Freshly dissected	BAM[8]
Odontotermes sp.	Macrotermitinae	Fungus	Wg	Ethanol-stored	JKUAT, Kenya
Alyscotermes trestus	Apicotermitinae	(Soil)[6]	Wg	Ethanol-stored	JKUAT, Kenya
Cubitermes ugandensis	Termitinae	Soil	Hg	In the laboratory 2[4]	Lhiranda Hill, Kakamega, Kenya
Ophiotermes sp.	Termitinae	Soil	Wg	Ethanol-stored	Kalunja Gl., Kakamega,

					Kenya
Amitermes meridionalis	Termitinae	Grass	Wg	Ethanol-stored	Finness River, Litchfield NP, Darwin
Microcerotermes sp.	Termitinae	Wood	Wg	Ethanol-stored	JKUAT, Kenya
Nasutitermes corniger	Nasutitermitinae	Wood	Hg[3]	In the laboratory 1	Rudolf H. Scheffrahn
Nasutitermes takasagoensis	Nasutitermitinae	Wood	Hg	In the laboratory 1	Gaku Tokuda
Trinervitermes sp.	Nasutitermitinae	Grass	Wg	Freshly dissected	JKUAT, Kenya

[1]…Whole gut

[2]…At room temperature in the dark; in polyethylene containers on a diet of pine wood and water

[4]…At room temperature in the dark; in polyethylene containers; regularly parts of the nest material were removed and replaced with fresh soil

[3]…Hindgut

[5]…Section of the gut

[6]…not clear

[7]…At 27°C and 72% rH; in polyethylene containers on a diet of dry wood; Termites are given occasionally a few drops of water

[8]…Permanent termite cultures from the Bundesanstalt für Materialforschung und -prüfung Berlin, Germany

[9]…Fungus-cultivating, *Termitomyces* spp. in special combs in the nests

[10]…At 27°C and 60% rH, under a 12 h/12 h LD light regimen; in polyethylene containers on a diet of autoclaved hay, which was replaced three times per week; water was supplied *ad libitum* through bottles attached to the nest container

Pyrotag sequencing and processing

Depending on gut size, 3–10 individual hindgut sections were homogenized in 1× PBS using sterile Micropistill sticks (Eppendorf). DNA was extracted with phenol–chloroform using the bead-beating protocol of Henckel *et al.*, (1999) and precipitated with two volumes of polyethylene glycol. The V3–V4 region of the bacterial 16S rRNA gene was amplified using the primer set 343Fmod–784Rmod and a high-fidelity polymerase (Herculase II Fusion Enzyme with dNTPs Combo Kit, Agilent) under the conditions as described in Chapter 2. Each primer had an additional, sample-specific 6-bp barcode at the 5' end, which differed by at least 2 bp between samples and contained no homopolymers. The amplicons were photometrically quantified (NanoDrop, Thermo Fisher Scientific, Germany) and mixed in equimolar amounts before further analysis. Adaptor ligation, subsequent amplification, and pyrosequencing (454 GS FLX with Titanium technology, Roche) were done by a commercial service (GATC Biotech, Konstanz, Germany; Agowa, Berlin, Germany).

Pyrotag data was pre-processed using the mothur software suite (version 1.15.0; Schloss *et al.*, 2009) and purged applying stringent conditions (reads >200 bp; no ambiguous bases, etc.) as described previously (Chapter 2). Sequences were aligned against the SILVA 102 non-redundant database (Pruesse *et al.*, 2007) using the SINA aligner. The taxonomy of the pyrotags was assigned using the Naïve Bayesian Classifier implemented in the mothur software (confidence threshold of 60%) and a manually edited reference database (Chapter 2), containing all bacterial isolates, all uncultivated bacteria from intestinal environments, and at least 3 representative sequences from every other lowest-level group in the SILVA database.

Statistics

All statistic analyses were carried out using *R*, version 2.13.1 (R Development Team Core, 2009) with the packages vegan and entropy. Prior to the community analyses, all samples were normalized based on the smallest number of sequences per insect gut (approximately 2000 sequences for *Cubitermes ugandensis*). Dimension reduction was performed by pair-wise comparison based on the Bray-Curtis dissimilarity coefficient and subsequent non-metric multidimensional data scaling (NMDS) of the resulting distance matrix. To test whether diet or evolution of the host influences the insect microbiota, we performed both analysis of variance using distance matrices (ADONIS) and multi response permutation procedure (MRPP).

For further analysis of the resulting dissimilarities between the different insect microbiota, we performed step-wise artificial reduction in resolution ranging from 0.1 to 10% relative abundance (so-called jack-knifing). Every taxon abundance in each sample below the regarded threshold was replaced by zero. Subsequently, the whole dataset was renormalized based on the current smallest number of sequences per sample in the data set. The corresponding NMDS plots were visually checked to find the threshold abundance that still ensures the pattern in the NMDS plotting. The corresponding algorithm was written in *S* and *R* programming languages.

For a detailed analysis of the Bray-Curtis coefficient between the samples we analyzed the mathematical structure of the coefficient. Oksanen *et al.* (2010) described the following basal parameters for the coefficient in the *R* package vegan:

$$A=\sum_{i=1}^{N} x_{ij} \qquad (1) \qquad B=\sum_{i=1}^{N} x_{ik} \qquad (2)$$

$$J=\sum_{i=1}^{N} \min(x_{ij},x_{ik}) \qquad (3)$$

Where A is the sum of all abundances in the sample j, B the sum of all abundances in sample k, and J the sum of the minima of shared taxa abundances of both samples. By using these parameters the Bray-Curtis similarity s_{BC} and dissimilarity d_{BC}, respectively, is obtained:

$$s_{BC}=\frac{2 \cdot J}{A+B} \qquad (4) \qquad d_{BC}=1-s_{BC} \qquad (5)$$

However, these terms do not allow testing for the individual taxon contribution. Since a complete deletion of the taxon would also have an influence on the sum terms A and B of the samples, it is not possible to address taxon contribution with already published methods.

If the entire taxon was left out of the analysis, this would influence the whole term by also influencing the sums A and B of each sample. Therefore we determined A and B independently and analyzed the partial similarities of a taxon:

$$\sigma_{i,BC}=\frac{2 \cdot \min(x_{ij},x_{ik})}{A+B} \qquad (6)$$

Where $\sigma_{i,BC}$ is the partial similarity caused by the taxon i. The sum all $\sigma_{i,BC}$ equals the Bray-Curtis similarity. Drawback of the minimum term $\min(x_{ij},x_{ik})$ is that if one sample lacks a complete taxon (e.g. $x_{ij} = 0$) the minimum equals zero and therefore the $\sigma_{i,BC}$ equals zero as well. Since we additionally wanted to quantify the contribution of a taxon on the dissimilarity, we needed a bidirectional measure. In order to achieve this, we defined a partial dissimilarity measure:

$$\delta_{i,BC} = \frac{\max\left(x_{ij}, x_{ik}\right) - \min(x_{ij}, x_{ik})}{A+B} \qquad (7)$$

Where $\max(x_{ij}, x_{ik})$ is the maximum abundance of the taxon in both samples j and k. Also the sum of all $\delta_{i,BC}$ equals the Bray-Curtis dissimilarity. By subtracting $\delta_{i,BC}$ from $\sigma_{i,BC}$ we get a bidirectional $\delta_{i,BC,eff}$ measure for each taxon:

$$\delta_{i,BC,eff} = \sigma_{i,BC} - \delta_{i,BC} = \frac{3 \cdot \min(x_{ij}, x_{ik}) - \max(x_{ij}, x_{ik})}{A+B} \qquad (8)$$

Where $\delta_{i,BC,eff}$ is a bidirectional measure of similarity ranging from -1 to 1. A negative value is defined as caused dissimilarity and a positive value as similarity. For illustration, we multiplied these values by 100%. Finally, we sorted these values on the basis of their absolute values and took the upper 10 as the most influential. This procedure was written as an algorithm in *S* and *R* programming languages.

To identify the core microbiota, we checked for the total presence of taxa in a predefined subset of our dataset. If a taxon was present in all the samples of the predefined subsets, it was regarded as part of the core microbiota. The corresponding algorithm was written in *S* and *R* programming languages.

Results

Pyrotag library characteristics and diversity measures

After amplification of the bacterial 16S rRNA genes pyrotag sequencing of the V3–V4 region was carried out. Trimming and quality control resulted in removal of 10.3–26.6% of the reads from each dataset, resulting in sequence libraries of 2050–53,000 reads per sample (for details, see Supplementary Table 4). The data for the hindgut of *N. corniger* was taken from a previously published study (Chapter 2). Classification of the bacterial 16S gene reads in all the samples led to 90–550 genera (Table 2). The lowest number of genera (91) was detected in the drywood termite *Coptotermes niger*. Accordingly, this termite also had the lowest evenness (0.44) indicating only a few but prominent bacterial groups. The coverage of the samples ranged from 64% to 90%. In general, the average coverage and diversity of the gut microbiota was slightly higher in cockroaches than in termites. Therefore, the bacterial groups were more evenly distributed in the cockroaches than in the termites (0.72 and 0.62, respectively). Interestingly, besides the enormous number of about 100,000 reads, the genus coverage of the blaberid cockroach *Eublaberus posticus* was still only at 81%. This is a very good example illustrating the huge diversity existing in gut communities. The large diversity especially manifests in the rare bacterial groups, i.e., 75% of all the detected genera in all the samples showed a relative abundance of only 0.26% (details not shown).

Table 2: Coverage, diversity, similarity, and evenness of the bacterial hindgut communities in the different insect samples.

Host of microbiota	**Number of genera**[a]	**Estimated coverage**[b] **(%)**	**Diversity**[c]	**Evenness**[d]
E. capucina	232	72.7	4.37	0.76
S. lateralis	186	81.8	3.96	0.73
S. macroptera	135	88.4	3.59	0.71
H. flexivitta	177	69.5	4.46	0.80
E. chopardi	200	80.7	4.14	0.75
E. floridiana	354	89.7	3.92	0.66
D. punctuata	161	87.0	3.89	0.75
O. orientalis	291	77.0	4.36	0.73
R. maderae	268	86.7	4.22	0.74
E. posticus	416	80.8	3.98	0.64
Panchlora sp.	212	67.2	3.64	0.63
S. lampyridiformis	217	75.7	4.08	0.72

B. orientalis	246	75.2	3.86	0.67
P. angustupennis	202	64.5	4.25	0.74
S. esakii	296	82.2	4.22	0.72
C. punctulatus	180	75.3	3.84	0.70
M. darwiniensis	137	71.7	3.00	0.57
H. sjoestedti	272	80.7	3.69	0.63
R. santonensis	112	80.2	2.85	0.58
C. niger	91	81.2	2.06	0.44
Z. nevadensis	278	81.0	3.76	0.64
H. mossambicus	204	72.8	3.57	0.63
I. marginipennis	299	82.8	3.10	0.53
N. jouteli	276	81.4	3.70	0.64
M. bellicosus	260	78.5	3.58	0.62
Odontotermes sp.	211	66.1	3.80	0.66
Microtermes sp.	307	79.1	4.42	0.74
C. ugandensis	211	69.2	4.31	0.75
Microcerotermes sp.	291	74.0	3.27	0.55
Ophiotermes sp.	328	72.9	4.13	0.68
A. meridionalis	354	82.0	3.47	0.57
A. trestus	550	75.3	4.45	0.67
N. corniger	175	64.2	3.28	0.58
N. takasagoensis	198	73.5	2.82	0.50
Trinervitermes sp.	232	80.0	3.81	0.67
Pachnoda sp.	339	80.3	4.37	0.72
A. domesticus	104	80.6	3.39	0.70
G. assimilis	190	78	3.33	0.61

[a]…Lowest-level of the reference database
[b]…Based on Chao1 (Chao, 1984)
[c]…Non-parametric Shannon index (since the coverage was less than 100%; Chao and Shen, 2003)
[d]…Evenness (Legendre and Legendre, 1998)

Bacterial community structure

Although the bacterial diversity of cockroach and termite guts is in a comparable range, the structure of their gut communities is completely different. This is already obvious at phylum level (Fig. 1). First, there is a prominent increase of Spirochaetes in all lower termites (up to 64%), wood-feeding higher (up to 68%) and the wood-feeding cockroach *Cryptocercus punctulatus*. Additionally, the TG3 or Fibrobacteres increased from virtual absence in relative abundance to higher only in the higher termites feeding on cellulosic diets. Members of the Elusimicrobia phylum are highly abundant only in lower termites (up to 13%) but are present in all Dictyoptera, albeit in fewer numbers. However, Elusimicrobia are absent in the outgroup (Gryllidae). With some exceptions Bacteroidetes are numerically less important in the termites and Fusobacteria are mainly found in the cockroaches.

Our pyrotag classification approach allows us not only to compare the phylum-level distribution of bacteria in dictyopteran hindguts but also investigate lower taxonomic levels, i.e. genus level (Fig. 2). The selected bacterial lineages represent the different patterns occurring in the Dictyoptera. Some bacteria are present in all Dictyoptera (Paludibacter) but can accumulate in specific hosts like Desulfovibrio 1 and Endomicrobia culminating in the lower termites. There are bacteria mostly prominent in the cockroaches, but showing lower or virtually no abundance in the termites like an uncultured group of Marinilabiaceae or a special group of Fusobacteria. Supporting the close clustering of fungus-cultivating termites to the cockroaches (Fig. 3) can be explained by, e.g., Desulfovibrio 3 or Alistipes accumulating mostly in the mentioned dictyopteran hosts. Furthermore, there are bacterial taxa almost exclusively obtained from particular dictyopteran host intestines, e.g., Candidatus Tammella and the uncultured 54 group of Lachnospiraceae in Macrotermitinae or Turicibacter in Termitinae. Members of Fibrobacteres Termite Cluster I are accumulating in higher termites feeding on cellulose-rich diets but are absent in soil-feeding termites.

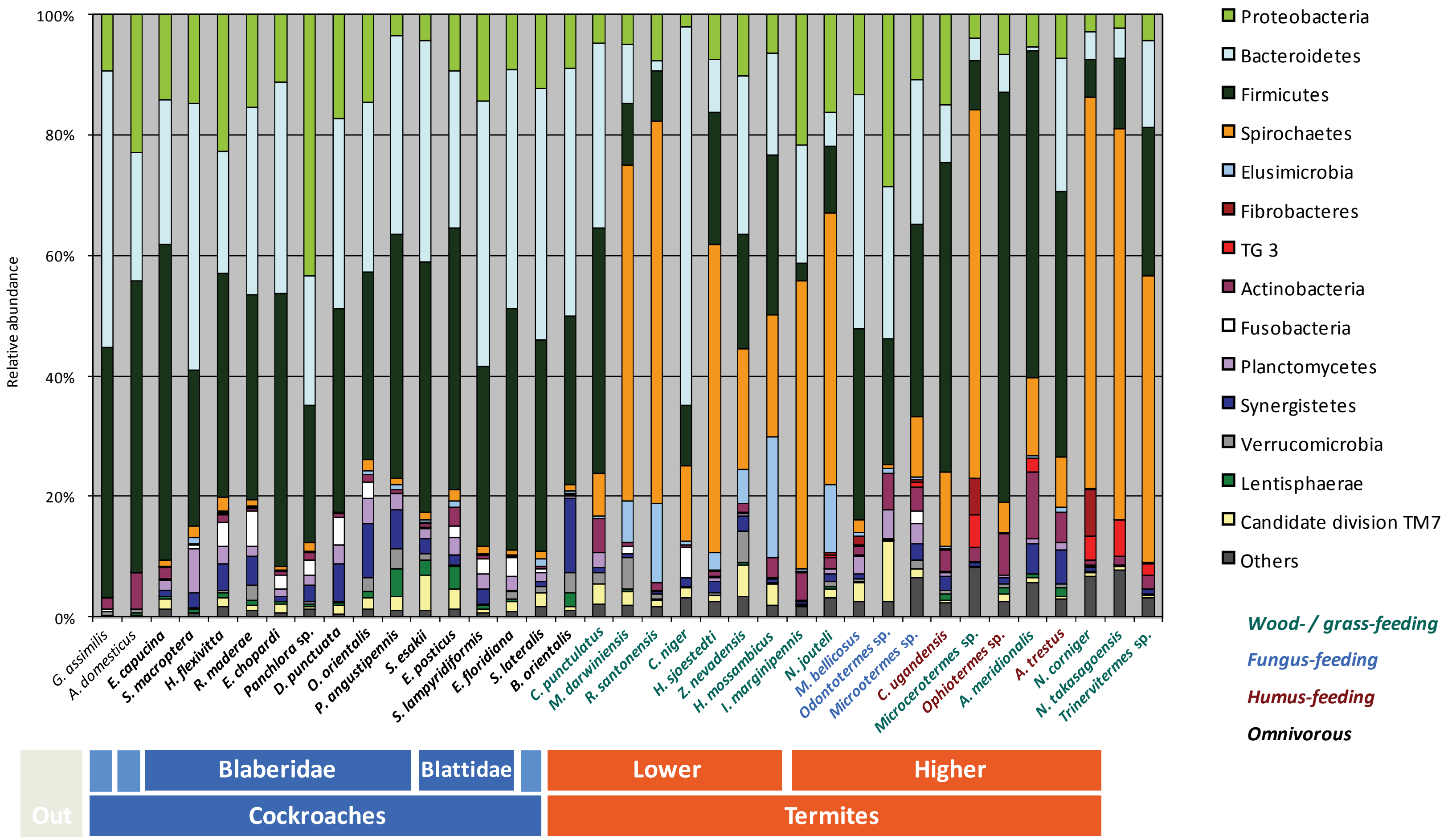
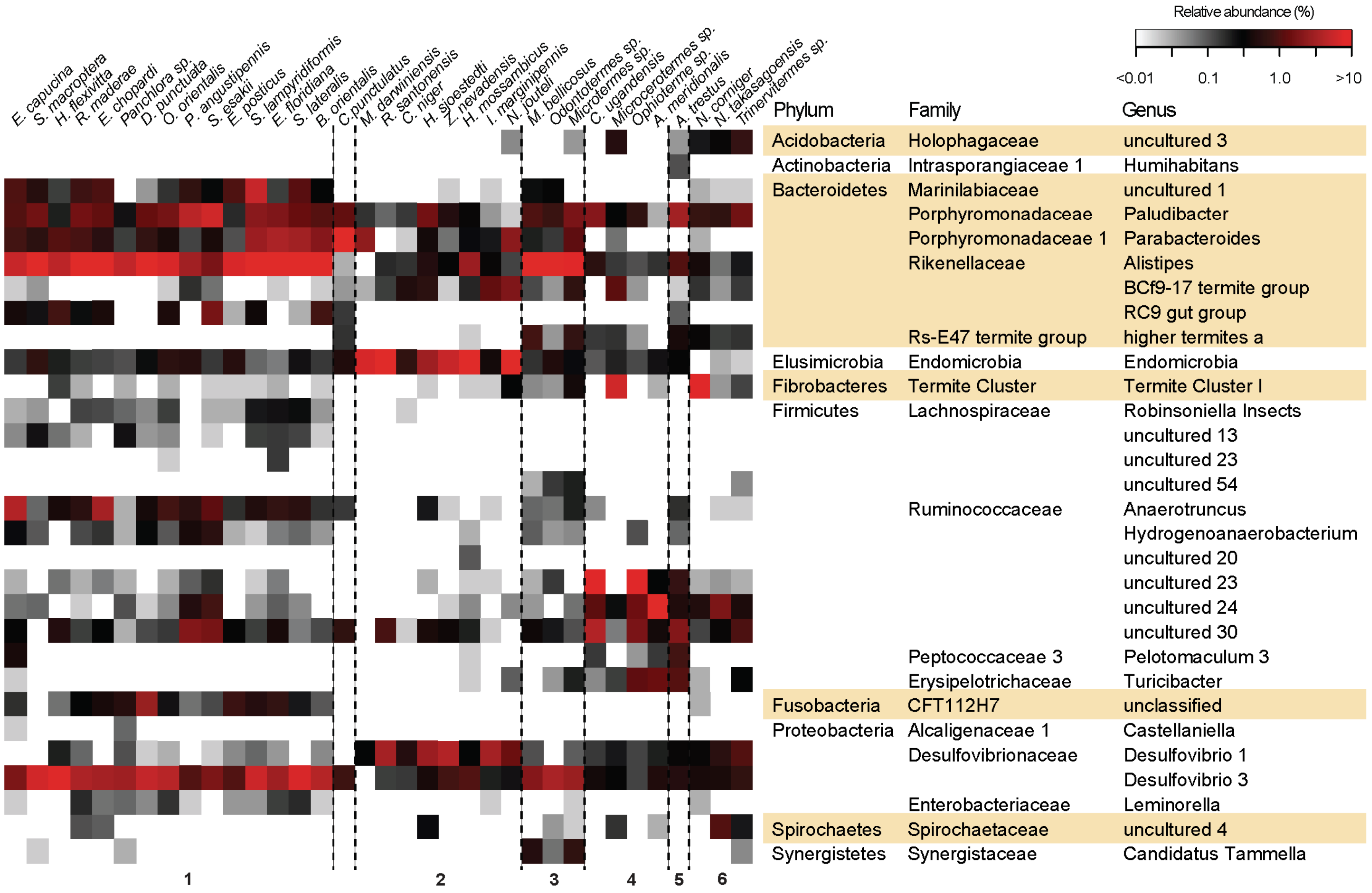


Figure 1: Phylum-level overall distribution of bacterial gut microbiota within the *Dictyoptera*. Feeding traits are color-coded.



Phylum	Family	Genus
Acidobacteria	Holophagaceae	uncultured 3
Actinobacteria	Intrasporangiaceae 1	Humihabitans
Bacteroidetes	Marinilabiaceae	uncultured 1
	Porphyromonadaceae	Paludibacter
	Porphyromonadaceae 1	Parabacteroides
	Rikenellaceae	Alistipes
		BCf9-17 termite group
		RC9 gut group
	Rs-E47 termite group	higher termites a
Elusimicrobia	Endomicrobia	Endomicrobia
Fibrobacteres	Termite Cluster	Termite Cluster I
Firmicutes	Lachnospiraceae	Robinsoniella Insects
		uncultured 13
		uncultured 23
		uncultured 54
	Ruminococcaceae	Anaerotruncus
		Hydrogenoanaerobacterium
		uncultured 20
		uncultured 23
		uncultured 24
		uncultured 30
	Peptococcaceae 3	Pelotomaculum 3
	Erysipelotrichaceae	Turicibacter
Fusobacteria	CFT112H7	unclassified
Proteobacteria	Alcaligenaceae 1	Castellaniella
	Desulfovibrionaceae	Desulfovibrio 1
		Desulfovibrio 3
	Enterobacteriaceae	Leminorella
Spirochaetes	Spirochaetaceae	uncultured 4
Synergistetes	Synergistaceae	Candidatus Tammella

↑

Figure 2: Frequency of selected bacterial lineages in the Dictyoptera. The dotted lines divide major phylogenetic groups among the dictyopteran hosts:

1…cockroaches; 2…lower termites; 3…Macrotermitinae; 4…Termitinae; 5…Apicotermitinae; 6…Nasutitermitinae. Data is log10-transformed and zero values are considered as NA.

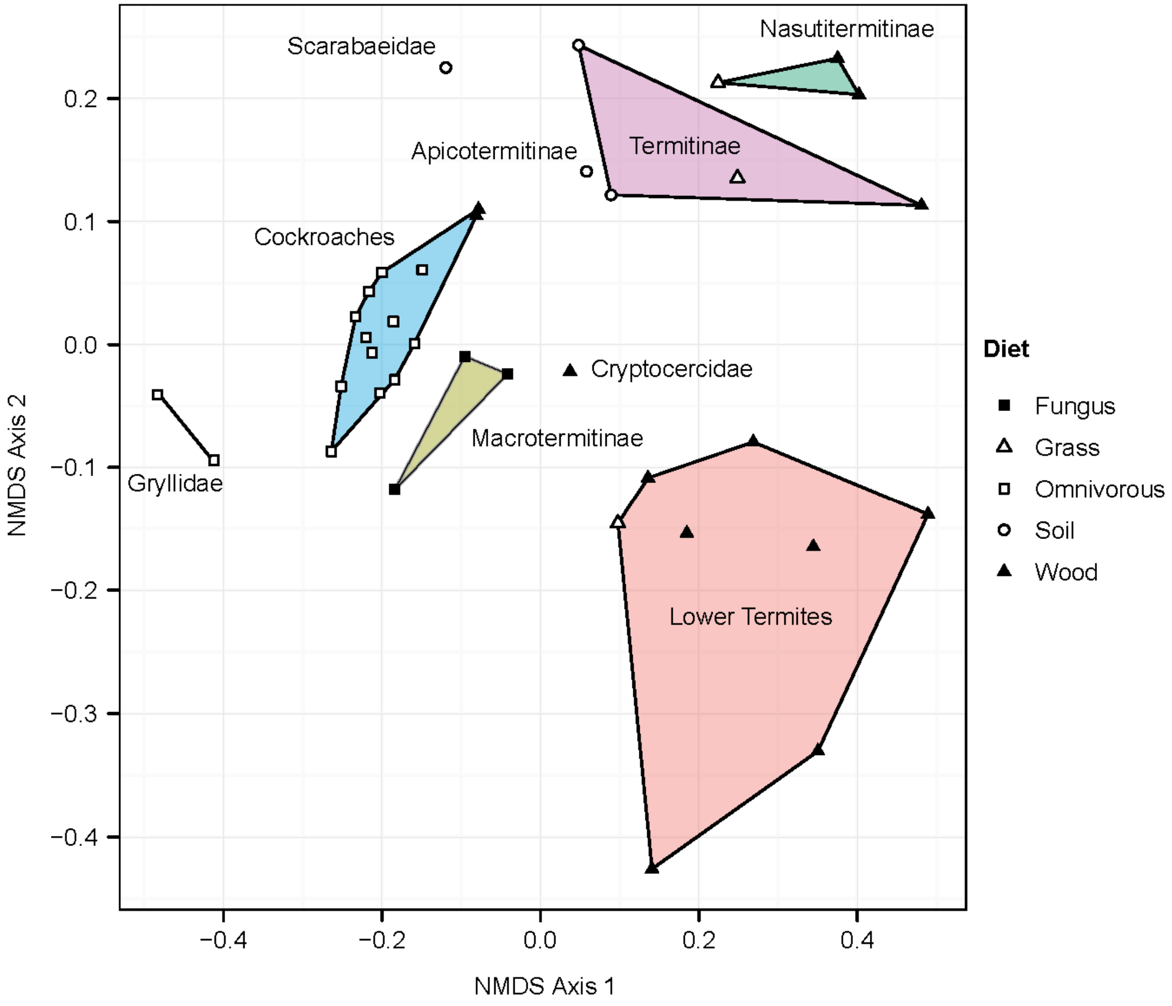


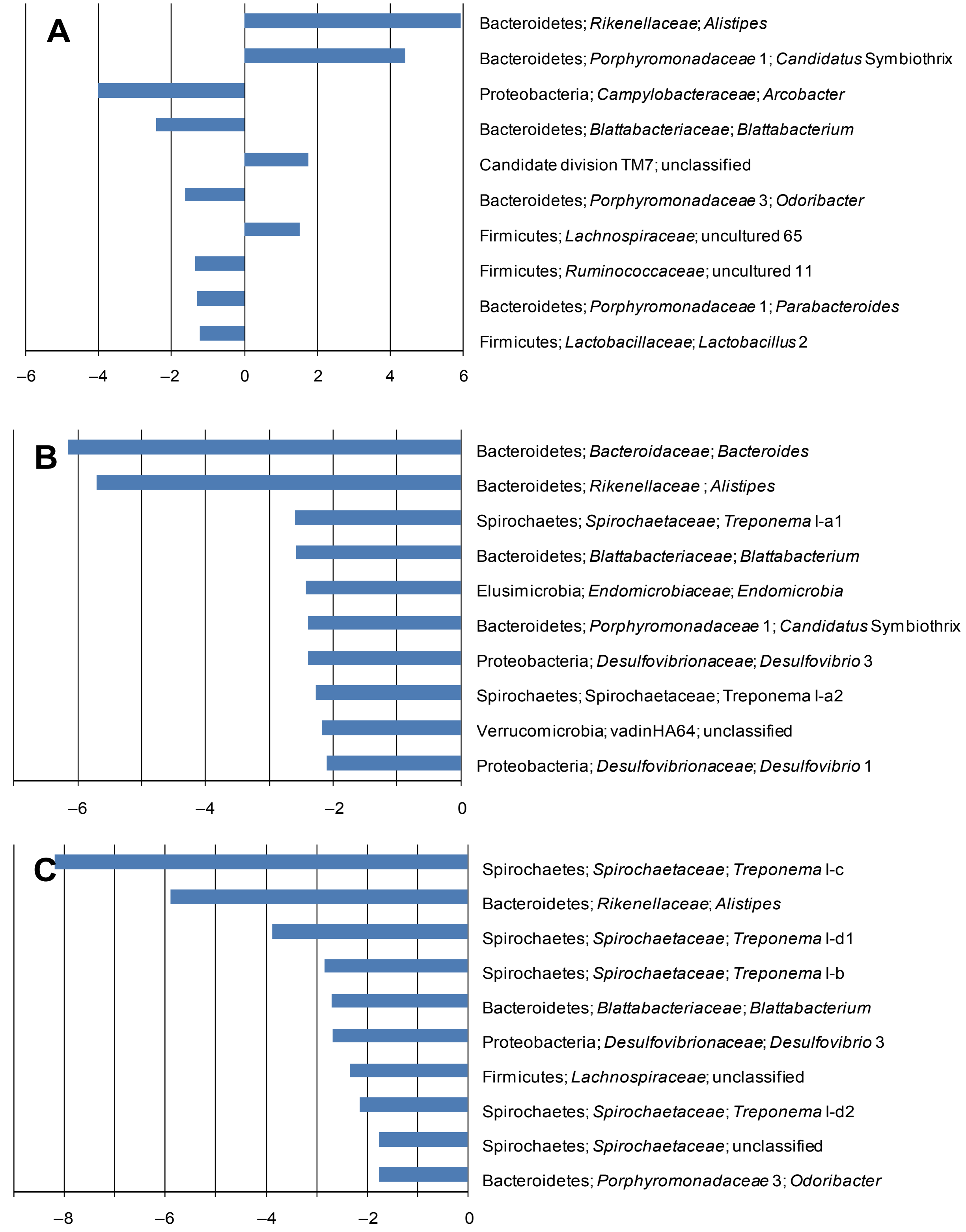
Figure 3: Non-metric multidimensional scaling (NMDS) based on a Bray-Curtis dissimilarity distance matrix.

Species belonging to the identical phylogenetic group are connected and the areas are colored. Two Gryllidae species and the larva of *Pachnoda* sp. were used as outgroup. The feeding traits are indicated by different symbols.

Cluster analyses

The different patterns shown in Fig. 2 already indicate an evolutionary framework in the gut microbiota of dictyopteran species. Performing a genus-level cluster analysis, i.e., non-metric multidimensional scaling (NMDS) based on a Bray-Curtis dissimilarity matrix, visualized a clear clustering of the gut microbiota concerning the phylogeny of the host organism (Fig. 3; color-shaded areas). Cockroaches are distinctly separated from the lower termites that form a rather loose cluster. Higher termites constitute discrete clusters based on their subfamily level revealing the fungus cultivators clearly separated from the other higher termite subfamilies and affiliating them more to the cockroaches. Despite the closer phylogenetic relationship to cockroaches and lower termites, the wood-feeding cockroach *Cryptocercus punctulatus* falls in between all the dictyopteran species. Higher termites sharing similar feeding habits seem also to form cluster. To test the significance of the clustering, we applied ADONIS and MRPP analyses. Both were resulting in p-values <0.001.

To check the stability of the particular clustering in the NMDS analysis and to understand which bacterial groups are responsible for the dissimilarities, we performed a jack-knifing analysis. The clustering was consistent until the removal of bacterial taxa having ≤ 1.7% relative abundance (details not shown), indicating again the importance of low-abundant groups in the shaping of gut communities. These taxa are indicated / highlighted in Fig. 2 and Supplementary Table 4. Additionally, we checked each taxon for its contribution to the Bray-Curtis (dis-)similarity in a pair wise comparison of the gut microbiota of representative dictyopteran hosts. Many of the taxa identified in the jack-knifing analysis add also to the Bray-Curtis (dis-)similarities. Noteworthy, most of the taxa in all the pair wise comparisons contributed rather to dissimilarities between the gut samples (Fig. 4; negative percentage values). This again shows how clearly different the clusters of cockroaches, lower, and higher termites are. The genus Alistipes appears only in higher abundance in cockroaches and fungus-cultivating higher termites (Supplementary Table 4), hence this genus contributes to similarities (Fig. 4A; positive percentage values). Comparing the cockroaches with representatives of the other higher and the lower termites revealed different treponemes as responsible taxa for the clustering (Fig. 4A–C). The composition of treponemes is also relevant for the differentiation of lower and higher termites and the wood-feeding cockroach *C. punctulatus* (Fig. 4D–H). In general, some bacterial taxa seem to be responsible for the overall clustering scheme in Fig. 3, e.g., the different treponemal genera, *Alistipes*, *Bacteroides*, and *Blattabacterium*.



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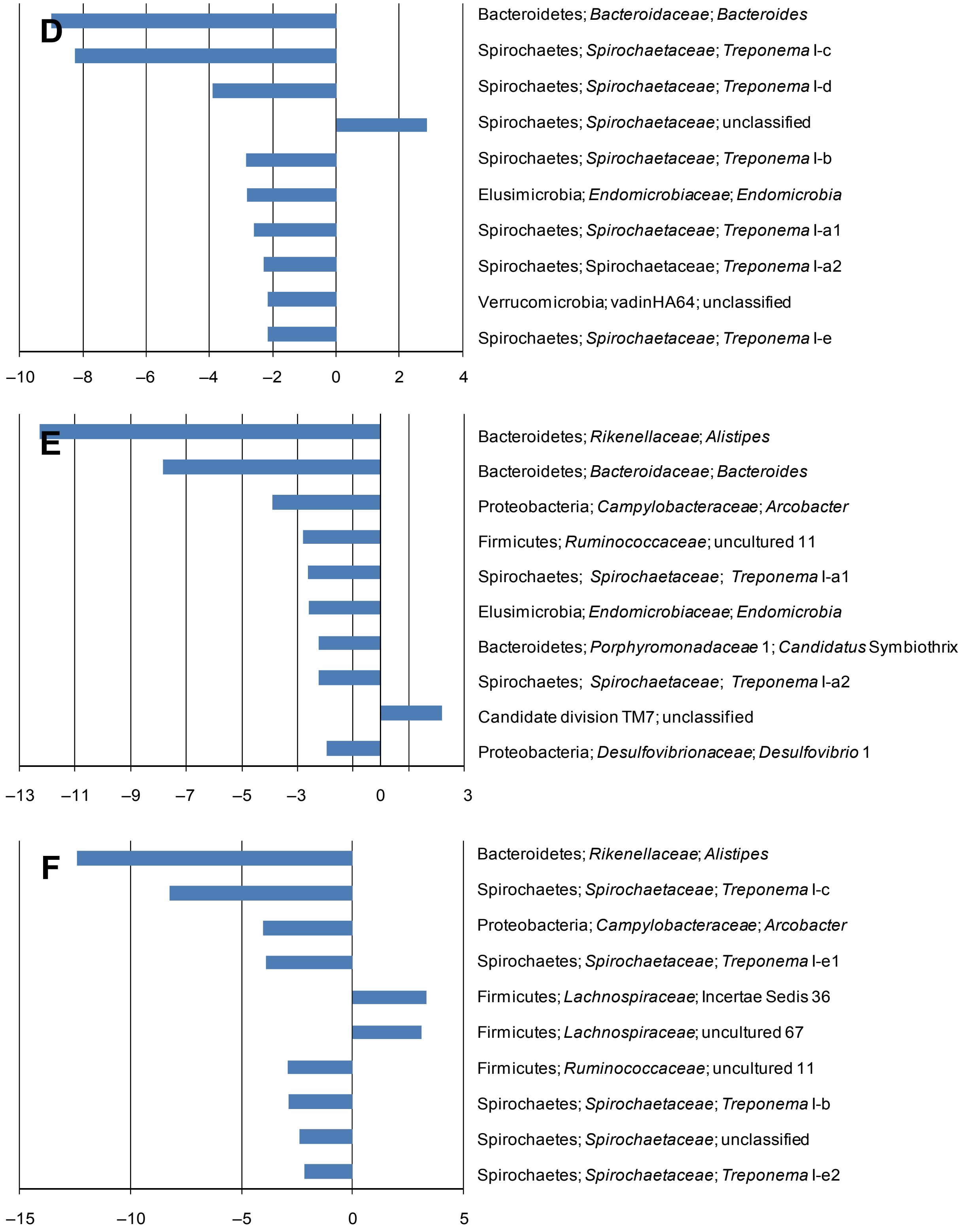

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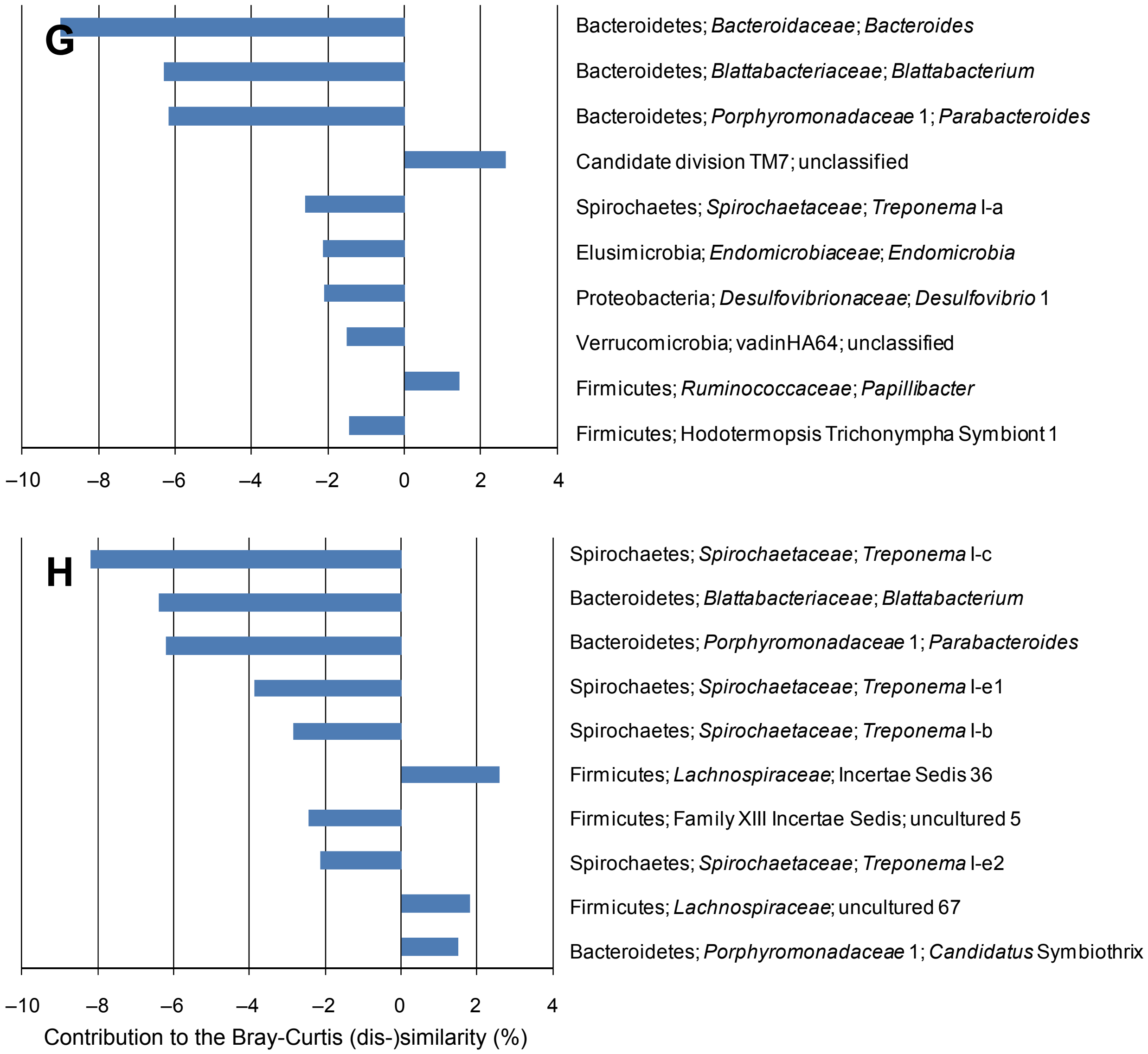

Figure 4 Contribution of the ten most important effective taxa to the Bray-Curtis (dis-)similarity in a pair wise comparison of the gut microbiota of representative dictyopteran hosts.

A…*S. lateralis* + *M. bellicosus*; B…*S. lateralis* + *Z. nevadensis*; C…*S. lateralis* + *Trinervitermes* sp.; D…*Trinervitermes* sp. + *Z. nevadensis*; E…*M. bellicosus* + *Z. nevadensis*; F…*Trinervitermes* sp. + *M. bellicosus*; G…*C. punctulatus* + *Z. nevadensis*; H…*C. punctulatus* + *Trinervitermes* sp.

Core microbiota

The analysis of the effective taxa responsible for the clustering in Fig. 3 already indicated some important bacterial groups (Fig. 4). Furthermore, we wanted to know what taxa the core microbiota is composed of, meaning the presence of a bacterial taxon in all the samples of cockroach, lower, and higher termite host organism. At a first glance, termites—lower or higher—share only half the number of core genera than the individuals among cockroaches (~10 and 21, respectively; Fig. 5). Only three taxa are shared by all intestinal tracts of the dictyopteran species, namely two uncultured groups from *Lachnospiraceae* and *Synergistaceae* and members of the TM7 Candidate division (Table 3). Lower termites share less taxa with the cockroaches than higher termites although the latter are phylogenetically farther related. Astonishingly, lower and higher termites only share two taxa (uncultured groups of *Coriobacteriaceae* and Family XIII Incertae Sedis of Firmicutes). Because of the exceptional position of *Cryptocercus punctulatus*, we omitted this sample from the core microbiota analysis. *C. punctulatus* shares all the core taxa of cockroaches and lower termites with the exception of a *Rikenellaceae* group and *Desulfovibrio* 1, respectively.

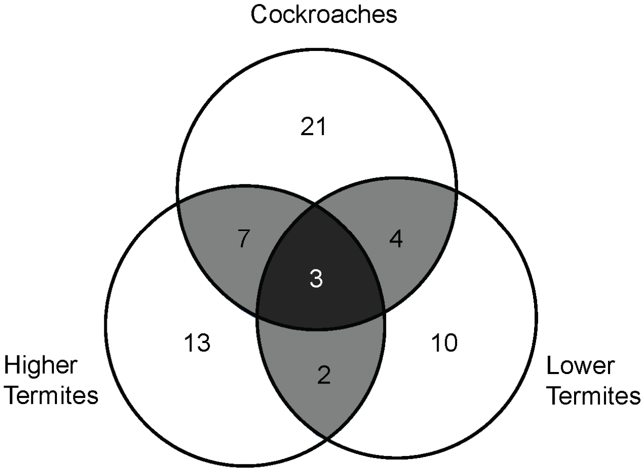

Figure 5: Venn diagram based on Table 3 showing the core microbiota (presence of a bacterial taxon in all the samples).

Due to the exceptional position of *Cryptocercus punctulatus*, it was omitted from this analysis.

Table 3 Selected core microbiota taxa between the cockroaches and the lower and higher termites. Unclassified taxa are not shown. ***…not found in Cryptocercus punctulatus

	Cockroach	**Lower termites**	**Higher termites**
Cockroach	Bacteroidetes; *Blattabacteriaceae*; *Blattabacterium*		
	Bacteroidetes; *Porphyromonadaceae*; *Paludibacter*		
	Bacteroidetes; *Porphyromonadaceae* 1; *Dysgonomonas*		
	Bacteroidetes; *Porphyromonadaceae* 1; *Parabacteroides*		
	Bacteroidetes; *Rikenellaceae*; P1_32 Panesthia***		
	Bacteroidetes; *Rikenellaceae*; Rs-D38 termite group		
	Firmicutes; *Lachnospiraceae*; *Catabacter*		
	Firmicutes; *Ruminococcaceae*; Incertae Sedis 4		
	Firmicutes; *Ruminococcaceae*; insect guts a		
	Firmicutes; *Ruminococcaceae*; uncultured 11		
	Firmicutes; *Ruminococcaceae*; uncultured 36		
	Firmicutes; *Veillonellaceae*; uncultured 7		
	Planctomycetes; vadinHA49; unclassified		
	Elusimicrobia; *Endomicrobiaceae*; *Endomicrobia*	Elusimicrobia; *Endomicrobiaceae*; *Endomicrobia*	
	Bacteroidetes; *Rikenellaceae*; *Alistipes*		Bacteroidetes; *Rikenellaceae*; *Alistipes*
	Firmicutes; *Lachnospiraceae*; Incertae Sedis 36		Firmicutes; *Lachnospiraceae*; Incertae Sedis 36
	Firmicutes; *Lachnospiraceae*; uncultured 65		Firmicutes; *Lachnospiraceae*; uncultured 65
	Proteobacteria; *Desulfovibrionaceae*; *Desulfovibrio* 3		Proteobacteria; *Desulfovibrionaceae*; *Desulfovibrio* 3
	Candidate division TM7; unclassified	Candidate division TM7; unclassified	Candidate division TM7; unclassified
	Firmicutes; *Lachnospiraceae*; uncultured 67	Firmicutes; *Lachnospiraceae*; uncultured 67	Firmicutes; *Lachnospiraceae*; uncultured 67
	Synergistetes; *Synergistaceae*; uncultured 6	Synergistetes; *Synergistaceae*; uncultured 6	Synergistetes; *Synergistaceae*; uncultured 6
Lower		Proteobacteria; *Desulfovibrionaceae*; *Desulfovibrio* 1***	
		Proteobacteria; Rickettsiales; *Candidatus* Hepatincola	
		Spirochaetes; *Spirochaetaceae*; *Treponema* I-a	
		Spirochaetes; *Spirochaetaceae*; *Spirochaeta* 2	
		Actinobacteria; *Coriobacteriaceae*; uncultured 10	Actinobacteria; *Coriobacteriaceae*; uncultured 10
		Firmicutes; Family XIII Incertae Sedis; uncultured 5	Firmicutes; Family XIII Incertae Sedis; uncultured 5
Higher			Bacteroidetes; *Porphyromonadaceae* 1; Cluster V
			Firmicutes; *Ruminococcaceae*; uncultured 12
			Firmicutes; *Ruminococcaceae*; uncultured 30
			Proteobacteria; Rs-K70 termite group; unclassified

Discussion

Evolutionary vs. dietary patterns

Analyzing a broad range of cockroaches and termites yielded an enormous amount of data and insights into the hindgut microbiota of *Dictyoptera*. It is already well established that symbionts of gut protists co-evolve with the insect host or the protist cell (Noda *et al.*, 2007; Ikeda-Ohtsubo and Brune, 2009; Desai *et al.*, 2010). Patterns of evolutionary inheritance of selected bacterial lineages for representative groups (presence / absence or numerical preference) of *Dictyoptera* were also supported by our investigations, too (Fig. 2).

While evolutionary patterns become quite clear in Fig. 3, one has to be cautious to distinguish dietary bacterial community patterns in the *Dictyoptera* since with evolution of the Isoptera and its (sub-)families their food has changed several times, too. Nevertheless, we want to discuss some emerging patterns. The fungus-cultivating higher termites cluster very closely to the omnivorous cockroaches (Fig. 3). This is not astonishing since these termites actually feed on both, fungus-infested and pre-digested wood particles. Hence, their diet is not only cellulose-rich but also rich in nitrogen (proteins) compared to the nitrogen-deficient, wood-feeding lower termites. Thus, Macrotermitinae exhibit a rather omnivorous lifestyle. Carbon isotope studies revealed, that *Macrotermes* sp. rather feed on the fungus itself whereas other fungus-cultivators more feed on the cellulose provided in the fungal gardens (Hyodo *et al.*, 2011). The same is true for the wood-feeding cockroaches *Salganea esakii* and *Panesthia angustipennis*, which feed on fungus-pervaded rotten wood. However, an affiliation to Macrotermitinae is not clearly recognizable. More putative dietary clusters can be found in the wood-feeding and the grass-feeding higher termites (Fig. 3). They form separate but tight clusters to the wood- or grass-feeding lower termites. The main reason for the separation from the lower termites is the loss of the cellulolytic gut flagellates in the higher termites leading to another microbiota compensating for cellulose digestion. Most noteworthy is the soil-feeder cluster. Even the larva of a far-distantly related beetle (*Pachnoda* sp.) groups loosely to the soil-feeding higher termites, indicating diet to be a strong discriminator for the bacterial gut microbiota besides evolutionary aspects. Furthermore, only very specific bacterial groups seem to be able to help the insect host to thrive on a recalcitrant diet like soil or humus. ADONIS and MRPP analyses both support the dietary patterns with highly significantly p-values (<0.001). However, the Gryllidae outgroup argues against a food pattern. These are also omnivorous insects but they do not cluster as close to the cockroaches as the fungus-cultivating termites. On the other hand, Gryllidae species do not harbor some of the bacterial lineages that are "specific" in the *Dictyoptera* like representatives of the Elusimicrobia phylum and many others (Supplementary Table 4).

Our results show that the gut microbiota of dictyopteran species is not only shaped by insect host evolution but also by the respective diet. This can happen quite immediately; the termite gut microbiota of *Nasutitermes takasagoensis* is fast and drastically responds to different artificial diets (Miyata *et al.*, 2007).

Characteristics of the microbiota in cockroaches and termites

Cockroaches and termites differ not only phylogenetically or based on their great diet variety, but also on their social lifestyle. The latter led to a different digestive mutualism evolving with different stages of coprophagy in omnivorous cockroaches up to highly eusocial proctodeal trophallaxis in termites (Nalepa *et al.*, 2001). These established prerequisites for coevolution of host-specific gut symbionts like flagellates or flagellate-associated symbionts (see above). Therefore, we find bacterial lineages, e.g., Endomicrobia or *Desulfovibrio* 1, in all the *Dictyoptera* with hotspots only in particular host species. Hence, the cockroaches could have served as a bacterial reservoir for the phylogenetically related termites. The observation that some bacterial lineages seem to be absent in cockroaches or particular termites, e.g., *Candidatus* Tammella, could indicate a remaining problem with the detection limit—meaning these lineages are simply not uncovered even by pyrotag sequencing.

The coverage of the samples in this study ranged from 64% to 90% with slightly higher values in cockroaches than in termites. Also the bacterial groups showed a lower variation and were more evenly distributed (0.72 and 0.62, respectively). But the average diversity of cockroaches is still as high, even slightly higher, than in termites (4.1 and 3.6, respectively). This is a strong hint that cockroaches do not harbor a defined, specialized microbiota like termites but rather a wide-ranging microbial community in their guts. Hence, everything is equally distributed. Another indicator is the core microbiota: roaches have more taxa in common than the more specialized termites. The *Drosophila* gut flora shows only a less-diverse microbiota with Shannon indices of 0.7–1.5 (Wong *et al.*, 2011). It is assumed that the fruitfly gut environment is confronted permanent disturbances during development, leading to such low-diversity communities. Higher Shannon indices and evenness values are normal for other intestinal tracts like human gut microbiomes surveyed in Turnbaugh *et al.*, 2009 (4.63 ± 0.01 and 0.84 ± 0.001) suggesting humans to be even less adapted to special diets.

***Cryptocercus* – Living on the edge**

There were long debates over decades on the taxonomic and phylogenetic position of *C. punctulatus* to cockroaches and termites (reviewed in Lo and Eggleton, 2011). Molecular studies have included a number of host genes and dictyopteran taxa and have consistently recovered a termite-*Cryptocercus* clade (Lo *et al.*, 2000; Inward *et al.*, 2007; Legendre *et al.*, 2008). From the microbiological point of view many findings accumulate suggesting the genus *Cryptocercus* more to be a termite rather than a cockroach. With the exception of the higher termites, representatives of all other termite families and *Cryptocercus* harbor unique genera of parabasalid and oxymonad flagellates, exclusively linked to these hosts only (Cleveland *et al.*, 1934; Inoue *et al.*, 2000; Ohkuma *et al.*, 2009). Additionally, phylogenetic analyses of bacterial endosymbionts from *Mastotermes darwiniensis* and *Cryptocercus* reinforce the hypothesis that termites evolved from wood-feeding cockroaches (Lo *et al.*, 2003).

Cryptocercus shares many taxa of the core microbiota with cockroaches and lower termites (Table 3). However, one taxon each of cockroaches and lower termites are not found in *Cryptocercus*, pointing out the special in-between-position of this insect. Sometimes the *Cryptocercus* sample shows patterns of bacterial lineages resembling the cockroaches but at the same time also patterns that are found in the termites (Fig. 2). NMDS plotting of Bray-Curtis dissimilarity of the hindgut microbiota revealed again the position in between the termites and cockroaches but a closer relationship to lower and higher fungus-cultivating termites (Fig. 3). Therefore, our data adds to the hypothesis that *Cryptocercus* is rather a termite than a cockroach.

454 pyrotag sequencing – Sinner or saint

Despite the high abundance of Planctomycetes found in the P3 compartment of higher soil-feeding termites (Köhler *et al.*, 2008) and the fact that the termite hindgut microbiota is dominated by the P3 compartment (Chapter 2), Planctomycetes are missing. A thorough analysis of the obtained sequence data revealed a problem with a specific subgroup of the planctomycetes (Termite planctomycetes cluster; Köhler *et al.*, 2008) showing two mismatches of the reverse primer; a weak mismatch on the 5' end (-C**C**C vs. -C**U**C) and a second inside the primer (-G**G**A- vs. -G**A**A-). However, basal sequences of this planctomycetes group are still partially detected by this primer set but only to a minor percentage in relative abundance. For a further analysis of Planctomycetes, a modified primer set has to be used.

The deep sampling approach of pyrotag sequencing enables researchers to detect even very low-abundant, so-far undetected groups. Regarding the intracellular *Blattabacterium* symbionts, it was long believed that all but the most primitive termites have lost this symbiont residing in the fat body and considered responsible for remobilizing uric acid during times of high nitrogen demand (Sabree *et al.*, 2009). However, our results falsify that long-accepted dogma and provide room for new hypotheses. Peculiarly, in this study members of the genus *Blattabacterium* could be detected in most of the termite samples but not in *Mastotermes darwiniensis*. This could be due to several reasons. Comparing the presence and absence of rare bacterial taxa, i.e., 0.01-0.8% in termites, should be handled with care in pyrotag sequencing studies as well as in clone library studies since a lower detection limit of the method can be reached. Not only biological errors (very less fat body residues were in the hindgut homogenate) but also systematical errors like the noise at the lower end of detection should be considered.

This study elucidates the patterns of microbial evolution in the hindguts of a wide range of cockroaches and termites and provides many newly detected bacterial taxa in the *Dictyoptera*. It provides room for testing old and setting up new hypotheses: Food for thoughts.

References

Brune, A. (2006) Symbiotic associations between termites and prokaryotes. In: The Prokaryotes, 3rd ed., Volume 1: Symbiotic associations, Biotechnology, Applied Microbiology, Vol. 1 (Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, K-H., Stackebrandt, E. (eds.), Eds.), pp. 439-474. Springer, New York.

Chao, A. Nonparametric estimation of the number of classes in a population. (1984) Scan. J. Stat. 11, 265-270.

Chao, A., Shen, T.-J. (2003) Nonparametric estimation of Shannon's index of diversity when there are unseen species in sample. Environ. Ecolog. Stat. 10, 429-443.

Cleveland, L.R., Hall, S.R., Sanders, E.P., Collier, J. (1934) The wood-feeding roach Cryptocercus, its protozoa and the symbiosis between protozoa and roach. Mem. Am. Acad. Arts Sci. 17, 185-342.

Desai, M. S., Strassert, J. F. H., Meuser, K., Hertel, H., Ikeda-Ohtsubo, W., Radek, R., Brune, A. (2010) Strict cospeciation of devescovinid flagellates and Bacteroidales ectosymbionts in the gut of dry-wood termites (Kalotermitidae). Environ. Microbiol. 12, 2120-2132.

Henckel, T., Friedrich, M., Conrad, R. (1999) Molecular analyses of the methane-oxidizing microbial community in rice field soil by targeting the genes of the 16S rRNA, particulate methane monooxygenase, and methanol dehydrogenase. Appl. Environ. Microbiol. 65, 1980-1990.

Hongoh, Y., Deevong, P., Inoue, T., Moriya, S., Trakulnaleamsai, S., Ohkuma, M., Vongkaluang, C., Noparatnaraporn, N., Kudo, T. (2005) Intra- and interspecific comparisons of bacterial diversity and community structure support coevolution of gut microbiota and termite host. Appl. Environ. Microbiol. 71, 6590-6599.

Hongoh, Y., Ohkuma, M., Kudo, T. (2003) Molecular analysis of bacterial microbiota in the gut of the termite Reticulitermes speratus (Isoptera; Rhinotermitidae). FEMS Microbiol. Ecol. 44, 231-242.

Hyodo, F., Takematsu, Y., Matsumoto, T., Inui, Y., Itioka, T. (2011) Feeding habits of Hymenoptera and Isoptera in a tropical rain forest as revealed by nitrogen and carbon isotope ratios. Insect. Soc. 58, 417-426.

Ikeda-Ohtsubo, W., Brune, A. (2009) Cospeciation of termite gut flagellates and their bacterial endosymbionts: Trichonympha species and 'Candidatus Endomicrobium trichonymphae'. Mol. Ecol. 18, 332-342.

Inoue, T., Kitade, O., Yoshimura, T., Yamaoka, I. (2000) Symbiotic associations with protists. In: Termites: Evolution, Sociality, Symbiosis, Ecology, Vol. (Abe, T., Bignell, D.E., Higashi, M., Eds.), pp. 275-288. Kluwer Academic Publishers, Dordrecht.

Inward, D., Beccaloni, G., Eggleton, P. (2007) Death of an order: a comprehensive molecular phylogenetic study confirms that termites are eusocial cockroaches. Biol. Lett. 3, 331-335.

Keeling, P.J., Poulsen, N., McFadden, G.I. (1998) Phylogenetic diversity of parabasalian symbionts from termites, including the phylogenetic position of Pseudotrypanosoma and Trichonympha. J. Euk. Microbiol. 45, 643-650.

Köhler, T., Stingl, U., Meuser, K., Brune, A. (2008) Novel lineages of Planctomycetes densely colonize the alkaline gut of soil-feeding termites (*Cubitermes* spp.). Environ. Microbiol. 10, 1260-1270.

Legendre F, Whiting MF; Bordereau C; Cancello EM; Evans TA; Grandcolas P (2008) The phylogeny of termites (Dictyoptera: Isoptera) based on mitochondrial and nuclear markers: implications for the evolution of the worker and pseudergate castes, and foraging behaviors. Mol. Phylogenet. Evol. 48, 615-627.

Legendre, P., Legendre, L. (1998) Developments in Environmental Modelling. , Montreal (Quebec).

Lo N; Bandi C; Watanabe H; Nalepa C; Beninati T (2003) Evidence for co-cladogenesis between diverse dictyopteran lineages and their intracellular endosymbionts. Mol. Biol. Evol. 20, 907-913.

Lo, N., Eggleton, P. Termite phylogenetics and co-cladogenesis with symbionts. (2011) In: Biology of Termites: A Modern Synthesis, Vol. (Bignell, D.E., Roisin, Y., Lo, N., Eds.), pp. 27-50. Springer, Dordrecht.

Lo, N., Tokuda, G., Watanabe, H., Rose, H., Slaytor, M., Maekawa, K., Bandi, C., Noda, H. (2000) Evidence from multiple gene sequences indicates that termites evolved from wood-feeding cockroaches. Curr. Biol. 10, 801-804.

Miyata R, Noda N, Tamaki H, Kinjyo K; Aoyagi H; Uchiyama H; Tanaka H (2007) Influence of feed components on symbiotic bacterial community structure in the gut of the wood-feeding higher termite Nasutitermes takasagoensis. Biosci. Biotechnol. Biochem. 71, 1244-1251.

Nalepa, C.A., Bignell, D.E., Bandi, C. (2001) Detritivory, coprophagy, and the evolution of digestive mutualisms in Dictyoptera. Insect. Soc. 48, 194-201.

Noda, S., Hongoh, Y., Sato, T., Ohkuma, M. (2009) Complex coevolutionary history of symbiotic Bacteroidales bacteria of various protists in the gut of termites. BMC Evol. Biol. 9, 158.

Noda, S., Kitade, O., Inoue, T., Kawai, M., Kanuka, M., Hiroshima, K., Hongoh, Y., Constantino, R., Uys, V., Zhong, J., Kudo, T., Ohkuma, M. (2007) Cospeciation in the triplex symbiosis of termite gut protists (Pseudotrichonympha spp.), their hosts, and their bacterial endosymbionts. Mol. Ecol. 16, 1257-1266.

Ohkuma M; Noda S; Hongoh Y; Nalepa CA; Inoue T (2009) Inheritance and diversification of symbiotic trichonymphid flagellates from a common ancestor of termites and the cockroach Cryptocercus. Proc. R. Soc. B 276, 239-245.

Oksanen, J., Blanchet, F.G., Kindt, R., Legendre, P., O'Hara, R.B., Simpson, G.L., Solymos, P., Stevens, M.H.H., Wagner, H. (2010) vegan: Community Ecology Package. R package version 1.17-4. http://CRAN.R-project.org/package=vegan.

Pester, M., Brune, A. Expression profiles of fhs (FTHFS) genes support the hypothesis that spirochaetes dominate reductive acetogenesis in the hindgut of lower termites. (2006) Environ. Microbiol. 8, 1261-1270.

Pruesse, E., Quast, C., Knittel, K., Fuchs, B., Ludwig, W., Peplies, J., Glöckner, F.O. (2007) SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucleic Acids Res. 35, 7188-7196.

R Development Core Team (2009) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Sabree ZL; Kambhampati S; Moran NA (2009) Nitrogen recycling and nutritional provisioning by Blattabacterium, the cockroach endosymbiont. Proc. Natl. Acad. Sci. USA 106, 19521-19526.

Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., *et al.*, Van Horn, D.J., Weber, C.F. (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities.. Appl. Environ. Microbiol. 75, 7537-7541.

Schmitt-Wagner, D., Friedrich, M.W., Wagner, B., Brune, A. (2003) Phylogenetic diversity, abundance, and axial distribution of bacteria in the intestinal tract of two soil-feeding termites (Cubitermes spp.). Appl. Environ. Microbiol. 69, 6007-6017.

Shinzato, N; Muramatsu, M; Matsui, T; Watanabe, Y (2007) Phylogenetic analysis of the gut bacterial microflora of the fungus-growing termite Odontotermes formosanus. Biosci. Biotechnol. Biochem. 71, 906.

Turnbaugh, P.J., Hamady, M., Yatsunenko, T., Cantarel, B.L., Duncan, A., Ley, R.E., Sogin, M.L., Jones, W.J., Roe, B.A., Affourtit, J.P., Egholm, M., Henrissat, B., Heath, A.C., Knight, R., Gordon, J.I. (2009) A core gut microbiome in obese and lean twins. Nature 457, 480-484.

Wong, C.N., Ng, P., Douglas, A.E. (2011) Low-diversity bacterial community in the gut of the fruitfly Drosophila melanogaster. Environ. Microbiol. 13, 1889-1900.

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4 Persistence and development of bacterial lineages in the Dictyoptera – a matter of niches and feeding

Tim Köhler, Aram Mikaelyan, Katja Meuser, and Andreas Brune

Summary

Termites feed on diets consisting of lignocellulosic or humic substrates. They are divided into two groups – the more primitive "lower" termites, which possess cellulolytic gut flagellates, and the evolutionarily advanced "higher" termites, which lack such flagellates and have developed novel strategies to digest their respective diets. While the lower termites feed almost exclusively on wood, higher termites (family Termitidae), which make up about 80% of all termite species, comprise several feeding guilds of fungus-cultivating, soil-feeding, and secondarily wood-feeding forms. We conducted a comprehensive comparative analysis of the bacterial gut microbiota in representatives of all subfamilies and feeding guilds including cockroaches, combining 454 pyrotag sequencing. We revised the phylogeny of termite spirochetes and updated the information about the existing Fibrobacteres / TG3 sequences to enable a more precise assignment of the pyrotag sequences. Clear differences in community structure between the bacterial gut microbiota of dictyopteran species reflect the importance of the fiber-digesting flagellates as a bacterial habitat (e.g., the loss of the abundant endosymbiotic *Desulfovibrio* 1). The strong increase of potentially cellulolytic Fibrobacteres in wood-feeding higher termites and the decrease of Spirochaetes in soil-feeding termites correlate with the nutritional specialization of their termite host. Our results document the evolution of specific gut microbial communities in each lineage of termites and cockroaches and will help to better understand the function of the gut microbiota in the digestive process.

Introduction

The termites (Isoptera) are a group of hemimetabolous insects that belong to the superorder *Dictyoptera*, including also the cockroaches (Blattaria). Termites can be roughly divided into two groups: the primitive, flagellate-harboring lower (six families) and the more derived, flagellate-free higher termites (one family; Termitidae) (Engel and Krishna, 2004). These two groups vary significantly in the social organization, diversity of feeding guilds (Donovan *et al.*, 2001; Inward *et al.*, 2007) and gut structure (Noirot, 1995; Noirot, 2001). Cockroaches consist of six families and 29 subfamilies.

While the lower termites are restricted to a diet of wood, many lineages within the higher termites show specializations to a wide array of diets that can include soil (*Cubitermes* spp.), grass (*Trinervitermes* spp.), and fungus (*Macrotermes* spp.) in addition to wood (Donovan *et al.*, 2001). During the evolution of the termites, such dietary constrains have allowed specific modifications of the gut structure like a strong compartmentation (Noirot, 2001) that would aid in efficient utilization of complex plant-derived aromatic compounds (Watanabe and Tokuda, 2010), and a concomitant evolution of specific symbioses with numerous prokaryotic and eukaryotic groups (reviewed in Ohkuma and Brune, 2011). The diet of cockroaches differs significantly from that of termites since many cockroaches exhibit an omnivorous lifestyle and thrive on a wide variety of substances. One exception are wood-feeding cockroaches of the genus *Cryptocercus* and genera in the Blaberidae that developed the ability to digest cellulose independently (Klass *et al.*, 2008). Digestive mutualism in the *Dictyoptera* evolved with different stages of coprophagy in omnivorous cockroaches up to highly eusocial proctodeal trophallaxis in termites (Nalepa *et al.*, 2001).

The termite hindgut is physiologically and spatially heterogeneous and has numerous microhabitats that house well-adapted and niche-specialized symbionts. In the lower termites, one encounters different levels of obligate symbioses which involve mutualistic interactions between host, symbiotic protists, and their endosymbionts (Brune and Ohkuma, 2011 and references therein). These symbiotic protists have been shown to be play a crucial role in the nutrition of the host and are essential contributors to the depolymerization of their lignocellulosic diet. The higher termites, however, have lost these symbiotic flagellates during the course of evolution. This generated other niches in the hindgut. A metagenomic study suggests the possibility of bacterial symbionts having taken over the role of cellulolysis in higher termites in order to compensate for the loss of cellulolytic protists (Warnecke *et al.*, 2007).

To understand if the development of some of the microbial gut communities have been influenced not only by factors such host phylogeny, but also ecological properties of particular niches in the dictyopteran gut (e.g., microhabitat or diet-related factors) , we undertook an in-depth survey of the hindgut flora using pyrotag sequencing of the bacterial 16S rRNA genes.

Materials and Methods

Data Mining

This study bases on data collected in the scope of another survey (Digesting the diversity – Evolutionary patterns in the gut microbiota of termites and cockroaches, Chapter 3).

Phylogenetic analyses

Our curated reference database contains publicly available high-quality full-length 16S rRNA gene sequences that have been aligned according to the SILVA seed alignment (www.arb-silva.de; Pruesse *et al.*, 2007). This core of aligned sequences along with the node information from the guide tree in the SILVA database was used for the hierarchical classification of the pyrosequences obtained from the termites. Because of the bad phylogenetic resolution of Fibrobacteres and *Treponema* in the existing guide tree, and the high abundances of these groups in termite gut systems, we constructed new phylogenetic trees for these two groups using the *ARB* environment (Ludwig *et al.*, 2004). The phyML algorithm (with the HKY substitution model) with 100 bootstrap replicates was used for the calculation of the core tree for the *Treponema* sequences obtained from termite guts. The calculation used 1286 columns with 120 sequences after manual optimization of the alignment. The core tree for Fibrobacteres and TG3 based on 1194 columns and 65 sequences and was obtained using the same algorithm. Other sequences in the database belonging to the groups were added to their respective core trees by the quick add marked species feature in *ARB*. The node information was made available to the classifier for deeper and more accurate taxonomic assignment of the pyrotag sequences. The classified sequences were imported into *ARB* and using the quick add marked function to confirm the taxonomic position assigned by the classifier.

Results and Discussion

The pyrotag sequencing analysis of bacterial 16S rRNA genes in a wide variety of dictyopteran species revealed phylogenetic and dietary patterns (see Chapter 3). Here we focus on particular bacterial lineages possibly forming the basis of the clustering patterns and try to find answers for the arrangement in their respective insect host guts.

Fibrobacteres as putative cellulose degraders

Phylogenetic trees were constructed using different algorithms (neighbor-joining, parsimony, maximum-likelihood) to verify the branching patterns. The maximum-likelihood tree based on the bacterial 16S rRNA gene for the Fibrobacteres / TG3 group (Fig. 1) reveals clusters previously discussed in literature. The nomenclature of the lineages within this group follows that described by (Hongoh *et al.*, 2006b). While subphylum 1 from Fibrobacteres contains clones from the mammalian gut and a subcluster of sequences from a landfill site (McDonald *et al.*, 2008), subphylum 2 contains sequences exclusively from the termite guts.

The pyrotag survey of the gut microbiota of a wide variety of dictyopteran species could add to the knowledge about the distribution of Fibrobacteres /TG3 (Fig. 2). Fibrobacteres are very less abundant (<0.1% relative abundance) in only some cockroaches and lower termites with a small increase in abundance of subphylum 2 in the drywood termite Neotermes jouteli (0.3%). The latter termite showed also for all TG3 lineages a shift to slightly higher abundances. TG3 lineages are furthermore even less detected in the other lower termites and cockroaches. A completely different pattern is reflected in the higher termites. The subphylum 2 of Fibrobacteres is sharply increasing (up to 8% in N. corniger) in all higher termites feeding on a cellulose diet but is completely absent in the soil-feeding species. A similar motif is obtained from the TG3 lineages, with the exception of subphylum 1 Termite Cluster II that is found additionally in the two soil-feeding species investigated but not in the N. corniger and Trinervitermes species. The fungus feeders show a different scenario. While Macrotermes bellicosus enriches only Fibrobacteres subphylum 1 in its gut, Microtermes sp. harbors all other Fibrobacteres and TG3 lineages in a higher abundance. Odontotermes sp. only harbors Fibrobacteres, albeit in low number (<0.04% relative abundance).

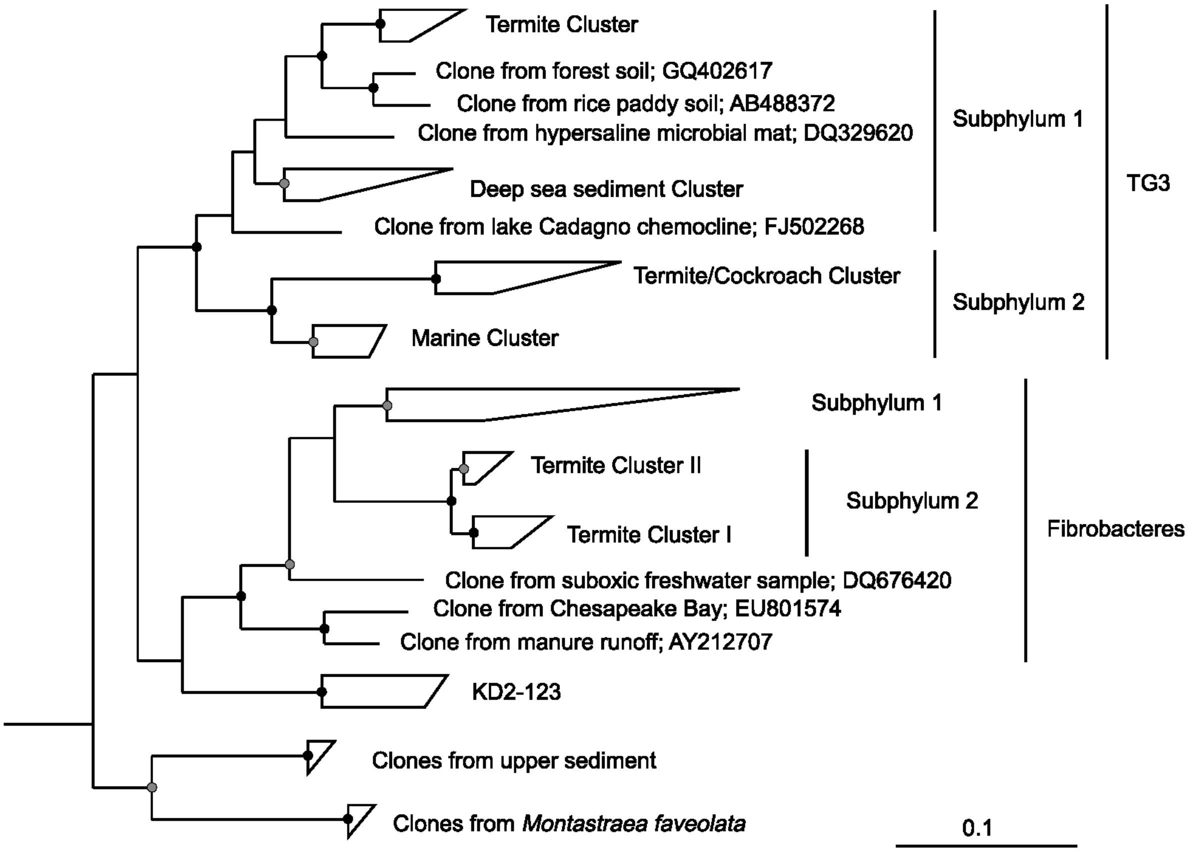


Figure 1: Maximum-likelihood core tree of the Fibrobacteres phylum. Bootstrap values are marked with gray (70–89% confidence) and black circles (90–100% confidence).

The enrichment of most of the Fibrobacteres and TG3 lineages in wood- and grass-feeding higher termites strongly suggests a function of cellulose decomposition of these bacteria since the flagellates helping lower termites to degrade cellulose are missing in the higher termites (Brune and Stingl, 2005). A metagenomic analysis of the luminal contents of the P3 compartment of a *Nasutitermes* sp. revealed the presence of numerous glycosyl hydrolases putatively involved in the degradation of (hemi-)celluloses, which were tentatively assigned to members of Fibrobacteres (Warnecke *et al.*, 2007). Our reanalysis of the clones obtained in that study revealed most of the clones actually belonging to TG3 subphylum 1 Termite Cluster1. This cluster also harbored most of the sequences obtained from our pyrotag sequencing survey. The differences in the presence of Fibrobacteres or TG3 in the fungus-cultivating termites further can be explained by their dietary preferences. Carbon isotope studies revealed that *Macrotermes* sp. rather feed on the fungus itself whereas other fungus-cultivators feed more on the degraded cellulose provided from the fungi (Hyodo *et al.*, 2011).

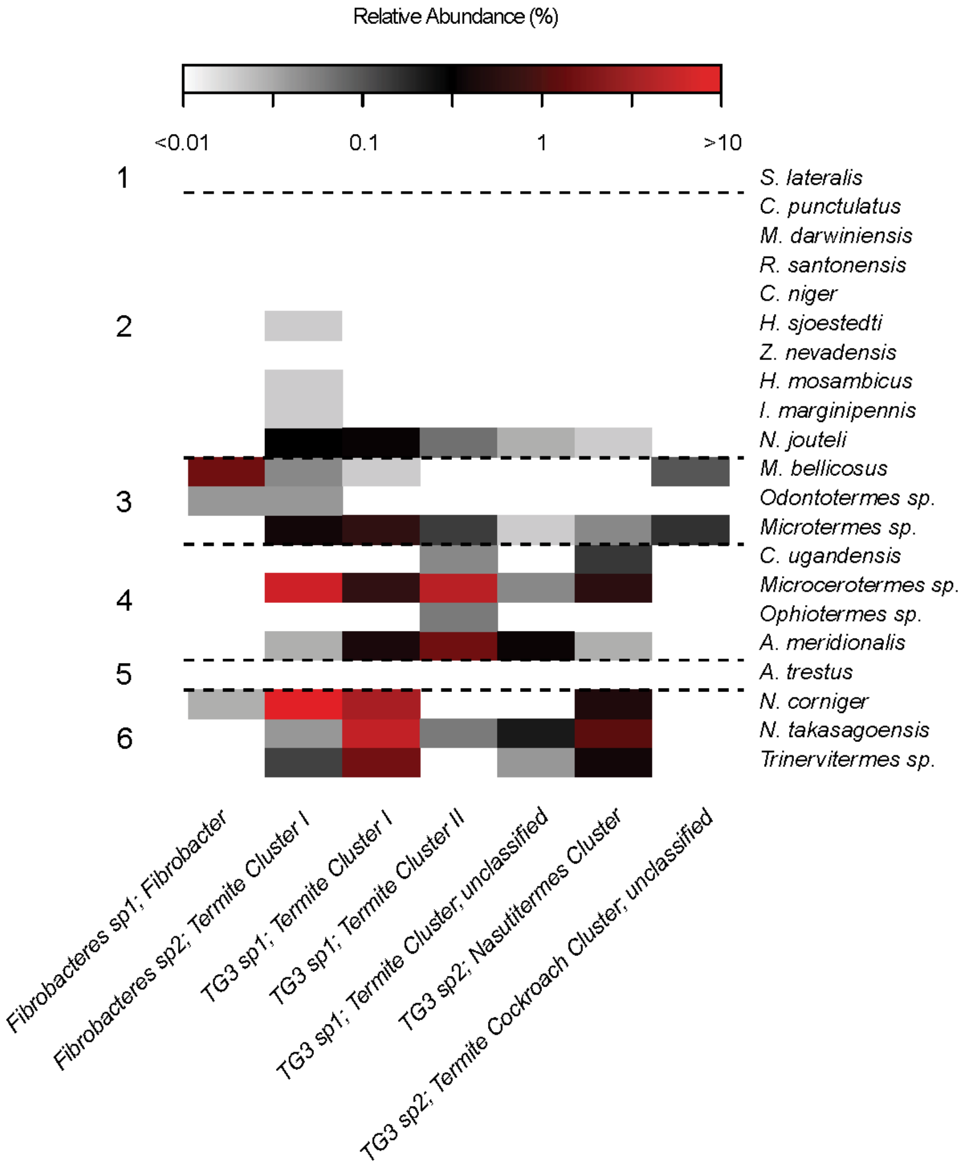


Figure 2: Frequency of the subgroups of Fibrobacteres phylum.

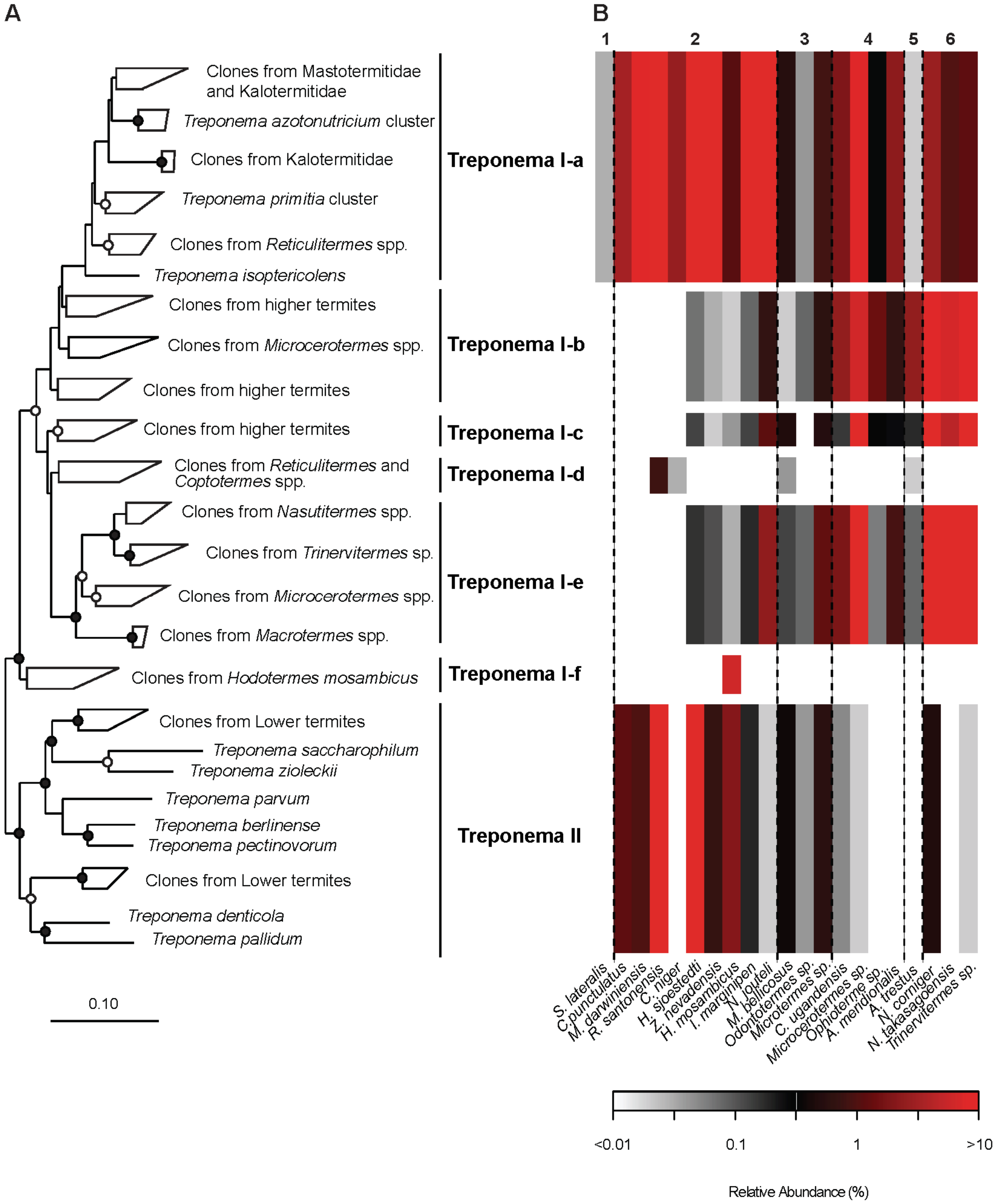
The dotted lines divide major phylogenetic groups among the dictyopteran hosts: 1…cockroach; 2…lower termites; 3…Macrotermitinae; 4…Termitinae; 5…Apicotermitinae; 6…Nasutitermitinae.

Spirochetes as niche colonizers and putative cellulose degraders

Phylogenetic trees were constructed using different algorithms (neighbor-joining, parsimony, maximum-likelihood) to verify the branching patterns. The maximum-likelihood tree based on the bacterial 16S rRNA gene revealed two separate *Treponema* groups, *Treponema* I exclusively consisting of sequences and isolates obtained termite guts and *Treponema* II harboring treponemes from different habitats (Fig. 3). The *Treponema* I group revealed many subclusters (a through f). *Treponema* I-a contained sequences sampled exclusively from lower termites. This cluster also harbored distinct lineages bearing cultured representatives of Spirochaetes from termite guts (Graber *et al.*, 2004; Dröge *et al.*, 2008). We named these distinct lineages after the respective isolates therein. Other *Treponema* I subclusters consisted only of uncultured representatives from the termite guts such as I-b and I-c (from higher termites), and I-d (from lower termites). The I-e subcluster formed a distinct lineage containing clones mostly from higher termites that are known to feed on a diet composed of lignocellulose, but also contains a smaller number of sequences from other higher termites. Treponema I-f cluster is basal to the other lineages discussed above, and exclusively contains clones from *Hodotermes mossambicus*.

Pyrotag sequencing broadened the information about spirochetes in cockroaches and termites. The *Treponema* I-a group, comprised so-far solely of sequences of the guts of lower termites, was now also detected in higher termites (up to 8% relative abundance in the wood-feeding *Microcerotermes* sp.). The same scenario occurred for so-far higher termite clusters (Treponema I-b, c, and e), where pyrosequencing also revealed sequences from the guts of lower termites, albeit in much lower numbers. The *Treponema* I-f is absolutely distinct and pyrotag sequences were exclusively found in *Hodotermes mossambicus*. All the treponemal groups were also detected in cockroaches but in very low numbers leading to apparent absence in some cockroaches (see Supplementary Table 4 in Chapter 3).

Spirochetes do not reflect the termite phylogeny, since Treponema I-f, constituted of clones obtained from *Hodotermes mossambicus*, is very basal in the tree but then higher and lower termite clusters alternate. Members of the Treponema I-c and I-e could serve as cellulose degrader. Glycosyl hydrolases were tentatively assigned to members of the Spirochaetes in *Nasutitermes* sp. (Warnecke *et al.*, 2007). Representatives of the *Treponema* I-a are further known to attach to protist cells (Noda *et al.*, 2003; Wenzel *et al.*, 2003; Yang *et al.*, 2005). Additionally, in the group *Treponema* II we also detected sequences from ectosymbiotic spirochetes attached to oxymonad protists (Iida *et al.*, 2000). All these spirochete groups should have colonized other niches in higher termites due to the lack of flagellates. Another possible niche for spirochetes could be the colonization of the gut wall. There is already information in the literature accumulating (Bignell *et al.*, 1980; Czolij *et al.*, 1985). The differences between lower and higher termites like the evident loss of flagellates in the higher termites suggest that the termites favored particular spirochetes due to niche selection.



← **Figure 3:** Phylogenetic analysis of the *Treponema*.

A. Maximum-likelihood core tree. Bootstrap values are marked with open (70–89% confidence) and closed circles (90–100% confidence). B. Frequency of the subgroups of *Treponema*. The dotted lines divide major phylogenetic groups among the dictyopteran hosts: 1…cockroach; 2…lower termites; 3…Macrotermitinae; 4…Termitinae; 5…Apicotermitinae; 6…Nasutitermitinae.

Other putatively attached microbial lineages

Bacteroidetes Cluster V

Representatives of the Bacteroidetes Cluster V (Hongoh *et al.*, 2005; Noda *et al.*, 2006) were present in all *Dictyoptera* hosts sampled (<3% relative abundance, Fig. 4) . A dramatic increase to nearly 60% was encountered in *Coptotermes niger*. Modestly elevated abundances (4–7%) were detected in the two higher termite species *Macrotermes bellicosus* and *Alyscotermes trestus* both feeding on a cellulose-rich diet, the wood-feeding cockroaches *Salganea esakii* and *Panesthia angustipennis*, and two other cockroaches.

The Bacteroidetes Cluster V harbors many sequences obtained mostly from both flagellate-associated—hence restricted to lower termites—ectosymbionts like *Candidatus* Armantifilum devescovinae (named in Desai *et al.*, 2010 and also found in Noda *et al.*, 2006) and *Candidatus* Symbiothrix dinenymphae (Hongoh *et al.*, 2007b). An exception is *Candidatus* Azobacteroides pseudotrichonymphae (Hongoh *et al.*, 2008) which is an endosymbiont of the protist *Pseudotrichonympha grassii* making up the bulk of the protist microbiota in the subterranean termite *Coptotermes formosanus* (Yoshimura, 1995). In *Coptotermes formosanus* Bacteroidetes Cluster V bacteria account for 70–80% of the bacterial cells in the total gut (Noda *et al.*, 2005). Our data from a related termite species of the genus *Coptotermes* nicely fit this known relative abundance and suggest a flagellate-association in *C. niger*, too. Furthermore, representatives of Bacteroidetes Cluster V found in the gut walls of many lower termites (Nakajima *et al.*, 2005; Nakajima *et al.*, 2006) suggest a general attachment feature of these bacteria. Other studies encountered relatives of Bacteroidetes Cluster V also in gut homogenates of a higher termites (Schmitt-Wagner *et al.*, 2003; Deevong *et al.*, 2006; Hongoh *et al.*, 2006b) It is possible that these bacteria are reliant on attachment sites for not getting lost through the gut passage

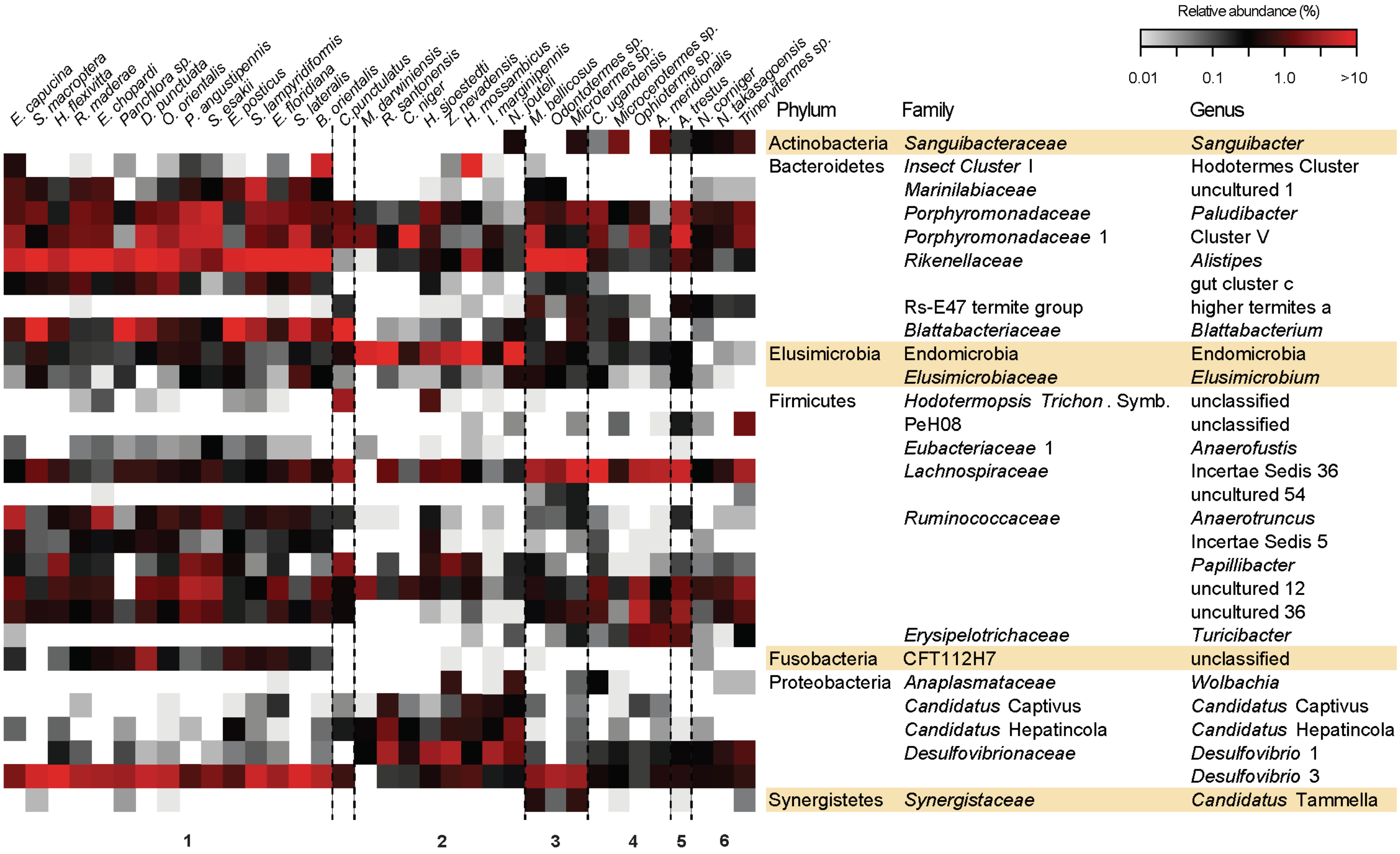


Figure 4: Frequency of selected bacterial lineages in the *Dictyoptera*.

The dotted lines divide major phylogenetic groups among the dictyopteran hosts: 1…cockroaches; 2…lower termites; 3…Macrotermitinae; 4…Termitinae; 5…Apicotermitinae; 6…Nasutitermitinae. Data is log10-transformed and zero values (white) are considered as NA.

Candidatus Tammella

The *Candidatus* Tammella was reported as motility ectosymbionts of a flagellate found in the drywood termite *Cryptotermes cavifrons* (Hongoh *et al.*, 2007c). We encountered related sequences in very low abundance (< 0.05%, Fig. 4) and close to the noise range of pyrosequencing (see Chapter 2) in some guts of different cockroach families, only one lower drywood termite (*Neotermes jouteli*), and some higher termite species belonging to different subfamilies and all feeding on a cellulose-based diet (*Microcerotermes* sp., *Apicotermes* sp., and *Trinervitermes* sp.). However, there was an increase in most of the fungus-cultivating termites.

Since cockroaches lack flagellates existing in termites (Brune and Stingl, 2005) the localization of *Candidatus* Tammella is unknown. In drywood termites these bacteria seem not to be restricted to flagellate-attachments; they were also recorded from the gut wall of *Neotermes koshunensis* (Nakajima *et al.*, 2006). This suggests an apparent attached lifestyle in drywood termites. However, the ancestor of the flagellate-associated bacteria is suggested to be a free-living gut bacterium (Hongoh *et al.*, 2007c). There is also a bulk of information about *Candidatus* Tammella relatives obtained from gut homogenates of the higher termites *Microcerotermes* spp. (Hongoh *et al.*, 2005; Deevong *et al.*, 2006), *Termes comis* (Thongaram *et al.*, 2005), and the fungus-cultivating termite *Macrotermes gilvus* homogenate (Hongoh *et al.*, 2006). However, the sampling of the guts in the mentioned studies does not allow for a localization in higher termites but the increase in relative abundance within the fungus-cultivating termites strongly suggests an important function of these bacteria, providing opportunities for further investigation. Interestingly, *Candidatus* Tammella relatives were obtained in clone libraries from two different *Reticulitermes* spp. (*R. flavipes*, Fisher *et al.*, 2007 and *R. speratus,* Hongoh *et al.*, 2003). The first cited study did not mention this group in the paper and there was only one singleton from 1344 sequences found in *R. speratus*, indicating very low abundance of this group in lower termites close to the detection limit. Additionally, we found one consistent mismatch at the 5' end of the reverse primer used. That could lead to an underestimation in the pyrotag dataset. However, we still could target these sequences suggesting this mismatch is not crucial for primer binding under the relaxed PCR conditions used.

Sanguibacter spp.

The genus *Sanguibacter* (Actinobacteria) seemed to be absent (<0.01% relative abundance, Fig. 4) in nearly all the cockroaches and lower termites with the exception of one drywood termite *Neotermes jouteli* (0.4%). Most of the higher termite species harbored these bacteria, however, the overall relative abundance of these bacteria was very low (mostly <1%).

Comparing the data collected from the P3 hindgut compartment of *Nasutitermes corniger* to the purely luminal sample of the P3 gut compartment from Warnecke *et al.* (2007) allowed some careful inferences regarding the putative gut wall localization (see Chapter 2). The genus *Sanguibacter* was one of the bacteria that arose. All *Sanguibacter* isolates (Actinobacteria) known so far are aerobic or facultatively anaerobic (Kim *et al.*, 2008; Huang *et al.*, 2005; Khan *et al.*, 2009, allowing the prerequisite for possible gut wall colonizers.

Due to the overall low relative abundance of the genus *Sanguibacter* in all the sampled insect guts, a sampling bias cannot be excluded although the primer set fits exactly.

Anaerofustis spp.

Sequences belonging to the genus *Anaerofustis* could be amplified from nearly all cockroach guts. Moreover, they could be retrieved from half of the lower termites but close to the detection noise (0.01–0.03% relative abundance) and only in one higher termite *Alyscotermes trestus* (Fig. 4).

The only isolate from this bacterial group is *Anaerofustis stercorihominis* obtained from human feces (Finegold *et al.*, 2004). This group seems usually to be obtained from different mammal feces (Ley *et al.*, 2008) but was so far not established in termite gut systems. However, they are found in the gut wall fraction of the lower termite *R. speratus* (Nakajima *et al.*, 2005) and the gut homogenate of the fungus-cultivating termite *Macrotermes gilvus* (Hongoh *et al.*, 2006).

Endosymbiotic bacteria and their relatives

Representatives of *Desulfovibrio* 1

Desulfovibrio 1 relatives were present in all lower termites (Fig. 4). Despite the formation of only a minor population (<0.2% relative abundance) in some cockroaches and all higher termites—with the exception of a soil-feeding *Odontotermes* species—, they were enriched in the lower termites (up to 4%).

Within the group Desulfovibrio 1 there is *Candidatus* Desulfovibrio trichonymphae, an endosymbiont of the flagellate *Trichonympha agilis* from *Reticulitermes speratus* (Sato *et al.*, 2009). In this termite it sums up to 2% of the prokaryotic gut microbiota. We could verify this percentage with about 3% from our analysis and a different termite of the same genus. *Trichonympha* spp. flagellates occur in four different termite families (Termopsidae, Rhinotermitidae, Kalotermitidae, and Hodotermitidae) and also in the wood-feeding cockroach *Cryptocercus*. It is reasonable that *Candidatus* Desulfovibrio trichonymphae or its relatives could infest protist cells in all these termite families leading to the high relative abundances we obtained. However, the absence in *Cryptocercus punctulatus* (this study) contradicts this hypothesis. Comprehensive analyses of *Trichonympha* spp. of different termites have to be analyzed by clone libraries or FISH to answer this question.

Candidatus Hepatincola

Sequences assigned to *Candidatus* Hepatincola could be encountered in nearly all the samples used. However, this group accumulated only in all lower termites and interestingly slightly in the *Nasutitermitinae*.

Candidatus Hepatincola (Rickettsiales) was first described to colonize the endothelium of the hepatopancreas of the common woodlouse, Porcellio scaber (Wang *et al.*, 2004). This assumption is reasonable since relatives of this group colonize the hindgut wall. It cannot be excluded that members of this group have an intracellular lifestyle because Rickettsiales usually are intracellular symbionts or pathogens. The increase in abundance in the lower termites could suggest that these bacteria colonized—at least partially—protists. A good support is the study of Yang and coworkers (2005). They sampled different fractions of the gut of *Reticulitermes santonensis* and *Candidatus* Hepatincola related sequences were associated to the protozoa fraction. Additionally, colleagues of our group found related sequences from picked flagellates (*Devescovina* spp.) from different species of the drywood termite *Cryptotermes* (unpublished data). It remains open if these bacteria are endo- or ectosymbionts of such flagellates.

The gut microbiota of dampwood and drywood termites

Comparison revealed that both feeding guilds share many bacterial taxa but several lineages were abundant in drywood termites. One interesting "uncultured 11" group (*Lachnospiraceae*) showed 1.6% relative abundance in *Zootermopsis nevadensis* but was nearly absent or had <0.1% (*Trinervitermes* sp.) in all the other dictyopteran species (Table 1). The same scenario was visible with the "group aa" (Bacteroidetes) occurring highest in *Hodotermopsis sjoestedti* (~1%). The groups having a slightly higher abundance in drywood termites were also present in other termites suggesting no specific adaptation of the drywood termites. Interestingly, the M2PB4-61 termite group (*Rikenellaceae*) showed only elevated relative abundance in *Incisitermes marginipennis* (1.5%) and selected higher termites.

The M2PB4-61 termite group was so-far only found in drywood and higher termites (Hongoh *et al.*, 2005; Hongoh *et al.*, 2006; Hongoh *et al.*, 2006b; Hongoh *et al.*, 2007;

Warnecke *et al.*, 2007). No obvious pattern emerges in the results for dampwood and drywood termites. However, the dampwood and drywood dietary clusters found in the non-metric multidimensional data scaling (NMDS) are significantly different (tested by analysis of variance using distance matrices and multi response permutation procedure, see Chapter 3). Hence, not single taxa but the sum of presence-absence and relative abundance of all bacterial groups add to the clustering of these feeding guilds. With the help of statistical methods such hypotheses can be tested.

Conclusion

Many of the mentioned bacterial lineages (e.g., Fibrobacteres, *Treponema*, Bacteroidetes Cluster V) seem to be ubiquitous, albeit very rare in most of the *Dictyoptera* and exploiting specific niches only in exclusive phylogenetic or dietary groups of host guts. A reasonable example is the *Treponema* I, that developed different subclusters in lower and higher termites pointing to niches like the presence or absence of flagellate cells in the hindgut. Already Noda and colleagues (2009) stated for the Bacteroidales cluster V, that the gut could serve as a reservoir of diverse bacteria for associations with the protist cells.

Table 1: Relative abundance of selected bacterial lineages from dampwood and drywood termites (bold) and other dictyopteran hosts.

Taxon	**Relative abundance (%)**																				
	S_late	C_pur	M_dar	R_san	C_nig	**HS***	**ZN***	H_mo	**IM***	**NJ***	M_bel	Odont	Microt	C_ug	Micro	Ophiol	A_me	Apicot	N_co	N_tak	Triner
Bacteroidetes; COB P4-1 termite group; unclassified	0	0	1.12	0	0	**0**	**0.01**	0	**0.14**	**0.04**	0.02	0.04	0.04	0.1	0.08	0	0	0.49	0.54	0.43	1.07
Bacteroidetes; *Porphyromonadaceae* ; *Paludibacter*	1.38	1.25	0.16	0.08	0.15	**1.6**	**0.5**	0.35	**0.04**	**0.02**	0.99	0.76	1.75	2.1	0.31	0.64	0.03	3.16	0.73	0.63	1.56
Bacteroidetes; *Porphyromonadaceae* 1; *Dysgonomonas*	2.71	0.15	0.53	0.01	2.59	**1.04**	**0.07**	0	**0.05**	**0.03**	0.12	0.15	4.74	0	0.03	0	0.01	0.03	0.05	0.01	1.21
Bacteroidetes; *Rikenellaceae* ; M2PB4-61 termite group	0.1	0.39	0.2	0	0	**0.02**	**0.02**	0.02	**1.52**	**0.24**	0.16	0.07	0.39	1.08	0.77	0.06	0	0.17	0.4	1.02	1.73
Bacteroidetes; Rs-E47 termite group; group aa	0.02	0.04	0	0	0	**1.02**	**0.04**	0.05	**0**	**0**	0.01	0	0	0.05	0	0	0	0	0	0	0.08
Firmicutes; *Enterococcaceae* ; *Enterococcus* 2	0.03	0	0	0	0	**0.07**	**0.08**	0.38	**0.03**	**0**	0.03	0	0	0	0	0	0	0	0.05	0	0
Firmicutes; Family XIII Incertae Sedis; uncultured 6	0	0	0	0.64	0	**0.01**	**0.01**	0	**0.04**	**0.04**	0.79	0.36	0	0.1	0	0.08	0.07	0	0	0.01	0.04
Firmicutes; Lachnospiraceae; Incertae Sedis 24	1.28	0.01	0	0	0.02	**0.11**	**0.07**	0	**0.02**	**0**	0.06	0.07	0.02	0.05	0.01	0.01	0	0	0	0	0
Firmicutes; Lachnospiraceae; uncultured 11	0	0	0.03	0	0	**0.02**	**1.55**	0.05	**0.01**	**0**	0.04	0.07	0	0.05	0.03	0	0.01	0	0.03	0.07	0.13
Firmicutes; Ruminococcaceae; Incertae Sedis 4	0.88	0.83	0.05	0.04	0	**0.15**	**0.19**	0.26	**0.01**	**0.02**	0.22	0.4	0.09	0.05	0.01	0.43	0.08	0.33	0.03	0.02	0.05
Firmicutes; Ruminococcaceae; Incertae Sedis 8	0	0.15	0.14	0.39	0.02	**0.05**	**0.39**	0.02	**0.01**	**0**	0.02	0	0.27	0.49	0.13	0.93	0.99	0.97	0	0.08	0.19
Firmicutes; Ruminococcaceae; uncultured 25	0.08	1.34	0	0.04	0	**0.13**	**0.05**	0.19	**0.02**	**0**	0.4	0.11	0.05	0.15	0.02	0.06	0.1	0.14	0.08	0.04	0.09
Firmicutes; Ruminococcaceae; uncultured 30	0.06	0.64	0	0.91	0.02	**0.44**	**0.37**	0.21	**0.02**	**0.01**	0.37	0.22	0.11	3.91	0.06	1.75	0.39	2.01	0.13	0.34	0.96
Firmicutes; Ruminococcaceae; uncultured 35	0	0.61	0.05	0.16	0.1	**0.16**	**0.24**	0.18	**0.01**	**0**	0.16	0.11	0.02	0.83	0.01	1.48	0.26	1.64	0	0.15	0.35
Firmicutes; *Peptococcaceae* 2; *Dehalobacter*	0	0.15	0	0.01	0	**0.25**	**0.29**	0	**0**	**0.01**	0	0	0.02	0	0	0	0	0	0	0	0
Firmicutes; Veillonellaceae; uncultured 7	2.28	0.39	0	0	0.03	**0.33**	**0.67**	0.18	**0.03**	**0.05**	1.02	1.23	1.04	0	0.03	0.01	0	0	0.03	0	0

* HS….*Hodotermopsis sjoestedti*; ZN…*Zootermopsis nevadensis*; IM…*Incisitermes marginipennis*; NJ…*Neotermes jouteli*.

References

Amend, A.S., Seifert, K.A., Bruns, T.D. (2010) Quantifying microbial communities with 454 pyrosequencing: does read abundance count?. Mol. Ecol.

Bignell, D.E., Oskarsson, H., Anderson, J.M. (1980) Specialization of the hindgut wall for the attachment of symbiotic microorganisms in a termite *Procubitermes aburiensis*. Zoomorphology 96, 103-112.

Brune, A., Ohkuma, M. (2011) Role of the termite gut microbiota in symbiotic digestion. In: Biology of Termites: A Modern Synthesis, Vol. (D.E. Bignell, Y. Roisin, N. Lo, eds, Eds.), pp. 439-475. Springer, Dordrecht.

Brune, A., Stingl, U. (2005) Prokaryotic symbionts of termite gut flagellates: phylogenetic and metabolic implications of a tripartite symbiosis. In: Molecular Basis of Symbiosis, Vol. 41 (Overmann, J., Eds.), pp. 39-60. Springer, Berlin.

Czolij, R., Slaytor, M., O'Brien, R.W. (1985) Bacterial flora of the mixed segment and the hindgut of the higher termite *Nasutitermes exitiosus* Hill (Termitidae, Nasutitermitinae). Appl. Environ. Microbiol. 49, 1226-1236.

Deevong, P., Hongoh, Y., Inoue, T., Trakulnaleamsai, S., Kudo, T., Noparatnaraporn, N., Ohkuma, M. (2006) Effect of temporal sample preservation on the molecular study of a complex microbial community in the gut of the termite *Microcerotermes* sp.. Microbes Environ. 21, 78-85.

Desai, M. S., Strassert, J. F. H., Meuser, K., Hertel, H., Ikeda-Ohtsubo, W., Radek, R., Brune, A. (2010) Strict cospeciation of devescovinid flagellates and *Bacteroidales* ectosymbionts in the gut of dry-wood termites (*Kalotermitidae*). Environ. Microbiol. 12, 2120-2132.

Donovan, S.E; Eggleton, P., Bignell, D.E. (2001) Gut content analysis and a new feeding group classification of termites. Ecol. Entomol. 26, 356-366.

Dröge, S., Rachel, R., Radek, R., König, H. (2008) *Treponema isoptericolens* sp. nov., a novel spirochaete from the hindgut of the termite *Incisitermes tabogae*. Int. J. Syst. Evol. Microbiol. 58, 1079-1083.

Dunbar, J., Ticknor, L.O., Kuske, C.R. (2001) Phylogenetic specificity and reproducibility and new method for analysis of terminal restriction fragment profiles of 16S rRNA genes from bacterial communities. Appl. Environ. Microbiol. 67, 190-197.

Engel, S. E., Krishna, K. (2004) Family-group names for termites (Isoptera). Am. Mus. Nov. , 1-9.

Finegold, S.M., Lawson, P.A., Vaisanen, M.L., Molitoris, D.R., Song, Y., Liu, C., Collins, M.D. (2004) *Anaerofustis stercorihominis* gen. nov., sp. nov., from human feces. Anaerobe 10, 41-45.

Fisher M; Miller D; Brewster C; Husseneder C; Dickerman A (2007) Diversity of gut bacteria of *Reticulitermes flavipes* as examined by 16S rRNA gene sequencing and amplified rDNA restriction analysis. Curr. Microbiol. 55, 254-259.

Gomez-Alvarez, V., Teal, T.K., Schmidt, T.M. (2009) Systematic artifacts in metagenomes from complex microbial communities.. ISME J. 3, 1314-1317.

Graber, J.R., Leadbetter, J.R., Breznak, J.A. (2004) Description of *Treponema azotonutricium* sp. nov. and *Treponema primitia* sp. nov., the first spirochetes isolated from termite guts. Appl. Environ. Microbiol. 70, 1315-1320.

Henckel, T., Friedrich, M., Conrad, R. (1999) Molecular analyses of the methane-oxidizing microbial community in rice field soil by targeting the genes of the 16S rRNA, particulate methane monooxygenase, and methanol dehydrogenase. Appl. Environ. Microbiol. 65, 1980-1990.

Hongoh Y; Ekpornprasit L; Inoue T; Moriya S; Trakulnaleamsai S; Ohkuma M; Noparatnaraporn N; Kudo T (2006) Intracolony variation of bacterial gut microbiota among castes and ages in the fungus-growing termite *Macrotermes gilvus*. Mol. Ecol. 15, 505-516.

Hongoh, Y., Deevong, P., Hattori, S., Inoue, T., Noda, S., Noparatnaraporn, N., Kudo, T., Ohkuma, M. (2006) Phylogenetic diversity, localization and cell morphologies of the candidate phylum TG3 and a subphylum in the phylum *Fibrobacteres*, recently found bacterial groups dominant in termite guts. Appl. Environ. Microbiol. 72, 6780-6788.

Hongoh, Y., Deevong, P., Hattori, S., Inoue, T., Noda, S., Noparatnaraporn, N., Kudo, T., Ohkuma, M. (2006) Phylogenetic diversity, localization and cell morphologies of the candidate phylum TG3 and a subphylum in the phylum *Fibrobacteres*, recently found bacterial groups dominant in termite guts. Appl. Environ. Microbiol. 72, 6780-6788.

Hongoh, Y., Deevong, P., Inoue, T., Moriya, S., Trakulnaleamsai, S., Ohkuma, M., Vongkaluang, C., Noparatnaraporn, N., Kudo, T. (2005) Intra- and interspecific comparisons of bacterial diversity and community structure support coevolution of gut microbiota and termite host. Appl. Environ. Microbiol. 71, 6590-6599.

Hongoh, Y., Ohkuma, M., Kudo, T. (2003) Molecular analysis of bacterial microbiota in the gut of the termite *Reticulitermes speratus* (Isoptera; Rhinotermitidae). FEMS Microbiol. Ecol. 44, 231-242.

Hongoh, Y., Sato, T., Noda, S., Ui, S., Kudo, T., Ohkuma, M. (2007) *Candidatus* Symbiothrix dinenymphae: bristle-like *Bacteroidales* ectosymbionts of termite gut protists. Environ. Microbiol. 9, 2631-2635.

Hongoh, Y., Sharma, V.K., Prakash, T., Noda, S., Toh, H., Taylor, T.D., Kudo, T., Sakaki, Y., Toyoda, A., Hattori, M., Ohkuma, M. (2008) Genome of an endosymbiont coupling N_2 fixation to cellulolysis within protist cells in termite gut. Science 322, 1108-1109.

Hongoh, Y; Sato, T; Dolan, M; Noda, S; Ui, S; Kudo, T; Ohkuma, M; (2007) The motility symbiont of the termite gut flagellate *Caduceia versatilis* is a member of the "*Synergistes*" group. Appl. Environ. Microbiol. 73, 6270-6276.

Hongoh, Y; Sato, T; Dolan, M; Noda, S; Ui, S; Kudo, T; Ohkuma, M; (2007) The motility symbiont of the termite gut flagellate *Caduceia versatilis* is a member of the "*Synergistes*" group. Appl. Environ. Microbiol. 73, 6270-6276.

Hooper, S.D., Raes, J., Foerstner, K.U., Harrington, E.D., Dalevi, D., Bork, P. (2008) A Molecular Study of Microbe Transfer between Distant Environments.. PLoS ONE 3, e2607.

Huang, Y., Dai, X., He, L., Wang, Y.N., Wang, B.J., Liu, Z., Liu, S.J. (2005) *Sanguibacter marinus* sp. nov., isolated from coastal sediment. Int. J. Syst. Evol. Microbiol. 55, 1755-1758.

Husseneder, C., Ho, H.-Y., Blackwell, M. (2010) Comparison of the bacterial symbiont composition of the Formosan Subterranean Termite from its native and introduced range. Open Microbiol. J. 4, 53-66.

Hyodo, F., Takematsu, Y., Matsumoto, T., Inui, Y., Itioka, T. (2011) Feeding habits of Hymenoptera and Isoptera in a tropical rain forest as revealed by nitrogen and carbon isotope ratios. Insect. Soc. 58, 417-426.

Iida, T., Ohkuma, M., Ohtoko, K., Kudo, T. (2000) Symbiotic spirochetes in the termite hindgut: phylogenetic identification of ectosymbiotic spirochetes of oxymonad protists. FEMS Microbiol. Ecol. 34, 17-26.

Inward, D.J.G., Vogler, A.P., Eggleton, P. (2007) A comprehensive phylogenetic analysis of termites (Isoptera) illuminates key aspects of their evolutionary biology. Mol. Phylogenet. Evol. 44, 953-967.

Khan, S.T., Harayama, S., Tamura, T., Ando, K., Takagi, M., Kazuo, S.Y. (2009) *Paraoerskovia marina* gen. nov., sp. nov., an actinobacterium isolated from marine sediment. Int. J. Syst. Evol. Microbiol. 59, 2094-2098.

Kim, M.K., Pulla, R.K., Kim, S.Y., Yi, T.H., Soung, N.K., Yang, D.C. (2008) *Sanguibacter soli* sp. nov., isolated from soil of a ginseng field. Int. J. Syst. Evol. Microbiol. 58, 538-541.

Klass, K-D., Nalepa, C., Lo, N. (2008) Wood-feeding cockroaches as models for termite evolution (Insecta: Dictyoptera): Cryptocercus vs. Parasphaeria boleiriana. Mol. Phylogenet. Evol. 46, 809-817.

Köhler, T., Stingl, U., Meuser, K., Brune, A. (2008) Novel lineages of *Planctomycetes* densely colonize the alkaline gut of soil-feeding termites (*Cubitermes* spp.). Environ. Microbiol. 10, 1260-1270.

Kunin, V., Engelbrektson, A., Ochman, H., Hugenholtz, P. (2010) Wrinkles in the rare biosphere: pyrosequencing errors lead to artificial inflaation of diversity estimates.. Environ. Microbiol. 12, 118-123.

Kunin, V., Hugenholtz, P. (2010) PyroTagger: A fast, accurate pipeline for analysis of rRNA amplicon pyrosequence data. The Open Journal 1, 1-8.

Lane, D.J. (1991) 16S/23S rRNA sequencing. In: Nucleic acids techniques in bacterial systematics, Vol. (Stackebrandt, E., Goodfellow, M., Eds.), pp. 115-175. John Wiley & Sons, Chichester.

Lefebvre, T., E. Miambi; A. Pando; M. Diouf; C. Rouland-Lefèvre (2009) Gut-specific actinobacterial community structure and diversity associated with the wood-feeding termite species, Nasutitermes corniger (Motschulsky) described by nested PCR-DGGE analysis . Insect. Soc. 56, 269-276.

Ley, R.E., Hamady, M., Lozupone, C., Turnbaugh, P.J., Ramey, R.R., Bircher, J.S., Schlegel, M.L., Tucker, T.A., Schrenzel, M.D., Knight, R., Gordon J.I. (2008) Evolution of Mammals and Their Gut Microbes. Science 320, 1647-1651.

Lozupone, C., Hamady, M., Knight, R. (2006) UniFrac - An online tool for comparing microbial community diversity in a phylogenetic context.. BMC Bioinform. 7, .

Lozupone, C., Knight, R. (2005) UniFrac: a New Phylogenetic Method for Comparing Microbial Communities.. Appl. Environ. Microbiol. 71, 8228-8235.

Ludwig, W., Strunk, O., Westram, R., Richter, L., Meier, H. and 27 other authors (2004) ARB: a software environment for sequence data. Nucleic Acids Res. 32, 1363-1371.

Maekawa, K., Matsumoto, T., Nalepa, C.A. (2008) Social biology of the wood-feeding cockroach genus *Salganea*. Insect. Soc. , .

McDonald, J.E., Lockhart, R.J., Cox, M.J., Allison, H.E., McCarthy, A.J. (2008) Detection of novel *Fibrobacter* populations in landfill sites and determination of their relative abundance via quantitative PCR. Environ. Microbiol. 10, 1310-1319.

McKenna, P., Hoffmann, C., Minkah, N., Aye, P.P., Lackner, A., Liu, Z., Lozupone, C.A., Hamady, M., Knight, R., Bushman, F.D. (2008) The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis.. PLoS Pathog. 4, e20.

Miyata R, Noda N, Tamaki H, Kinjyo K; Aoyagi H; Uchiyama H; Tanaka H (2007) Influence of feed components on symbiotic bacterial community structure in the gut of the wood-feeding higher termite *Nasutitermes takasagoensis*. Biosci. Biotechnol. Biochem. 71, 1244-1251.

Morales, S.E., Cosart, T.F., Johnson, J.V., Holben, W.E. (2009) Extensive Phylogenetic Analysis of a Soil Bacterial Community Illustrates Extreme Taxon Evenness and the Effects of Amplicon Length, Degree of Coverage, and DNA Fractionation on Classification and Ecological Parameters.. Appl. Environ. Microbiol. 75, 668-675.

Nakajima H; Hongoh Y; Noda S; Yoshida Y; Usami R; Kudo T; Ohkuma M (2006) Phylogenetic and morphological diversity of *Bacteroidales* members associated with the gut wall of termites. Biosci. Biotechnol. Biochem. 70, 211-218.

Nakajima, H., Hongoh, Y., Usamib, R., Kudo, T., Ohkuma, M. (2005) Spatial distribution of bacterial phylotypes in the gut of the termite *Reticulitermes speratus* and the bacterial community colonizing the gut epithelium. FEMS Microbiol. Ecol. 54, 247-255.

Nalepa, C.A., Bignell, D.E., Bandi, C. (2001) Detritivory, coprophagy, and the evolution of digestive mutualisms in Dictyoptera. Insect. Soc. 48, 194-201.

Noda S; Iida T; Kitade O; Nakajima H; Kudo T; Ohkuma M (2005) Endosymbiotic *Bacteroidales* bacteria of the flagellated protist *Pseudotrichonympha grassii* in the gut of the termite *Coptotermes formosanus*. Appl. Environ. Microbiol. 71, 8811-8817.

Noda S; Inoue T; Hongoh Y; Nalepa CA; Vongkaluang C; Kudo T; Ohkuma M (2006) Identification and characterization of ectosymbionts of distinct lineages in *Bacteroidales* attached to flagellated protists in the gut of termites and a wood-feeding cockroach. Environ. Microbiol. 8, 11-20.

Noda, S., Hongoh, Y., Sato, T., Ohkuma, M. (2009) Complex coevolutionary history of symbiotic Bacteroidales bacteria of various protists in the gut of termites. BMC Evol. Biol. 9, 158.

Noda, S., Ohkuma, M., Yamada, A., Hongoh, Y., Kudo, T. (2003) Phylogenetic position and in situ identification of ectosymbiotic spirochetes on protists in the termite gut. Appl. Environ. Microbiol. 69, 625-633.

Noirot, C. (1995) The gut of termites (isoptera). Comparative anatomy, systematics, phylogeny. I. Lower termites. Ann. Soc. Entomol. Fr. (N.S.) 31, 197-226.

Noirot, C. (2001) The gut of termites (isoptera). Comparative anatomy, systematics, phylogeny. II. Higher termites (termitidae). Ann. Soc. Entomol. Fr. (N.S.) 37, 431-471.

Ohkuma, M., Brune, A. (2011) Diversity, structure, and evolution of the termite gut microbial community. In: Biology of Termites: A Modern Synthesis, Vol. (D.E. Bignell, Y. Roisin, N. Lo, eds, Eds.), pp. 413-438. Springer, Dordrecht.

Oksanen, J., Blanchet, F.G., Kindt, R., Legendre, P., O'Hara, R.B., Simpson, G.L., Solymos, P., Stevens, M.H.H., Wagner, H. (2010) vegan: Community Ecology Package. R package version 1.17-4. http://CRAN.R-project.org/package=vegan.

Pellens R., Grandcolas P., Silva-Neto I.D.D. (2002) A new and independently evolved case of xylophagy and the presence of intestinal flagellates in the cockroach Parasphaeria boleiriana (Dictyoptera, Blaberidae, Zetoborinae) from the remnants of the Brazilian Atlantic forest. Can. J. Zool. 80, 350-359.

Pester, M., Brune, A. (2006) Expression profiles of *fhs* (FTHFS) genes support the hypothesis that spirochaetes dominate reductive acetogenesis in the hindgut of lower termites. Environ. Microbiol. 8, 1261-1270.

Pruesse, E., Quast, C., Knittel, K., Fuchs, B., Ludwig, W., Peplies, J., Glöckner, F.O. (2007) SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucleic Acids Res. 35, 7188-7196.

Quince, C., Lanzén, A., Curtis, T.P., Davenport, R.J., Hall, N., Head, I.M., Read, L.F., Sloan, W.T. (2009) Accurate determination of microbial diversity from 454 pyrosequencing data.. Nat. Methods 6, 639-641.

R Development Core Team (2009) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Sato T; Hongoh Y; Noda S; Hattori S; Ui S; Ohkuma M (2009) *Candidatus* Desulfovibrio trichonymphae, a novel intracellular symbiont of the flagellate *Trichonympha agilis* in termite gut. Environ. Microbiol. 11, 1007-1015.

Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., Hartmann, M., Hollister, E.B., Lesniewski, R.A., Oakley, B.B., Parks, D.H., Robinson, C.J., Sahl, J.W., Stres, B., Thallinger, G.G., Van Horn, D.J., Weber, C.F. (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities.. Appl. Environ. Microbiol. 75, 7537-7541.

Schmitt-Wagner, D., Friedrich, M.W., Wagner, B., Brune, A. (2003) Phylogenetic diversity, abundance, and axial distribution of bacteria in the intestinal tract of two soil-feeding termites (*Cubitermes* spp.). Appl. Environ. Microbiol. 69, 6007-6017.

Sogin ML, Morrison HG, Huber JA, Welch DM, Huse SM, Neal PR, Arrieta JM, Herndl GJ. (2006) Microbial diversity in the deep sea and the underexplored "rare biosphere". Proc. Natl. Acad. Sci. USA 103, 12115-12120.

Stingl, U., Radek, R., Yang, H., Brune, A. (2005) '*Endomicrobia*': Cytoplasmic symbionts of termite gut protozoa form a separate phylum of prokaryotes. Appl. Environ. Microbiol. 71, 1473-1479.

Thongaram, T., Hongoh, Y., Kosono, S., Ohkuma, M., Trakulnaleamsai, S., Noparatnaraporn, N., Kudo, T. (2005) Comparison of bacterial communities in the alkaline gut segment among various species of higher termites. Extremophiles 9, 229-238**.**

Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R. (2007) Naive Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. Appl. Environ. Microbiol. 73, 5261-5267.

Wang, Y., Stingl, U., Anton-Erxleben, F., Zimmer, M., Brune, A. (2004) '*Candidatus* Hepatincola porcellionum' gen. nov., sp. nov., a new, stalk-forming lineage of Rickettsiales colonizing the midgut glands of a terrestrial isopod. Arch. Microbiol. 181, 299-304.

Warnecke F., Luginbühl, P., Ivanova, N., et al. Hugenholtz P; Leadbetter JR (2007) Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature 450, 560-565.

Watanabe, H., Tokuda, G. (2010) Cellulolytic systems in insects. Annu. Rev. Entomol. 55, 609-632.

Weisburg, W.G., Barns, S.M., Pelletier, D.A., Lane, D.J. (1991) 16S ribosomal DNA amplification for phylogenetic study. J. Bacteriol. 173, 697-703.

Wenzel, M., Radek, R., Brugerolle, G., König, H. (2003) Identification of the ectosymbiotic bacteria of *Mixotricha paradoxa* involved in movement symbiosis. Eur. J. Protistol. 39, 11-24.

Yang, H., Schmitt-Wagner, D., Stingl, U., Brune, A. (2005) Niche heterogeneity determines bacterial community structure in the termite gut (*Reticulitermes santonensis*). Environ. Microbiol. 7, 916-932.

Yoshimura, T. (1995) Contribution of the protozoan fauna to nutritional physiology of the lower termite, *Coptotermes formosanus* Shiraki (Isoptera: Rhinotermitidae). Wood Research 82, 68-129.

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5 General Discussion

A long-time debate about the phylogeny of cockroaches and termites could be resolved by thorough molecular analyses (Inward *et al.*, 2007; Legendre *et al.*, 2008). Additionally, more and more evidences were emerging in the literature that the gut microbiota of termites evolves with their insect or protist hosts (Ohkuma and Brune, 2011). The studies within this thesis could contribute to the knowledge that termites harbor a distinct microbiota specific even between different gut compartments in one termite host. Furthermore, the results allowed testing and positively answering the hypothesis of evolutionary and dietary patterns formed by the gut microbiota in the *Dictyoptera*.

The significance and aspects of the results reported in the individual chapters of this work were discussed already in their respective context. The following discussion directs more to general aspects about prerequisites and difficulties using pyrotag sequencing and general implications of the results obtained in this work.

Clone library data as prerequisite for next-generation sequencing surveys

An advantage of the pyrotag sequencing analysis is the fast data generation and the deep sampling size, i.e. low-abundant species can be detected (Sogin, 2006). Using the vast amount of data and analyzing it statistically helps in finding biologically relevant patterns between environments (Kuczynski *et al.*, 2010). However, a big drawback of the method can appear by analyzing the data on the taxonomic level, i.e. after classification of the reads. The *Naïve Bayesian Classifier* of the Ribosomal Database Project (RDP) online platform (Wang *et al.*, 2007) is mostly used in diversity studies (e.g., Fierer *et al.*, 2010). The classification of the pyrotag sequences down to low taxonomic levels (genus), however, strongly depends on the quality of the database the pyrotag sequences are compared to (Werner *et al.*, 2011). The keyword "quality" here includes two aspects: first the quality of the sequences (length, ambiguous bases, chimeric, well taxonomically classified) and second the availability of related sequences from the sampled environments. Shortcomings in one of these two factors lead to dissatisfying results, such as 60% unclassified sequences already on family level in arctic environments (Bowman *et al.*, 2011) simply due to the lack of related sequences in the reference database.

In case of the termites, the microbial composition of the gut microbiota has been investigated for representatives of all the major families and feeding traits (e.g., Hongoh *et al.*, 2003; Schmitt-Wagner *et al.*, 2003; Shinzato *et al.*, 2007; Warnecke *et al.*, 2007). This is a very good backbone for the pyrotag sequencing survey of this study. Furthermore, using a manually extended and refined database for classification resulted in improved genus assignments of the pyrotag sequences in this study (Chapter 2 and Chapter 3).

Precautions in pyrotag sequencing analyses

Although widely used in microbial ecology, pyrotag sequencing still has its problems, and many precautions have to be considered in the (pre)treatment of samples and data.

It already starts with the storage of the environmental sample. When stored in ethanol, comparable samples (termite *Coptotermes formosanus* sampled in different regions) exhibited a dramatic increase of gram positive bacteria like Firmicutes and Actinobacteria (Husseneder *et al.*, 2010). This can be also due to different cell lysis protocols The samples stored in ethanol investigated in Chapter 3 probably did not show such an artifact. Although most of the samples indeed show an increase in Firmicutes, it certainly is a real microbial community pattern. *Microcerotermes* sp. was stored in ethanol, too but has less Firmicutes and from all subfamilies and feeding traits also freshly dissected species were sampled showing similar bacterial compositions. Another study investigating the temporal sample preservation of the termite *Microcerotermes* sp. encountered remarkably changes of some taxonomic groups after one-month acetone preservation (Deevong *et al.*, 2006). Therefore DNA should preferably be extracted from fresh samples or as soon as possible.

Another important aspect is the DNA concentration estimation before pyrosequencing. In this study the amplicons were quantified photometrically by NanoDrop technology (Thermo Fisher Scientific), leading to a wide range in the number of reads (2,000–53,000; Chapter 2 and Chapter 3). More appropriate are DNA binding fluorophor-based assays like PicoGreen or SYBR Green having a more accurate DNA detection.

Pyrosequencing has a low intrinsic error rate of ca. 1% (Gilles *et al.*, 2011). However, sequencing noise can artificially inflate the bacterial diversity in the sample and can lead to wrong interpretations of the rare biosphere (Quince *et al.*, 2009; Kunin *et al.*, 2010). Therefore stringent quality trimming of the pyrotag reads is necessary. To even further reduce introduced sequencing errors, all statistical analyses in the studies presented in this thesis were based on taxonomic classification, i.e., genus level. Hence, read errors will not lead to overestimation of the microbial communities.

The concept of core microbiota

For understanding stable, consistent components across complex microbial communities the concept core microbiota or microbiome is used. Usually the core microbiota is defined by bacterial groups shared by similar environments (Turnbaugh *et al.*, 2009). However, there are even more definitions of a core microbiota (Shade and Handelsman, 2011). It has been proposed that core species associated with a specific habitat are likely critical to important functions. In this survey, core microbiota was defined as taxa present in all host guts after normalization. Interestingly, cockroaches and termites exhibit very few core genera (Chapter 3). Termites—lower or higher—share only half the number of core genera than the individuals among cockroaches. Only three taxa are shared by all intestinal tracts of the dictyopteran species. Finally, lower and higher termites only share two taxa. This suggests that cockroaches do not harbor a defined, specialized microbiota like termites but rather a wide-ranging microbial community in their guts. Hence, cockroaches share more core genera that could be rather common gut inhabitants. For lower termites it is likely due to both dietary preferences of the insect host and the presence / absence of particular niches, i.e. all species feed on wood and rely on cellulose-degrading protist cells. A relative within the core genus *Desulfovibrio* 1 in lower termites is *Candidatus* Desulfovibrio trichonymphae, an endosymbiont of the flagellate *Trichonympha agilis* from *Reticulitermes speratus* (Sato *et al.*, 2009). *Trichonympha* spp. flagellates occur in four different termite families and it is reasonable, that *Candidatus* Desulfovibrio trichonymphae or its relatives could colonize protist cells in all these termite families.

Seed of termite gut-associated bacteria already in the cockroaches

Cockroaches and termites differ fundamentally in their dietary and social lifestyle. The latter led to a different digestive mutualism evolving with different stages of coprophagy in omnivorous cockroaches up to highly eusocial proctodeal trophallaxis in termites (Nalepa *et al.*, 2001). This established prerequisites for a constant reinoculation of the digestive systems of the insect host and a coevolution host-specific gut symbionts like flagellates or flagellate-associated symbionts. Some of these flagellates in termites and wood-feeding cockroaches of the *Cryptocercus* genus coevolve with their insect host (Keeling *et al.*, 1998; Ohkuma *et al.*, 2009). Additionally, the bacterial symbionts of such flagellates like *Endomicrobia* (Ikeda-Ohtsubo and Brune, 2009) or relatives of the Bacteroidetes Cluster V (Noda *et al.*, 2009; Desai *et al.*, 2010) have been shown to coevolve with their protist host.

The accumulation of so many tight relationships between host, symbiotic protists, and their endosymbionts raises the question for their evolutionary origin. The results of this thesis could verify and add to the knowledge of the presence of so-far nearly only flagellate-associated bacterial lineages (Chapter 4). In the study of Ikeda-Ohtsubo *et al.* (2010) relatives of the obligate endosymbiotic, flagellate-associated *Endomicrobia* were found in defaunated termites and also cockroaches lacking these flagellates. This suggests free-living ancestors of *Endomicrobia* already in the gut of a common ancestor of cockroaches and termites. Further indications of the gut serving as a reservoir of diverse bacteria for associations with protist cells were discussed by Noda *et al.* (2009) (Noda *et al.*, 2009). All these finding including several consistent groups revealed in this study suggest that already the cockroaches serving as a bacterial reservoir for the phylogenetically related termites. Many of the found bacterial lineages seem to be ubiquitous, albeit very rare in most of the *Dictyoptera* species but are exploiting specific niches only in exclusive phylogenetic or dietary groups of host guts.

Future perspectives

This work provides deep insights in the microbial gut communities of cockroaches and termites and elucidates the patterns of microbial evolution, niche determination and dietary influences. Many new bacterial taxa were detected in the Dictyoptera. However, describing the bacterial communities in termites and cockroaches is only the first step toward a better understanding of the functions of the respective microorganisms. This study provides room for testing old and setting up new hypotheses: *Food for thoughts.*

References

Bowman, J.S., Rasmussen, S., Blom, N., Deming, J.W., Rysgaard, S., Sicheritz-Ponten, T. (2011) Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. ISME J

Deevong, P., Hongoh, Y., Inoue, T., Trakulnaleamsai, S., Kudo, T., Noparatnaraporn, N., Ohkuma, M. (2006) Effect of temporal sample preservation on the molecular study of a complex microbial community in the gut of the termite *Microcerotermes* sp.. Microbes Environ. 21, 78-85.

Desai, M. S., Strassert, J. F. H., Meuser, K., Hertel, H., Ikeda-Ohtsubo, W., Radek, R., Brune, A. (2010) Strict cospeciation of devescovinid flagellates and *Bacteroidales* ectosymbionts in the gut of dry-wood termites (*Kalotermitidae*). Environ. Microbiol. 12, 2120-2132.

Fierer, N., Lauber, C.L., Zhou, N., McDonald, D., Costello, E.K., Knight, R. (2010) Forensic identification using skin bacterial communities. Proc. Natl. Acad. Sci. U.S.A. 107, 6477-6481.

Gilles, A., Meglécz, E., Pech, N., Ferreira, S., Malausa, T., Martin, J.F. (2011) Accuracy and quality assessment of 454 GS-FLX Titanium pyrosequencing. BMC Genomics

Hongoh, Y., Ohkuma, M., Kudo, T. (2003) Molecular analysis of bacterial microbiota in the gut of the termite *Reticulitermes speratus* (Isoptera; Rhinotermitidae). FEMS Microbiol. Ecol. 44, 231-242.

Husseneder, C., Ho, H.-Y., Blackwell, M. (2010) Comparison of the bacterial symbiont composition of the Formosan Subterranean Termite from its native and introduced range. Open Microbiol. J. 4, 53-66.

Ikeda-Ohtsubo, W., Brune, A. (2009) Cospeciation of termite gut flagellates and their bacterial endosymbionts: *Trichonympha* species and '*Candidatus* Endomicrobium trichonymphae'. Mol. Ecol. 18, 332-342.

Ikeda-Ohtsubo, W., Faivre, N., Brune, A. (2010) Putatively free-living '*Endomicrobia*' – ancestors of the intracellular symbionts of termite gut flagellates?. Environ. Microbiol. 2, 554-559.

Inward, D., Beccaloni, G., Eggleton, P. (2007) Death of an order: a comprehensive molecular phylogenetic study confirms that termites are eusocial cockroaches. Biol. Lett. 3, 331-335.

Inward, D.J.G., Vogler, A.P., Eggleton, P. (2007) A comprehensive phylogenetic analysis of termites (Isoptera) illuminates key aspects of their evolutionary biology. Mol. Phylogenet. Evol. 44, 953-967.

Keeling, P.J., Poulsen, N., McFadden, G.I. (1998) Phylogenetic diversity of parabasalian symbionts from termites, including the phylogenetic position of Pseudotrypanosoma and Trichonympha. J. Euk. Microbiol. 45, 643-650.

Kuczynski, J., Liu, Z., Lozupone, C., McDonald, D., Fierer, N., Knight, R. (2010) Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. Nat. Meth. 7, 813-819.

Kunin, V., Engelbrektson, A., Ochman, H., Hugenholtz, P. (2010) Wrinkles in the rare biosphere: pyrosequencing errors lead to artificial inflaation of diversity estimates.. Environ. Microbiol. 12, 118-123.

Legendre F, Whiting MF; Bordereau C; Cancello EM; Evans TA; Grandcolas P (2008) The phylogeny of termites (Dictyoptera: Isoptera) based on mitochondrial and nuclear markers: implications for the evolution of the worker and pseudergate castes, and foraging behaviors. Mol. Phylogenet. Evol. 48, 615-627.

Nalepa, C.A., Bignell, D.E., Bandi, C. (2001) Detritivory, coprophagy, and the evolution of digestive mutualisms in Dictyoptera. Insect. Soc. 48, 194-201.

Noda, S., Hongoh, Y., Sato, T., Ohkuma, M. (2009) Complex coevolutionary history of symbiotic Bacteroidales bacteria of various protists in the gut of termites. BMC Evol. Biol. 9, 158.

Ohkuma M; Noda S; Hongoh Y; Nalepa CA; Inoue T (2009) Inheritance and diversification of symbiotic trichonymphid flagellates from a common ancestor of termites and the cockroach *Cryptocercus*. Proc. R. Soc. B 276, 239-245.

Ohkuma, M., Brune, A. (2011) Diversity, structure, and evolution of the termite gut microbial community. In: Biology of Termites: A Modern Synthesis, Vol. (D.E. Bignell, Y. Roisin, N. Lo, eds, Eds.), pp. 413-438. Springer, Dordrecht.

Quince, C., Lanzén, A., Curtis, T.P., Davenport, R.J., Hall, N., Head, I.M., Read, L.F., Sloan, W.T. (2009) Accurate determination of microbial diversity from 454 pyrosequencing data.. Nat. Methods 6, 639-641.

Sato T; Hongoh Y; Noda S; Hattori S; Ui S; Ohkuma M (2009) *Candidatus* Desulfovibrio trichonymphae, a novel intracellular symbiont of the flagellate *Trichonympha agilis* in termite gut. Environ. Microbiol. 11, 1007-1015.

Schmitt-Wagner, D., Friedrich, M.W., Wagner, B., Brune, A. (2003) Phylogenetic diversity, abundance, and axial distribution of bacteria in the intestinal tract of two soil-feeding termites (*Cubitermes* spp.). Appl. Environ. Microbiol. 69, 6007-6017.

Shade, A., Handelsman, J. (2011) Beyond the Venn diagram: the hunt for a core microbiome. Environ. Microbiol.

Shinzato, N; Muramatsu, M; Matsui, T; Watanabe, Y (2007) Phylogenetic analysis of the gut bacterial microflora of the fungus-growing termite *Odontotermes formosanus*. Biosci. Biotechnol. Biochem. 71, 906-912.

Sogin ML, Morrison HG, Huber JA, Welch DM, Huse SM, Neal PR, Arrieta JM, Herndl GJ. (2006) Microbial diversity in the deep sea and the underexplored "rare biosphere". Proc. Natl. Acad. Sci. USA 103, 12115-12120.

Turnbaugh, P.J., Hamady, M., Yatsunenko, T., Cantarel, B.L., Duncan, A., Ley, R.E., Sogin, M.L., Jones, W.J., Roe, B.A., Affourtit, J.P., Egholm, M., Henrissat, B., Heath, A.C., Knight, R., Gordon, J.I. (2009) A core gut microbiome in obese and lean twins. Nature 457, 480-484.

Wang, Q., Garrity, G.M., Tiedje, J.M., Cole, J.R. (2007) Naive Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. Appl. Environ. Microbiol. 73, 5261-5267.

Warnecke F., Luginbühl, P., Ivanova, N., et al. Hugenholtz P; Leadbetter JR (2007) Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature 450, 560-565

Werner, J.J., Koren, O., Hugenholtz, P., Desantis, T.Z., Walters, W.A., Caporaso, J.G., Angenent, L.T., Knight, R., Ley, R.E. (2011) Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. ISME J

6 Summary

This thesis comprises an array of studies about the bacterial gut microbiota in cockroaches and termites belonging to the superorder *Dictyoptera*. A high-throughput sequencing method, namely 454 pyrotag sequencing, was established and tested to analyzing bacterial 16S rRNA genes in intestinal tracts of insects. For this purpose the microbial communities within the gut compartments of the higher wood-feeding termite *Nasutitermes corniger* were investigated. In addition, physicochemical gut conditions of this termite were measured. Furthermore, a broad survey of specimen covering all families and subfamilies of cockroaches and lower and higher termites, including all known feeding habits, was conducted to investigate evolutionary and dietary patterns of their gut microbiota.

The comprehensive study linking physicochemical gut conditions with the structure of the microbial communities in the different gut compartments of *N. corniger* revealed the dilated hindgut paunch (P3) as the densest colonized gut compartment dominating the whole microbial gut community. This compartment accumulates high hydrogen partial pressures (up to 12 kPa), which was apparently produced by the dense community of Spirochaetes and Fibrobacteres dominating also the gut of other *Nasutitermes* species. All other compartments such as the alkaline P1 (average pH 10.0) comprised small but distinct populations characteristic for each gut region. Finally, similarities in the microbial communities of posterior hindgut and crop suggested that proctodeal trophallaxis or coprophagy is present also in higher termites.

The study of the *Dictyoptera* hindgut microbiota could show that the cockroach microbial gut community is more diverse and less specialized than that of the termites. Both differ significantly in their composition already on phylum level. The emerging patterns document a long history of (co)evolution of the gut microbiota with their dictyopteran host species. This resulted in clear and distinct clustering of the hosts concerning their phylogenetic relationship and dietary demands. Many of the bacterial lineages causing this clustering (e.g., Fibrobacteres, *Treponema*, and Bacteroidetes Cluster V) seem to be ubiquitous, albeit very rare in most of the *Dictyoptera*. The gut could serve as a reservoir of diverse bacteria that seem to exploit specific niches only in exclusive phylogenetic or dietary groups of host guts. Furthermore, the analyses could add to the inherent peculiar position of the wood-feeding cockroach *Cryptocercus punctulatus* sharing many microbial core taxa with the cockroaches, lower, and the higher termites. Statistical analyses verified the phylogenetic position of *Cryptocercus* hindgut microbiota in between the termites and cockroaches.

7 Zusammenfassung

Diese Arbeit umfasst eine Reihe von Studien über die bakterielle Darmmikrobiota von Schaben und Termiten, die der Superordnung *Dictyoptera* zuzuordnen sind. Zunächst wurde eine Hochdurchsatz-Sequenziermethode für Insektendarmbakterien etabliert und am Beispiel der höheren, holzfressenden Termite *Nasutitermes corniger* getestet. Hierbei wurden die mikrobiellen Gemeinschaften der einzelnen Darmkompartimente dieser Termite anhand der bakteriellen 16S-rRNA-Gene untersucht. Anschließend wurde eine ausgedehnte Studie von Vertretern aller Familien und Subfamilien der Schaben und Termiten, sowie aller Ernährungstypen dieser Insekten durchgeführt, um evolutionäre sowie nahrungsabhängige Muster der Darmmikrobiota zu untersuchen.

Die umfassende Studie zur Zusammensetzung der Mikrobiota verschiedener Darmkompartimente der Termite *N. corniger* wurde mit der Messung physikochemischer Parameter des Darms verknüpft. Die im am dichtest besiedelten P3 gefundenen Bakterien dominieren die mikrobielle Darmgemeinschaft. Die ausgeprägte Akkumulation an Wasserstoffpartialdruck (bis zu 12 kPa) im P3 ist vermutlich der Produktion durch Spirochaetes und Fibrobacteres zuzuschreiben, die dieses Kompartiment dominieren. Alle anderen Darmkompartimente von *N. corniger*—so auch das alkalische P1 (mittlerer pH 10,0)—weisen im Vergleich zum P3 klar unterschiedliche, wenngleich auch zahlenmäßig geringere mikrobielle Gemeinschaften auf. Die Gemeinsamkeiten der Mikrobiota zwischen den posterioren Darmkompartimenten und dem Kropf deuten darauf hin, dass proktodeale Trophallaxis oder Koprophagie als Verhaltensweise auch bei höheren Termiten vorkommt.

Der Vergleich der Darmmikrobiota verschiedener *Dictyoptera*-Spezies zeigte, dass die mikrobiellen Gemeinschaften im Schabendarm diverser und weniger spezialisiert sind als in Termiten und sich bereits auf Phylumebene signifikant unterscheiden. Die Verteilung einzelner bakteriellen Linien dokumentieren eine (Ko-)Evolution der Darmmikrobiota mit deren Insekten-Wirtsspezies. Dies zeichnet sich in ausgeprägten Gruppierungen der Wirte bezüglich deren phylogenetischen Verwandtschaft und Nahrungsmustern aus. Viele der für die Gruppierung verantwortlichen bakteriellen Linien (z.B. Fibrobacteres, *Treponema* und Bacteroidetes Cluster V) scheinen in unterschiedlicher Anzahl in allen *Dictyoptera* vorhanden zu sein. Der Darm könnte als Reservoir für verschiedenste Bakterien dienen, die sich als Besiedler von Nischen ausgewählter Wirte (phylogenetisch oder nahrungsabhängig) anreichern und entfalten können. Statistische Analysen bestätigten die phylogenetische Position der Darmmikrobiota von *Cryptocercus* zwischen der von Termiten und Schaben.

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Zuallererst möchte ich bei Prof. Andreas Brune für dieses ergiebige und sehr interessante Thema meiner Doktorarbeit sowie das Erstgutachten bedanken. Bei Fragen und Sorgen wusste ich in ihm einen guten Diskussionspartner.

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Und ich möchte alle grüßen, die mich kennen…

9 Erklärung der Eigenständigkeit

Ich versichere, dass ich meine Dissertation

„Diversity and evolutionary patterns in the bacterial gut microbiota of termites and cockroaches"

selbständig und ohne unerlaubte Hilfe angefertigt habe und mich keiner als der von mir ausdrücklich bezeichneten Quellen und Hilfen bedient habe. Diese Dissertation wurde in der jetzigen oder einer ähnlichen Form noch bei keiner anderen Hochschule eingereicht und hat noch keinen sonstigen Prüfungszwecken gedient.

Marburg, Oktober 2011

10 Abgrenzung der Eigenleistung

Soweit nicht anders erwähnt, wurden alle Experimente von mir selbst geplant und durchgeführt, sowie anschließend in Form eines Manuskriptes ausgewertet.

Im Kapitel „Physicochemical gradients and deep sequencing of the bacterial microbiota indicate functional compartmentation in the gut of the termite Nasutitermes corniger“ half C.D. bei der Präparation der Termitendarmkompartimente zur DNA-Extraktion und HPLC-Analyse. Letztere wurde durch C.D. durchgeführt und ausgewertet. C.D. führte die statistischen Analysen durch und war weitgehend an der Erstellung des Manuskriptes beteiligt. R.H.S. stellte die Termiten und das Darmübersichtsbild zur Verfügung. Das finale Manuskript entstand unter Mitarbeit von CD. und A.B. Zusätzliche Unterstützung leistete Katja Meuser bei der DNA-Probenvorbereitung zur Pyrosequenzierung.

Im Kapitel „Digesting the diversity – Evolutionary patterns in the gut microbiota of termites and cockroaches“ half C.D. maßgeblich bei der Durchführung der statistischen Analysen und deren Auswertung. Rüdiger Plarre stellte einige der analysierten Termiten zur Verfügung. Zusätzliche Hilfe leisteten Christine Schauer bei der Präparation mancher Schaben und Katja Meuser bei der DNA-Probenvorbereitung zur Pyrosequenzierung sowie Sequenzierung der COII-Gene der Schaben und Termiten.

Das Kapitel „Persistence and development of bacterial lineages in the Dictyoptera – a matter of niches and feeding“ wurde unterstützt durch die phylogenetische Analyse und Neuklassifizierung der *Treponema* sowie Fibrobacteres / TG3 durch A.M.

11 Curriculum Vitae

Ausbildung

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09.1988 – 07.1992	**132. Polytechnische Oberschule, Dresden**

Jobs / Praktika

05.2007 – 09.2007	**Max-Planck-Institut für terrestr. Mikrobiologie, Marburg** Hilfswissenschaftler; molekularbiologische Untersuchung der Reaktionen von Bakterien auf Sauerstoff im Termitendarm
11.2005 – 02.2006	**Institut für medizinische Mikrobiologie, TU Dresden**
	Studentische Hilfskraft; molekularbiologische Untersuchung der Diversität von Archaen in Talsperrensedimenten
10.2004 – 03.2005	**Max-Planck-Institut für terrestr. Mikrobiologie, Marburg**
	Praktikum in der Abteilung Biogeochemie; molekularbiologische Untersuchung der Phylogenie, Abundanz und Verteilung von Planktomyzeten im Darm von bodenfressenden Termiten

08.2004 – 10.2004	**elbion AG, Radebeul** Praktikum in der Abteilung für Molekularbiologie; Untersuchung des Einflusses von Testsubstanzen auf die cAMP- und TNFα-Produktion menschlicher Blutzellen; Optimierung von Assays
01.2004 – 04.2004	**Akademisches Auslandsamt, TU Dresden** Studentische Hilfskraft; Organisation einer Einweihungsfeier und Anfangsbetreuung ausländischer Studierender
03.2003 – 02.2006	**Club Aquarium e.V.** Studentenclub; Organisation und Bardienst
09.2000 – 08.2001	**Kinderladen Schildkröte e.V., Dresden** Freiwilliges Soziales Jahr; Betreuung und Begleitung von z.T. körperlich und geistig behinderten Kindern, Kenntnisse der Montessori-Pädagogik

Zusätzliche Qualifikationen / Interessen

Workshops:	Wissenschaftliches Präsentieren und Schreiben, Fluoreszenz-In-Situ-Hybridisierungen, Mikrosensoren, Proteinaufreinigung
Fremdsprachen:	Englisch – fließend in Wort und Schrift Französisch – gute Kenntnisse
EDV:	MS-Office- und Linux-Anwendungen – sehr gute Kenntnisse Programmierung – Grundkenntnisse in Perl, R, bash, awk, etc.
Interessen:	Lesen, Spazieren, Snooker, Musik (Mitglied einer Band), Jonglieren

Marburg, 12. Dezember 2011

Supplementary Table 4 from Chapter 2: Distribution and relative abundance of the pyrotag reads in all samples.

	Relative abundance of bacterial groups (%)								
	Nasutitermes corniger							*N. takasa-goensis*	*N.* sp.
Taxon	Crop 12891 reads	Midgut 14175 reads	P1 8379 reads	P3 24029 reads	P4 25957 reads	P5 3270 reads	Hindgut 3704 reads	Hindgut 16619 reads	P3[a] 1252 reads
1_Proteobacteria;1_Deltaproteobacteria;1_Desulfobacterales;1_Nitrospinaceae;Candidatus_Entotheonella	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified	0.00	0.00	0.00	0.00	0.03	0.00	0.03	0.00	0.00
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_14	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_2	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_23	0.58	0.07	0.17	0.15	2.96	3.24	0.92	0.07	0.64
Acidobacteria;Holophagae;Holophagales;Holophagaceae;unclassified	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.04	0.00
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_3	0.16	0.08	0.35	0.37	0.25	0.43	0.22	0.33	1.68
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_5	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Acidobacteria;unclassified;unclassified;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_2	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_3	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;Salana	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Brevibacteriaceae;Brevibacterium	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;Brachybacterium	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;Dermabacter	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Frankiaceae;Frankia	0.00	0.00	0.01	0.00	0.00	0.03	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Agromyces_2	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;unclassified	0.11	0.01	0.06	0.00	0.01	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_1	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_21	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_sanguinis	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Marmoricola	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Nocardioides	0.00	0.04	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Myceligenerans_xiligouense	0.00	0.00	0.01	0.02	0.02	0.03	0.03	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;unclassified	0.00	0.00	0.00	0.01	0.05	0.00	0.00	0.04	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Xylanimonas_	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Aestuariimicrobium	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Sanguibacteraceae;Sanguibacter	6.73	0.90	17.97	1.17	4.97	10.40	0.35	0.43	0.00
Actinobacteria;Actinobacteria;Actinomycetales;unclassified;unclassified	1.62	0.47	4.61	0.47	3.75	3.49	0.08	0.70	0.00
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptacidiphilus	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_8	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unclassified	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_1	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_atypicum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_spheniscorum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;unclassified	0.00	0.01	0.01	0.02	0.01	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_1	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Dietziaceae;Dietzia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Mycobacteriaceae;Mycobacterium	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_2	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_2;unclassified;unclassified	0.02	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonosporaceae_bacteria_a	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinocorallia	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00

Actinobacteria;Actinobacteria;AKIW543;unclassified;unclassified	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;marine_group	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;unclassified	0.02	0.01	0.02	0.01	0.18	0.00	0.00	0.02	0.00
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_10	0.26	0.13	0.17	0.19	5.00	0.37	0.24	0.14	0.00
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_11	0.00	0.01	0.04	0.01	0.08	0.03	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;RL185-aaj71c12;unclassified;unclassified	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Solirubrobacterales;Patulibacteraceae;Patulibacter	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Solirubrobacterales;Solirubrobacteriaceae;Solirubrobacter	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Actinobacteria;Actinobacteria;Solirubrobacterales;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Actinobacteria;Actinobacteria;unclassified;unclassified;unclassified	0.95	0.34	3.02	0.22	1.74	3.12	0.03	0.16	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.06	0.08	0.05	0.06	0.05	0.12	0.03	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;CAP-aah99b04;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;COB_P4-1_termite_group;unclassified	0.42	0.01	0.00	0.34	0.25	0.61	0.54	0.43	0.16
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_cluster_a;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;3M1PL1-52_termite_group	0.04	0.00	0.00	0.02	0.03	0.06	0.00	0.02	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Wood_feeding_roaches	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;unclassified	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.03	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_a	0.51	0.02	0.01	0.21	0.29	1.47	0.03	0.09	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_b	0.32	0.05	0.01	0.42	0.67	0.80	0.51	1.62	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_c	0.00	0.01	0.00	0.01	0.04	0.00	0.03	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Alkaliflexus	0.26	0.04	0.01	0.01	0.76	0.34	0.03	0.00	0.96
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured_1	0.00	0.00	0.00	0.02	0.00	0.06	0.03	0.02	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Nearly_all_Termite_Cluster;unclassified	0.00	0.00	0.00	0.01	0.00	0.03	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;p-2534-18B5_gut_group;termite_group_a	0.02	0.00	0.00	0.00	0.00	0.09	0.00	0.01	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Paludibacter	0.78	0.11	0.11	0.33	0.93	0.76	0.73	0.62	0.64
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Candidatus_Symbiothrix	0.47	0.07	0.01	0.39	0.01	1.35	0.38	0.51	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Dysgonomonas	0.06	0.11	0.01	0.03	0.06	0.03	0.05	0.01	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Parabacteroides	0.11	0.11	0.10	0.08	0.11	0.24	0.03	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Tannerella	0.03	0.01	0.00	0.12	0.00	0.09	0.00	0.16	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;unclassified	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Odoribacter	0.02	0.01	0.00	0.00	0.01	0.03	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Shelfordella_cluster_a	0.00	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella_7	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;ratAN060301C;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	0.35	0.28	0.17	0.17	0.52	0.52	0.40	0.07	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;BCf9-17_termite_group	0.22	0.10	0.19	0.17	0.04	0.28	0.16	0.04	0.16
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_c	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;M2PB4-61_termite_group	0.48	0.11	0.07	0.26	0.03	0.28	0.40	1.01	0.40
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;P1_32_Panesthia	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rs-D38_termite_group	0.12	0.03	0.01	0.10	0.13	0.15	0.08	0.07	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;unclassified	0.02	0.04	0.08	0.02	0.03	0.03	0.05	0.04	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;vadinBC27_wastewater-sludge_group	0.09	0.00	0.00	0.04	0.00	0.03	0.13	0.16	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_bb	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;higher_termites_a	0.06	0.00	0.01	0.05	0.02	0.06	0.35	0.14	1.36
Bacteroidetes;Bacteroidia;Bacteroidales;unclassified;unclassified	0.14	0.07	0.06	0.07	0.12	0.18	0.16	0.15	0.00
Bacteroidetes;Bacteroidia;Bacteroidales;vadinHA21;unclassified	0.50	0.02	0.00	0.23	0.16	0.34	0.16	0.05	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;Blattabacterium	0.70	0.85	0.73	0.46	0.62	0.92	0.05	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;Owenweeksia	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Flavobacterium_1	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_1	0.03	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Cloacibacterium	0.00	0.01	0.00	0.00	0.01	0.03	0.00	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;unclassified	0.00	0.01	0.01	0.00	0.00	0.03	0.00	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;uncultured_a	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00
Bacteroidetes;Flavobacteria;Flavobacteriales;unclassified;unclassified	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;SB-1;unclassified	0.06	0.01	0.00	0.01	0.02	0.06	0.00	0.01	0.00

Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_3	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;unclassified;unclassified	0.04	0.00	0.00	0.02	0.00	0.00	0.00	0.03	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;vadinHA17;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;WCHB1-69;unclassified	0.12	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Sediminibacterium	0.19	0.00	0.01	0.00	0.04	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;unclassified	0.06	0.00	0.00	0.00	0.00	0.03	0.11	0.01	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_10	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_11	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_12	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_2	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;uncultured_1	0.98	0.01	0.01	0.02	0.16	0.06	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_3;Hymenobacter	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;Sphingobacteria;unclassified;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteroidetes;unclassified;unclassified;unclassified;unclassified	0.05	0.07	0.07	0.02	0.05	0.15	0.05	0.06	0.00
BD1-5;unclassified;unclassified;unclassified;unclassified	0.01	0.00	0.01	0.01	0.01	0.09	0.00	0.00	0.00
Candidate_division_BRC1;unclassified;unclassified;unclassified;unclassified	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Candidate_division_OD1;unclassified;unclassified;unclassified;unclassified	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Candidate_division_OP11;unclassified;unclassified;unclassified;unclassified	0.45	0.06	0.05	0.07	0.59	1.90	0.22	0.01	0.00
Candidate_division_OP3;unclassified;unclassified;unclassified;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Candidate_division_SR1;unclassified;unclassified;unclassified;unclassified	0.40	0.05	0.02	0.07	0.82	1.96	0.30	0.00	0.00
Candidate_division_TM7;unclassified;unclassified;unclassified;unclassified	1.26	0.20	0.32	0.43	4.34	3.94	0.62	0.57	0.00
Chlorobi;Chlorobia;Chlorobiales;BSV26;unclassified	0.06	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Chlorobi;Chlorobia;Chlorobiales;OPB56;unclassified	0.01	0.00	0.01	0.00	0.00	0.00	0.08	0.03	0.08
Chlorobi;Chlorobia;Chlorobiales;SJA-28;unclassified	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.03	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_1	0.07	0.00	0.00	0.00	0.02	0.03	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_11	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_3	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_4	0.03	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_5	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_4	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chloroflexi;Thermomicrobia;JG30-KF-CM45;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Chloroflexi;TK10;unclassified;unclassified;unclassified	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chloroflexi;vadinBA26;unclassified;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.05	0.00
Cyanobacteria;Cyanobacteria;Cyanobacteriales;4C0d-2;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16
Cyanobacteria;Cyanobacteria;Cyanobacteriales;ML635J-21;unclassified	0.19	0.05	0.14	0.18	0.17	0.28	0.22	0.12	0.88
Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Mucispirillum	0.01	0.03	0.05	0.05	0.02	0.00	0.00	0.03	0.08
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_I_[Endomicrobia]	0.21	0.30	0.14	0.22	0.46	0.37	0.00	0.03	0.08
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_III_[Elusimicrobium]	0.07	0.02	0.00	0.02	0.11	0.15	0.03	0.01	0.00
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;unclassified	0.00	0.01	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Fibrobacteres;Fibrobacteres_sp1;Fibrobacterales;Fibrobacteraceae;Fibrobacter	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Fibrobacteres;Fibrobacteres_sp2;Fibrobacteres_sp2;Termite_Cluster;Termite_Cluster_I	6.63	1.09	2.08	5.08	6.01	10.64	8.13	0.04	2.64
Firmicutes;Bacilli;Apr-15;unclassified;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_14	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_5	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_17	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;unclassified	0.01	0.00	0.01	0.00	0.01	0.00	0.00	0.01	0.00
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_2	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_5	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Lysinibacillus	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;unclassified	0.00	0.01	0.01	0.02	0.01	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_1	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_1	0.02	0.03	0.00	0.00	0.01	0.00	0.03	0.00	0.00

Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_2	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Bacillales;unclassified;unclassified	0.02	0.05	0.13	0.01	0.03	0.00	0.00	0.02	0.00
Firmicutes;Bacilli;Bacillales_1;Bacillaceae;Bacillus_1	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;16d63.751;unclassified	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Catellicoccus_marimammalium;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_2	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_3	0.01	0.03	0.06	0.01	0.02	0.03	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_4	0.01	0.01	0.11	0.00	0.00	0.03	0.00	0.01	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_5	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;unclassified	0.02	0.01	0.06	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_sp._R-25205	0.02	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;unclassified	0.01	0.08	0.05	0.01	0.02	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;uncultured_a	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_1	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_2	0.18	0.21	0.30	0.14	0.13	0.12	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_4	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_6	0.01	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;unclassified	0.04	0.04	0.02	0.03	0.05	0.00	0.08	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_2	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;PeH08;unclassified	0.40	0.47	4.56	0.08	0.25	0.46	0.03	0.00	0.16
Firmicutes;Bacilli;Lactobacillales;Rs-D42;unclassified	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Sl_24;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_1	0.02	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactovum	12.16	0.23	0.48	0.10	0.19	0.15	0.00	0.01	0.00
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;unclassified	8.18	0.20	0.26	0.07	0.14	0.03	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_1	0.33	0.05	0.10	0.02	0.03	0.03	0.00	0.00	0.00
Firmicutes;Bacilli;Lactobacillales;unclassified;unclassified	0.78	0.75	4.55	0.16	0.37	0.80	0.11	0.01	0.00
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Hepialus;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Bacilli;unclassified;unclassified;unclassified	0.09	0.13	0.63	0.05	0.05	0.00	0.08	0.01	0.00
Firmicutes;Bacilli;VAN12;unclassified;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_1	0.04	0.01	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_8	0.02	0.00	0.00	0.00	0.00	0.00	0.03	0.02	0.00
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;unclassified	0.03	0.06	0.07	0.03	1.70	0.12	0.00	0.06	0.00
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Pseudoramibacter	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;unclassified	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;uncultured	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Anaerovorax_	0.00	0.00	0.00	0.00	0.07	0.00	0.13	0.08	0.08
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_3	0.02	0.00	0.02	0.00	0.18	0.03	0.00	0.04	0.00
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;unclassified	0.09	0.04	0.06	0.08	0.17	0.09	0.08	0.26	0.00
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_5	0.22	0.14	0.12	0.20	3.64	0.37	0.13	0.62	0.00
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_6	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Catabacter	0.01	0.00	0.00	0.00	0.01	0.00	0.03	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Coprococcus_1	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_11	0.01	0.01	0.01	0.00	0.01	0.03	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_24	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_31	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_34	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_36	0.33	1.04	1.17	0.30	0.80	0.24	0.32	0.59	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_6	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Mmba_A01b	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Parasporobacterium-Sporobacterium	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_higher_Termites	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_Insects	0.02	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;unclassified	0.59	2.90	3.77	0.24	0.71	0.37	0.40	0.36	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_10	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_11	0.00	0.01	0.01	0.00	0.00	0.00	0.03	0.07	0.40

Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_13	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_4	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_54	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_62	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_65	0.29	0.13	0.18	0.32	0.92	0.46	0.43	0.13	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_67	10.15	73.43	4.09	1.80	2.68	3.09	0.84	2.18	0.24
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Sporacetigenium_mesophilum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;unclassified	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_3	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerotruncus	0.00	0.02	0.02	0.05	0.01	0.03	0.00	0.02	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Butyricicoccus_pullicaecorum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_alkalicellulosi	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_straminisolvens	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Fastidiosipila	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_1	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.49	0.16
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_3	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_4	0.03	0.01	0.01	0.04	0.24	0.03	0.03	0.02	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_5	0.02	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_6	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_7	0.00	0.01	0.00	0.00	0.03	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_8	0.02	0.01	0.02	0.11	0.26	0.06	0.00	0.09	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;insect_guts_a	0.05	0.06	0.05	0.05	0.10	0.03	0.35	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Papillibacter	0.05	0.01	0.00	0.01	0.04	0.09	0.05	0.13	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_1	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.02	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_2	0.07	0.01	0.04	0.02	0.65	0.21	0.08	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Sporobacter	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Termite_group_aaa	0.05	0.07	0.05	0.06	0.08	0.06	0.03	0.02	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;unclassified	0.26	0.23	0.14	0.22	1.61	0.43	0.27	1.23	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_11	0.03	0.13	0.10	0.06	0.13	0.03	0.11	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_12	4.43	0.21	0.21	0.61	0.25	5.02	0.70	0.85	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_13	0.00	0.01	0.00	0.01	0.01	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_23	0.01	0.00	0.00	0.00	0.01	0.00	0.03	0.04	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_24	0.62	0.08	0.13	0.25	1.70	0.34	0.49	1.81	0.16
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_25	0.00	0.00	0.00	0.00	0.02	0.00	0.08	0.04	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_29	0.02	0.00	0.00	0.00	0.02	0.00	0.03	0.32	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_30	0.05	0.00	0.01	0.04	0.27	0.00	0.13	0.37	0.16
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_35	0.01	0.00	0.00	0.01	0.04	0.00	0.00	0.14	0.00
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_36	0.40	0.02	0.00	0.07	0.01	0.18	0.08	0.52	0.00
Firmicutes;Clostridia_1;Clostridiales;unclassified;unclassified	0.46	0.85	0.38	0.21	1.76	0.34	0.16	0.47	0.00
Firmicutes;Clostridia_2;Clostridiales;Peptococcaceae;Desulfitibacter	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Pelospora	0.01	0.00	0.00	0.02	0.01	0.00	0.03	0.01	0.00
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_1	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.00
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_2	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;unclassified	0.00	0.00	0.00	0.01	0.03	0.00	0.00	0.02	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_2	0.02	0.00	0.00	0.04	0.06	0.00	0.03	0.04	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_5	0.07	0.08	0.04	0.27	0.66	0.06	0.16	0.62	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Desulfosporosinus	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;uncultured_gut_Group_A	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.08
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Desulfotomaculum_4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Sporotomaculum_syntrophicum	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;unclassified	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00

Firmicutes;Clostridia_2;Clostridiales_1;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acetonema_a	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Dendrosporobacter	0.01	0.00	0.04	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Thermosinus	0.04	0.04	0.01	0.09	0.01	0.18	0.24	0.01	0.08
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;unclassified	0.00	0.00	0.01	0.00	0.03	0.00	0.05	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_6	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_7	0.02	0.04	0.13	0.05	0.03	0.00	0.03	0.00	0.00
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_8	0.00	0.00	0.02	0.00	0.05	0.03	0.00	0.01	0.00
Firmicutes;Clostridia_2;unclassified;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Turicibacter	0.33	0.80	13.38	0.14	0.18	0.15	0.03	0.01	0.00
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;unclassified	0.04	0.00	0.04	0.00	0.00	0.00	0.00	0.01	0.00
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_2	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_3	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.01	0.00
Firmicutes;Mollicutes;unclassified;unclassified;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes;unclassified;unclassified;unclassified;unclassified	0.48	1.04	3.90	0.23	0.42	0.49	0.13	0.41	0.00
Fusobacteria;Fusobacteria;Fusobacteriales;boneC3G7;unclassified	0.00	0.01	0.04	0.00	0.02	0.00	0.00	0.00	0.00
Fusobacteria;Fusobacteria;Fusobacteriales;CFT112H7;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Fusobacterium_1	0.01	0.00	0.02	0.01	0.02	0.00	0.00	0.00	0.00
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Sebaldella	0.02	0.01	0.00	0.00	0.02	0.00	0.05	0.01	0.00
Fusobacteria;Fusobacteria;Fusobacteriales;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00
Lentisphaerae;Lentisphaeria;055B07-P-DI-P58;unclassified;unclassified	0.02	0.01	0.05	0.02	0.12	0.15	0.00	0.00	0.00
Lentisphaerae;Lentisphaeria;CVer-1_termite_group;unclassified;unclassified	0.00	0.01	0.00	0.00	0.03	0.00	0.05	0.00	0.00
Lentisphaerae;Lentisphaeria;CVer-2_termite_group;unclassified;unclassified	0.01	0.01	0.00	0.00	0.11	0.00	0.00	0.00	0.00
Lentisphaerae;Lentisphaeria;RFP12_gut_group;unclassified;unclassified	0.00	0.00	0.00	0.02	0.07	0.03	0.00	0.00	0.00
Lentisphaerae;Lentisphaeria;unclassified;unclassified;unclassified	0.05	0.01	0.01	0.12	0.45	0.24	0.03	0.01	0.00
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;Victivallis	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Lentisphaerae;Lentisphaeria;WCHB1-25;unclassified;unclassified	0.05	0.01	0.00	0.02	0.25	0.15	0.00	0.04	0.00
NPL-UPA2;unclassified;unclassified;unclassified;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Planctomycetes;BD7-11;unclassified;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Planctomycetes;Phycisphaerae;mle1-8;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pirellula	0.02	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Termite_planctomycete_cluster	0.02	0.01	0.01	0.03	0.46	0.21	0.05	0.00	0.00
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;unclassified	0.02	0.01	0.01	0.01	0.25	0.18	0.03	0.02	0.00
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Planctomycetes;vadinHA49;unclassified;unclassified;unclassified	0.06	0.06	0.05	0.07	0.10	0.06	0.13	0.00	0.00
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_3	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;uncultured_2	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Brucella	0.02	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_3	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_9	0.05	0.00	0.01	0.00	0.02	0.03	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_20	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_21	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;unclassified;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;BCf3-20;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_12	0.03	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_4	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Nitrobacter	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;unclassified	0.26	0.00	0.06	0.01	0.05	0.15	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Methylobacterium	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Microvirga	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Catellibacterium	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Roseobacter_clade_Ketogulonicigenium	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;unclassified	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;uncultured_19	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidicaldus	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Marispirillum_indicum	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Thalassospira	0.01	0.02	0.00	0.00	0.01	0.00	0.00	0.01	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;unclassified	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_2	0.80	0.08	0.16	0.26	0.12	1.16	0.59	0.26	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;Wolbachia	0.01	0.01	0.01	0.01	0.02	0.00	0.00	0.02	0.00
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Captivus;Candidatus_Captivus	0.01	0.04	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Hepatincola;Candidatus_Hepatincola	0.03	0.09	0.04	0.06	0.05	0.06	0.03	0.00	0.00
Proteobacteria;Alphaproteobacteria;Rickettsiales;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium_2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_2	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_3	0.27	0.00	0.00	0.00	0.09	0.06	0.00	0.01	0.00
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_4	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified	0.04	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;Sphingomonadales;unclassified;unclassified	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Proteobacteria;Alphaproteobacteria;unclassified;unclassified;unclassified	0.04	0.02	0.01	0.02	0.04	0.03	0.00	0.02	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Achromobacter_3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_1	0.05	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;unclassified	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_2;Cupriavidus	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax_7	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Alicycliphilus	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium	0.02	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquamonas	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Giesbergeria	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga_1	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga_5	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified	0.01	0.00	0.01	0.01	0.00	0.09	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_25	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum_1	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia_6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Oxalobacter	0.00	0.00	0.00	0.01	0.00	0.00	0.03	0.00	0.08
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified	0.02	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified;unclassified	0.04	0.01	0.00	0.00	0.09	1.38	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas	0.24	0.01	0.05	0.00	0.02	0.06	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;uncultured_1	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;Methyloversatilis	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;uncultured	0.02	0.02	0.04	0.01	0.02	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Dechloromonas_1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Lower_termite_Cluster	0.00	0.01	0.00	0.01	0.01	0.00	0.03	0.01	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Propionivibrio	0.02	0.00	0.04	0.05	0.05	0.09	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;unclassified	0.02	0.02	0.00	0.00	0.00	0.03	0.05	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_1	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;unclassified;unclassified	0.02	0.03	0.00	0.02	0.03	0.12	0.05	0.02	0.00
Proteobacteria;Betaproteobacteria;SC-I-84;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Betaproteobacteria;unclassified;unclassified;unclassified	0.17	0.04	0.01	0.03	0.06	0.24	0.03	0.01	0.00
Proteobacteria;Deltaproteobacteria;43F-1404R;unclassified;unclassified	0.00	0.00	0.00	0.02	0.03	0.00	0.00	0.01	0.00
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.02	0.00
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiferula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobotulus	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.03	0.03	0.01	0.00
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00

Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfohalobiaceae_2;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_1	0.49	0.07	0.13	0.55	1.60	0.55	0.35	0.58	0.16
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_2	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_3	0.12	0.17	0.24	0.36	0.22	0.31	0.43	0.45	0.16
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;unclassified	0.08	0.02	0.04	0.08	0.46	0.12	0.00	0.05	0.00
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;unclassified;unclassified	0.00	0.02	0.01	0.00	0.13	0.00	0.00	0.02	0.00
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;GR-WP33-58;unclassified	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;Phaselicystidaceae;Phaselicystis	0.04	0.00	0.00	0.02	0.00	0.00	0.00	0.02	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium_2	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified;unclassified	0.02	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_5;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Deltaproteobacteria;Rs-K70_termite_group;unclassified;unclassified	0.25	0.14	0.37	1.62	0.15	0.49	0.51	0.58	2.24
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.01	0.00
Proteobacteria;Deltaproteobacteria;unclassified;unclassified;unclassified	0.01	0.00	0.00	0.01	0.02	0.00	0.00	0.09	0.00
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0.01	0.00	0.00	0.00	0.00	0.06	0.13	0.00	0.00
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum	0.09	0.16	0.07	0.06	0.13	0.06	0.03	0.00	0.00
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Rs-M59_termite_group	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Proteobacteria;Epsilonproteobacteria;unclassified;unclassified;unclassified	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Frateuria	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudomonas_cissicola	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas	0.03	0.00	0.00	0.00	0.01	0.03	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0.02	0.01	0.02	0.01	0.02	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Aeromonadales;Aeromonadaceae;Aeromonas_2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Aeromonadales;Succinivibrionaceae;unclassified	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;B38;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Enteric_Bacteria_cluster	0.20	0.06	0.07	0.06	0.06	0.18	0.03	0.02	0.00
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Leminorella	0.02	0.00	0.02	0.01	0.00	0.00	0.03	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;unclassified	0.02	0.03	0.08	0.02	0.01	0.00	0.08	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;unclassified	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Xenorhabdus_nematophila	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;unclassified;unclassified	0.01	0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae;Pseudospirillum	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Acinetobacter	0.02	0.00	0.00	0.01	0.03	0.03	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Cellvibrio	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_13	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_2	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.05	0.00	0.00
Proteobacteria;Gammaproteobacteria_1;unclassified;unclassified;unclassified	0.00	0.01	0.00	0.01	0.01	0.00	0.05	0.00	0.00
Proteobacteria;Gammaproteobacteria_2;Methylococcales;Methylococcaceae_2;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_6	0.02	0.00	0.04	0.00	0.02	0.03	0.00	0.00	0.00
Proteobacteria;TA18;unclassified;unclassified;unclassified	0.09	0.01	0.00	0.01	0.34	0.09	0.00	0.01	0.00
Proteobacteria;unclassified;unclassified;unclassified;unclassified	0.05	0.04	0.04	0.04	0.13	0.09	0.16	0.13	0.00
Spirochaetes;Spirochaetes;FGL12-B44;unclassified;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Rs-H88_termite_group	0.00	0.01	0.00	0.00	0.08	0.00	0.03	0.01	0.08
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;uncultured_3	0.02	0.00	0.00	0.07	0.07	0.06	0.05	0.10	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;M2PT2-76_termite_group	0.12	0.01	0.42	0.56	0.02	0.09	0.13	0.13	0.88
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Kalotermitidae_Cluster	0.12	0.08	0.14	0.41	0.20	0.09	0.11	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_I	0.01	0.05	0.02	0.05	0.02	0.09	0.00	0.01	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_II	0.09	0.02	0.17	0.20	0.02	0.06	0.24	0.01	0.08
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Reticulitermes_Cluster	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Rhinotermitidae_Cluster_Qadd	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_1	0.02	0.01	0.02	0.10	0.06	0.03	0.00	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_2	0.22	0.03	0.06	0.17	0.47	0.18	0.13	0.16	0.08
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_sp_Kalotermes	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I	0.02	0.01	0.00	0.02	0.01	0.00	0.00	0.02	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Clu	1.18	0.27	1.17	3.77	2.06	1.28	7.32	5.71	9.50
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Clu	0.02	0.01	0.06	0.09	0.22	0.03	0.03	0.20	0.00

Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Clu	0.07	0.04	0.07	0.18	0.15	0.09	0.30	0.22	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.46	0.33	0.51	1.28	0.95	0.40	0.86	0.97	0.48
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.23	0.14	0.13	0.35	0.20	0.31	0.35	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.10	0.10	0.11	0.25	0.27	0.09	0.78	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.00	0.00	0.00	0.01	0.00	0.00	0.30	0.02	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.02	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.17	0.15	0.11	0.38	0.22	0.21	0.00	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Clus	0.06	0.04	0.06	0.15	0.13	0.15	0.38	0.02	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Microcerotermes_Cl	0.16	0.08	0.11	0.41	0.28	0.15	0.00	0.01	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Mixed_Higher_Term	0.20	0.07	0.32	0.30	0.32	0.03	0.24	0.50	0.40
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster	0.00	0.00	0.01	0.07	0.12	0.00	0.03	0.05	0.24
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	1.06	0.32	0.98	2.19	1.14	1.01	1.54	0.28	0.96
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	0.00	0.02	0.01	0.02	0.03	0.06	0.08	0.40	0.16
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	0.05	0.01	0.08	0.13	0.06	0.06	0.22	0.14	0.56
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	4.96	1.07	5.04	24.06	8.38	7.34	22.84	39.96	19.89
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	1.55	0.49	1.17	6.14	2.68	1.74	5.62	1.51	2.16
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Terr	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.03	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Microcerote	0.02	0.03	0.06	0.07	0.06	0.00	0.00	0.01	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	0.06	0.02	0.04	0.11	0.08	0.18	0.11	0.03	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	0.00	0.01	0.00	0.02	0.03	0.00	0.11	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	1.39	0.40	1.36	5.45	1.91	2.05	7.29	0.42	0.72
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	0.00	0.00	0.00	0.02	0.01	0.00	0.05	0.00	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	2.19	0.54	1.99	5.06	1.93	2.69	12.01	3.86	0.40
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	0.01	0.00	0.00	0.00	0.00	0.00	0.05	0.11	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Clus	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermiti	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Treponema_2	0.00	0.01	0.00	0.01	0.00	0.00	0.46	0.01	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Trinervitermes_cluster_a	0.12	0.21	0.24	0.40	0.29	0.31	0.35	1.43	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;unclassified	1.91	1.25	2.39	5.82	3.74	3.18	5.43	11.52	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_4	0.00	0.01	0.02	0.10	0.01	0.03	0.00	1.05	0.64
Spirochaetes;Spirochaetes;Spirochaetales;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Synergistetes;Synergistia;Synergistales;Synergistaceae;Candidatus_Tammella	0.00	0.01	0.02	0.01	0.03	0.00	0.00	0.00	0.00
Synergistetes;Synergistia;Synergistales;Synergistaceae;unclassified	0.01	0.00	0.00	0.00	0.02	0.03	0.08	0.00	0.00
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_6	0.21	0.27	0.68	0.33	1.64	0.31	0.65	0.09	0.08
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_I	5.72	1.22	7.08	16.38	6.16	4.62	3.56	5.10	47.12
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_II	0.19	0.15	0.19	0.20	0.15	0.15	0.00	0.07	0.00
TG3;TG3;TG3_sp1;Termite_Cluster;unclassified	0.08	0.07	0.05	0.10	0.12	0.00	0.00	0.21	0.00
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;Nasutitermes_Cluster	0.38	0.08	0.24	0.82	0.28	0.21	0.49	1.13	1.36
TG3;TG3;unclassified;unclassified;unclassified	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Verrucomicrobia;OPB35_soil_group;unclassified;unclassified;unclassified	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0.02	0.01	0.01	0.05	0.15	0.18	0.08	0.01	0.00
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;unclassified	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Verrucomicrobia;Opitutae;vadinHA64;unclassified;unclassified	0.02	0.03	0.00	0.01	0.03	0.00	0.03	0.00	0.00
Verrucomicrobia;Spartobacteria;Chthoniobacter;unclassified;unclassified	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;unclassified;unclassified	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Akkermansia	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;Prosthecobacter	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
unclassified;unclassified;unclassified;unclassified;unclassified	2.44	0.74	2.05	0.63	0.91	1.22	0.97	1.14	0.00

Supplementary Table 4 from Chapter 3: Distribution and relative abundance of the pyrotag reads in all samples.

	Relative abundance (%)													
Taxon	E. capucina	S. lateralis	S. macroptera	H. flexivitta	E. chopardi	E. floridiana	D. punctuata	O. orientalis	R. maderae	E. posticus	P. spec	S. lampyridif	B. orientalis	P. angu. H1
1_Proteobacteria;1_Deltaproteobacteria;1_Desulfobacterales;1_Nitrospinaceae;Candidatus_Entotheonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0.06
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Chloroacidobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Solibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Terriglobus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0.04
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_22	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_23	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_26	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_27	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_31	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;Holophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;Ilumatobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;marine_group	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Candidatus_Microthrix;Candidatus_Microthrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Iamiaceae;Iamia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;marine_group_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;marine_group_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_4;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_5;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_6;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Actinobacteria;Actinobacteria;Actinomycetales;Acidothermaceae;Acidothermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_2	0.02	0	0	0	0.06	0	0.05	0.1	0.01	0.08	0.03	0	0	0.06
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_3	0	0	0	0	0	0.02	0	0.01	0.03	0.02	0.05	0	0.01	0
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;Salana	0	0	0	0	0	0	0	0	0	0.11	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;unclassified	0.02	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Brevibacteriaceae;Brevibacterium	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0.02
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Actinotalea	0	0	0	0	0	0	0	0	0	0	0.16	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas_2	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Oerskovia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0.08	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Demequina;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;Brachybacterium	0	0	0	0	0	0	0.02	0	0	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales;Dermacoccaceae;Demetria	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Dermacoccaceae;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Frankiaceae;Frankia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_saxobsidens	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Humihabitans	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Janibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Lapillicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Terrabacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Terracoccus_sp_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Quadrisphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Agromyces_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Frigoribacterium_2	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Humibacter_albus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leucobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Microbacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Pseudoclavibacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Kocuria_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;unclassified	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Yaniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nakamurellaceae;Nakamurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Kribbella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Marmoricola	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Nocardioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonospiraceae;Cellulosimicrobium_	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Myceligenerans_xiligouense	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Xylanimonas_	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Aestuariimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Brooklawnia_cerclae	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Tessaracoccus	0.05	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Sanguibacteraceae;Sanguibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;unclassified;unclassified	0.93	0.11	0	0.43	0.01	0.02	0	0.04	0.02	0.62	0.08	0	0	0.09
Actinobacteria;Actinobacteria;Actinomycetales;uncultured_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Catenulisporaceae;Catenulispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptacidiphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_1	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unclassified	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unpublished_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Actinospicaceae;Actinospica	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_1	0.02	0.11	0.12	0.14	0.06	0	0.07	0.05	0	0.02	0.27	0.06	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_atypicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_spheniscorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;unclassified	0	0.03	0.02	0	0.01	0	0.04	0.03	0.01	0.01	0.03	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Dietziaceae;Dietzia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Millisia_brevis;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Mycobacteriaceae;Mycobacterium	0.03	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae_1;Gordonia	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_1;Amycolatopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_1;Saccharopolyspora	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_2;Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_3;Goodfellowiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_4;Crossiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_4;Kutzneria_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Segniliparaceae;Segniliparus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Tsukamurellaceae;Tsukamurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;unclassified;unclassified	0.03	0	0	0.14	0.03	0	0	0	0	0	0.08	0.06	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;uncultured;unclassified	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_3;PeM15;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_3;Sporichthyaceae;Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinoplanes_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinoplanes_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Dactylosporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Krasilnikovia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Luedemannella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonosporaceae_bacteria_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Nocardiopsaceae;Nocardiopsis_1	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Microbispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Sphaerisporangium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Streptosporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinoallomurus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinocorallia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;AKIW543;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Aeriscardovia_aeriphila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium_2	0	0	0	0.07	0	0	0	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium_4	0.02	0	0	0.07	0.01	0	0	0.08	0	0.28	0	0.02	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Gardnerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia_criceti	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;unclassified	0.13	0	0	0	0	0.03	0	0.37	0.07	1.48	0.08	0.06	0.02	0
Actinobacteria;Actinobacteria;Bogoriella_caseilytica;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;marine_group	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;unclassified	0.02	0	0	0	0	0.01	0	0.04	0.04	0.02	0.03	0	0.02	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_10	0.28	0.08	0.04	0.21	0.31	0.13	0.44	0.46	0.35	0.38	0.3	0.28	0.07	0.33
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_11	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_8	0.02	0	0	0	0	0	0	0	0	0	0	0.04	0.01	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Actinobacteria;Actinobacteria;MB-A2-108;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;RL185-aaj71c12;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteriaceae;Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;0319-6M6;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;288-2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;480-2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Conexibacteraceae;Conexibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Patulibacteraceae;Patulibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Solirubrobacteriaceae;Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;TM146;unclassified	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;YNPFFP1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;unclassified;unclassified;unclassified	0.07	0	0	0.07	0	0	0	0.03	0.02	0.02	0	0.02	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.93	1.85	3.81	0.35	0.6	1.42	0.93	1.61	0.21	0.05	0.03	1.4	0.51	0.04
Bacteroidetes;Bacteroidia;Bacteroidales;CAP-aah99b04;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;COB_P4-1_termite_group;unclassified	0.61	0	0	0.21	0.32	0.15	0.09	0.21	0.11	0.02	0	0.92	0.45	0.74
Bacteroidetes;Bacteroidia;Bacteroidales;gir-aah93h0;unclassified	0	0	0	0	0	0.01	0	0.01	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_cluster_a;unclassified	2.08	0	0	0.57	2.19	5.83	0	0.48	0.41	0.11	0.11	0.14	0.11	1.24
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;3M1PL1-52_termite_group	0	0	0	0	0	0	0	0	0	0	0	0	0	0.91
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Hodotermes_Cluster	0.48	0	0	0	0	0.05	0	0.02	0.01	0.01	0.03	0	5.93	0.13
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.09	0.19
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Wood_feeding_roaches	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;unclassified	0.18	0	0.32	0	0	0	0	0.01	0	0	0	0	0	0.06
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_a	1	0	0.36	0.43	0.99	0.16	0.49	0.85	0.21	0.02	0.05	0.22	0.55	1.43
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_b	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_c	0.08	0.08	0.18	0.07	0	0.44	0	0	0.01	0	0	0.02	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Alkaliflexus	0	0.1	0.06	0	0	0.05	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured_1	0.98	1.09	0.54	0.14	0.97	0.14	0.04	0.16	0.82	1	0	5.31	0.31	0.65
Bacteroidetes;Bacteroidia;Bacteroidales;MgMjR-022;unclassified	0.1	0	0	0	0	0	0	0.03	0	0	0	0	0	0.33
Bacteroidetes;Bacteroidia;Bacteroidales;Nearly_all_Termite_Cluster;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;p-2534-18B5_gut_group;termite_group_a	0	0	0	0	0	0.01	0	0	0	0	0	0	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Paludibacter	1.05	1.38	1.57	0.21	1.27	1.87	1.33	1.67	1.6	0.18	0.24	2.14	1.06	4.39
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;unclassified	0	0	0	0	0	0	0	0	0.02	0	0	0	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Candidatus_Symbiothrix	2.54	4.83	0.36	1.06	1.55	1.03	4.85	2.61	1.63	0.07	0.03	1.47	0.72	5.3
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Dysgonomonas	0.23	2.71	3.85	1.84	1.18	1.74	1.26	1.25	1.22	0.7	1.95	2.77	1	0.19
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Parabacteroides	0.86	3.15	0.59	1.06	0.56	3.63	0.67	0.44	0.91	0.11	0.14	2.83	2.13	0.13
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Tannerella	0.15	0.31	0.22	0.21	0.15	0.08	0.33	0.16	0.17	0.01	0.03	0.14	0.01	0.11
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;unclassified	0.27	0.13	0.14	0.14	0.31	0.1	0.18	0.09	0.06	0.1	0.27	0.59	0.01	0.24
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_2;Cubitermes_Cluster_A	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_2;Proteiniphilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Butyricimonas	0	0	0	0	0	0	0	0	0.02	0	0	0.08	0.35	0

Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Odoribacter	0	3.49	0.22	0.07	0	0.14	0	0	0	0	0	0	0.1	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Shelfordella_cluster_a	0.03	0.34	0.95	0.14	2.15	0.14	0	0.26	0.18	0.12	0.05	0.88	3.71	0.07
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;unclassified	0.02	0	0.02	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;uncultured_b	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;uncultured_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;ratAN060301C;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	5.42	12.17	11.56	4.68	13.03	16.65	14.26	7.19	12.41	7.04	4.87	13.29	15.35	3.11
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;BCf9-17_termite_group	0.02	0	0.04	0	0	0.02	0	0.02	0.01	0.01	0	0	0.02	0.17
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_a	0.02	0	0.36	0	0	0.01	0	0.03	0.35	0.01	0	0.33	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_c	0.27	0.95	0.46	0.64	0.22	0.39	0.98	1.9	1.12	0.1	0.49	1.02	0.16	0.2
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;M2PB4-61_termite_group	0.02	0.1	0	0	0	0.01	0	0.71	0.02	0.01	0	0.02	0.01	0.54
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;P1_32_Panesthia	0.8	0.29	2.12	1.49	0.38	1.81	0.65	2	6.23	0.42	1.33	1.77	0.27	2.76
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;RC9_gut_group	0.4	0.03	0.24	0.85	0.44	0.01	0	0.45	0.26	0.03	0	0.37	0.86	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_1	0.03	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_3	0.02	0	0.02	0.07	0	0.01	0.02	0.02	0.01	0	0	0	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_4	0.02	0	0	0	0.15	0	0	0	0.02	0	0	0	0	0.02
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rs-D38_termite_group	0.05	0.19	0.18	0.21	0.63	0.12	0.28	0.69	0.22	0.07	0.24	0.49	0.19	0.2
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;unclassified	1.16	0.61	1.03	1.28	1.85	0.84	0.63	1.15	1.62	0.45	0.89	1.57	0.55	1.46
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;vadinBC27_wastewater-sludge_group	0	0	0	0	0.03	0.05	0	0.02	0	0	0	0	0	1.56
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_aa	0	0.02	0	0	0.01	0.02	0	0.01	0	0.01	0.03	0.02	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_bb	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;higher_termites_a	0	0	0	0	0	0.01	0	0	0.01	0	0	0	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;unclassified	0	0.02	0	0	0.01	0.01	0	0	0	0	0	0	0.01	0
Bacteroidetes;Bacteroidia;Bacteroidales;S24-7;unclassified	0.05	0	0	0	0.06	0	0	0	0	0.18	0.24	0.14	0	0.06
Bacteroidetes;Bacteroidia;Bacteroidales;unclassified;unclassified	0.73	0.75	0.85	0.64	0.44	0.86	0.37	0.89	0.6	0.48	1.06	1.38	0.92	1.3
Bacteroidetes;Bacteroidia;Bacteroidales;uncultured_bacterium_Cylindroiulus_2;unclassified	0	0.61	0.02	0	0.06	0.16	0.07	0.03	0.08	0	0	0.16	0.24	0
Bacteroidetes;Bacteroidia;Bacteroidales;vadinHA21;unclassified	2.09	0.55	0.16	1.98	5.17	0.09	0.72	0.28	0.02	0.06	0	0.04	3.28	1.37
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;Blattabacterium	0.85	5.33	13.54	0.99	0.15	0.7	3.17	0.85	0.16	14.09	8.74	3.34	1.26	0.59
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;unclassified	0	0	0	0	0	0.01	0	0	0.01	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Flavobacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Galbibacter_mesophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Lutaonella_thermophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Bergeyella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_12	0	0	0	0	0	0	0	0.01	0	0	0	0.16	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_5	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_molle	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_pallidum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_soldanellicol	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_sp._CCUG_15624	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Elizabethkingia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Empedobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;unclassified	0.02	0	0	0	0	0	0	0	0	0.01	0.16	0.04	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;uncultured_a	0	0	0	0.07	0	0.04	0	0.09	0.07	0.05	0.03	0.04	0.11	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Wautersiella_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Weeksella	0.08	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Bacteroidetes;Flavobacteria;Flavobacteriales;unclassified;unclassified	0.05	0.02	0.02	0	0	0.04	0	0	0.02	0.05	0.03	0.02	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;SB-1;unclassified	0	0	0	0.85	0	0	0.07	1.53	0	0.08	0	0	0.02	1.13
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Mucilaginibacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Mucilaginibacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Nubsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;ST-12K33;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;vadinHA17;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.09
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;WCHB1-69;unclassified	0	0.02	0	0	0	0	0	0.01	0	0	0	0	0.3	0.13
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Niabella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	1.58
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.06
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_1;Flexibacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_2;Sporocytophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;unclassified;unclassified	0	0	0	0	0	0.02	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;unclassified;unclassified;unclassified	0	0.02	0.02	0	0	0.04	0	0.01	0	0	0	0	0	0.06
Bacteroidetes;unclassified;unclassified;unclassified;unclassified	0.2	0.22	0.3	0.14	0.07	0.69	0.05	0.35	0.22	0.27	0.38	0.71	0.32	0.39
Bacteroidetes;VC2.1_Bac22;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0.02
BD1-5;unclassified;unclassified;unclassified;unclassified	0.12	0.08	0	0.07	0.13	0.17	0.02	0.02	0.03	0.01	0.11	0.02	0	0
Candidate_division_BRC1;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_OD1;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_OP10;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_OP11;unclassified;unclassified;unclassified;unclassified	0.42	0.56	0.14	0.35	0.1	0.11	0.21	0.33	0.3	0.55	0.22	0.04	0.17	0.19
Candidate_division_SR1;unclassified;unclassified;unclassified;unclassified	0	0.51	0	0	0	0.07	0	0.01	0	0.06	0.16	0	0.06	0
Candidate_division_TM6;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_TM7;unclassified;unclassified;unclassified;unclassified	1.59	2.18	0.06	1.49	1.37	1.6	1.51	1.77	0.9	3.23	0.57	0.75	0.72	2.39
Chlamydiae;Chlamydiae;Chlamydiales;cvE6;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Candidatus_Protochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Neochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus_Rhabdochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlorobi;Chlorobia;Chlorobiales;OPB56;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlorobi;Chlorobia;Chlorobiales;SJA-28;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Chloroflexi;Chloroflexales;Chloroflexaceae;Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Gitt-GS-136;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;JG37-AG-4;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;KD4-96;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Ktedonobacter;Ktedonobacter;Ktedonobacter;Ktedonobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;S085;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Thermomicrobia;AKYG1722;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Thermomicrobia;JG30-KF-CM45;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Thermomicrobia;Sphaerobacteridae;Sphaerobacterales;Sphaerobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;TK10;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;unclassified;unclassified;unclassified;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;vadinBA26;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;4C0d-2;unclassified	0	0	0.04	0	0	0	0	0	0.01	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;Chloroplast;Chloroplast	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;ML635J-21;unclassified	0	0	0	0	0	0.01	0	0.01	0.02	0	0	0.02	0.01	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;MLE1-12;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionII;SubgroupII_Chroococcidiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionIII;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionIV;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionV;Stigonema	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;WD272;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02

Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Mucispirillum	0.03	0.8	0.63	0	0.1	0.14	0.04	0.23	0.13	0.04	0.65	0.29	0.1	0.22
Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;unclassified	0	0.02	0	0	0	0	0	0.02	0	0	0	0	0	0.02
Deinococcus-Thermus;Deinococcus-Thermus;Deinococcales;Deinococcaceae;Deinococcus	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0
Deinococcus-Thermus;Deinococcus-Thermus;Deinococcales;Trueperaceae;Truepera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_I_[Endomicrobia]	0.15	0.24	0.63	0.21	0.13	0.06	0.26	0.59	0.14	0.55	0.11	0.08	0.15	0.54
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_III_[Elusimicrobium]	0.03	0.96	0.4	0.07	0.01	0.02	0	0.03	0.1	0.38	0.16	0.08	0.3	0.3
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;unclassified	0.02	0	0	0	0	0.01	0	0	0	0.01	0	0	0.09	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;uncultured_d	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fibrobacteres;Fibrobacteres_sp1;Fibrobacterales;Fibrobacteraceae;Fibrobacter	0.02	0	0	0.14	0	0.01	0	0.01	0.02	0.08	0	0	0	0
Fibrobacteres;Fibrobacteres_sp2;Fibrobacteres_sp2;Termite_Cluster;Termite_Cluster_I	0	0	0	0.14	0	0.03	0	0.03	0.03	0.02	0.03	0.02	0.02	0
Fibrobacteres;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Apr-15;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_11	1.45	0	0	0	0	0	0.02	0	0	0.01	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_12	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_3;Bacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_5;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_6;Bacillus_2	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Family_XII_Incertae_Sedis;Exiguobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Listeriaceae;Brochothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Listeriaceae;Listeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_1;Oxalophagus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Brevibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Cohnella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_16	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Caryophanon	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_1	0	0.06	0.04	0	0.01	0.01	0	0	0	0	0	0.02	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_2	0	0.02	0.02	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Firmicutes;Bacilli;Bacillales_2;Thermoactinomycetaceae;Shimazuella	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Firmicutes;Bacilli;Lactobacillales;16d63.751;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;Eremococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Carnobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Carnobacterium_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Trichococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Catellicoccus_marimammalium;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_2	0.23	0.03	0	0.78	1.77	0.04	1.94	0.21	0.74	4.52	0.32	0.75	0.46	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_4	0.07	0.34	0.81	0.07	0.19	0.09	1.84	0.06	0.13	0.05	0.3	0.45	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_5	0.02	0.05	0	0.21	0.81	0.02	0.04	0.06	0.39	0.05	0.6	0.26	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_7	0	0.02	0	0	0	0	0	0	0	0.01	0.05	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Pilibacter	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;unclassified	0.1	0.22	0.04	0.28	0.71	0.35	1.56	0.14	0.51	0.11	0.08	1.57	0.17	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Vagococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;Enterococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;Enterococcus_3	0.05	0	0	0	0	0	0.09	0	0	0.01	0	0	0.01	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;unclassified	0	0	0	0	0.01	0	0	0.01	0.02	0.02	0	0	0.01	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_1	0	0	0.04	0	0.07	0	0.19	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_sp._R-25205	0	0	0	0	0.01	0.01	0	0	0.02	0	0	0.04	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;unclassified	0	0	0.02	0	0.79	0.01	0.02	0.03	0.21	0.03	0.05	0.12	0.02	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;uncultured_a	0	0	0	0	0.07	0	0	0.01	0.04	0.01	0	0.04	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcus_phoeniculicola;unclassified	0	0	0	0	0	0	0	0	0.02	0.01	0	0.02	0	0
Firmicutes;Bacilli;Lactobacillales;Hodotermopsis_Trichonympha_Symbiont_1;unclassified	0	0	0	0	0.09	0.01	0.02	0.01	0.02	0.03	0	0.04	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_1	0.35	0	0	0.14	0.09	0	0.02	0.67	0.23	0.46	0	0.06	0.01	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_2	0.07	2.41	2.89	0	0.09	0	0.02	0	0.02	0.02	0	0	0.06	0.02
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_3	0.25	0.08	0.06	0	0.1	0	0	0.15	0.01	0.22	0.08	0.02	0.01	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_4	1.91	0	0.14	1.35	0.52	0.02	0.46	1.67	1.45	1.5	0.19	1.49	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_5	4.52	0	0	0.35	1.71	0.02	0.02	0.32	0.07	1.39	0.08	0.1	0.05	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_6	0	0.02	0	0	0.46	0	0.02	0.02	0.02	0.01	0	0	0.01	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_9	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_sp_a	0	0.1	0	0	0	0	0	0	0	0	0	0	0.22	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Paralactobacillus	0	0.19	0	0	0	0	0	0	0	0	0	0	0.07	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Pediococcus	0.17	0.88	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;unclassified	1.54	0.47	2.1	0.57	0.31	0.02	0.77	1.08	1.18	0.81	0.32	0.73	0.05	0.02
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Fructobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Hm_96	0	0	0	0	0	0	0.02	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;HsjTcB_43	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	0	0	0.02	0	0.01	0	0	0	0	0	0	0.35	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc_fallax	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Oenococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;unclassified	0	0	0	0	0	0	0.04	0	0.02	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_1	0.02	0	0	0	0.01	0	0.54	0.03	0.02	0	0	0.04	0.01	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_2	0	0	0	0	0	0.01	0	0	0	0	0	0.02	0.02	0
Firmicutes;Bacilli;Lactobacillales;PeH08;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Rs-D42;unclassified	0	0	0	0	0	0.01	0	0	0.02	0.02	0.03	0.02	0.01	0
Firmicutes;Bacilli;Lactobacillales;Sl_24;unclassified	0	0	0	0.07	0.01	0.05	0	0.08	0.07	0.11	0.08	0.04	0.04	0
Firmicutes;Bacilli;Lactobacillales;Sl_99;unclassified	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_1	0	0.03	0.16	0	0.03	0.11	1.59	0.02	0.55	0.01	0.51	0.06	1.62	0.02
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_2	0.02	0	0.08	0	0.01	0.03	0.19	0.01	0.11	0	0.08	0.04	0	0.02
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_3	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactovum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;unclassified	0	0	0	0.07	0	0.03	0.42	0.01	0.12	0.01	0.16	0	0.07	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;unclassified;unclassified	0.56	0.22	1.8	1.84	4.81	0.3	1.72	0.93	1.92	1.43	1.14	0.69	0.32	0.02
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Hepialus;unclassified	0	0	0	0	0	0.01	0	0	0.01	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Pachnoda_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;unclassified;unclassified;unclassified	0.03	0	0.02	0.07	0.01	0	0	0.02	0.02	0.02	0.03	0.04	0.02	0.02
Firmicutes;Bacilli;VAN12;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;CK-1C4-19;unclassified;unclassified;unclassified	0.02	0	0	0.21	0.19	0.03	0.33	0.02	0.01	0.09	0.19	0.02	0	0.02

Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Anaerobacter_polyendosporus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_6	0	0.47	0	0	0	0.74	0	0	0	0.01	0	0.02	0	0.11
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_8	0.02	0.47	0	0.43	0.01	0.97	0	0.02	1.41	0.03	1.98	0.06	0.05	0.17
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;unclassified	0	0.03	0	0.07	0	0.07	0	0.03	0.06	0	0.05	0	0.01	0.04
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_2;Alkaliphilus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Dethiosulfatibacter_aminovoran;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Anaerofustis	0.08	0.02	0	0	0.07	0.02	0.05	0.03	0.05	0.05	0.03	0.1	0	0.04
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_1	0	0	0	0.07	0.03	0	0.04	0.02	0.07	0.02	0	0.02	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_2	0.03	0	0	0	0.01	0	0	0.01	0	0.01	0	0.02	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Pseudoramibacter	0.05	0	0	0.07	0	0.02	0.04	0.09	0	0	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;unclassified	0.18	0.02	0	0.21	0.34	0.01	0.12	0.21	0.02	0.2	0.3	1	0.02	0.09
Firmicutes;Clostridia_1;Clostridiales;Family_XI_Incertae_Sedis;Anaerococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XI_Incertae_Sedis;Tissierella_3	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Anaerovorax_	0.02	0.05	0	0	0.24	0.02	0.05	0.05	0.02	0.03	0.03	0	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_2	0	0.05	0	0	0	0	0	0	0	0.09	0	0	0.05	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_3	0	0.14	0.02	0	0.01	0.01	0	0.13	0	0.01	0.11	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;unclassified	0.4	0.1	0	0.14	0.04	0.16	0.14	0.15	0.04	0.16	0.08	0.1	0.34	0.07
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_1	0	0	0	0.21	0	0.01	0	0.09	0.05	0.01	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_4	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_5	0.23	0.45	0.04	0.5	0.59	0.42	0.19	0.48	0.46	0.67	0.03	0.33	0.1	1.35
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_6	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Gracilibacteraceae;Lutispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Gracilibacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Anaerostipes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Butyrivibrio_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Butyrivibrio_fibrisolvens	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Catabacter	0.33	0.21	0.14	1.13	0.34	0.13	0.68	0.28	0.4	0.67	0.14	0.16	0.16	0.43
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Clostridiales_bacterium_HAW-EB17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Coprococcus_1	0	0.06	0	0	0	0.02	0	0.15	0	0.01	0	0	0.06	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Hespellia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_11	0	0.05	0	0.14	0	0.08	0	0.01	0	0.02	0.05	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_13	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_16	0	0	0	0	0.01	0	0	0.01	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_18	0	0	0	0	0	0	0	0	0.01	0.01	0	0	0	0.04
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_24	0.02	1.28	0.24	0.07	1	1.16	0.47	1.46	1.39	0.77	0.49	1.83	0.5	0.02
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_25	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_26	0	0	0	0	0	0	0.05	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_3	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_30	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_31	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_32	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_34	0.05	0.05	0	0.07	0.16	0.25	0.16	0.05	0.71	0.08	0.16	0.02	0.22	0.02
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_35	0.02	0.03	0	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_36	0.32	1.06	1.41	0.71	0.09	0.51	0.74	0.5	0.14	0.21	0.73	0.28	0.44	0.43
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_8	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Marvinbryantia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Mmba_A01b	0	0.02	0.02	0.07	0	0.03	0	0	0	0	0.14	0	0	0.02
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Parasporobacterium-Sporobacterium	0	0	0	0.14	0.03	0	0.02	0.03	0.06	0.01	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_higher_Termites	0	0	0	0	0	0	0	0.01	0	0	0	0	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_Insects	0.03	0.26	0.04	0	0.12	0.24	0.05	0.14	0.13	0.03	0.08	0.22	0.04	0

Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;unclassified	6.26	6.78	4.78	4.39	3.99	11.09	1.63	2.36	2.68	2.79	2.57	2.79	3.64	1.98
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_1	0.48	0.03	0	0	0	0.12	0	0.01	0	0	0	0	0.07	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_10	0.03	0	0	0	0.37	0.02	0.02	0.03	0.01	0.19	0	0.26	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_11	0.02	0	0	0	0	0	0	0.02	0	0.01	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_13	0.05	0.13	0.24	0.07	0.01	0.15	0.04	0.05	0.03	0.01	0.24	0.14	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_14	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_22	0	0	0	0	0	0	0.04	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_23	0	0	0	0	0	0.15	0	0.02	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_27	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_31	0	0.02	0	0	0	0.02	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_47	0	0	0	0	0	0.01	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_48	0.03	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_50	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_51	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_54	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_56	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_58	0.1	0.02	0	0.07	0.34	0.02	0	0.03	0.02	0.05	0.03	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_59	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_6	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_61	0	0	0	0	0.04	0.09	0	0.01	0.18	0.01	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_62	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_63	0	0	0	0	0	0.01	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_64	0	0.05	0	0	0	0.04	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_65	5.1	3.47	1.63	4.54	4.49	3.12	4.61	3.28	3.24	10.56	4.22	4.68	3.55	3.78
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_66	0.12	0	0.06	0	0.03	0.05	0.04	0	0.02	0.03	0.03	0.02	0	0.06
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_67	0.38	0.67	0.73	0.14	0.37	0.36	0.35	0.32	0.21	0.61	0.24	0.67	0.69	1.26
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_68	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_1	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_3	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_5	0.6	0.11	0.04	0.71	0.35	0.01	0.05	0	0.38	0.02	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Sporacetigenium_mesophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;unclassified	1.03	1.93	0.16	0.21	1.12	0.32	0.05	0.01	0.59	0.28	0.03	0.08	0.22	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_2	0	0	0	0	0	0	0	0.01	0.01	0.01	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_3	0.15	0.11	0	0	0	0.03	0	0	0	0	0	0	0.05	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Acetanaerobacterium	0.02	0	0	0	0.01	0	0	0	0	0	0	0	0.01	0.02
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerofilum	0	0	0	0	0	0.02	0.02	0	0	0	0	0	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerotruncus	4.07	0.58	0.08	0.43	3.21	0.67	0.4	0.87	0.58	0.17	0.03	0.49	0.16	0.57
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Butyricicoccus_pullicaecorum	0	0.02	0	0	0	0	0	0.01	0	0	0.03	0	0	0.02
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_alkalicellulosi	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_clariflavum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_straminisolvens	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ethanoligenens	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Fastidiosipila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	0.27	0.08	0.1	0	0.16	0.06	0.28	0.1	0.12	0.03	0.03	0.02	0.04	0.43
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_1	0.1	0.18	0	0	0	0.2	0	0.02	0.02	0.09	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_3	0.02	0.11	0	0	0	0.01	0	0.01	0	0.01	0	0.2	0.71	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_4	0.08	0.88	0.38	0.07	0.78	0.53	0.23	0.11	0.19	0.43	0.14	0.2	0.76	0.89
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_5	0.47	0.35	0.08	0.07	0.24	0.17	0.53	0.42	0.37	0.3	0.38	0.1	0.22	0.06
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_6	0.13	0.14	0	0.21	0.25	0.37	0.18	0.44	0.17	0.03	0.05	0	0.25	0.02
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_7	0	0.03	0	0	0	0.02	0	0.09	0.01	0.02	0.05	0	0.01	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_8	0	0	0	0	0.01	0.13	0	0	0.01	0.03	0	0	0.17	0.07
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;insect_guts_a	1.96	2.01	1.8	2.06	2.56	2.72	3.61	4.51	2.15	2.68	1.41	4.66	1.41	0.35
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Oscillibacter	0.02	0	0	0	0.01	0.02	0	0	0.01	0	0	0	0	0.04
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Oscillospira	0	0	0	0	0	0.06	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Papillibacter	0.25	0	0.1	1.98	0.18	0.19	0.07	0.2	0.21	0.39	0	0.04	0.05	1.8
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_1	0.68	0	0	0.07	0.97	0.83	0	0.09	0	0.55	0.03	0.06	0	0.04
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_2	0.1	0.13	0	0.07	0	0.03	0.11	0	0.01	0.03	0	0	0.04	0

Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Sporobacter	0	0	0	0.07	0.03	0	0	0.01	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Termite_group_aaa	0	0	0	0.07	0	0.02	0	0.03	0.02	0.01	0.03	0.02	0.06	0.87
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;unclassified	3.55	0.98	0.71	2.62	2.03	2.33	1.38	1.62	1.46	1.01	0.46	1.12	3.71	6.66
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_10	0.07	0	0	0.28	0.18	0.17	0	0.01	0.05	0.01	0	0	0.11	0.41
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_11	1.15	1.01	3.01	0.92	0.63	1.33	1.24	0.58	1.02	0.28	0.87	0.81	0.51	1.59
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_12	1.38	0.1	0.18	0.92	0.74	1.5	1.49	1.3	0.63	0.2	0	0.28	1.15	3.86
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_13	0	0	0	0	0	0	0.04	0.01	0.02	0	0	0	0.07	0.02
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_23	0.03	0	0	0.07	0.06	0.06	0	0.03	0.03	0.01	0.03	0.02	0.01	0.09
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_24	0.07	0.05	0.08	0	0.01	0.09	0.02	0.05	0.02	0.01	0.11	0.04	0	0.5
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_25	0.53	0.08	0.02	1.35	0.35	0.54	0.14	0.99	0.92	0.11	0.08	0.02	0.27	0.89
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_26	0	0	0	0	0.01	0	0	0	0.01	0.01	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_27	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_28	0.4	0.22	0.08	0.28	0.47	0.45	0.49	0.51	0.4	0.18	0.03	0.43	0.57	0.65
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_29	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_30	0.33	0.06	0	0.5	0.31	0.43	0.12	0.15	0.14	0.29	0.03	0.14	0.12	1.97
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_33	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_34	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_35	0.25	0	0	0.21	0.12	0.62	0.04	0.02	0.03	0.08	0	0.02	0.05	0.61
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_36	0.86	0.26	0.46	0.5	0.5	0.75	0.79	0.35	0.33	0.2	0.11	0.14	0.71	1.54
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_9	0	0	0	0	0	0	0.07	0	0.02	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;unclassified;unclassified	0.83	0.22	0.2	0.57	0.74	0.83	0.09	0.38	0.28	0.42	0.35	0.31	0.37	1.26
Firmicutes;Clostridia_1;unclassified;unclassified;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Peptococcaceae;Desulfitibacter	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Pelospora	0.13	0	0	0.07	0.03	0.01	0	0.02	0	0	0	0	0	0.02
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_1	0.08	0	0	0	0.09	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_2	0.18	0	0	0	0	0	0.02	0	0	0	0	0	0	0.04
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_3	0	0.02	0	0	0	0	0.04	0.01	0.01	0.01	0	0	0.01	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;unclassified	0.85	0	0	0.71	0.15	0.07	0.02	0.05	0.02	0.03	0.03	0	0	0.43
Firmicutes;Clostridia_2;Clostridiales_1;Heliobacteriaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;OPB54;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;P._palm_C;A_51	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;Thermincola	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;unclassified	0.18	0.16	0.06	0.07	0.12	0.05	0	0.16	0.02	0.02	0	0.06	0.09	0.33
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_2	1.41	0.03	0.1	0.28	0.5	0.21	0.07	0.15	0.11	0.11	0	0.06	0.22	1.78
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_3	0.23	0	0	0	0	0.02	0	0	0	0	0	0	0.02	0.02
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_4	0.07	0.02	0	0	0	0.03	0.07	0.09	0.01	0.03	0	0	0.05	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_5	0.02	0	0	0	0.04	0	0	0.03	0.05	0.02	0.03	0	0.01	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Dehalobacter	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Desulfosporosinus	0.03	0	0	0.07	0.06	0.02	0.02	0.03	0.01	0	0	0	0.01	0.02
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;uncultured_gut_Group_A	0	0	0	0	0	0	0	0	0.01	0	0	0.02	0	0.02
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Desulfotomaculum_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Pelotomaculum_3	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04
Firmicutes;Clostridia_2;Clostridiales_1;unclassified;unclassified	0.07	0	0	0.07	0	0	0	0	0.02	0.01	0	0	0.01	0.07
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acetonema_a	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acidaminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaeroarcus-Anaeromusa	0	0.14	0	0	0	0	0	0.01	0	0	0.19	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaerospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaerovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Dendrosporobacter	0.17	0.02	0.04	0.14	0.1	0.04	0.07	0.15	0.25	0.07	0	0.02	0.01	0.57
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Megamonas	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Phascolarctobacterium	0.28	0.4	0	0.43	0.44	0.95	0	0.15	1.11	4.35	0.54	0.14	1.23	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Sporomusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Succinispira_mobilis	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0.02
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Thermosinus	0	0	0	0	0	0	0	0.01	0.01	0	0	0	0.01	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;unclassified	0	0	0	0.07	0.03	0.07	0	0.04	0.14	0.26	0.08	0.02	0.12	0.07
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_6	0	0	0	0	0	0.01	0	0	0.01	0.01	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_7	1.23	2.28	0.36	1.13	0.43	0.55	0.68	0.98	2.36	1.04	1.06	0.41	0.27	0.43
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_8	0.18	0.14	0.04	0.21	0.24	0.21	0.05	0.03	0.14	0.05	0.03	0	0.4	0.13
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Veillonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Thermoanerobacterales;Thermoanaerobacteraceae;Gelria	0	0	0	0	0.04	0	0	0.02	0	0.01	0	0	0	0.02
Firmicutes;Clostridia_2;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0.06
Firmicutes;Clostridia_3;Clostridiales;Syntrophomonadaceae;Dethiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Asteroleplasma	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Bulleidia_extructa	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Erysipelothrix	0	0	0	0	0	0.01	0	0.01	0.02	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Incertae_Sedis_8	0	0	0	0	0.04	0.02	0	0.01	0.02	0	0	0.02	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Turicibacter	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;uncultured_3	0	0.03	0	0	0	0	0	0	0.01	0	0	0.02	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_2	0.15	0.63	0	0.07	0.74	0.11	0	0.28	0.05	0.66	0.11	0	0.07	0.46
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_3	0.03	0	0	0	0	0	0	0	0	0.01	0	0	0.01	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;unclassified	0.07	0	0	0	0.01	0	0	0	0	0.02	0.05	0	0	0
Firmicutes;Mollicutes;Anaeroplasmatales;Anaeroplasmataceae;Anaeroplasma	0.02	0	0	0	0	0.49	0	0	0.01	0.02	0	0.06	0	0.02
Firmicutes;Mollicutes;EMP-G18;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Firmicutes;Mollicutes;Entomoplasmatales;Entomoplasmataceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Entomoplasmatales;Spiroplasmataceae;Spiroplasma_2	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;RF9;unclassified;unclassified	0	0	0	0	0.04	0.02	0	0.01	0	0	0	0	0	0
Firmicutes;Mollicutes;unclassified;unclassified;unclassified	0.02	0	0	0	0	0.02	0	0.02	0.01	0.11	0	0	0	0
Firmicutes;RF3;unclassified;unclassified;unclassified	0.02	0	0	0.07	0.03	0.02	0	0.03	0	0.1	0	0	0.07	0.09
Firmicutes;unclassified;unclassified;unclassified;unclassified	0.7	0.11	0.06	0.14	0.43	0.21	0	0.26	0.22	0.27	0.14	0.06	0.15	0.33
Fusobacteria;Fusobacteria;Fusobacteriales;ASCC02;unclassified	0.02	0	0	0.07	0.01	0.01	0	0.03	0.06	0.02	0.03	0.04	0.01	0
Fusobacteria;Fusobacteria;Fusobacteriales;boneC3G7;unclassified	0	0	0.02	0	0.03	0.13	0.04	0.03	0.03	0.03	0.08	0.04	0.02	0
Fusobacteria;Fusobacteria;Fusobacteriales;CFT112H7;unclassified	0.17	0.22	0	0.07	0.41	0.67	2.7	0.24	0.31	0.78	0.54	0.53	0.1	0.07
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Fusobacterium_1	0.02	0.14	0.46	0.5	0.97	1.4	0.23	0.01	1.48	0.22	0.41	1.08	0.02	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Ilyobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;unclassified	0	0.03	0	0.21	0.03	0	0.02	0.01	0.1	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Hados.Sed.Eubac.3;unclassified	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Sebaldella	0	0.1	0.06	0	0.28	0.57	0.02	0.35	0.03	0.7	1	0.47	0.02	0.06
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;unclassified;unclassified	0.03	0.13	0.12	3.26	0.62	0.48	1.51	2.02	3.76	0.23	0.24	0.33	0.07	0.02
Gemmatimonadetes;Gemmatimonadetes;AT425-EubC11_terrestrial_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;055B07-P-DI-P58;unclassified;unclassified	0	0	0	0	0.12	0	0	0.03	0	0.03	0	0	0	0
Lentisphaerae;Lentisphaeria;B01R017;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;BS5;unclassified;unclassified	0.22	0	0	0.21	0.21	0.01	0.02	0.24	0.09	0.92	0	0.02	0	0.52
Lentisphaerae;Lentisphaeria;c5LKS8;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;CVer-1_termite_group;unclassified;unclassified	0.1	0	0	0.28	0	0.01	0	0.04	0.48	1.28	0.03	0	0.69	0.93
Lentisphaerae;Lentisphaeria;CVer-2_termite_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.48
Lentisphaerae;Lentisphaeria;RFP12_gut_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;unclassified;unclassified;unclassified	0.03	0	0	0	0.09	0.01	0.02	0.3	0.16	0.44	0.03	0	0.32	0.85
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.09	0
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;Victivallis	0.07	0.02	0.5	0.43	0.12	0.27	0.37	0.38	0.1	0.49	0.19	0.45	1.03	1.43
Lentisphaerae;Lentisphaeria;WCHB1-25;unclassified;unclassified	0.07	0	0	0	0	0	0	0.03	0.01	0.62	0.05	0.06	0	0.43
Nitrospirae;Nitrospira;Nitrospirales;0319-6A21;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NPL-UPA2;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Planctomycetes;Phycisphaerae;CPla-3_termite_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;AKAU3564_sediment_group;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;ODP1230B30.02_sediment_group;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;AKYG587	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;CL500-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Pla1_lineage;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Pla4_lineage;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;CPla-4_termite_group	0.1	0	0	0.07	0	0	0	0.13	0	0.14	0	0.02	0	0.85
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Isosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir1_lineage	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir4_lineage	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pirellula	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Rhodopirellula	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Schlesneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Singulisphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Termite_planctomycete_cluster	0.33	0.22	0	0.78	0.04	0.16	0.16	0.2	0.51	0.79	0	0.1	0.07	1.17
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;unclassified	0.13	0.11	0	0.28	0.01	0.02	0.05	0.06	0.23	0.06	0	0	0.04	0.19
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_24	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_32	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_35	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_b	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Zavarzinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Planctomycetes;vadinHA49;unclassified;unclassified;unclassified	1.21	1.22	7.16	1.84	1.19	2.01	2.98	3.79	0.89	1.85	1.68	2.46	0.31	0.39
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_3	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Rhodobium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Aurantimonadaceae;Aurantimonas_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Brucella	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_2	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Aminobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Aminobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_loti	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_thiogangeticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Shinella_genera_incertae_sedis;Shinella_genera_incertae_sedis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;1174-901-12;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;alphaI_cluster_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;alphaI_cluster_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;BCf3-20;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;Chelatococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Afipia_1	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Afipia_birgiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Blastobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bosea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_japonicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_sp._CCBAU_61196	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Nitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Rhodoblastus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Rhodopseudomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0.27	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Prosthecomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Rhodomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae_1;Ancalomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Methylobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Microvirga	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylocystis_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylocystis_parvus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;unclassified;unclassified	0.02	0.05	0	0	0	0	0	0.14	0.08	0	0.24	0.02	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;Labrys	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;Pseudolabrys	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;DUNssu044;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Hyphomicrobium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Hyphomicrobium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Pedomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Methylobacteriaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Nordella;Nordella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Amaricoccus	0	0	0	0	0	0	0	0.01	0	0	0.05	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Palleronia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_1	0	0	0	0	0	0	0	0	0	0	0.14	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Rhodobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Roseobacter_clade_Ketogulonicigenium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;uncultured_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acetobacter	0	0.06	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidicaldus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidiphilium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidisoma	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Craurococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Rhodopila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Rubritepida	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;unclassified	0	0	0.1	0	0	0	0.04	0.02	0.02	0	0	0.02	0	0.06
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.09
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Marispirillum_indicum	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Telmatospirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Thalassospira	0.03	0.19	0.14	0.07	0.07	0.19	0.16	0.13	0.04	0.44	0.41	0.24	1.18	0.61
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;unclassified	0	0.02	0	0	0.03	0.03	0	0.07	0.01	0.04	0.03	0.02	0.06	0.09
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_2	0	0.02	0	0	0	0	0	0	0.01	0	0	0	0.04	0.07
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_a	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;unclassified;unclassified	0	0	0	0	0.01	0	0	0.03	0	0.02	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Candidatus_Alysiosphaera;Candidatus_Alysiosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;DA111;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;I-10;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;JG37-AG-20;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;MNH4;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;Azospirillum_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;Skermanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;wr0007;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;Wolbachia	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Captivus;Candidatus_Captivus	0	0	0	0	0	0.16	0	0.01	0.02	0.01	0	0.04	0.01	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Hepatincola;Candidatus_Hepatincola	0.07	0	0	0.07	0	0.01	0	0.01	0	0.36	0.03	0.04	0.06	0.02
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Midichloria;Candidatus_Midichloria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;Rickettsia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Ellin6055;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandarakinorhabdus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;unclassified;unclassified;unclassified	0.12	0.22	0	0.07	0.35	0.07	0	0.91	1.04	0.51	0.24	0.31	0.49	0.26
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Derxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Achromobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Bordetella_3	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Castellaniella	0.02	0	0	0	0	0	0	0.01	0	0	0.08	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;GKS98_freshwater_group	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Pandoraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_2;Ralstonia	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax_caeni	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caenimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_R	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ideonella_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Leptothrix_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ottowia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified	0	0	0	0.14	0	0	0.07	0.03	0.02	0	0.08	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_25	0.1	0.06	0.4	0	0.16	0.06	0.39	0.11	0.04	0.06	0.68	0.31	0.01	0.02
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_3	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xenophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified	0.05	0.02	0.14	0	0	0	0.02	0.01	0.02	0	0.03	0.02	0.02	0.02
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium	0.13	0.02	0.14	0	0	0.05	0.07	0.06	0	0.01	0.08	0.06	0.01	0.02
Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified;unclassified	0	0	0	0	0	0	0.02	0.01	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Leeia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Aquaspirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Microvirgula_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Stenoxybacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0.22	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;uncultured_1	0.02	0	0	0.21	0	0	0	0	0.01	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;uncultured_a	0	0	0	0	0	0	0	0	0	0	0.19	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas	0	0	0.18	0	0.01	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0

Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;Denitratisoma_oestradiolicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;unclassified	0.02	0.02	0	0	0	0	0	0	0	0	0.05	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azoarcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azoarcus_2	0.48	0.11	0	0	0.04	0	0	0	0	0	0.35	0.1	0	0.02
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;unclassified	0.3	0.06	0	0	0	0	0	0	0	0	0.16	0	0.01	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;uncultured	0	0	0.02	0.14	0	0	0	0	0	0	0	0.04	0.01	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Azonexus_caeni	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Dechloromonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;IC13_Millipede	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Lower_termite_Cluster	0	0	0	0.07	0	0.08	0	0.13	0.13	0.08	0.16	0.2	0.1	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Propionivibrio	0.02	0	0	0	0	0	0	0.01	0.01	0	0	0	0.01	0.06
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;unclassified	3.27	0	0	0	0	0.04	0	0.01	0.05	0.02	0.05	0.04	0.02	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_4	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;unclassified;unclassified	0.3	0.06	0	0.07	0.03	0.02	0	0.03	0.06	0.02	1.7	0.1	0.05	0
Proteobacteria;Betaproteobacteria;SC-I-84;unclassified;unclassified	0	0	0	1.42	0	0.01	0	0	0.49	0.01	0	0.06	0.01	0
Proteobacteria;Betaproteobacteria;TRA3-20;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;unclassified;unclassified;unclassified	1.4	0.05	0.06	0.57	0	0.02	0.04	0.69	0.53	0.06	1.6	0.26	0.04	0
Proteobacteria;Deltaproteobacteria;43F-1404R;unclassified;unclassified	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Bacteriovorax_2	0	0.05	0	0.28	0	0.06	0.02	0.01	0.02	0.05	0	0	0.01	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Peredibacter	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;unclassified	0	0.11	0	0.07	0.03	0.01	0	0.01	0.12	0.06	0.03	0.1	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;OM27_clade	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus	0.08	0.06	0.1	0.14	0.06	0.11	0.05	0.03	0.07	0.02	0	0.16	0.06	0.02
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;uncultured	0.07	0	0	0.07	0	0	0	0	0	0.01	0	0	0	0.17
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiferula	0.91	0.35	0.61	1.13	0.32	0.34	1.51	0.91	0.74	0.12	0.03	0.79	0.16	0.26
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobotulus	0	0.02	0.02	0.28	0.07	0	0.07	0.5	1.02	0.16	0	0.45	0.26	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina	0	0	0	1.77	0.91	0	0.16	0.62	0.03	0.07	0	0.45	0.09	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;unclassified	0.05	0.03	0	1.91	0.32	0.02	0.81	1.45	0.16	0.13	0.05	0.41	0.36	0.04
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus	0.61	0.1	1.33	0.78	0.4	0.49	0.77	0.38	0.41	1.96	0.11	0.55	0.2	0.02
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulforhopalus	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;unclassified	0	0	0	0	0	0.02	0	0.02	0.02	0.02	0	0.02	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_1	0	0	0	0.21	0	0.04	0.02	0.03	0.08	0.05	0.11	0.08	0.05	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_2	0.02	0.03	0.02	0	0.01	0.03	0	0.04	0.02	0.01	0	0.02	0.02	0.04
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_3	1.78	7.2	6.36	7.51	3.27	2.97	5.15	4.31	3.72	1.01	2.98	5.7	4.17	1.02
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_4	0.02	0.03	0.12	0	0.03	0.03	0	0.03	0.03	0.02	0	0.08	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_5	0.1	0	0	0	0	0.02	0	0.15	0.01	0.23	0.03	0	0.05	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;unclassified	0.02	0.27	0.02	0.07	0.06	0.08	0.04	0.05	0.02	0.01	0.05	0.08	0.05	0.02
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;unclassified;unclassified	0	0	0	0	0	0.06	0.02	0.03	0.01	0.02	0.03	0.02	0.01	0.07
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;GR-WP33-58;unclassified	0	0	0	0	0	0	0	0.23	0	0.04	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;0319-6G20;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Anaeromyxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Hyalangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Melittangium_boletus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Haliangiaceae;Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;JG37-AG-15;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;mle1-27;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Phaselicystidaceae;Phaselicystis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Byssovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_4;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_5;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Rs-K70_termite_group;unclassified;unclassified	1.1	0.87	3.33	1.28	0.75	0.95	1.44	0.62	1.19	0.09	0.11	1.77	0.04	0.07
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;unclassified;unclassified;unclassified	0	0.02	0	0.21	0.01	0.03	0.02	0.08	0.06	0.03	0.03	0.16	0.02	0.04
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0.55	0	0	0.43	0	0.1	0	0.11	0.13	0.1	28.3	0.12	0.05	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum	0.05	0	0	0.43	0.03	0.04	0	0.09	0.56	0.65	0	0.04	0.06	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Rs-M59_termite_group	0	0	0	0	0	0.01	0	0.02	0	0.01	0.03	0.02	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Hydrogenimonas_thermophila;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Nautiliales;Nautiliaceae;Thioreductor	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Epsilonproteobacteria;unclassified;unclassified;unclassified	0	0	0	0	0	0.01	0	0.02	0.02	0.01	0.03	0.02	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Arenimonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Dyella_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Dyella_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Frateuria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Leifsonia_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Luteimonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudomonas_cissicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Silanimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0	0.02	0.06	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Thermomonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;uncultured_3	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Xanthomonas_campestris	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Alteromonadales;Alteromonadaceae;Microbulbifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;B38;unclassified;unclassified	0	0	0	0	0	0.01	0	0	0.01	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Budvicia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Enteric_Bacteria_cluster	1.58	0.74	0.4	1.7	2.68	1.32	1.31	0.93	2.7	0.38	1.65	0.88	0.12	0.02
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Leminorella	0.02	0.18	0	0	0.07	0.14	0.05	0.16	0.18	0.04	0.08	0.04	0.02	0.02
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Pragia	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;unclassified	0.03	0.39	0.04	0.64	0.6	0.46	0.07	0.59	0.51	0.13	0.92	0.16	0.1	0.04
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Morganella	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Proteus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Providencia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;unclassified	0	0	0.02	0.07	0	0.06	0.14	0.02	0.14	0.2	0	0.02	0.01	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Xenorhabdus_nematophila	0	0	0	0	0	0	0	0	0.02	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;unclassified;unclassified	0	0.14	0.04	0.35	0.25	0.25	0.6	0.12	0.34	0.37	0.35	0.04	0.01	0.02
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae;Pseudospirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae_1;Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales_1;Halomonadaceae;Chromohalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales_4;Halomonadaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;Aggregatibacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;Chelonobacter_oris	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Gammaproteobacteria_1;PB1-aai25f07;unclassified;unclassified	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Acinetobacter	0.05	0	0	0	0	0	0	0	0	0	0.22	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Alkanindiges	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Perlucidibaca	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Azotobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Cellvibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_1	0	0	0	0	0	0	0	0	0	0	0.03	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_2	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_42	0	0.45	0.63	0.07	0.07	0.02	4.17	0.05	0	1.42	0.03	0	0.04	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_43	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;unclassified	0.1	0.14	0.28	0	0.21	0.03	0.04	0.03	0.01	0.14	0.24	0	0.47	0
Proteobacteria;Gammaproteobacteria_1;unclassified;unclassified;unclassified	0	0	0	0	0.04	0.03	0.04	0.01	0.06	0.06	0.08	0.06	0.01	0.02
Proteobacteria;Gammaproteobacteria_1;Vibrionales;Vibrionaceae;Photobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Aquicella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Coxiella	0.02	0.02	0.02	0	0.09	0.35	0	0.01	0.06	0.01	0.05	0.02	0.12	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Rickettsiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;unclassified	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Legionellaceae;Legionella_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Legionellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Gammaproteobacteria_2;NKB5;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;unclassified;unclassified;unclassified	0	0	0	0	0	0.08	0	0.02	0.01	0	0.03	0	0.01	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;Nevskia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;Steroidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;TA18;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;unclassified;unclassified;unclassified;unclassified	0.07	0.05	0.04	0.35	0.19	0.09	0.02	0.42	0.24	0.12	0.32	0.18	0.1	0.06
Spirochaetes;Spirochaetes;CW-1_termite_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;GZKB75;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Rs-H88_termite_group	0.08	0	0	0.28	0	0.01	0	0.54	0.02	0.17	0.05	0	0.04	0.06
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;unclassified	0	0	0	0	0	0	0	0.03	0	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;PL-11B10;unclassified	0	0	0	0	0	0	0	0	0	0.08	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Hodotermes_mossambicus_cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;M2PT2-76_termite_group	0	0	0	0	0	0	0	0	0	0.36	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Kalotermitidae_Cluster	0	0	0	0	0	0.02	0	0.03	0.08	0.02	0.05	0.04	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_I	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_II	0	0.03	0	0	0	0	0	0.02	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Reticulitermes_Cluster	0	0	0	0	0	0.01	0	0.02	0	0	0	0.02	0.01	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Rhinotermitidae_Cluster_Qadd	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_1	0	0.4	0.81	0	0	0	0	0.03	0.01	0.02	0.24	0.33	0.04	0.41
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_2	0.32	0.08	0.99	0.57	0.43	0.19	0	0.17	0.07	0.3	0.03	0	0.07	0.3
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_sp_Kalotermes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Nasutite	0	0	0	0	0	0	0	0.03	0.03	0.01	0	0	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Soil_Fee	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Trinervit	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster	0	0.03	0	0.21	0	0.04	0.02	0.05	0.04	0.05	0.08	0.06	0.04	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Kaloterm	0	0	0	0.14	0	0.02	0	0.03	0.04	0.03	0.03	0.08	0.01	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Mastote	0	0	0	0.07	0	0.06	0	0.17	0.07	0.09	0.22	0.14	0.04	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Reticulit	0.02	0	0	0.07	0.01	0.02	0	0.04	0.02	0.04	0.14	0.08	0.05	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0	0	0	0	0.01	0	0.01	0.02	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0	0	0	0.01	0.04	0	0.06	0.02	0.04	0	0.06	0.04	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Microcerotermes_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Mixed_Higher_Termite_Cluster	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0.07	0	0.03	0	0.02	0.06	0.02	0	0.02	0.02	0

Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0.01	0.01	0.01	0	0.02	0.01	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Microcerotermes_Cluste	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster	0	0	0	0	0	0	0	0.01	0	0	0	0.02	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Macroterr	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Microcero	0	0	0	0	0	0.01	0	0.01	0.02	0.01	0	0.02	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0.07	0	0.02	0	0.01	0.05	0.03	0.03	0.02	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Treponema_2	0.18	0	0	0.07	0.06	0.04	0	0.16	0.06	0.25	0.05	0.04	0.09	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Trinervitermes_cluster_a	0	0	0	0.14	0	0	0	0.01	0	0.01	0.03	0.02	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;unclassified	0.4	0.72	0.04	0.43	0.12	0.18	0	0.47	0.26	0.31	0.41	0.28	0.29	0.33
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_4	0	0	0	0	0.09	0	0	0	0.11	0	0	0	0.01	0
Spirochaetes;Spirochaetes;Spirochaetales;unclassified;unclassified	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Candidatus_Tammella	0	0	0.02	0	0	0	0	0.01	0	0	0.03	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Cloacibacillus	0	0	0	0	0.01	0	0	0	0	0	0	0	0.07	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Jonquetella	0.02	0.02	0	0	0	0	0.04	0.09	0.02	0.03	0	0.04	0.04	0.04
Synergistetes;Synergistia;Synergistales;Synergistaceae;Synergistes_jonesii	0	0	0	0	0	0	0	0.01	0.01	0.01	0.03	0	0.01	0.02
Synergistetes;Synergistia;Synergistales;Synergistaceae;unclassified	0.51	0.21	0.04	3.97	0.6	0.11	1.49	7.09	4.48	1.31	2.41	1.85	11.15	6.03
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_1	0	0.05	0	0	0	0	0	0.03	0	0	0	0.08	0.29	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_2	0.18	0	0	0	0	0	4.71	1.32	0.06	0.01	0.05	0	0.12	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_6	0.2	0.5	2.44	0.35	0.19	0.23	0.05	0.32	0.2	0.39	0.32	0.43	0.6	0.48
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_I	0	0	0	0.14	0	0.01	0	0.01	0.01	0.01	0	0.02	0.02	0
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_II	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TG3;TG3;TG3_sp1;Termite_Cluster;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;Nasutitermes_Cluster	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
TG3;TG3;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified;unclassified;unclassified;unclassified;unclassified	0.75	0.61	0.46	1.06	0.43	0.57	0.18	0.96	0.67	0.66	0.68	0.47	0.81	0.69
Verrucomicrobia;Acidimethylosilex;Termite_group_A;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	1.84
Verrucomicrobia;Acidimethylosilex;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;OPB35_soil_group;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0.02	0.02	0	0	0	0.02	0.04	0.13	0.03	0.02	0.11	0.02	0.01	0.39
Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Cerasicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;unclassified	0	0	0	0.07	0	0	0	0	0.01	0	0	0	0	0
Verrucomicrobia;Opitutae;unclassified;unclassified;unclassified	0.02	0	0	0.07	0	0	0.02	0	0.03	0	0.03	0	0.01	0.02
Verrucomicrobia;Opitutae;vadinHA64;unclassified;unclassified	0.02	0	0	0	0	0.01	0	0.06	0.44	0.06	0.27	0	0.07	0.65
Verrucomicrobia;Spartobacteria;Candidatus_Xiphinematobacter;Candidatus_Xiphinematobacter;Candidatus_Xiphinematobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;Chthoniobacter;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
Verrucomicrobia;Spartobacteria;DA101_soil_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;FukuN18_freshwater_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.09
Verrucomicrobia;Spartobacteria;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0.02
Verrucomicrobia;Spartobacteria;uncultured_1;unclassified;unclassified	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;zEL20;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;unclassified;unclassified;unclassified;unclassified	0	0.11	0.14	0	0	0	0.02	0	0.28	0	0	0	0.06	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;unclassified;unclassified	0	0.43	0.16	0	0	0	0	0.03	1.01	0.01	0	0.02	0.15	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Akkermansia	0	0.45	0.06	0.21	0	1.18	0.16	2.14	0.75	0.08	0	0.24	2.99	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;unclassified	0	0.02	0	0	0	0	0	0.02	0	0	0	0	0.01	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_1;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;Prosthecobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WCHB1-60;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table 4 from Chapter 3: Distribution and relative abundance of the pyrotag reads in all samples.

	Relative abundance (%)													
Taxon	S. esak. H1	C. punctulatu	M. darwiniensis	H. sjoestedti	R. santonensis	C. niger	Z. nevadensis	H. mosambic	I. marginipen	N. jouteli. 2. wg	M. bellicosus	Odontoterme	Microtermes. wg	C. ugandensis
1_Proteobacteria;1_Deltaproteobacteria;1_Desulfobacterales;1_Nitrospinaceae;Candidatus_Entotheonella	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium	0.03	0.03	0	0	0.01	0	0.02	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Chloroacidobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Koribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Solibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter	0.07	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Terriglobus	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified	0.01	0.01	0.04	0.12	0	0	0	0	0	0	0	0.04	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_12	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_17	0	0	0	0	0	0	0	0.02	0	0	0	0.04	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_18	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_22	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_23	0	0	0.12	0.41	0	0	0	0	0	0.06	0.01	0	0.11	0.15
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_26	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_27	0	0	0.01	0	0.07	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_31	0	0	0	0	0	0	0	0	0	0	0	0.15	0.07	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;Holophaga	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0.05	0	0	0.04	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;unclassified;unclassified;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;Ilumatobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;marine_group	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Candidatus_Microthrix;Candidatus_Microthrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Iamiaceae;Iamia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;marine_group_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;marine_group_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_4;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_5;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_6;unclassified	0.01	0.01	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Acidothermaceae;Acidothermus	0.01	0.01	0	0	0	0	0	0.03	0	0	0	0.04	0	0.24
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_2	0.04	0.06	0.01	0	0.13	0.03	0.01	0	0.01	0.03	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_3	0	0.94	0	0.08	0.07	0	0.07	0.06	2.57	0	0	0	0	0.05
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;unclassified	0	0	0.01	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;Salana	0	0.09	0	0.01	0	0	0.01	0.02	0	0	0	0	0	0.05
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales;Brevibacteriaceae;Brevibacterium	0	0	0	0	0	0	0	0.06	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas_1	0.01	0.06	0	0	0	0	0	0	0	0	0	0	0.04	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas_2	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Oerskovia	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;unclassified	0.01	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Demequina;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales;Dermacoccaceae;Demetria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Dermacoccaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Frankiaceae;Frankia	0	0.03	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_3	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_saxobsidens	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Geodermatophilus	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Modestobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Humihabitans	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Janibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Lapillicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Terrabacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Terracoccus_sp_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Kineosporia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Quadrisphaera	0	0	0	0	0	0	0	0	0	0	0	0.11	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;unclassified	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Agromyces_2	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Curtobacterium	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Frigoribacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Humibacter_albus	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leucobacter	0	0	0	0	0	0	0	0.02	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Microbacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Pseudoclavibacter_1	0	0.01	0	0	0	0	0.04	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;unclassified	0.05	0.19	0.03	0.01	0	0	0.04	0.06	0	0	0.01	0.07	0.04	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_17	0	0	0	0	0	0	0	0	0	0	0	0.15	0.04	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_21	0	0	0	0	0	0	0	0	0	0	0	0.07	0.25	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Citricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Kocuria_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Yaniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nakamurellaceae;Nakamurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Kribbella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Marmoricola	0.01	0	0	0	0	0.02	0	0	0	0	0.01	0.22	0.11	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Nocardioides	0	0	0.01	0	0	0	0	0	0	0	0.03	0.07	0.67	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonospiraceae;Cellulosimicrobium_	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Myceligenerans_xiligouense	0	0	0	0	0	0	0	0	0	0.01	0	0	0.04	0.05
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Xylanimonas_	0	0	0.04	0	0	0	0	0	0	0	0	0	0.02	0.15
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Aestuariimicrobium	0	0.01	0	0.01	0	0	0	0	0.01	0	0.01	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Brooklawnia_cerclae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Microlunatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Tessaracoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;unclassified	0	0	0	0	0	0	0	0	0.01	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales;Sanguibacteraceae;Sanguibacter	0	0	0	0	0	0	0	0	0	0.42	0	0	0.5	0.05
Actinobacteria;Actinobacteria;Actinomycetales;unclassified;unclassified	0.05	1.77	0.2	0.06	0.04	0	0.21	0	1.27	0.42	0.07	1.92	0.48	0.44
Actinobacteria;Actinobacteria;Actinomycetales;uncultured_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Catenulisporaceae;Catenulispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Kitasatospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptacidiphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05

Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_1	0	0	0	0	0	0	0	0	0	0	0	0.07	0.07	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_3	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_8	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0.05
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unpublished_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Actinospicaceae;Actinospica	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_1	0	0	0	0	0	0	0	0.05	0	0	0.01	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_5	0	0	0	0	0	0	0	0.69	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_atypicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_spheniscorum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;unclassified	0	0	0	0	0	0	0	0.46	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Dietziaceae;Dietzia	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Millisia_brevis;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Mycobacteriaceae;Mycobacterium	0.01	0	0	0	0	0	0	0	0	0	0	0.04	0	0.05
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Nocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae_1;Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_1;Amycolatopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_1;Saccharopolyspora	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_2;Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0.01	0.07	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_3;Goodfellowiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_4;Crossiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_4;Kutzneria_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Segniliparaceae;Segniliparus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Tsukamurellaceae;Tsukamurella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;uncultured;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_3;PeM15;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_3;Sporichthyaceae;Sporichthya	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinocatenispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinoplanes_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinoplanes_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Dactylosporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Krasilnikovia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Luedemannella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_8	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonosporaceae_bacteria_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;unclassified	0	0	0	0.01	0.03	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;uncultured	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Nocardiopsaceae;Nocardiopsis_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Microbispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Sphaerisporangium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Streptosporangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinoallomurus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinocorallia	0	0	0	0	0	0	0	0	0	0	0	0	0.23	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;unclassified;unclassified	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;AKIW543;unclassified;unclassified	0	0	0	0.01	0	0	0	0.02	0	0	0	0.07	0.02	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Aeriscardovia_aeriphila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium_4	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0.05
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Gardnerella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia_criceti	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;unclassified	0	0	0	0.04	0	0	0.02	0	0.02	0	0.04	0	0	0.05
Actinobacteria;Actinobacteria;Bogoriella_caseilytica;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;marine_group	0	0.24	0.01	0.01	0.03	0	0.01	0	0	0	0	0	0.19	0.49
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;unclassified	0.04	0	0	0.03	0	0	0.02	0.05	0.01	0.03	0.05	0.15	0.04	0.1
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_10	0.37	1.64	0.26	0.69	1.04	0.31	0.85	1.76	0.52	0.75	1.28	2.32	0.46	1.03
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_11	0	0	0	0.01	0.04	0	0.03	0.03	0.01	0.02	0.02	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0.39
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_9	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;MB-A2-108;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;RL185-aaj71c12;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.09	0
Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteriaceae;Rubrobacter	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;0319-6M6;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Solirubrobacterales;288-2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Solirubrobacterales;480-2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Conexibacteraceae;Conexibacter	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Patulibacteraceae;Patulibacter	0.01	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Solirubrobacteriaceae;Solirubrobacter	0	0	0	0	0	0	0	0	0	0	0	0.07	0.04	0
Actinobacteria;Actinobacteria;Solirubrobacterales;TM146;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Actinobacteria;Actinobacteria;Solirubrobacterales;YNPFFP1;unclassified	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0.1
Actinobacteria;Actinobacteria;unclassified;unclassified;unclassified	0.01	0.48	0.01	0.01	0	0	0.14	0.03	0.17	0.13	0.01	0.04	0.23	0.15
Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.14	0.01	0.03	0.1	0	0	17.59	0.38	0.83	0.06	0.76	0.15	0.23	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;CAP-aah99b04;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;COB_P4-1_termite_group;unclassified	1.01	0	1.12	0	0	0	0.01	0	0.14	0.04	0.02	0.04	0.04	0.1
Bacteroidetes;Bacteroidia;Bacteroidales;gir-aah93h0;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_cluster_a;unclassified	2.67	0	0	0.22	0	0	0.02	0	0.05	0	0.08	0.22	0	0.1
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;3M1PL1-52_termite_group	1.18	0	0	0	0	0.02	0.13	0.02	0	0	0.01	0	0	0.24
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Hodotermes_Cluster	0.06	0	0	0	0	0	0.04	11.19	0.01	0	0.02	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;unclassified	0.24	0.07	0.28	0	0	0.31	0.06	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Wood_feeding_roaches	0.56	0	0.24	0	0	0.1	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0.1
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_a	2.12	0.39	0.55	0.01	0	0	0.01	0.05	0.01	0.01	0.36	0.22	0.25	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_b	0	0	0	0.01	0	0	0	0	0.01	0.01	0	0.04	0.02	0.83
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_c	0	0	0	0.01	0	0	0.01	0	0	0	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Alkaliflexus	0	0	0	0	0	0	0	0	0	0.01	0	0	0.18	0.1
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured_1	0.28	0	0	0.01	0	0	0.02	0	0.02	0	0.26	0.33	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;MgMjR-022;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Nearly_all_Termite_Cluster;unclassified	0.12	0	0	0	0	0	0.02	0.18	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;p-2534-18B5_gut_group;termite_group_a	0	0	0.26	0.44	0	0.08	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Paludibacter	6.15	1.25	0.16	1.6	0.08	0.15	0.5	0.35	0.04	0.02	0.99	0.76	1.75	2.1
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;unclassified	0.02	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Candidatus_Symbiothrix	5.54	1.59	1.63	0.81	0.26	58.74	0.06	0.05	0.55	0.13	4.48	0.25	0.21	1.56
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Dysgonomonas	0.23	0.15	0.53	1.04	0.01	2.59	0.07	0	0.05	0.03	0.12	0.15	4.74	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Parabacteroides	0.44	12.23	2.36	0.39	0.01	0.02	0.07	0.27	0.22	2.22	0.21	0.15	1.2	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Tannerella	1.08	0.07	0.63	0.28	0	0	0.01	0.03	0.08	0	0.01	0.07	0.69	0.1
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;unclassified	0.21	0.07	0.11	0.15	0	0.03	0.01	0.02	0.04	0.01	0.01	0	0.05	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_2;Cubitermes_Cluster_A	0	0	0	0	0	0	0.01	0	0	0	0	0	0	1.47
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_2;Proteiniphilum	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Butyricimonas	0	0	0	0	0	0	0	0	0	0	0.06	0	0	0

Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Odoribacter	0	0	0	0	0.7	0	0	0	0	0.01	0.12	0	0.16	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Shelfordella_cluster_a	0.41	0	0	0.01	0	0	0.03	0	0.01	0	0.02	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;uncultured_b	0	0	0	0	0	0	0	0	0	0	0.84	0.07	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;uncultured_10	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;ratAN060301C;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	1.76	0.03	0.01	0.5	0.18	0.16	0.33	2.85	0.34	0.13	24.87	21.07	9.44	0.59
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;BCf9-17_termite_group	0.07	0.04	0.03	0.59	0.14	0.49	0.02	0.19	1.31	1.9	0.12	0.04	0.64	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_a	0.06	0.03	0	0	0	0	0.02	0	0	0	0.11	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_c	0.02	0	0	0.22	0	0	0.02	0	0.02	0	0.1	0.25	0.21	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;M2PB4-61_termite_group	0.6	0.39	0.2	0.02	0	0	0.02	0.02	1.52	0.24	0.16	0.07	0.39	1.08
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;P1_32_Panesthia	1.01	0	0.03	0.07	0	0	0.08	0.11	0.07	0	0.11	0	0	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;RC9_gut_group	1.71	0.15	0	0.01	0	0	0.01	0	0	0	0.01	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_1	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_3	0	0	0	0	0	0	0.01	0	0	0	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_4	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rs-D38_termite_group	0.1	0.04	0.01	0.25	0.07	0.07	0.05	0.02	6.16	0.13	0.07	0	0.05	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;unclassified	2.06	0.04	0.04	0.12	0.01	0.02	0.16	0.43	0.13	0.02	0.54	0.15	0.19	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;vadinBC27_wastewater-sludge_group	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0.34
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_aa	0	0.04	0	1.02	0	0	0.04	0.05	0	0	0.01	0	0	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_bb	0	0.03	0	0.04	0	0	0	0	0	0	0.32	0	0.16	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;higher_termites_a	0	0.16	0	0.01	0	0	0.01	0.02	0	0.01	0.85	0.04	0.67	0.15
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;unclassified	0	0	0	0.01	0	0	0	0.11	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;S24-7;unclassified	0.31	0.01	0	0	0	0	0.01	0	0	0	0.07	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;unclassified;unclassified	1.06	1.06	1.49	0.55	0.07	0.13	5.64	0.19	0.23	0.1	1.5	0.11	0.57	0.1
Bacteroidetes;Bacteroidia;Bacteroidales;uncultured_bacterium_Cylindroiulus_2;unclassified	0.01	0	0	0	0	0	0	0	0.01	0	0	0	0	0.05
Bacteroidetes;Bacteroidia;Bacteroidales;vadinHA21;unclassified	4.2	0.01	0.01	0.02	0.01	0	0.16	0	0	0.01	0.02	0.29	0	0.05
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;Blattabacterium	0.26	12.55	0	0.05	0.03	0.02	0.12	0	0.09	0.42	0.19	0	0.81	0.15
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;unclassified	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Flavobacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Galbibacter_mesophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Lutaonella_thermophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Myroides	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;unclassified	0	0	0.03	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Bergeyella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_11	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_5	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_8	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_molle	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_pallidum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_soldanellicol	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_sp._CCUG_15624	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Elizabethkingia	0	0	0	0	0	0	0	0.02	0	0	0.48	0.04	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Empedobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;unclassified	0	0.18	0.01	0.04	0.11	0	0.62	0.14	0.01	0	0.09	0.04	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;uncultured_a	0	0.01	0	0.04	0	0	0.1	0	7.43	0	0.04	0	0	0.1
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Wautersiella_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Weeksella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;unclassified;unclassified	0.01	0.04	0	0	0	0	0.04	0	0.04	0	0.07	0	0.02	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;SB-1;unclassified	0.18	0	0	0.02	0	0	0.01	0.02	0.01	0.01	0.31	0.25	0.5	0.1
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Mucilaginibacter_1	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Mucilaginibacter_2	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Nubsella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_1	0	0	0	0.01	0	0	0	0.02	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_3	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0

Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;ST-12K33;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;unclassified;unclassified	0.03	0	0.01	0	0	0	0	0	0	0	0.01	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;vadinHA17;unclassified	0.16	0	0	0	0	0	0.01	0	0	0	0	0	0.11	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;WCHB1-69;unclassified	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Niabella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Sediminibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;unclassified	0	0	0.03	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_12	0.01	0	0.01	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;uncultured_1	0	0	0	0	0	0	0	0	0	0.01	0	0	0.02	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_1;Flexibacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_2;Sporocytophaga	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;unclassified;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Bacteroidetes;unclassified;unclassified;unclassified;unclassified	0.31	0.13	0.04	0.12	0	0.08	0.33	0	0.15	0.04	0.24	0.11	0.21	0.1
Bacteroidetes;VC2.1_Bac22;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
BD1-5;unclassified;unclassified;unclassified;unclassified	0	0.04	0	0.01	0.16	0	0.15	0.06	0	0.03	0	0.04	0.05	0
Candidate_division_BRC1;unclassified;unclassified;unclassified;unclassified	0.01	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Candidate_division_OD1;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_OP10;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Candidate_division_OP11;unclassified;unclassified;unclassified;unclassified	0.3	0.66	0.13	0.15	0.32	1.42	0.41	0.19	0.03	0.5	1.42	1.92	3.68	0.24
Candidate_division_SR1;unclassified;unclassified;unclassified;unclassified	0.14	0.1	0.17	0.3	0.26	0	0.44	0	0.46	0.02	0.02	0	0	0.1
Candidate_division_TM6;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_TM7;unclassified;unclassified;unclassified;unclassified	5.9	3.48	2.4	0.87	1.08	1.7	5.21	3.5	0.06	1.55	3.2	9.83	1.4	0.39
Chlamydiae;Chlamydiae;Chlamydiales;cvE6;unclassified	0	0	0.03	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Candidatus_Protochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Neochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus_Rhabdochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chlorobi;Chlorobia;Chlorobiales;OPB56;unclassified	0.01	0.15	0	0.16	0	0	0.01	0.03	0	0	0	0	0.05	0.2
Chlorobi;Chlorobia;Chlorobiales;SJA-28;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Chloroflexi;Chloroflexales;Chloroflexaceae;Roseiflexus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Gitt-GS-136;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;JG37-AG-4;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0.1
Chloroflexi;KD4-96;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Ktedonobacter;Ktedonobacter;Ktedonobacter;Ktedonobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;S085;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Thermomicrobia;AKYG1722;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Chloroflexi;Thermomicrobia;JG30-KF-CM45;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0.05	0
Chloroflexi;Thermomicrobia;Sphaerobacteridae;Sphaerobacterales;Sphaerobacteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;TK10;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;vadinBA26;unclassified;unclassified;unclassified	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Cyanobacteria;Cyanobacteria;Cyanobacteriales;4C0d-2;unclassified	0	0.06	0	0	0	0	0.01	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;Chloroplast;Chloroplast	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;ML635J-21;unclassified	0	0.09	0	0.05	0.16	0.03	0.17	0.53	0.49	1.24	0.01	0	0.23	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;MLE1-12;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionII;SubgroupII_Chroococcidiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionIII;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionIV;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionV;Stigonema	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;WD272;unclassified	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0

Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Mucispirillum	0.35	0.04	0	0.1	0	0	0.05	0.05	0.16	0.08	0.27	1.34	2.02	0.15
Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;unclassified	0.01	0	0	0	0	0	0	0	0.01	0	0	0	0.05	0
Deinococcus-Thermus;Deinococcus-Thermus;Deinococcales;Deinococcaceae;Deinococcu	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus;Deinococcus-Thermus;Deinococcales;Trueperaceae;Truepera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_I_[Endomicrobia]	0.15	0.46	6.9	3.01	13.04	0.65	5.49	19.79	0.39	10.92	0.16	0.47	0.27	0.1
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_III_[Elusimicrobium]	0.21	0.04	0	0.02	0.08	0.02	0.16	0.03	0.02	0.47	0.46	0.29	0.14	0.29
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;unclassified	0	0	0.01	0.01	0	0.03	0	0.18	0.01	0.02	0	0	0	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;uncultured_d	0	0	0	0	0	0	0.02	0.02	0	0	0	0	0	0
Fibrobacteres;Fibrobacteres_sp1;Fibrobacterales;Fibrobacteraceae;Fibrobacter	0.1	0	0	0	0	0	0	0	0.01	0	1.53	0.04	0	0
Fibrobacteres;Fibrobacteres_sp2;Fibrobacteres_sp2;Termite_Cluster;Termite_Cluster_I	0.02	0	0	0.02	0	0	0.01	0.02	0.02	0.32	0.05	0.04	0.39	0
Fibrobacteres;unclassified;unclassified;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Apr-15;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Alicyclobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_11	0.01	0	0.01	0	0	0	0	0.08	0	0	0	0.15	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_4	0	0	0	0	0	0	0	0	0	0	0	0.11	0.07	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_5	0	0	0	0	0	0	0	0	0	0.02	0	0.04	0.04	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_6	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_7	0	0	0	0	0	0	0	0	0	0	0.01	0.04	0.18	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0.1
Firmicutes;Bacilli;Bacillales;Bacillaceae_3;Bacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_5;unclassified	0	0	0	0.01	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_6;Bacillus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Family_XII_Incertae_Sedis;Exiguobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Listeriaceae;Brochothrix	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Listeriaceae;Listeria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_1;Oxalophagus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Brevibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Cohnella	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_17	0.04	0	0	0	0.01	0	0	0	0	0	0	0.04	0.02	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_18	0.01	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Caryophanon	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_1	0	0	0	0	0	0	0	0	0	0	0	0	0.16	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_2	0	0	0	0	0	0	0	0	0	0	0	0	0.3	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_3	0	0	0.03	0	0	0	0	0	0	0	0	0	0.04	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_5	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_6	0	0	0	0	0	0	0	0	0	0	0	0.04	0.25	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Lysinibacillus	0.01	0	0	0	0	0	0	0	0	0	0	0.15	0.07	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;unclassified	0	0	0.01	0	0	0	0	0	0	0	0	0	0.55	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0.11	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_1	0	0	0	0	0	0	0	0	0	0	0	0.11	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;unclassified;unclassified	0	0	0.01	0	0	0	0	0	0	0.03	0	0.04	0.04	0.05
Firmicutes;Bacilli;Bacillales_2;Thermoactinomycetaceae;Shimazuella	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0

Firmicutes;Bacilli;Lactobacillales;16d63.751;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;Eremococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Carnobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Carnobacterium_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Trichococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Catellicoccus_marimammalium;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_2	0.01	0	0	0.07	0	0	0.08	0.38	0.03	0	0.03	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_3	0	0.07	0	0.02	0.04	0	0	0	0	0.68	0	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_4	0	0	0	0.04	0	0	0.01	0.11	0	0	0	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_5	0	0.07	0	0.01	0	0	0.01	0	0	0	0.01	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Pilibacter	0	0	0	0	0	0.2	0	0.02	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;unclassified	0.01	0.01	0	0	0	0	0.01	1.45	0.01	0	0.01	0	0	0.05
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Vagococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;Enterococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;Enterococcus_3	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_sp._R-25205	0	0	0	0.01	0	0.02	0.01	0	0	0	0	0	0.05	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;unclassified	0	0.01	0	0	0	0	0	0	0.01	0	0.02	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;uncultured_a	0	0	0	0.01	0	0	0	0.02	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcus_phoeniculicola;unclassified	0	0.01	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Hodotermopsis_Trichonympha_Symbiont_1;unclassified	0	2.83	0	0.99	0	0	0.01	0	0.01	0	0.01	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_1	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_2	0	0	0	0	0	0	0	0	0	0.08	0	0	0.04	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_3	0	0	0	0	0	0	0.01	0	0	0	0.01	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_4	0	0	0	0.01	0	0	0.02	0	0.01	0	0.04	0	0	0.05
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_5	0	0	0	0.02	0	0	0.04	0	0.02	0	0.01	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_sp_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Paralactobacillus	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Pediococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;unclassified	0	0	0	0.01	0	0	0.02	0	0	0.02	0.02	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Fructobacillus	0	0	0.36	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Hm_96	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;HsjTcB_43	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	0	1.89	0	0.04	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc_fallax	0	0.01	0	0	0	0	0	0	0	0	0	0	0.04	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Oenococcus	0	0	0	0.07	0	0	0	0.02	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;unclassified	0	0.12	0	0.37	0	0.08	0.01	0.02	0	0	0.02	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_1	0	0	0	0	0	0	0	2.09	0	0.01	0	1.92	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_2	0	0.16	0	1.28	0	0	0	0	0	0	0.02	0	0	0
Firmicutes;Bacilli;Lactobacillales;PeH08;unclassified	0	0	0	0	0	0	0	0.02	0	0.04	0	0	0.04	0
Firmicutes;Bacilli;Lactobacillales;Rs-D42;unclassified	0	0	0	0	0	0	0.01	0	0	0	0.02	0	0	0
Firmicutes;Bacilli;Lactobacillales;Sl_24;unclassified	0	0.01	0	0.09	0	0	0.02	0.08	0.02	0	0.07	0	0	0
Firmicutes;Bacilli;Lactobacillales;Sl_99;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_1	0.01	0	0	0.02	0	0	0.01	0	0.01	0	0.01	0.07	0	0.05
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_2	0.01	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_3	0	0.06	0.01	0.16	0.03	0.57	0.02	0.5	0	0	0	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactovum	0.05	0	0	0	0	0.21	0	0	0	0.06	0	0.33	1.45	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;unclassified	0	0	0	0.01	0	0	0	0.06	0	0.06	0.01	0.07	0.14	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0.01	0	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_2	0	0	0	0	0	0.13	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;unclassified;unclassified	0.01	0.55	0	0.33	0	0	0.13	1.61	0.08	0.14	0.09	0	0.27	0.15
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Hepialus;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Pachnoda_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;unclassified;unclassified;unclassified	0	0	0	0.01	0	0	0	0.02	0.01	0.04	0.01	0	0.12	0.1
Firmicutes;Bacilli;VAN12;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;CK-1C4-19;unclassified;unclassified;unclassified	0.01	0	0	0.01	0	0	0	0	0	0	0	0	0	0

Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Anaerobacter_polyendosporus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_1	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_11	0	0	0	0.09	0	0	0	0	0	0	0	0	0	0.1
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_6	0.04	0.01	0	0.01	0	0	0	0.02	0	0	0.06	0.44	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_8	0.51	0	0	0.02	0	0	0.04	0	0.04	0	0.04	0	0.04	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;unclassified	0.06	0.01	0.01	0.01	0	0.02	0.02	0.11	0	0.02	0.06	0.29	0.04	0.05
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_2;Alkaliphilus_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Dethiosulfatibacter_aminovoran;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Anaerofustis	0.32	0	0.03	0.01	0	0	0	0.02	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_1	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Pseudoramibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;unclassified	0.16	0	0	0.02	0	0	0.01	0	0.01	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XI_Incertae_Sedis;Anaerococcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XI_Incertae_Sedis;Tissierella_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Anaerovorax_	0.01	0.31	0.03	0.01	0	0	0.11	0	0	0	0.02	0.04	0	0.59
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_2	0	0	0	0	0	0	0.01	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_3	0.01	0	0	0	0	0.02	0	0	0	0.01	0	0.07	0.27	0.1
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;unclassified	0.03	0.69	0.21	0.16	0	0	0.19	0.22	0.73	0.07	0.17	0.04	0.09	0.73
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_1	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_4	0	0.09	0	0.04	0	0	0.01	0.11	0	0	0	0	0.07	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_5	1.46	5.81	2.42	2.81	0.47	0.36	1.63	4.72	0.11	0.27	0.06	0.54	0.67	0.73
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_6	0	0	0	0.01	0.64	0	0.01	0	0.04	0.04	0.79	0.36	0	0.1
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_a	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Gracilibacteraceae;Lutispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Gracilibacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Anaerostipes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Butyrivibrio_4	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Butyrivibrio_fibrisolvens	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Catabacter	0.44	0.66	0	0.1	0	0	0.02	0.14	0.02	0	0.21	0.15	0.09	0.1
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Clostridiales_bacterium_HAW-EB17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Coprococcus_1	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Hespellia	0	0.09	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_11	0	0	0	0.01	0	1.04	0	0.02	0	0	0.02	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_14	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_18	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_24	0.16	0.01	0	0.11	0	0.02	0.07	0	0.02	0	0.06	0.07	0.02	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_25	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_26	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_30	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_31	0	0.03	0	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_32	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_34	0.02	0.03	0	0.01	0.05	2.99	0.01	0	0	0.01	0.01	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_35	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_36	0.79	2.78	0	1.13	1.36	0.08	1.33	0.34	0.05	0.18	3.3	2.21	6.86	7.62
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Marvinbryantia	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Mmba_A01b	0.03	0	0	0	0	0	0.02	0	0	0	0.02	0	0.07	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Parasporobacterium-Sporobacterium	0	0	0	0	0	0	0	0	0	0	0	0.11	0.09	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_higher_Termites	0	0	0	0.02	0	0	0	0	0.01	0	0.01	0.04	0	2.98
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_Insects	0.03	0	0	0.01	0	0.02	0.01	0	0	0	0	0	0	0

Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;unclassified	1.72	2.08	0.32	2.1	0.13	0.31	0.68	0.93	0.22	0.19	2.47	1.49	1.63	2.54
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_1	0	0	0	0	0	0.02	0	0	0	0	0.01	0	0.09	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_11	0	0	0.03	0.02	0	0	1.55	0.05	0.01	0	0.04	0.07	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_13	0.02	0	0	0.01	0	0	0.01	0	0.01	0.01	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_22	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_23	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_27	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_31	0	0	0	0	0	0.13	0	0	0	0	0	0	0.5	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_4	0	0	0	0	0.25	0.02	0	0	0	0.01	0	0.04	0.32	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_47	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_48	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_50	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_51	0	0	0	0	0	0	0	0	0	0	0.14	0.51	0	0.2
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_54	0	0	0	0	0	0	0	0	0	0	0.03	0.15	0.21	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_56	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_58	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_59	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_61	0.03	0	0	0	0	0	0.01	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_62	0	0	0	0.05	0	0	0.02	0	0	0	0	0	0.09	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_63	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_64	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_65	6.17	0.61	0.01	1.15	0.43	0.29	0.81	0.91	0.22	0.07	2.15	1.63	0.64	2.64
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_66	0.05	0	0	0.01	0	0	0	0.02	0	0	0.14	0.04	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_67	0.59	2.34	0.09	1.24	0.21	0.47	0.16	0.62	0.16	3.01	3.19	0.29	2.71	2.15
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_68	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_1	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_3	0	0	0	0.11	0	0	0	0	0	0.03	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_5	0	0	0	0.01	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_6	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Sporacetigenium_mesophilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;unclassified	0	0	0	0.01	0	0	0.01	0	0.02	0	0.01	0.04	0.11	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0.18	0.21	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Acetanaerobacterium	0.01	0.03	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerofilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerotruncus	1.19	0.15	0.01	0.22	0.01	0	0.02	0	0.02	0	0.08	0.07	0.21	0.05
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Butyricicoccus_pullicaecorum	0	0.01	0	0.01	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_alkalicellulosi	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_clariflavum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_straminisolvens	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ethanoligenens	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Fastidiosipila	0	0	0	0	0	0	0.04	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	0.57	0	0	0.01	0	0	0	0.03	0.01	0	0.09	0.04	0.05	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_1	0.05	0.15	0.22	0.21	0.54	0	0.03	0.14	0	0.28	0.01	0	0.02	0.34
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_2	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_3	0.01	0	0	0	0	0	0.01	0	0	0	0.19	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_4	0.69	0.83	0.05	0.15	0.04	0	0.19	0.26	0.01	0.02	0.22	0.4	0.09	0.05
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_5	0.03	0	0	0.51	0	0	0.01	0	0.01	0	0.02	0	0.04	0.1
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_6	0.06	0	0	0	0	0	0.01	0.19	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_7	0.01	0.07	0	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_8	0.18	0.15	0.14	0.05	0.39	0.02	0.39	0.02	0.01	0	0.02	0	0.27	0.49
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;insect_guts_a	0.34	1.73	0	1.84	0.01	0	0.26	1.66	0.09	0.02	0.6	0.87	1.68	0.34
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Oscillibacter	0.03	0	0	0	0	0	0	0	0	0	0	0	0.05	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Oscillospira	0.01	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Papillibacter	1.26	2.03	0	0.65	0.11	0	1.59	0.67	0.01	0.18	0.25	0.04	0	0.15
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_1	0.2	0	0	0.01	0	0	0.01	0.1	0.02	0	0.58	0	0	0.1
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_2	0.01	0.21	0	0.05	0.09	0	0.01	0	0	0.01	0.01	0.04	0.07	0

Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Sporobacter	0.02	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Termite_group_aaa	0.44	0.46	1.2	0.45	0.17	0.03	1.69	0.59	0.02	0.43	0.04	0.07	0.12	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;unclassified	5.96	4.45	0.53	0.88	0.47	0.42	1.71	3.04	0.11	0.59	1.97	0.8	1.11	5.03
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_10	0.17	0.19	0	0.01	0	0	0	0.02	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_11	2.25	2.76	0	0.85	0.5	0.39	0.12	0.27	0.06	0.07	5.73	2.43	3.94	1.42
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_12	3.13	0.37	1.91	0.48	0.16	0.77	0.19	0.45	0.04	0.17	0.51	0.22	0.12	1.27
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_13	0.04	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_20	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_21	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_23	0.17	0	0	0.03	0	0	0.01	0.02	0.02	0	0.03	0.15	0	8.6
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_24	0.86	0.01	0	0.01	0	0	0.02	0.05	0	0.05	0.04	0	0.07	1.17
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_25	1.15	1.34	0	0.13	0.04	0	0.05	0.19	0.02	0	0.4	0.11	0.05	0.15
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_26	0.01	0.01	0	0	0	0	0	0.06	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_27	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_28	0.87	0.01	0	0.18	0	0	0.01	0.13	0.01	0	0.21	0.04	0.02	0.1
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_29	0.04	0.13	0.08	0.01	0.01	0	0.24	0	0	0	0.01	0.07	0	0.24
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_30	1.68	0.64	0	0.44	0.91	0.02	0.37	0.21	0.02	0.01	0.37	0.22	0.11	3.91
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_33	0.01	0.07	0.16	0.01	0	0	0.04	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_34	0	0	0	0	0.01	0	0.01	0.03	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_35	0.52	0.61	0.05	0.16	0.16	0.1	0.24	0.18	0.01	0	0.16	0.11	0.02	0.83
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_36	1.11	0.37	0	0.02	0	0	0.01	0.08	0.01	0.01	0.26	0.47	0.8	0.93
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;unclassified;unclassified	1.01	0.55	0.18	0.27	0.17	0.11	0.25	0.94	0.06	2.92	0.57	0.36	0.53	1.08
Firmicutes;Clostridia_1;unclassified;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Peptococcaceae;Desulfitibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Pelospora	0.08	0	0	0.1	0	0	0	0	0	0.01	0.02	0	0	0.15
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_1	0.01	0	0.03	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_2	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;unclassified	0.48	0	0.08	0.05	0	0	0	0.02	0	0	0	0.18	0	0.24
Firmicutes;Clostridia_2;Clostridiales_1;Heliobacteriaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;OPB54;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;P._palm_C;A_51	0.02	0	0	0	0	0.03	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;Thermincola	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;unclassified	0.01	0	0	0.02	0	0	0	0.1	0	0	0.07	0.07	0.02	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_2	1.03	0.1	0	0.05	0.09	0	0	0.42	0.01	0	0.31	0.15	0.16	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_3	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_4	0.05	0	0	0	0	0	0	0.1	0	0	0.02	0	0	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_5	0.01	0	0	0	0	0	0.12	0.05	0	0.5	0.17	0	0.07	0.39
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Dehalobacter	0.01	0.15	0	0.25	0.01	0	0.29	0	0	0.01	0	0	0.02	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Desulfosporosinus	0.11	0	0	0.03	0	0	0.01	0	0	0	0.02	0.04	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;unclassified	0.02	0.07	0.01	0.05	0.07	0	0.08	0.02	0	0.02	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;uncultured_gut_Group_A	0	0	0.22	0	0	0	0.01	0	0.01	0	0.01	0.11	0	1.17
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Desulfotomaculum_4	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Pelotomaculum_3	0.01	0	0	0	0	0	0	0.02	0	0	0	0	0	0.15
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;unclassified;unclassified	0.03	0.01	0.07	0.02	0	0	0.01	0.02	0	0.01	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acetonema_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acidaminococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaeroarcus-Anaeromusa	0	0	0	0.01	0	0	0.01	0	0	0	0	0	0.04	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaerospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaerovibrio	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Dendrosporobacter	0.41	0	0	0.01	0	0	0.01	0	0.01	0	0.06	0.07	0.23	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Megamonas	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Phascolarctobacterium	0	0	0	0.05	0	0	0.04	0	0.04	0	0.05	0	0	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Propionispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Sporomusa	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Succinispira_mobilis	0	0.01	0	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Thermosinus	0	0	0	0	0	0	0	0	0	0.02	0.31	0.07	0.87	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;unclassified	0.01	0.42	0	0.09	0	0	0.18	0.1	0.09	0.11	0.05	0	0.04	0.05
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_6	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_7	0.4	0.39	0	0.33	0	0.03	0.67	0.18	0.03	0.05	1.02	1.23	1.04	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_8	0.4	0	0	0.01	0	0	0	0.08	0	0	0	0	0	0.2
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Veillonella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Thermoanerobacterales;Thermoanaerobacteraceae;Gelria	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;unclassified;unclassified;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Firmicutes;Clostridia_3;Clostridiales;Syntrophomonadaceae;Dethiobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Asteroleplasma	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Bulleidia_extructa	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Erysipelothrix	0.03	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Incertae_Sedis_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Turicibacter	0	0	0	0	0	0	0	0.02	0	0.09	0	0.04	0.21	0.05
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;unclassified	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;uncultured_9	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_2	0.55	0	0	0.02	0.01	0	0	0	0.01	0	0.01	0	0.05	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_3	0	0.01	0	0.01	0	0	0.76	0.13	0	0	0	0	0	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;unclassified	0	0.04	0	0	0	0	0.44	0.3	0.01	0	0.01	0	0	0
Firmicutes;Mollicutes;Anaeroplasmatales;Anaeroplasmataceae;Anaeroplasma	0.01	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Mollicutes;EMP-G18;unclassified;unclassified	0	0	0	0.01	0	0	0	0.18	0	0	0	0	0	0
Firmicutes;Mollicutes;Entomoplasmatales;Entomoplasmataceae;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Entomoplasmatales;Spiroplasmataceae;Spiroplasma_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;uncultured_1	0	0.04	1.67	0	0	0.08	0	0.02	0.01	0	0	0	0	0
Firmicutes;Mollicutes;RF9;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Firmicutes;Mollicutes;unclassified;unclassified;unclassified	0	0.03	0	0	0	0	0.47	0.1	0	0	0.02	0	0.02	0.05
Firmicutes;RF3;unclassified;unclassified;unclassified	0.02	0.22	0	0	0	0	0.21	0.03	0	0	0.17	0	0	0
Firmicutes;unclassified;unclassified;unclassified;unclassified	0.41	0.18	0.07	0.18	0.75	0.85	0.87	0.45	0.07	0.34	3.46	0.22	0.27	0.39
Fusobacteria;Fusobacteria;Fusobacteriales;ASCC02;unclassified	0.01	0	0.03	0.01	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;boneC3G7;unclassified	0	0	0	0.02	0	0	0.01	0	0.01	0	0.02	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;CFT112H7;unclassified	0.12	0	0	0	0	0	0.01	0	0.01	0	0.01	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Fusobacterium_1	0	0	0	0	0	0	0.01	0	0.01	0.02	0	0	0.02	0.05
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Ilyobacter	0	0	0.57	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;unclassified	0	0	0.05	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Hados.Sed.Eubac.3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Sebaldella	0.02	0	0	0.03	0	4.98	0.01	0	0	0	0	0	1.86	0.05
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;unclassified;unclassified	0.08	0	0.58	0.05	0	0.02	0.06	0	0.15	0	0.07	0	0.02	0.15
Gemmatimonadetes;Gemmatimonadetes;AT425-EubC11_terrestrial_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;055B07-P-DI-P58;unclassified;unclassified	0.3	0	0.14	0.02	0.04	0.02	0.29	0	0	0.15	0	0	0	0
Lentisphaerae;Lentisphaeria;B01R017;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;BS5;unclassified;unclassified	0.09	0	0	0.01	0	0	0.03	0	0.02	0	0.02	0	0	0
Lentisphaerae;Lentisphaeria;c5LKS8;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;CVer-1_termite_group;unclassified;unclassified	0.21	0	0	0.02	0	0	0.02	0	0.02	0	0.02	0	0	0.59
Lentisphaerae;Lentisphaeria;CVer-2_termite_group;unclassified;unclassified	0.24	0	0	0	0	0	0.02	0.02	0	0	0	0	0	0.29
Lentisphaerae;Lentisphaeria;RFP12_gut_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;unclassified;unclassified;unclassified	0.71	0	0.26	0.02	0	0	0.02	0	0.01	0.2	0.01	0.11	0.02	0.15
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;Victivallis	0.36	0	0	0.02	0	0	0.02	0	0.01	0	0.11	0.07	0	0.05
Lentisphaerae;Lentisphaeria;WCHB1-25;unclassified;unclassified	0.44	0	0	0	0	0	0.07	0	0	0.01	0.05	0	0.04	0
Nitrospirae;Nitrospira;Nitrospirales;0319-6A21;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NPL-UPA2;unclassified;unclassified;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0

Planctomycetes;Phycisphaerae;CPla-3_termite_group;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;AKAU3564_sediment_group;unclassified	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;ODP1230B30.02_sediment_group;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;AKYG587	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;CL500-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Pla1_lineage;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Pla4_lineage;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;CPla-4_termite_group	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Isosphaera	0.01	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir1_lineage	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir4_lineage	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pirellula	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Rhodopirellula	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Schlesneria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Singulisphaera	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Termite_planctomycete_cluster	0.57	0.76	0.04	0.07	0.08	0	0.01	0	0	0.01	0.36	0.62	1.03	0.29
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;unclassified	0.02	0.01	0.04	0.02	0.01	0	0	0.02	0	0.01	0.07	0.11	0.32	0.15
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_23	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_24	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_32	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_35	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_b	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Zavarzinella	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;unclassified;unclassified;unclassified;unclassified	0	0.03	0	0	0	0	0	0.11	0	0	0	0	0	0
Planctomycetes;vadinHA49;unclassified;unclassified;unclassified	0.47	1.68	0	0.48	0.01	0.08	0.4	0.02	0.11	0.81	2.46	3.95	1.87	0.05
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter	0	0	0	0	0	0	0	0.06	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium	0.01	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_3	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_5	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;uncultured_2	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Rhodobium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Aurantimonadaceae;Aurantimonas_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Brucella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_5	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_9	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Aminobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Aminobacter_2	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0

Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_loti	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_thiogangeticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;unclassified	0.01	0.01	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_2	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_20	0	0	0	0	0	0	0	0.29	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_21	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_23	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;unclassified	0	0	0	0	0	0	0	0.02	0	0	0	0.04	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Shinella_genera_incertae_sedis;Shinella_genera_incertae_sedis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;1174-901-12;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;alphaI_cluster_1;unclassified	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;alphaI_cluster_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;BCf3-20;unclassified	0	0	0.01	0	0.01	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;Chelatococcus_2	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;uncultured_3	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Afipia_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Afipia_birgiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Blastobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bosea	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_12	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_japonicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_sp._CCBAU_61196	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Nitrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Rhodoblastus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Rhodopseudomonas	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;unclassified	0.01	0	0	0	0	0	0	0.08	0	0.01	0	0.04	0	0.15
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Prosthecomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Rhodomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae_1;Ancalomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Methylobacterium	0	0	0	0.01	0	0	0	0	0	0	0	0.15	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Microvirga	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylocystis_3	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylocystis_parvus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;unclassified;unclassified	0	0.01	0.05	0	0.03	0	0.04	0.02	0	0	0.02	0.04	0.02	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;Labrys	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;Pseudolabrys	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_1	0.01	0	0	0	0.05	0	0.06	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;DUNssu044;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Hyphomicrobium_1	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Hyphomicrobium_2	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Pedomicrobium	0	0	0.01	0	0.04	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Methylobacteriaceae;uncultured	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Nordella;Nordella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Amaricoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Palleronia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_3	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Rhodobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Roseobacter_clade_Ketogulonicigenium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;uncultured_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidicaldus	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidiphilium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidisoma	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidocella	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Craurococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Rhodopila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_2	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Rubritepida	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;unclassified	0.02	0	0	0	0.01	0	0.01	0	0	0	0	0.07	0.04	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_3	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Marispirillum_indicum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Telmatospirillum	0	0.01	0	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Thalassospira	0.4	0.12	0.01	0.15	0.03	0	0.01	0.1	0.01	0.01	0.02	0.36	0.18	0.15
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;unclassified	0.04	0.01	0	0.01	0	0	0.01	0	0	0.06	0.01	0.04	0.04	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_2	0.08	0.07	0	0.07	0.01	0	0.15	0.06	0.13	2.31	0.01	0	0.37	0.15
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0.01	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Candidatus_Alysiosphaera;Candidatus_Alysiosphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;DA111;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;I-10;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;JG37-AG-20;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;MNH4;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;Azospirillum_1	0	0	0	0.01	0	0	0	0.02	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;Skermanella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;wr0007;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;Wolbachia	0	0	0	0	0	0	0.67	0	0.01	0.79	0	0	0.07	0.29
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Captivus;Candidatus_Captivus	0	0.04	0.01	0.02	0.67	0.05	0.09	0.74	0.52	0.35	0.07	0	0.05	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Hepatincola;Candidatus_Hepatincola	0	0.21	0.36	0.12	1.58	0.31	0.64	0.61	0.35	1.7	0.01	0	0.07	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Midichloria;Candidatus_Midichloria	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;Rickettsia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;unclassified;unclassified	0	0.01	0	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Ellin6055;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium_2	0.01	0	0	0	0	0	0	0.05	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandarakinorhabdus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium_1	0	0	0.01	0.01	0	0	0	0.03	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_2	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_3	0.01	0	0	0	0	0	0	0.03	0	0.01	0	0.15	0.05	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis_1	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified	0.02	0	0	0	0	0	0	0	0	0	0	0.07	0.05	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;unclassified;unclassified;unclassified	0.14	0.45	0	0.1	0.01	0.02	0.12	0.08	0.12	0.53	0.42	0.18	0.27	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Derxia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Achromobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Alcaligenes	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Bordetella_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Castellaniella	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;GKS98_freshwater_group	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;unclassified	0.01	0	0.01	0	0	0	0	0.06	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_1	0.05	0	0	0	0	0	0	0	0	0	0	0.04	0.02	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Pandoraea	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;unclassified	0.02	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_2;Ralstonia	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax_caeni	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caenimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_2	0	0	0	0	0	0	0	0	0	0	0.11	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_6	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_R	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia	0	0.01	0	0.01	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ideonella_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Leptothrix_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ottowia	0	0	0	0	0	0	0	0	0.02	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Schlegelella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified	0	0	0.01	0	0	0	0	0.03	0.06	0	0.01	0.29	0.11	0.29
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_25	0.01	0	0	0	0	0	0	0.1	0.01	0	0.04	0	0.39	0.05
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xenophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Oxalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified	0	0	0	0.16	0	0	0.01	0.1	0.02	0.07	0.02	0	0.12	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium	0.02	0	0	0	0	0	0	0	0	0.01	0.02	0.11	0.28	0
Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0.01	0.01	0	0.02	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Leeia	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Aquaspirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Microvirgula_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Stenoxybacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;uncultured_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas	0	0	0	0	0	0	0	0	0	0.03	0	0	0.05	0
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;unclassified	0	0	0	0.01	0	0	0	0	0	0	0	0.04	0	0

Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;Denitratisoma_oestradiolicum	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;unclassified	0	0	0.01	0.01	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azoarcus_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azoarcus_2	0.01	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azovibrio	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;unclassified	0	0.09	0.03	0	0	0	0	0	0	0.04	0	0.07	0	0.05
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;uncultured	0	0.15	3.2	0.84	0.21	0	0.3	0	0.01	0.43	0.02	0	0.04	0.44
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Azonexus_caeni	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Dechloromonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;IC13_Millipede	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Lower_termite_Cluster	0	0.03	0	0.42	0.51	0.02	0.6	0.03	12.09	0.25	0.14	0.04	0.09	0.29
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Propionivibrio	0.22	0.86	0.07	0.48	0.21	0.15	0.55	0	0.18	0.91	0.01	0	0.11	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;unclassified	0	0	0.18	0.04	0	0	0.07	0.35	0.4	0.17	0.02	1.38	0.09	0.98
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0.18	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;unclassified;unclassified	0.01	0.09	0.3	0.07	0.01	0.15	0.05	0.3	0.12	0.69	0.05	2.72	0.34	2.15
Proteobacteria;Betaproteobacteria;SC-I-84;unclassified;unclassified	0	0	0	0.01	0	0.31	0	0.02	0.01	0	0.02	1.23	0	4.89
Proteobacteria;Betaproteobacteria;TRA3-20;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;unclassified;unclassified;unclassified	0.05	0.01	0.01	0.09	0	0.03	0.04	0.4	0.06	0.27	0.07	1.12	0.07	0.29
Proteobacteria;Deltaproteobacteria;43F-1404R;unclassified;unclassified	0.22	0	0	0.01	0	0	0	0	0	0	0	0	0	0.15
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Bacteriovorax_2	0	0.07	0	0	0	0	0.01	0	0	0	0	0	0.02	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Peredibacter	0	0.04	0	0	0	0	0.01	0	0	0	0	0	0.02	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;unclassified	0.02	0.24	0	0	0	0	0.04	0	0	0.06	0	0	0.02	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;OM27_clade	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus	0.05	0	0	0.01	0	0.02	0	0	0.03	0.02	0.02	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;uncultured	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiferula	0.13	0	0	0.04	0	0	0.02	0.03	0.02	0.01	0.05	0	0	0.1
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobotulus	0.02	0	0	0	0	0	0.02	0	0.01	0	0.01	0.15	0	0.05
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina	0	0	0	0.01	0	0	0.01	0	0.01	0	0.02	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;unclassified	0.06	0	0.01	0.01	0	0	0.02	0	0.02	0	0.05	0	0	0.05
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus	0.02	0	0	0.04	0	0	0.06	0	0.04	0	0.03	0.4	0.04	0.49
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulforhopalus	0	0	0	0	0	0	0	0	0	0	0	0.22	0.05	0.39
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;unclassified	0	0	0	0.01	0	0	0.01	0	0	0	0.02	0	0	0.05
Proteobacteria;Deltaproteobacteria;Desulfobacterales;unclassified;unclassified	0	0	0	0	0	0	0.01	0	0	0	0.02	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_1	0.02	0	0.32	2.82	3.24	0.51	4.09	0.32	3.21	1.43	0.11	0	0.09	0.15
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_2	0.01	0	0	0.03	0	0	0	0.06	0	0	0	0.04	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_3	1.84	0.8	0	0.41	0.14	0.15	0.86	1.02	0.21	0.24	2.07	3.52	2.78	0.39
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_4	0.02	0	0	0.01	0	0	0	0	0	0	0.02	0.33	0.05	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_5	0.04	0	0	0	0	0	0.01	0.03	0	0	0	0.25	0	0.05
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;unclassified	0.05	0	0.03	0.02	0.03	0	0.02	0.05	0.01	0.02	0.01	0.15	0.05	0.2
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;unclassified;unclassified	0.22	0	0	0.01	0	0	0	0.03	0	0	0	0	0.02	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;GR-WP33-58;unclassified	0.04	0.09	0	0.01	0	0	0	0	0	0	0	0	0	0.05
Proteobacteria;Deltaproteobacteria;Myxococcales;0319-6G20;unclassified	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Anaeromyxobacter	0.02	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Hyalangium	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Melittangium_boletus	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;unclassified	0	0	0	0.01	0	0.02	0.03	0.02	0	0	0.01	0	0.02	0.1
Proteobacteria;Deltaproteobacteria;Myxococcales;Haliangiaceae;Haliangium	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;JG37-AG-15;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;mle1-27;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Phaselicystidaceae;Phaselicystis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Byssovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium_2	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified;unclassified	0.02	0	0.03	0.01	0	0.03	0.01	0	0	0	0	0	0	0.64
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_3;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_4;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_5;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Proteobacteria;Deltaproteobacteria;Rs-K70_termite_group;unclassified;unclassified	0.03	0.79	0.01	0.63	0	0.16	0.61	0.06	0.41	0.38	0.8	1.63	2.25	0.05
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus	0	0	0	0	0	0	0	0	0	0	0	0	0.11	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;unclassified;unclassified;unclassified	0.03	0	0	0.05	0	0.02	0.03	0	0.03	0.01	0.03	0	0.11	0.05
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0	0	0	0.12	0	0	0.1	0	0.09	0.01	7.86	3.59	0.62	0.39
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum	0	0	0	0.17	0	0	0.13	0	2.02	4.21	0.23	5.69	0.16	0.05
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Rs-M59_termite_group	0	0	0	0	0.54	0	0.06	0	1.06	0.05	0.02	0	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Hydrogenimonas_thermophila;unclassified;unclassified	0	0	0	0	0	0	0	0	0.01	0.01	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Nautiliales;Nautiliaceae;Thioreductor	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0
Proteobacteria;Epsilonproteobacteria;unclassified;unclassified;unclassified	0	0	0	0.01	0	0	0.01	0	0.03	0.03	0.02	0	0	0.05
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Arenimonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Dyella_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Dyella_4	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Frateuria	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Leifsonia_a	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Luteimonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudomonas_cissicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas	0.01	0	0.11	0	0.01	0	0	0	0	0	0	0	0.05	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter_1	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter_2	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Silanimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0	0	0	0	0	0	0	0	0	0.01	0	0.04	0.04	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Thermomonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Xanthomonas_campestris	0	0	0	0	0	0	0	0	0	0	0	0.36	0	0
Proteobacteria;Gammaproteobacteria_1;Alteromonadales;Alteromonadaceae;Microbulbifer	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;B38;unclassified;unclassified	0	0	0	0	0	0	0	0.02	0	0	0.01	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Budvicia	0	0	0	0	0	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Enteric_Bacteria_cluster	0.03	0	0	0.03	0.04	0	0.04	0.51	0.04	0.03	0.17	1.41	0.16	0.15
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Leminorella	0.01	0	0	0.01	0	0	0.01	0	0.02	0.01	0.01	0	0.02	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Pragia	0	0	0	0.05	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;unclassified	0.01	0.01	0	0.02	0	0	0.05	0.02	0.02	0.02	0.02	0.04	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Morganella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Proteus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Providencia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;unclassified	0	0	0	0.02	0	0	0.02	0	0.01	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Xenorhabdus_nematophila	0.01	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;unclassified;unclassified	0.01	0	0	0.02	0	0	0.01	0	0.02	0.01	0.02	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae;Pseudospirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae_1;Marinomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales_1;Halomonadaceae;Chromohalobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales_4;Halomonadaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0	0.11	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;Aggregatibacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;Chelonobacter_oris	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;PB1-aai25f07;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Acinetobacter	0	0	0	0.08	0	0	0.01	0.37	0	0	0	0.11	0.05	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Alkanindiges	0	0	0	0	0	0	0	0	0	0	0.03	0.04	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Perlucidibaca	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Azotobacter_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Cellvibrio	0	0	0	0	0	0	0	0	0	0	0	0	0.09	0

Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_13	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_2	0	0	0	0	0	0	0	0	0	0	0.36	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_4	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_42	0	0	0	0	0	0	0.04	0	0.01	0	0.06	0	0	0.1
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_43	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;unclassified	0	0.04	0	0.01	0	0	0.01	0.03	0.01	0	0.03	0	0	0.05
Proteobacteria;Gammaproteobacteria_1;unclassified;unclassified;unclassified	0	0.03	0	0.01	0	0	0.01	0	0	0	0	0	0.04	0.05
Proteobacteria;Gammaproteobacteria_1;Vibrionales;Vibrionaceae;Photobacterium_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Aquicella	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Coxiella	0	0	0	0	0	0	0.02	0.02	0	0	0.02	0	0.05	0.1
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Rickettsiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Legionellaceae;Legionella_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Legionellaceae;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;NKB5;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;unclassified;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;Nevskia	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;Steroidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_6	0.01	0	0.01	0	0.03	0.02	0.01	0	0	0	0	0	0.02	0
Proteobacteria;TA18;unclassified;unclassified;unclassified	0	0.03	0	0	0	0	0.03	0	0	0	0	0	0.05	0
Proteobacteria;unclassified;unclassified;unclassified;unclassified	0.07	0.28	0.01	0.19	0.14	0.05	0.19	0.14	0.14	1.04	0.12	1.31	0.11	0.15
Spirochaetes;Spirochaetes;CW-1_termite_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0.39
Spirochaetes;Spirochaetes;GZKB75;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Rs-H88_termite_group	0.11	0	0	0.16	0.01	0	0.13	0.06	0.01	0	0.01	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;unclassified	0	0.07	0	0	0	0	0.12	0.29	0	0	0	0	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;uncultured_3	0	0.03	0	0.01	0.04	0	0	0.13	0	0	0.01	0	0	0.29
Spirochaetes;Spirochaetes;Spirochaetales;PL-11B10;unclassified	0	0.13	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Hodotermes_mossambicus_cluster	0	0	0	0	0	0	0	6.23	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;M2PT2-76_termite_group	0	0	0	0	0	0	0.01	0	0.01	0.02	0	0	0.18	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Kalotermitidae_Cluster	0	0.03	0	0.13	0	0	0.04	0	4.33	4.78	0.01	0	0.05	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_I	0	0	3.12	0.12	1.32	0.28	0.14	2.17	0	1.2	0	0	0.11	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_II	0	0.01	0	0	0.79	6.44	0.04	0	0.01	0.02	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Reticulitermes_Cluster	0	0	0.03	0.22	0.38	0	0.84	0.03	0.01	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Rhinotermitidae_Cluster_Qadd	0	0	0	0.12	0.28	0	0	0	0	0.1	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_1	0.47	0.01	0	0.01	0	0	0	0	0	0.05	0.05	0.22	3.45	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_2	0.32	0.01	0.51	0.68	0.22	0.33	0.25	0.16	0.51	0.26	0.04	0.04	0.11	0.93
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_sp_Kalotermes	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I	0	0	0	0	0	0.49	0	0.02	0	0.05	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Nasutite	0	0	0	0.05	0	0	0.02	0	0.06	0.31	0.02	0.04	0.18	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Soil_Fee	0	0	0	0.01	0	0	0.01	0.02	0.01	0.03	0	0.04	0.05	2.1
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Trinervit	0	0	0	0.01	0	0	0	0	0.01	0.04	0	0	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster	0	1.46	3.29	3.7	2.93	2.58	1.64	0.8	8.66	6.55	0.33	0	0.6	1.47
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Kaloterm	0.01	0.01	0.14	0.21	0	0	0.07	0.02	5.94	5.06	0.02	0.04	0.09	0.1
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Mastote	0	0	5.77	0.54	0	0	0.27	0.03	20.99	4.34	0.1	0	0.07	0.24
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Reticulit	0	0.86	0	10.8	17.72	0	4.44	0	0.19	0.04	0.07	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0.92	0	2.83	1.55	0	2.28	0.24	0.08	0	0.01	0	0	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0	0	0.01	0	0	0.01	0	0.05	4.06	0	0	0.05	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0	0.01	5.58	16.39	0.03	5.09	0.02	0.26	2.81	0.02	0	0.04	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Microcerotermes_Cluster	0	0	0	0	0	0	0	0	0	0.25	0	0	0.14	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Mixed_Higher_Termite_Cluster	0	0	0	0	0	0	0	0	0	0.05	0	0	0.21	0.34
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster	0	0	28.28	0.09	0	0.13	0.01	0	0	0.01	0	0	0.04	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster	0	0	0	0	0	0	0.01	0	0	0.7	0.01	0.04	0.34	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0.01	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0.15	0	0	0.08	0	0.12	1.11	0.1	0	0.62	0.15

Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0.01	0	0	0.01	0	0.04	0.51	0.02	0	0.25	0.15
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0	0.01	0	0.01	0	0	0	0.02	1.56
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Microcerotermes_Cluste	0	0	0	0	0	0	0	0.03	0	0.08	0	0.04	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster	0	0	0	0	0	0	0	0.02	0	0.03	0	0	0.04	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Macroterr	0	0	0	0.01	0	0	0	0	0.01	0	0.35	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Microcero	0	0	0	0.05	0	0	0.01	0	0.06	0.74	0.07	0	0.35	0.1
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0.07	0	0	0.01	0	0.06	0.39	0.06	0	0.12	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0.25	0	0	0	0.01	0	0.04	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0	0.03	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0.54	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Treponema_2	0	1.19	1	20.99	18.86	0	0.7	2.03	0.19	0.02	0.38	0.04	0.58	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Trinervitermes_cluster_a	0	0	0	0.02	0	0	0.01	0	0.02	0.11	0	0	0.19	0.05
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;unclassified	0.32	2.26	13.56	4.17	2.21	2.25	3.77	8.09	6.17	11.55	0.36	0.04	1.93	4.06
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_2	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_4	0	0	0	0.27	0	0	0	0	0	0.01	0	0.04	0.02	0
Spirochaetes;Spirochaetes;Spirochaetales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Candidatus_Tammella	0	0	0	0	0	0	0	0	0	0	0.51	0.07	0.64	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Cloacibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Jonquetella	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Synergistes_jonesii	0.01	0	0	0	0	0	0	0	0	0	0.01	0	0	0.05
Synergistetes;Synergistia;Synergistales;Synergistaceae;unclassified	1.73	0	0.03	0.11	0	0	0.13	0.34	0.06	0.01	0.13	0	0.07	0.29
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_2	0	0	0	0	0	0	0.01	0.14	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_6	0.68	0.86	0.46	1.93	0.47	1.44	2.4	0.1	0.37	1.39	0.36	0.07	1.98	2.1
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_I	0	0	0	0.01	0	0	0	0	0	0.35	0.02	0	0.64	0
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_II	0	0	0	0	0	0	0	0	0	0.07	0	0	0.14	0.05
TG3;TG3;TG3_sp1;Termite_Cluster;unclassified	0	0	0	0	0	0	0	0	0	0.03	0	0	0.02	0
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;Nasutitermes_Cluster	0	0	0	0.01	0.01	0	0.01	0	0	0.02	0	0	0.05	0.15
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;unclassified	0	0	0	0	0	0	0	0	0	0	0.1	0	0.16	0
TG3;TG3;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
unclassified;unclassified;unclassified;unclassified;unclassified	0.41	0.83	1.4	1.42	0.76	1.71	2.19	1.17	0.76	0.72	0.89	0.11	1.04	1.32
Verrucomicrobia;Acidimethylosilex;Termite_group_A;unclassified;unclassified	0.49	0.22	0.03	0	0.59	0	0.24	0	0	0	0	0	0	0
Verrucomicrobia;Acidimethylosilex;unclassified;unclassified;unclassified	0.01	0	0	0	0.03	0	0	0	0	0	0	0	0	0
Verrucomicrobia;OPB35_soil_group;unclassified;unclassified;unclassified	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0.18	0.01	0.58	0.16	0.13	0.08	0.19	0.02	0.06	0.01	0.03	0.04	0.21	0.1
Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Cerasicoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;unclassified;unclassified;unclassified	0.01	0	0.01	0.01	0	0	0.02	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;vadinHA64;unclassified;unclassified	0.33	0.45	4.59	0.16	0.17	0	4.26	0.11	0.07	0.8	0.24	0	1.29	0
Verrucomicrobia;Spartobacteria;Candidatus_Xiphinematobacter;Candidatus_Xiphinematobacter;Candidatus_Xiphinematobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;Chthoniobacter;unclassified;unclassified	0.09	1.04	0	0	0	0.08	0.24	0.02	0	0	0	0.11	0.02	0.29
Verrucomicrobia;Spartobacteria;DA101_soil_group;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;FukuN18_freshwater_group;unclassified;unclassified	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;unclassified;unclassified;unclassified	0.04	0.04	0	0	0	0	0.16	0	0	0	0	0	0	0.1
Verrucomicrobia;Spartobacteria;uncultured_1;unclassified;unclassified	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;zEL20;unclassified;unclassified	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;unclassified;unclassified;unclassified;unclassified	0	0.04	0	0	0	0	0.01	0	0	0	0.01	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;unclassified;unclassified	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Akkermansia	0	0	0	0.01	0	0	0.02	0	0.01	0	0.02	0.04	0	0.05
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_1;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;Prosthecobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;uncultured_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WCHB1-60;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table 4 from Chapter 3: Distribution and relative abundance of the pyrotag reads in all samples.

	Relative abundance (%)										
Taxon	**Microceroter. wg**	**Ophioterme**	**A. meridi**	**Apicotermes**	**N. corniger**	**N. takasag**	**Trinervite**	**P. paradoxa**	**Pachnoda. 18**	**A. domesticus**	**G. assimilis**
1_Proteobacteria;1_Deltaproteobacteria;1_Desulfobacterales;1_Nitrospinaceae;Candidatus_Entotheonella	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium	0	0	0.02	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Chloroacidobacterium	0	0	0.03	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Koribacter	0	0.08	0.02	0.02	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus_Solibacter	0	0.02	0	0.02	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Terriglobus	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified	0.01	0	0.01	0.02	0.03	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_1	0	0.02	0.03	0.06	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_12	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_14	0	0	0	0	0.03	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_17	0	0.05	0.01	0.01	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_18	0	0.02	0.03	0.01	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_22	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_23	0.26	0	0.16	0.85	0.92	0.07	0.11	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_26	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_27	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_31	0.01	0.02	0.01	0.05	0	0	0	0	0.34	0	0
Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;uncultured_9	0	0.01	0.04	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;Holophaga	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;unclassified	0.02	0	0	0	0	0.03	0	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_3	0.53	0	0	0.04	0.22	0.34	0.72	0	0	0	0
Acidobacteria;Holophagae;Holophagales;Holophagaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;Ilumatobacter	0	0	0	0.02	0	0	0	0	0.13	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;marine_group	0	0	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;unclassified	0	0	0	0	0	0	0	0	0.1	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_3	0	0	0	0.01	0	0	0	0	0.12	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Acidimicrobiaceae_1;uncultured_4	0	0	0	0.01	0	0	0	0	0.15	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Candidatus_Microthrix;Candidatus_Microthrix	0	0	0	0.01	0	0	0	0	0.03	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;Iamiaceae;Iamia	0	0	0	0	0	0	0	0	0.07	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;marine_group_1;unclassified	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;marine_group_2;unclassified	0	0	0	0	0	0	0	0	0.61	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;unclassified;unclassified	0	0.04	0	0.02	0	0	0	0	0.1	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_2;unclassified	0	0	0	0	0	0	0	0	0.03	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_3;unclassified	0	0	0	0	0	0	0	0	0.04	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_4;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_5;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Acidimicrobiales;uncultured_6;unclassified	0	0.29	0.02	0.11	0	0	0	0	0.08	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Acidothermaceae;Acidothermus	0	0.96	0.03	0.38	0	0	0.01	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_2	0	0.01	0.04	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces_3	0	0	0	0	0.03	0	0	0	0	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;unclassified	0	0	0.02	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;Salana	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Beutenbergiaceae;unclassified	0	0	0	0	0	0	0	0	0.11	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Brevibacteriaceae;Brevibacterium	0	0	0	0	0	0	0	0.01	0	0.02	0.09
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Actinotalea	0	0	0	0	0	0	0	0	0.03	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas_1	0	0.01	0	0.01	0	0	0	0	0.03	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas_2	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Oerskovia	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;unclassified	0	0	0	0	0	0	0	0	0.02	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales;Demequina;unclassified	0	0	0	0	0	0	0	0	0.06	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;Brachybacterium	0	0	0	0	0	0	0	0	0.01	0.02	0.01

Actinobacteria;Actinobacteria;Actinomycetales;Dermacoccaceae;Demetria	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Dermacoccaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Frankiaceae;Frankia	0	0.11	0	0.05	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_2	0	0	0	0.05	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_3	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus_saxobsidens	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Geodermatophilus	0	0	0	0.05	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Modestobacter	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;unclassified	0	0	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Humihabitans	0	0	0	0.11	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Janibacter	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Lapillicoccus	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Terrabacter	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;Terracoccus_sp_a	0	0.01	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae_1;unclassified	0	0	0	0.09	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Kineosporia	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Quadrisphaera	0	0	0	0.11	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Agromyces_2	0	0	0	0.01	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Curtobacterium	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Frigoribacterium_2	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Humibacter_albus	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_1	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia_7	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leucobacter	0	0.01	0	0.02	0	0	0	0	0	0	0.06
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Microbacterium	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Pseudoclavibacter_1	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;unclassified	0.01	0	0	0.02	0	0	0	0	0.03	0	0.02
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_1	0	0	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;uncultured_2	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_17	0	0	0	0	0	0	0	0	0	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_18	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_21	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter_5	0	0	0.01	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Citricoccus	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Kocuria_2	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Nesterenkonia	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Rothia	0	0	0.04	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;unclassified	0	0	0	0.01	0	0	0	0	0	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Yaniella	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nakamurellaceae;Nakamurella	0	0	0	0	0	0	0	0	1.68	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Aeromicrobium	0	0	0	0.01	0	0	0	0	0.05	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Kribbella	0	0	0	0.03	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Marmoricola	0	0	0	0.05	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Nocardioides	0	0.05	0	0.19	0	0	0.01	0	0.24	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonospiraceae;Cellulosimicrobium_	0	0	0.01	0.01	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Myceligenerans_xiligouense	0	0	0	0	0.03	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;unclassified	0	0	0.01	0.03	0	0.04	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Xylanimonas_	0	0.02	0	0.07	0	0.01	0.1	0	0.28	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Aestuariimicrobium	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Brooklawnia_cerclae	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Microlunatus	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Tessaracoccus	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;Sanguibacteraceae;Sanguibacter	1.64	0	1.44	0.15	0.35	0.43	0.86	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales;unclassified;unclassified	0.4	0.14	6.54	0.44	0.08	0.72	0.3	0	1.58	0	0
Actinobacteria;Actinobacteria;Actinomycetales;uncultured_1;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Catenulisporaceae;Catenulispora	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Kitasatospora	0	0.02	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptacidiphilus	0	0	0	0.01	0	0.01	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_1	0	0.02	0	0.04	0	0	0.01	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_10	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_11	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_2	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_3	0	0	0	0.04	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_6	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_8	0	0.01	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;Streptomyces_9	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unclassified	0	0.08	0	0.09	0	0.01	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales_1;Streptomycetaceae;unpublished_a	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Actinospicaceae;Actinospica	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_1	0	0	0.04	0	0	0	0	0	0.14	1.27	4.92
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_5	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_7	0	0	0	0	0	0	0	0	0	0.07	0.05
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_8	0	0	0	0	0	0	0	0	0	0	0.02
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_atypicum	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;Corynebacterium_spheniscorum	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;unclassified	0	0	0	0	0	0	0	0	0.01	0.3	0.78
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Corynebacteriaceae;uncultured_2	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Dietziaceae;Dietzia	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Millisia_brevis;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Mycobacteriaceae;Mycobacterium	0	0.06	0	0.08	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Nocardia	0	0	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_1	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;Rhodococcus_2	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae;unclassified	0	0	0	0	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Nocardiaceae_1;Gordonia	0	0	0	0	0	0	0	0	0.02	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_1;Amycolatopsis	0	0	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_1;Saccharopolyspora	0	0	0.01	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_2;Pseudonocardia	0	0.06	0.01	0.14	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_3;Goodfellowiella	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_4;Crossiella	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Pseudonocardiaceae_4;Kutzneria_2	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Segniliparaceae;Segniliparus	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;Tsukamurellaceae;Tsukamurella	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales_2;unclassified;unclassified	0	0.01	0	0.01	0	0	0.15	0	0.01	0	0.01
Actinobacteria;Actinobacteria;Actinomycetales_2;uncultured;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_3;PeM15;unclassified	0	0	0	0	0	0	0	0	0.31	0	0
Actinobacteria;Actinobacteria;Actinomycetales_3;Sporichthyaceae;Sporichthya	0	0	0	0	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinocatenispora	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinoplanes_1	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Actinoplanes_6	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Dactylosporangium	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Krasilnikovia	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Luedemannella	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_1	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_7	0	0	0	0.01	0	0	0	0	0.01	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonospora_8	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;Micromonosporaceae_bacteria_a	0	0.04	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;unclassified	0	0.02	0	0.11	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Micromonosporaceae;uncultured	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Nocardiopsaceae;Nocardiopsis_1	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Microbispora	0	0	0.01	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Sphaerisporangium_2	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;Streptosporangium	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Streptosporangiaceae;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinoallomurus	0	0.04	0	0.04	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinocorallia	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_1	0	0	0	0.02	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_3	0	0	0	0.01	0	0	0	0	0	0	0

Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_5	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;Actinomadura_8	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;Thermomonosporaceae_2;unclassified	0	0.14	0	0.15	0	0	0.02	0	0	0	0
Actinobacteria;Actinobacteria;Actinomycetales_4;unclassified;unclassified	0	0.01	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;AKIW543;unclassified;unclassified	0	0.02	0.08	0.31	0	0.01	0	0	0.59	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Aeriscardovia_aeriphila	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium_2	0	0	0	0	0	0	0.02	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium_4	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Gardnerella	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia_criceti	0	0	0	0	0	0	0.03	0	0	0	0
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;unclassified	0	0	0	0	0.13	0	0.02	0	0	0	0
Actinobacteria;Actinobacteria;Bogoriella_caseilytica;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;marine_group	0	2.8	0.13	0.26	0	0	0.01	0	0.07	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;unclassified	0.01	0.06	0.27	0.17	0	0.02	0	0.02	0.08	0.02	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_10	0.12	0.42	2.19	0.25	0.24	0.14	0.22	0	0.1	0	0.01
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_11	0.01	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_12	0	0.02	0	0.02	0	0	0.01	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_8	0	0	0.04	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;MB-A2-108;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;RL185-aaj71c12;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteriaceae;Rubrobacter	0	0	0	0.07	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;0319-6M6;unclassified	0	0.02	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;288-2;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;480-2;unclassified	0	0	0	0.21	0	0	0	0	0.16	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Conexibacteraceae;Conexibacter	0	0	0.01	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Patulibacteraceae;Patulibacter	0	0	0	0.04	0	0	0	0	0.07	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;Solirubrobacteriaceae;Solirubrobacter	0	0.01	0	0.1	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;TM146;unclassified	0	0.13	0.01	0	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;unclassified;unclassified	0	0.08	0.02	0.04	0	0	0	0	0.02	0	0
Actinobacteria;Actinobacteria;Solirubrobacterales;YNPFFP1;unclassified	0	1.01	0.07	0.21	0	0	0	0	0	0	0
Actinobacteria;Actinobacteria;unclassified;unclassified;unclassified	0.34	0.1	0.25	0.11	0.03	0.15	0.46	0	0.31	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.03	0.02	0	0	0.03	0	0	0.01	0.1	3.74	1.62
Bacteroidetes;Bacteroidia;Bacteroidales;CAP-aah99b04;unclassified	0	0	0	0.02	0	0.01	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;COB_P4-1_termite_group;unclassified	0.08	0	0	0.49	0.54	0.43	1.07	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;gir-aah93h0;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_cluster_a;unclassified	0	0	0	0	0.08	0	0	0	0.25	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;3M1PL1-52_termite_group	0	0.91	0.02	0.29	0	0.02	0.2	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Hodotermes_Cluster	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;unclassified	0	0.14	0	0.01	0	0.04	0.01	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Insect_Cluster_I;Wood_feeding_roaches	0	0	0	0	0	0.01	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;unclassified	0	0	0	0	0	0.03	0	0	0.04	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_a	0.01	0	0	0.1	0.03	0.09	0.88	0	0.03	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_b	0.01	0.04	0	0.84	0.51	1.62	0.98	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;M2PB4-65_termite_group;uncultured_c	0	0	0	0	0.03	0	0.17	0	0.01	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Alkaliflexus	0.01	0	0.04	0	0.03	0	0.19	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;unclassified	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured_1	0	0	0	0	0.03	0.02	0.02	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;MgMjR-022;unclassified	0	0.04	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Nearly_all_Termite_Cluster;unclassified	0.02	0.01	0	0	0	0	0.19	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;p-2534-18B5_gut_group;termite_group_a	0	0	0	0	0	0.01	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Paludibacter	0.31	0.64	0.03	3.16	0.73	0.63	1.56	0	0.21	0.05	0.01
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Candidatus_Symbiothrix	0.08	3.03	0.18	6.75	0.38	0.51	1.84	0	0	0.05	0.06
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Dysgonomonas	0.03	0	0.01	0.03	0.05	0.01	1.21	0	0.05	6.77	2.11
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Parabacteroides	0.07	0	0	0	0.03	0	0	0	0.31	5.62	3.43
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;Tannerella	0.11	0.17	0.01	2.55	0	0.16	0.87	0	0.01	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_1;unclassified	0	0	0	0.06	0	0	0	0.01	0.02	0.67	0.43
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_2;Cubitermes_Cluster_A	0	0.31	0	0.39	0	0	0.01	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_2;Proteiniphilum	0	0	0	0	0	0	0	0	1.33	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Butyricimonas	0	0	0	0	0	0	0	0	0	0	0.07

Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Odoribacter	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;Shelfordella_cluster_a	0	0	0	0	0.03	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;unclassified	0	0	0	0	0	0	0	0	0	0.02	0
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae_3;uncultured_b	0	0	0	0	0	0	2.11	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;uncultured_10	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;ratAN060301C;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	0.15	0.11	0.16	1.03	0.4	0.07	0.22	0	3.83	13.04	10.61
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;BCf9-17_termite_group	1.17	0.04	0	0.02	0.16	0.04	0.15	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_a	0	0	0	0	0	0	0	0	0	0.37	0.06
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;gut_cluster_c	0	0	0	0	0	0	0	0	0.12	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;M2PB4-61_termite_group	0.77	0.06	0	0.17	0.4	1.02	1.73	0	0.02	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;P1_32_Panesthia	0	0	0	0	0.03	0	0	0	0.01	5.62	0.69
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;RC9_gut_group	0	0	0	0.09	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_1	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_3	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rikenella_4	0	0	0	0	0	0	0	0	0	0.53	0.01
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Rs-D38_termite_group	0.03	0	0	0	0.08	0.07	0.7	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;unclassified	0.04	0	0	0.09	0.05	0.04	0.01	0	0.14	4.51	1.25
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;vadinBC27_wastewater-sludge_group	0	0.13	0	0.53	0.13	0.17	0.13	0	0.1	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_aa	0	0	0	0	0	0	0.08	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;group_bb	0	0	0	0	0	0	0.02	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;higher_termites_a	0.16	0.04	0	0.41	0.35	0.14	0.16	0	0.01	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;Rs-E47_termite_group;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;S24-7;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;unclassified;unclassified	0.04	0.13	0.01	0.37	0.16	0.15	0.04	0	0.07	1.04	0.75
Bacteroidetes;Bacteroidia;Bacteroidales;uncultured_bacterium_Cylindroiulus_2;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Bacteroidetes;Bacteroidia;Bacteroidales;vadinHA21;unclassified	0.01	0.14	0	0.02	0.16	0.05	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;Blattabacterium	0.46	0	0.03	0	0.05	0	0	0.05	0.08	0	0.04
Bacteroidetes;Flavobacteria;Flavobacteriales;Blattabacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Flavobacterium_2	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Galbibacter_mesophilus	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Lutaonella_thermophila	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;Myroides	0	0	0	0	0	0	0	0	0	0	0.04
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_1;unclassified	0	0	0	0	0	0	0	0	0.03	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Bergeyella	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_1	0.01	0.01	0	0.01	0	0	0	0.02	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_11	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_12	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_5	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_8	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_molle	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_pallidum	0.01	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_soldanellicol	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Chryseobacterium_sp._CCUG_15624	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Cloacibacterium	0	0	0.02	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Elizabethkingia	0	0.04	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Empedobacter_1	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;unclassified	0.16	0	0.12	0.03	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;uncultured_a	0	0	0	0	0.08	0	0	0	0	3.47	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Wautersiella_1	0	0.01	0	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae_2;Weeksella	0	0.01	0.01	0	0	0	0	0	0	0	0
Bacteroidetes;Flavobacteria;Flavobacteriales;unclassified;unclassified	0.02	0	0	0.01	0	0	0	0	0.03	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;SB-1;unclassified	0	0.12	0.02	3.51	0	0.01	0.16	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Mucilaginibacter_1	0	0	0	0.01	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Mucilaginibacter_2	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Nubsella	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_1	0	0	0	0.13	0	0	0	0	0	0	0.01
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_2	0	0.01	0	0	0	0	0	0	0	0	0.02
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;Sphingobacterium_3	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;Sphingobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0

Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;ST-12K33;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;unclassified;unclassified	0	0	0	0.15	0	0.02	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;vadinHA17;unclassified	0	0	0	0	0	0.01	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_1;WCHB1-69;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Niabella	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;Sediminibacterium	0	0	0.01	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;unclassified	0.01	0.05	0	0.01	0.11	0.01	0	0	0.01	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_11	0	0	0	0	0	0	0	0	0.02	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_12	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Chitinophagaceae;uncultured_6	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;Saprospiraceae;uncultured_1	0.01	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_2;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_1;Flexibacter_1	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;Cytophagaceae_2;Sporocytophaga	0	0	0	0	0	0	0	0	0	0	0
Bacteroidetes;Sphingobacteria;Sphingobacteriales_3;unclassified;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Bacteroidetes;Sphingobacteria;unclassified;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Bacteroidetes;unclassified;unclassified;unclassified;unclassified	0.04	0.05	0	0.84	0.05	0.06	0	0	0.03	0.28	0.14
Bacteroidetes;VC2.1_Bac22;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
BD1-5;unclassified;unclassified;unclassified;unclassified	0	0.01	0	0	0	0	0	0	0	0	0
Candidate_division_BRC1;unclassified;unclassified;unclassified;unclassified	0	0	0.01	0	0	0	0	0	0	0	0
Candidate_division_OD1;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_OP10;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_OP11;unclassified;unclassified;unclassified;unclassified	0.23	0.42	0.35	0.49	0.22	0.01	0.11	0	0.01	0	0
Candidate_division_SR1;unclassified;unclassified;unclassified;unclassified	0.04	0.1	0.15	0.21	0.3	0	0.11	0	0	0	0
Candidate_division_TM6;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Candidate_division_TM7;unclassified;unclassified;unclassified;unclassified	0.22	1.35	0.85	0.43	0.62	0.57	0.43	0	0.49	0.02	0.04
Chlamydiae;Chlamydiae;Chlamydiales;cvE6;unclassified	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Candidatus_Protochlamydia	0	0	0.02	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Neochlamydia	0	0	0	0.01	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus_Rhabdochlamydia	0	0	0	0	0	0	0	0	0	0	0
Chlamydiae;Chlamydiae;Chlamydiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Chlorobi;Chlorobia;Chlorobiales;OPB56;unclassified	0.12	0.01	0	0.07	0.08	0.03	0	0	0	0	0
Chlorobi;Chlorobia;Chlorobiales;SJA-28;unclassified	0.19	0	0	0	0	0.03	0	0	0	0	0
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured_11	0	0	0	0	0	0	0	0	0.12	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0	0	0	0	0	0	0	0	0.02	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_1	0	0	0	0	0	0	0	0	0.03	0	0
Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured_4	0	0	0	0.02	0	0	0	0	0	0	0
Chloroflexi;Chloroflexi;Chloroflexales;Chloroflexaceae;Roseiflexus	0	0	0	0.03	0	0	0	0	0.01	0	0
Chloroflexi;Gitt-GS-136;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0.24	0	0
Chloroflexi;JG37-AG-4;unclassified;unclassified;unclassified	0	1.2	0	0	0	0	0	0	0	0	0
Chloroflexi;KD4-96;unclassified;unclassified;unclassified	0	0.01	0	0.1	0	0	0	0	0.49	0	0
Chloroflexi;Ktedonobacter;Ktedonobacter;Ktedonobacter;Ktedonobacter	0	0.02	0.14	0.02	0	0	0	0	0	0	0
Chloroflexi;S085;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0.02	0	0
Chloroflexi;Thermomicrobia;AKYG1722;unclassified;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Chloroflexi;Thermomicrobia;JG30-KF-CM45;unclassified;unclassified	0	0	0	0.06	0	0	0	0	0.52	0	0
Chloroflexi;Thermomicrobia;Sphaerobacteridae;Sphaerobacterales;Sphaerobacteraceae	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi;TK10;unclassified;unclassified;unclassified	0	0.02	0	0	0	0	0	0	0.01	0	0
Chloroflexi;unclassified;unclassified;unclassified;unclassified	0	0	0	0.1	0	0	0	0	0	0	0
Chloroflexi;vadinBA26;unclassified;unclassified;unclassified	0	0.04	0.01	0.32	0	0.05	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;4C0d-2;unclassified	0	0	0	0	0	0	0	0	0.01	0	0.08
Cyanobacteria;Cyanobacteria;Cyanobacteriales;Chloroplast;Chloroplast	0	0	0	0	0	0	0	0.01	0	0.05	0.04
Cyanobacteria;Cyanobacteria;Cyanobacteriales;ML635J-21;unclassified	0.54	0	0.01	0.01	0.22	0.12	0.02	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;MLE1-12;unclassified	0	0	0.02	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionII;SubgroupII_Chroococcidiopsis	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionIII;uncultured	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionIV;unclassified	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;SubsectionV;Stigonema	0	0	0.03	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria;Cyanobacteria;Cyanobacteriales;WD272;unclassified	0	0.01	0.03	0.01	0	0	0	0	0	0	0

Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Mucispirillum	0.09	0.01	0.03	0.13	0	0.03	0.1	0	0.18	0.21	0.04
Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus;Deinococcus-Thermus;Deinococcales;Deinococcaceae;Deinococcu	0	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus;Deinococcus-Thermus;Deinococcales;Trueperaceae;Truepera	0	0	0	0	0	0	0	0	0.06	0	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_I_[Endomicrobia]	0.2	0.12	0.24	0.33	0	0.03	0.02	0.02	0.17	0	0.01
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Lineage_III_[Elusimicrobium]	0.02	0.01	0.03	0.33	0.03	0.01	0	0	0.11	0	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;uncultured_d	0	0	0	0	0	0	0	0	0	0	0
Fibrobacteres;Fibrobacteres_sp1;Fibrobacterales;Fibrobacteraceae;Fibrobacter	0	0	0	0	0.03	0	0	0	0	0	0
Fibrobacteres;Fibrobacteres_sp2;Fibrobacteres_sp2;Termite_Cluster;Termite_Cluster_I	6.22	0	0.03	0	8.13	0.04	0.13	0	0.01	0	0
Fibrobacteres;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Apr-15;unclassified;unclassified	0	0	0	0	0	0.01	0.01	0	0	0	0
Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Alicyclobacillus	0	0	0.06	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_10	0	0.01	0	0	0	0	0	0	0	0	1.38
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_11	0	2.1	0.22	0.1	0	0.04	0.05	0	0	0	0.01
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_12	0	0.11	0	0	0	0	0	0	0.02	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_14	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_3	0	0.62	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_4	0	1.89	0.01	0.08	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_5	0	0.45	0.25	0.03	0	0	0	0	0.01	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_6	0	0.13	0.01	0.02	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus_7	0	0	0	0.02	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae;unclassified	0	0.25	0.03	0.03	0	0	0	0.01	0.21	0	5.34
Firmicutes;Bacilli;Bacillales;Bacillaceae_3;Bacillus	0	0.02	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_5;unclassified	0	0.02	0	0.02	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Bacillaceae_6;Bacillus_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Family_XII_Incertae_Sedis;Exiguobacterium	0	0	0	0	0	0	0	0	0.01	0	0
Firmicutes;Bacilli;Bacillales;Listeriaceae;Brochothrix	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Listeriaceae;Listeria	0	0	0	0	0	0	0	0	0	0.02	0.09
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_1;Oxalophagus	0	0	0.03	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Brevibacillus	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Cohnella	0	0.05	0.02	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_1	0	0	0	0.01	0	0	0	0	0.01	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_12	0	0	0.03	0	0	0	0	0	0	0	0.01
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_13	0	0.01	0	0	0	0	0.01	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_15	0	0	0.03	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_16	0	0	0.03	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_17	0	0	0.01	0	0	0.01	0	0	0.03	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_18	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_19	0	0.01	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_7	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;Paenibacillus_8	0	0.02	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Paenibacillaceae_2;unclassified	0	0.17	0.35	0	0	0.01	0.01	0	0.01	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Caryophanon	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_2	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_3	0	0.08	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_5	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Incertae_Sedis_6	0.01	0	0.04	0.01	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;Lysinibacillus	0	0	0	0.01	0	0	0	0	0.07	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;unclassified	0.01	0	0	0.02	0	0	0	0	0	0	0.01
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_1	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_2	0	0	0	0	0	0	0	0	0	0	0.21
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Planococcaceae_2;uncultured_5	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;unclassified	0	0	0.09	0	0	0	0	0	0.01	0	0
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_1	0.01	0.04	0	0	0.03	0	0	0	0	8.67	4.41
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus_2	0	0	0	0	0	0	0	0.01	0	0.05	0.17
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;unclassified	0	0	0	0	0	0	0	0	0	0.16	0.25
Firmicutes;Bacilli;Bacillales;unclassified;unclassified	0.04	0.19	0.02	0.02	0	0.01	0.08	0	0.05	0	0.06
Firmicutes;Bacilli;Bacillales_2;Thermoactinomycetaceae;Shimazuella	0	0	0	0.01	0	0	0	0	0	0	0

Firmicutes;Bacilli;Lactobacillales;16d63.751;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;Eremococcus	0	0	0	0	0	0	0	0	0	0	0.01
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Carnobacterium_1	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Carnobacterium_3	0	0	0.02	0	0	0	0	0	0	0.18	0
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Trichococcus_1	0	0.02	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Catellicoccus_marimammalium;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_2	0	0	0	0	0.05	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_3	0.03	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_4	0.01	0	0	0.02	0	0.01	0.02	0.05	0	0.14	0.16
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_5	0	0	0	0	0.03	0	0	0.01	0.01	0.99	0.48
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus_7	0	0	0	0	0	0	0	0.27	0	3.37	0.16
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Pilibacter	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;unclassified	0	0.01	0	0.27	0.03	0	0.02	0.05	0	1.53	0.54
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Vagococcus	0	0	0	0.02	0	0	0	0	0	0	0.21
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;Enterococcus_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;Enterococcus_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;Enterococcus_sp._R-25205	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;unclassified	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcaceae_2;uncultured_a	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Enterococcus_phoeniculicola;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Hodotermopsis_Trichonympha_Symbiont_1;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_2	0.08	0	0.01	0	0	0	0	0.15	0.01	0	0.07
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_3	0	0	0	0	0	0	0	66.37	0.01	0	0.82
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_4	0	0	0	0	0.03	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_5	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_6	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_9	0	0	0	0	0	0	0	0.03	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus_sp_a	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Paralactobacillus	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Pediococcus	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;unclassified	0.02	0	0	0	0.08	0	0	7.85	0	0	0.07
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Fructobacillus	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Hm_96	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;HsjTcB_43	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc_fallax	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Oenococcus	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_1	0	0	0	0	0	0	0	0	0	0.02	0.15
Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella_2	0	0	0	0	0.08	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;PeH08;unclassified	0.07	0	0.01	0.21	0.03	0	1.53	0	0.07	0	0
Firmicutes;Bacilli;Lactobacillales;Rs-D42;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Sl_24;unclassified	0	0	0	0	0.03	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Sl_99;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_1	0	0.01	0	0.05	0.03	0.01	2.52	0.02	0.01	0.09	19.62
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_2	0	0	0	0	0	0	0	0.02	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus_3	0	0	0	0.01	0	0.01	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactovum	0.18	0.02	0.04	0.85	0	0.01	0.43	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0	0.04	0.02	0	0	0	0	0.01	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;unclassified	0.07	0	0	0.89	0	0	0.09	0	0	0	0.05
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_1	0.03	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;unclassified;unclassified	0.18	0.01	0.06	1.23	0.11	0.01	0.29	0.01	0	0.37	0.38
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Hepialus;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;Lactobacillales;uncultured_bacterium_Pachnoda_1;unclassified	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Bacilli;unclassified;unclassified;unclassified	0.16	0.04	2.27	0.87	0.08	0.01	0.01	0	0.07	0	0.35
Firmicutes;Bacilli;VAN12;unclassified;unclassified	0	0.02	0	0.01	0	0	0	0	0	0	0
Firmicutes;CK-1C4-19;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0.01	0	0.05	0.32

Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Anaerobacter_polyendosporus	0	0	0	0	0	0	0.05	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_1	0.03	0	0	0.02	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_11	0	0	0.02	0.03	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_6	0	0.01	0	0	0	0.02	0	0.02	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Clostridium_8	0	0.11	0.06	0.11	0.03	0.03	0	0	0.01	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;Oxobacter	0	0	0.03	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_1;unclassified	0.03	0.17	0.07	0.11	0	0.05	0.08	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Clostridiaceae_2;Alkaliphilus_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Dethiosulfatibacter_aminovoran;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Anaerofustis	0	0	0	0.01	0	0	0	0	0.02	0	0.01
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Eubacterium_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;Pseudoramibacter	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Eubacteriaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XI_Incertae_Sedis;Anaerococcus_1	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XI_Incertae_Sedis;Tissierella_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Anaerovorax_	0	0.38	0.02	0.13	0.13	0.08	0.12	0	0.14	0.51	0.21
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_1	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_2	0	0	0	0	0	0	0.01	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Eubacterium_3	0.01	0.12	0	0.14	0	0.04	0.03	0	0.01	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;Mogibacterium	0	0	0	0	0	0	0.08	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;unclassified	0.02	0.75	0.27	0.7	0.08	0.26	0.28	0	0.06	0.07	0.18
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_4	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_5	0.18	1.58	1.38	0.74	0.13	0.62	0.36	0	0.1	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_6	0	0.08	0.07	0	0	0.01	0.04	0	0.14	0	0
Firmicutes;Clostridia_1;Clostridiales;Family_XIII_Incertae_Sedis;uncultured_a	0	0	0	0	0	0	0	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Gracilibacteraceae;Lutispora	0	0	0	0	0	0	0	0	0.01	0	0
Firmicutes;Clostridia_1;Clostridiales;Gracilibacteraceae;unclassified	0	0.04	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Anaerostipes	0	0	0	0	0	0	0	0	0	0	0.04
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Butyrivibrio_4	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Butyrivibrio_fibrisolvens	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Catabacter	0.01	0.13	0.17	0.02	0.03	0.01	0.01	0	0.18	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Clostridiales_bacterium_HAW-EB17	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Coprococcus_1	0	0	0	0	0.03	0	0	0	0.02	0.28	0.28
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Hespellia	0	0	0	0.1	0	0	0	0	0.13	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_11	0	0	0.14	0.05	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_13	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_14	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_16	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_18	0	0	0	0	0	0	0	0	0	0.25	0.2
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_24	0.01	0.01	0	0	0	0	0	0	0.09	0.12	0.08
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_25	0	0	0	0.02	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_26	0	0	0	0	0	0	0	0	0.03	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_30	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_31	0	0	0	0.03	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_32	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_34	0	0.02	0	0	0.03	0.01	0.01	0	0	0	0.02
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_35	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_36	0.63	3.79	4.25	5.57	0.32	0.58	3.27	0	2.76	0.9	0.79
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_8	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Incertae_Sedis_9	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Marvinbryantia	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Mmba_A01b	0	0.06	0	0.02	0	0	0	0	0.05	0.18	0.14
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Parasporobacterium-Sporobacterium	0	0.75	0	0	0	0	0	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella	0	0	0	0	0	0	0	0	0	1.06	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_higher_Termites	0	7.03	0	0.14	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;Robinsoniella_Insects	0	0	0	0	0	0	0	0	0.01	0.23	0.07

Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;unclassified	0.27	2.39	0.63	2.54	0.4	0.33	0.73	0	2.64	7.44	5.57
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_1	0	0.01	0	0	0	0	0	0	0	0.02	0.01
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_10	0	0	0.02	0.06	0.03	0	0	0	0	0.12	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_11	0.03	0	0.01	0	0.03	0.07	0.13	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_13	0.01	0	0	0	0	0	0	0	0.05	0	0.05
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_14	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_22	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_23	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_27	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_31	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_4	0.01	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_47	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_48	0	0.02	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_50	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_51	0	0	0.01	0.02	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_54	0	0	0	0	0	0	0.05	0	0	0	0.03
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_56	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_58	0	0	0	0	0	0	0	0	0	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_59	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_6	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_61	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_62	0	0	0	0	0	0	0	0	0.01	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_63	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_64	0	0	0	0.02	0	0	0	0	0.02	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_65	0.07	7.06	1.85	4.02	0.43	0.13	0.39	0	9.73	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_66	0	0.12	0.01	0.07	0	0	0.06	0	0.03	0	0
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_67	4.33	2.07	1.87	2.11	0.84	2.2	3.49	0.01	4.27	0.02	0.07
Firmicutes;Clostridia_1;Clostridiales;Lachnospiraceae;uncultured_68	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_1	0	0	0	0	0	0	0	0.1	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_5	0	0	0	0	0	0	0	2.51	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Incertae_Sedis_6	0	0	0	0.01	0	0	0	0.02	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;Sporacetigenium_mesophilum	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;unclassified	0	0.01	0	0	0	0	0	20.18	0.01	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Peptostreptococcaceae;uncultured_3	0	0	0	0	0	0	0	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Acetanaerobacterium	0	0.02	0	0.06	0	0	0	0	0.04	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerofilum	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Anaerotruncus	0.01	0	0.01	0.17	0	0.02	0.02	0	0.17	0.12	0.04
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Butyricicoccus_pullicaecorum	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_alkalicellulosi	0	0	0.01	0.01	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_clariflavum	0	0.05	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Clostridium_straminisolvens	0	0.06	0	0	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ethanoligenens	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Fastidiosipila	0	0	0	0	0.03	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	0	0.11	0	0.08	0	0	0	0	0.42	0.12	0.04
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_1	0	0.04	0.06	0.11	0	0.49	0.96	0	0.08	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_2	0	0	0.01	0	0	0	0.08	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_3	0	0	0.02	0	0.03	0	0	0	0.02	0.07	0.01
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_4	0.01	0.43	0.08	0.33	0.03	0.02	0.05	0	0.35	0.12	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_5	0	0.01	0.01	0	0.03	0	0	0	0.28	0.02	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_6	0	0	0	0	0.03	0	0	0	0.16	0.05	0.06
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_7	0.01	0.02	0	0	0	0	0	0	0	0.07	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Incertae_Sedis_8	0.13	0.93	0.99	0.97	0	0.08	0.19	0	0.12	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;insect_guts_a	0.03	0.01	0.05	0	0.35	0.01	0.03	0	0.13	4.09	0.68
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Oscillibacter	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Oscillospira	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Papillibacter	0.01	0.01	0.03	0.11	0.05	0.1	0.06	0	0.2	0	0.01
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_1	0	0.01	0	0	0.08	0.02	0.71	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Ruminococcus_2	0.01	0	0	0	0.08	0	0.03	0	0.03	0	0

Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Sporobacter	0	0	0.02	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;Termite_group_aaa	0.09	0	0	0	0.03	0.02	0.02	0.01	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;unclassified	0.23	7.64	5.26	3.8	0.27	1.32	1.03	0	5.47	0.46	0.28
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_10	0	0	0	0	0	0	0	0	0.01	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_11	0.04	0.31	0.12	0.54	0.11	0.01	0.04	0	2.46	3.35	0.9
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_12	0.18	2.29	0.31	1.4	0.7	0.85	2.2	0	1.24	0.02	0.01
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_13	0.01	0.06	0	0	0	0.01	0.01	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_21	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_23	0.01	8.55	0.31	0.71	0.03	0.04	0.03	0	0.12	0.02	0.01
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_24	0.26	1.47	25.94	0.47	0.49	1.84	0.45	0	0.3	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_25	0.02	0.06	0.1	0.14	0.08	0.04	0.09	0	0.44	0	0.01
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_26	0	0	0.03	0.03	0	0	0	0	1.07	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_27	0	0.02	0	0	0	0	0	0	0	3.37	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_28	0	0.1	0.07	0.06	0	0.01	0	0	1.8	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_29	0.01	0.27	0.22	0.37	0.03	0.32	0.75	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_30	0.06	1.75	0.39	2.01	0.13	0.34	0.96	0	4.04	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_33	0	0.08	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_34	0	0.04	0	0.02	0	0	0	0	0.12	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_35	0.01	1.48	0.26	1.64	0	0.15	0.35	0	1.19	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_36	0.04	4.22	0.68	2.51	0.08	0.52	1.06	0	0.87	0.02	0.98
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_5	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_8	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;Ruminococcaceae;uncultured_9	0	0	0	0	0	0	0.02	0	0	0	0
Firmicutes;Clostridia_1;Clostridiales;unclassified;unclassified	0.29	0.91	0.25	0.72	0.16	0.48	0.26	0	2.33	0.02	0.04
Firmicutes;Clostridia_1;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Peptococcaceae;Desulfitibacter	0	0.02	0.01	0.01	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Pelospora	0.01	0.01	0	0.05	0.03	0.01	0.01	0	0.01	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_1	0	0.02	0	0.11	0.03	0.03	0.03	0.01	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_2	0	0	0	0.02	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;Syntrophomonas_3	0	0	0	0.02	0	0	0	0	0.02	0	0
Firmicutes;Clostridia_2;Clostridiales;Syntrophomonadaceae;unclassified	0.01	0.52	0.03	0.35	0	0.02	0	0.05	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Heliobacteriaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;OPB54;unclassified	0	0.05	0.42	0.02	0	0	0	0	0.01	0	0
Firmicutes;Clostridia_2;Clostridiales_1;P._palm_C;A_51	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;Thermincola	0	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;unclassified	0	0.02	0	0.04	0	0.02	0	0	0.19	0.05	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_2	0	0.19	0.04	0.25	0.03	0.04	0.02	0	0.98	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_3	0	0	0.01	0.03	0	0	0	0	0.11	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_4	0	0	0	0	0	0	0	0	0	0	0.01
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_1;uncultured_5	0.07	0.24	0.02	0.5	0.16	0.62	0.3	0	0.07	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Dehalobacter	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;Desulfosporosinus	0	0	0	0.05	0	0	0	0	0.07	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;unclassified	0	0	0	0.02	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_2;uncultured_gut_Group_A	0	1.02	0.02	0.01	0	0	0	0	1.04	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Desulfotomaculum_4	0	0	0	0	0	0	0.01	0	0.05	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;Pelotomaculum_3	0	0.04	0.15	0.87	0	0	0	0	0.14	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Peptococcaceae_3;unclassified	0	0	0	0	0	0.01	0.01	0	0.02	0	0
Firmicutes;Clostridia_2;Clostridiales_1;unclassified;unclassified	0	0.01	0	0.02	0	0.01	0	0	0.09	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acetonema_a	0.01	0	0	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Acidaminococcus	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaeroarcus-Anaeromusa	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaerospora	0	0	0.01	0.02	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Anaerovibrio	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Dendrosporobacter	0.01	0.01	0.05	0.11	0	0.01	0.01	0	0.08	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Megamonas	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Phascolarctobacterium	0	0	0	0	0	0	0	0	0	0.05	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Propionispora	0	0	0	0	0	0	0	0	0.03	0	0

Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Sporomusa	0	0.01	0.02	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Succinispira_mobilis	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Thermosinus	0.01	0	0.18	0.02	0.24	0.01	0.04	0	0.03	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;unclassified	0.01	0	0.1	0.11	0.05	0	0	0	0.3	0	0.01
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_6	0	0	0.01	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_7	0.03	0.01	0	0	0.03	0	0	0	0.32	2.33	2.05
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;uncultured_8	0	0.01	0	0.17	0	0.01	0.02	0	0.47	0	0
Firmicutes;Clostridia_2;Clostridiales_1;Veillonellaceae;Veillonella	0	0	0.02	0.01	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;Thermoanerobacterales;Thermoanaerobacteraceae;Gelria	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Clostridia_2;unclassified;unclassified;unclassified	0.01	0	0	0.01	0	0.01	0	0	0	0	0
Firmicutes;Clostridia_3;Clostridiales;Syntrophomonadaceae;Dethiobacter	0	0.04	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Asteroleplasma	0	0	0	0	0	0	0.23	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Bulleidia_extructa	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Erysipelothrix	0	0.01	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Incertae_Sedis_8	0	0.06	0	0	0	0	0	0	0	0.18	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Turicibacter	0.14	1.24	1.39	1.07	0.03	0.01	0.32	0	2.29	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;unclassified	0	0.01	0.09	0	0	0.01	0.04	0	0.01	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;uncultured_9	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_2	0	0	0.01	0	0.05	0	0	0	0.12	0	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma_3	0	0	0	0	0	0.01	0	0	0	0	0
Firmicutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;unclassified	0	0	0.04	0	0	0	0	0	0.01	0	0
Firmicutes;Mollicutes;Anaeroplasmatales;Anaeroplasmataceae;Anaeroplasma	0	0	0	0	0	0	0	0	0.04	0	0
Firmicutes;Mollicutes;EMP-G18;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Entomoplasmatales;Entomoplasmataceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Entomoplasmatales;Spiroplasmataceae;Spiroplasma_2	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;Mycoplasmatales;Mycoplasmataceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Firmicutes;Mollicutes;RF9;unclassified;unclassified	0	0.06	0	0.01	0	0	0	0	0	0	0.01
Firmicutes;Mollicutes;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0.31	0	0
Firmicutes;RF3;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0.27	0	0
Firmicutes;unclassified;unclassified;unclassified;unclassified	0.31	0.32	2.98	1.98	0.13	0.39	0.25	0	0.69	0.07	0
Fusobacteria;Fusobacteria;Fusobacteriales;ASCC02;unclassified	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;boneC3G7;unclassified	0.01	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;CFT112H7;unclassified	0	0	0	0	0.03	0	0	0	0.17	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Fusobacterium_1	0	0	0	0	0	0	0	0	0	0.39	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Ilyobacter	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;unclassified	0	0	0	0	0.03	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Hados.Sed.Eubac.3;unclassified	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Sebaldella	0.01	0	0	0	0.05	0.01	0	0	0.01	0.07	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;unclassified	0.01	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;uncultured_5	0	0	0	0	0	0	0	0	0	0	0
Fusobacteria;Fusobacteria;Fusobacteriales;unclassified;unclassified	0	0	0	0	0.08	0	0	0	0.18	0.09	0
Gemmatimonadetes;Gemmatimonadetes;AT425-EubC11_terrestrial_group;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0.1	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0	0	0	0.04	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_3	0	0.01	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured_7	0	0	0	0.01	0	0	0	0	0.72	0	0
Lentisphaerae;Lentisphaeria;055B07-P-DI-P58;unclassified;unclassified	0	0.04	0	0.1	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;B01R017;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;BS5;unclassified;unclassified	0	0	0	0	0	0	0	0	0.3	0	0
Lentisphaerae;Lentisphaeria;c5LKS8;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;CVer-1_termite_group;unclassified;unclassified	0	0.31	0.07	0.62	0.05	0	0.02	0	0	0	0
Lentisphaerae;Lentisphaeria;CVer-2_termite_group;unclassified;unclassified	0	0.58	0.32	0.63	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;RFP12_gut_group;unclassified;unclassified	0	0	0.01	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;unclassified;unclassified;unclassified	0.01	0.15	0.12	0.05	0.03	0.01	0.06	0	0	0	0
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;Victivallis	0	0	0.12	0	0	0	0	0	0.12	0	0.36
Lentisphaerae;Lentisphaeria;WCHB1-25;unclassified;unclassified	0.01	0.01	0.04	0.01	0	0.04	0	0	0	0	0
Nitrospirae;Nitrospira;Nitrospirales;0319-6A21;unclassified	0	0	0	0	0	0	0	0	0	0	0
Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	0	0	0	0	0	0	0	0	0	0	0
NPL-UPA2;unclassified;unclassified;unclassified;unclassified	0	0.05	0	0	0	0	0	0	0	0	0

Planctomycetes;Phycisphaerae;CPla-3_termite_group;unclassified;unclassified	0	0.12	0	0.01	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;AKAU3564_sediment_group;unclassified	0	0.01	0	0	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;ODP1230B30.02_sediment_group;unclassified	0	0.01	0	0.03	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;AKYG587	0	0	0	0	0	0	0	0	0.06	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;CL500-3	0	0	0	0	0	0	0	0	0.35	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Planctomycetes;Phycisphaerae;Phycisphaerales;unclassified;unclassified	0	0.05	0	0.24	0	0	0	0	0	0	0
Planctomycetes;Phycisphaerae;Pla1_lineage;unclassified;unclassified	0	0.01	0	0	0	0	0	0	0	0	0
Planctomycetes;Pla4_lineage;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula	0	0	0	0	0	0	0	0	0.07	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;CPla-4_termite_group	0	0.01	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata	0	0	0	0.05	0	0	0	0	0.02	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Isosphaera	0	0	0.03	0.02	0	0	0	0	0.02	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir1_lineage	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pir4_lineage	0	0	0	0.01	0	0	0	0	0.24	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pirellula	0	0	0	0.03	0	0	0	0	0.02	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces_1	0	0	0	0	0	0	0	0	0.12	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces_2	0	0	0	0	0	0	0	0	0.04	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Rhodopirellula	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Schlesneria	0	0	0	0.01	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Singulisphaera	0	0	0.01	0.04	0	0	0	0	0.02	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Termite_planctomycete_cluster	0.02	0.04	0.11	0.5	0.05	0	0	0	0.39	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;unclassified	0.01	0.04	0.22	0.21	0.03	0.02	0.02	0	0.11	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_16	0	0	0	0.01	0	0	0	0	0.05	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_18	0	0.01	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_2	0	0	0.03	0	0	0.01	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_21	0	0	0	0.01	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_23	0	0	0	0.02	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_24	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_32	0	0	0	0	0	0	0	0	0.05	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_35	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_5	0	0	0	0.01	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_8	0	0	0	0	0	0	0	0	0.03	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;uncultured_b	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Zavarzinella	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes;unclassified;unclassified;unclassified;unclassified	0	0	0.06	0	0	0	0	0	0	0	0
Planctomycetes;vadinHA49;unclassified;unclassified;unclassified	0.06	0.1	0.3	0.01	0.13	0	0	0	1.48	0	0.04
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter	0	0.01	0	0	0	0	0	0	0.18	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium	0	0	0	0.03	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;unclassified	0	0	0	0	0	0	0	0	0.06	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_4	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;uncultured_5	0	0.01	0.04	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;uncultured_1	0	0.02	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Rhodobium_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Aurantimonadaceae;Aurantimonas_3	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Brucella	0	0.02	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;Ochrobactrum_3	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Brucellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_5	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_7	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;Devosia_9	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Hyphomicrobiaceae;uncultured_2	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Aminobacter_1	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Aminobacter_2	0	0	0	0	0	0	0	0	0.01	0	0

Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_12	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_5	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_8	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_9	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_loti	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;Mesorhizobium_thiogangeticum	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Phyllobacteriaceae;unclassified	0	0	0	0.02	0	0	0	0	1.54	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_11	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_19	0	0	0	0	0	0	0	0	0	0	0.02
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_20	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_21	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;group_23	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Rhizobiaceae;unclassified	0	0	0	0.02	0	0	0	0	0.05	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;Shinella_genera_incertae_sedis;Shinella_genera_incertae_sedis	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_1;unclassified;unclassified	0	0	0	0.01	0	0	0	0	1.92	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;1174-901-12;unclassified	0	0.01	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;alphaI_cluster_1;unclassified	0	0.05	0.05	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;alphaI_cluster_2;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;BCf3-20;unclassified	0	0	0.86	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;Chelatococcus_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Beijerinckiaceae;uncultured_3	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Afipia_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Afipia_birgiae	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Balneimonas	0	0	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Blastobacter	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bosea	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_10	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_12	0	0.01	0.06	0.04	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_2	0	0.02	0.01	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_4	0	0	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_6	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_japonicum	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Bradyrhizobium_sp._CCBAU_61196	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Nitrobacter	0	0	0	0	0	0.01	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Rhodoblastus	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;Rhodopseudomonas	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;unclassified	0.01	0.94	0.18	0.68	0	0	0	0	0.02	0.09	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Bradyrhizobiaceae;uncultured_3	0	0	0	0.01	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Prosthecomicrobium	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Rhodomicrobium	0	0.04	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;Rhodoplanes	0	0.01	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Hyphomicrobiaceae_1;Ancalomicrobium	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Methylobacterium	0	0	0.12	0.06	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;Microvirga	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylobacteriaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylocystis_3	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylocystis_parvus	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;Methylosinus	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Methylocystaceae_1;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;unclassified;unclassified	0	0	0.1	0.04	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;Labrys	0	0.01	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;Pseudolabrys	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;unclassified	0	0.01	0.02	0.04	0	0	0	0	0.06	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_1	0	0.12	0.01	0.07	0	0	0	0	0.06	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_2	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_2;Xanthobacteraceae;uncultured_3	0	0.14	0.03	0.1	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;DUNssu044;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Hyphomicrobium_1	0	0	0	0.01	0	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Hyphomicrobium_2	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;Pedomicrobium	0	0.02	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Hyphomicrobiaceae;unclassified	0	0	0.01	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Methylobacteriaceae;uncultured	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhizobiales_3;Nordella;Nordella	0	0	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Amaricoccus	0	0	0	0	0	0	0	0	0.22	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Palleronia	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_1	0	0	0	0	0	0	0	0	0.38	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_3	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Paracoccus_5	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Rhodobacter_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Roseobacter_clade_Ketogulonicigenium	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;Rubellimicrobium	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;unclassified	0.01	0	0	0	0	0	0	0	1.01	0	0
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae_1;uncultured_23	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acetobacter	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidicaldus	0	0.01	0.05	0.02	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidiphilium	0	0	0.02	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidisoma	0	0	0	0	0	0	0	0	4.3	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Acidocella	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Craurococcus	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Rhodopila	0	0	0.02	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_1	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Roseomonas_4	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;Rubritepida	0	0	0.02	0.02	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;unclassified	0	0.02	0.07	0.1	0	0	0	0.01	0.79	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_2	0	0	0.02	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_3	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Acetobacteraceae;uncultured_4	0	0	0.03	0.05	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Marispirillum_indicum	0	0	0	0	0.05	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Telmatospirillum	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;Thalassospira	0	0.11	0.03	0.12	0	0.01	0	0	0.07	0	0.04
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;unclassified	0.01	0.01	0	0.02	0	0	0	0	0	0.42	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_2	0.25	0.02	0.09	0.21	0.59	0.25	0.03	0	0	0	0.22
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;Rhodospirillaceae;uncultured_a	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_1;unclassified;unclassified	0	0.02	0.01	0	0.03	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Candidatus_Alysiosphaera;Candidatus_Alysiosphaera	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;DA111;unclassified	0	0.1	0.05	0.15	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;I-10;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;JG37-AG-20;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;MNH4;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;Azospirillum_1	0.01	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;Skermanella	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;Rhodospirillaceae_2;unclassified	0	0	0	0	0	0	0	0	0	0.05	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0.02	0
Proteobacteria;Alphaproteobacteria;Rhodospirillales_2;wr0007;unclassified	0	0	0.04	0.04	0	0	0	0	0.09	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Anaplasmataceae;Wolbachia	0.01	0	0	0	0	0.02	0.02	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Captivus;Candidatus_Captivus	0.01	0.12	0.05	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Hepatincola;Candidatus_Hepatincola	0.04	0	0.03	0.01	0.03	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Candidatus_Midichloria;Candidatus_Midichloria	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;Rickettsia	0	0	0	0.04	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Rickettsiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Ellin6055;unclassified	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;uncultured_3	0	0	0	0	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium_2	0	0.04	0	0.02	0	0	0	0	0.12	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandarakinorhabdus	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium_1	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_2	0	0.02	0	0.09	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_3	0	0.82	1	0.03	0	0.01	0	0	0.01	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_4	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas_6	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified	0	0	0.01	0.02	0	0	0	0	0.04	0	0
Proteobacteria;Alphaproteobacteria;Sphingomonadales;unclassified;unclassified	0	0.02	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Alphaproteobacteria;unclassified;unclassified;unclassified	0.07	0.04	0.05	0.12	0	0.02	0.02	0	0.08	0.99	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Derxia	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Achromobacter_2	0	0	0	0.04	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Alcaligenes	0	0	0	0	0	0	0	0	0	0	0.1
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Bordetella_3	0	0	0	0	0	0	0	0	0.22	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;Castellaniella	0	0	0	0	0	0	0	0	0.91	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;GKS98_freshwater_group	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae_1;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_1	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Burkholderia_3	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;Pandoraea	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_1;unclassified	0	0	0	0	0	0	0.18	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae_2;Ralstonia	0	0.14	0.24	0.01	0	0	0.01	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax_caeni	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Alicycliphilus	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caenimonas	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_3	0	0	0	0	0	0	0	0	1.82	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_6	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas_R	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia	0	0.01	0	0.37	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ideonella_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Leptothrix_2	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ottowia	0	0.04	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas	0	0.01	0.02	0	0	0.01	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Schlegelella	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0	0.01	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified	0.01	0.11	0.08	1.1	0	0	0.02	0	0.08	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_17	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_20	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_25	0	0	0	0	0	0	0	0	0.15	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_3	0	0	0	0	0	0	0	0	0.12	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;uncultured_a	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax_2	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xenophilus	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia_1	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Oxalobacter	0.04	0	0	0	0.03	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified	0.01	0	0	0.04	0	0	0	0	0.11	0.05	0.01
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;uncultured_11	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium	0	0	0	0	0	0	0	0	0.18	0	0
Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0.03	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Leeia	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Aquaspirillum	0	0	0	0	0	0	0	0	0	0	0.01
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Microvirgula_1	0	0	0	0	0	0	0	0.01	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;Stenoxybacter	0	0	0.02	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;unclassified	0	0	0	0	0	0	0	0	0	0.18	2.11
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae_1;uncultured_a	0	0	0	0	0	0	0	0	0	0.49	2.9
Proteobacteria;Betaproteobacteria;Neisseriales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0.06
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;uncultured_1	0	0	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;Denitratisoma_oestradiolicum	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_1;uncultured_5	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azoarcus_1	0	0	0	0	0	0	0	0	0.07	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azoarcus_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;Azovibric	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;unclassified	0	0	0	0.04	0	0	0	0	0.58	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_2;unculturec	0	0.07	0.03	0.16	0	0	0.18	0	1.52	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Azonexus_caeni	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Dechloromonas_1	0	0	0	0	0	0.01	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;IC13_Millipede	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Lower_termite_Cluster	0.06	0	0.01	0.01	0.03	0.01	0.01	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;Propionivibric	0.01	0.01	0	0.02	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;unclassified	0.04	0.62	0.02	0.2	0.05	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_1	0	0	0	0.15	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae_3;uncultured_4	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Betaproteobacteria;Rhodocyclales;unclassified;unclassified	0.06	0.55	0	0.17	0.05	0.02	0.01	0	0.08	0	0
Proteobacteria;Betaproteobacteria;SC-I-84;unclassified;unclassified	0	0.23	0	0.02	0	0.01	0.01	0	0.07	0	0
Proteobacteria;Betaproteobacteria;TRA3-20;unclassified;unclassified	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Betaproteobacteria;unclassified;unclassified;unclassified	0.02	0.05	0	0.05	0.03	0.01	0	0	0	0	0.01
Proteobacteria;Deltaproteobacteria;43F-1404R;unclassified;unclassified	0	0.01	0	0.07	0	0.01	0.01	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Bacteriovorax_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Peredibacter	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;unclassified	0.01	0.02	0.16	0	0	0.01	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;OM27_clade	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus	0.01	0	0	0.03	0	0.02	0.01	0	0.05	0	0
Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;uncultured	0	0.1	0.04	0.05	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiferula	0	0	0	0	0	0	0	0	0.12	0	0.01
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobotulus	0	0	0	0	0.08	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina	0	0	0	0	0.03	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;unclassified	0.01	0	0	0	0.03	0.01	0	0	0.01	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus	0	0.05	0.13	0.05	0.03	0.01	0	0	0.83	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulforhopalus	0	0.12	0.04	0	0	0	0.01	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;unclassified	0	0	0	0	0.03	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_1	0.22	0.13	0.21	0.35	0.35	0.58	1.04	0.01	0	0	0.01
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_2	0.02	0.01	0	0.1	0	0	0	0	0.16	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_3	0.29	0.13	0.47	0.51	0.43	0.44	0.65	0	2.23	1.02	0.26
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_4	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_5	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;unclassified	0.03	0.1	0.01	0.09	0	0.06	0.03	0	0.03	0.02	0.02
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;unclassified;unclassified	0.02	0	0	0	0	0.02	0.02	0	0.01	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter_2	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;GR-WP33-58;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;0319-6G20;unclassifiec	0	0.05	0	0.03	0	0	0	0	0.01	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Anaeromyxobacter	0	0	0	0.04	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Hyalangium	0.01	0.01	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Melittangium_boletus	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;unclassifiec	0	0.04	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Haliangiaceae;Haliangium	0	0	0	0.02	0	0	0	0	0.03	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;JG37-AG-15;unclassified	0	0	0	0.01	0	0	0	0	0.03	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;mle1-27;unclassified	0	0.02	0.03	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Phaselicystidaceae;Phaselicystis	0	0.01	0	0	0	0.02	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Byssovorax	0	0	0.03	0.01	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium_2	0	0.01	0.06	0.28	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;unclassified	0	0	0	0	0	0	0	0	0.09	0	0

Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified;unclassified	0	0.1	0	0.05	0	0.02	0.01	0	0.22	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_3;unclassified	0	0	0	0.01	0	0	0	0	0.01	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_4;unclassified	0	0.01	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Myxococcales;uncultured_5;unclassified	0	0	0	0	0	0.01	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Rs-K70_termite_group;unclassified;unclassified	2.52	0.25	0.25	0.08	0.51	0.59	1.33	0	1.01	0	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus	0	0	0	0.02	0	0.01	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Deltaproteobacteria;unclassified;unclassified;unclassified	0.02	0.01	0.01	0	0	0.07	0	0	0	0	0.01
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0.01	0	0	0	0.13	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum	0.12	0.02	0	0	0.03	0	0	0	0.36	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Rs-M59_termite_group	0	0	0	0	0	0.01	0.79	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Campylobacterales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Hydrogenimonas_thermophila;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;Nautiliales;Nautiliaceae;Thioreductor	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Epsilonproteobacteria;unclassified;unclassified;unclassified	0.01	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Arenimonas_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Dyella_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Dyella_4	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Frateuria	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Leifsonia_a	0	0	0	0	0	0	0	0	0	0	0.01
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Luteimonas_1	0	0	0	0	0	0	0	0	0.43	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudomonas_cissicola	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas	0	0.01	0	0.01	0	0	0	0	0.01	0.16	0.05
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Silanimonas	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0.01	0.01	0	0.09	0	0	0	0	0	0	0.35
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Thermomonas_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;unclassified	0	0	0	0.01	0	0	0	0	0	0	0.03
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;uncultured_3	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Xanthomonas_campestris	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Alteromonadales;Alteromonadaceae;Microbulbifer	0	0	0	0	0	0	0	0	0.11	0	0
Proteobacteria;Gammaproteobacteria_1;B38;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Budvicia	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Enteric_Bacteria_cluster	0.04	0.06	0.1	0.14	0.03	0.02	0	1.16	0.04	0.44	7.86
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Leminorella	0.01	0	0	0	0.03	0	0	0.05	0	0	0.01
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;Pragia	0	0	0	0	0	0	0	0	0	3.61	0.42
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae;unclassified	0.01	0	0	0	0.08	0	0	0.21	0.01	0.25	1.68
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Morganella	0	0	0	0	0	0	0	0	0	0	2.26
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Proteus	0	0	0	0	0	0	0	0	0	0	0.1
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Providencia	0	0	0	0	0	0	0	0	0	0.09	0.29
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;unclassified	0	0	0	0	0	0	0	0	0.2	0.25	0.37
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;Enterobacteriaceae_1;Xenorhabdus_nematophila	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Enterobacteriales;unclassified;unclassified	0.01	0	0	0.01	0	0	0	0.01	0.04	0.37	0.57
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae;Pseudospirillum	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales;Oceanospirillaceae_1;Marinomonas	0	0	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales_1;Halomonadaceae;Chromohalobacter	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Oceanospirillales_4;Halomonadaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;Aggregatibacter_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;Chelonobacter_oris	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;unclassified	0	0	0	0	0	0	0	0	0	0.07	0.27
Proteobacteria;Gammaproteobacteria_1;Pasteurellales;Pasteurellaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;PB1-aai25f07;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Acinetobacter	0	0.02	0.02	0	0	0	0	0.01	0	0	0.68
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Alkanindiges	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;Perlucidibaca	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Moraxellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Azotobacter_1	0	0.44	0.05	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Cellvibrio	0	0	0	0	0	0	0	0	0	0	0

Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_13	0	0	0	0	0	0	0	0	0	0	0.01
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_16	0	0	0.02	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_2	0	0	0	0	0.03	0	0	0	0.01	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_4	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_42	0	0.01	0	0	0	0	0	0	0	0.46	0.17
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_43	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;Pseudomonas_5	0	0	0	0	0	0	0	0	0.33	0	0
Proteobacteria;Gammaproteobacteria_1;Pseudomonadales;Pseudomonadaceae;unclassified	0	0.04	0.01	0	0.05	0	0	0	0.03	0	0.01
Proteobacteria;Gammaproteobacteria_1;unclassified;unclassified;unclassified	0	0	0	0	0.05	0	0	0	0.04	0.28	1.88
Proteobacteria;Gammaproteobacteria_1;Vibrionales;Vibrionaceae;Photobacterium_1	0	0.04	0.05	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Aquicella	0	0	0	0.01	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Coxiella	0	0	0.05	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;Rickettsiella	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Coxiellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Legionellaceae;Legionella_1	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Legionellales;Legionellaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;NKB5;unclassified;unclassified	0	0	0.03	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0.02	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;Nevskia	0	0.02	0.01	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;Steroidobacter	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;unclassified	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_3	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_5	0	0	0	0	0	0	0	0	0.01	0	0
Proteobacteria;Gammaproteobacteria_2;Xanthomonadales;Sinobacteraceae;uncultured_6	0	0.01	0.01	0.02	0	0	0	0	0.02	0	0
Proteobacteria;TA18;unclassified;unclassified;unclassified	0.01	0.05	0.03	0.03	0	0.01	0	0	0	0	0
Proteobacteria;unclassified;unclassified;unclassified;unclassified	0.04	0.04	0.05	0	0.16	0.11	0.01	0	0.05	0	0
Spirochaetes;Spirochaetes;CW-1_termite_group;unclassified;unclassified	0.03	0.01	0	0.06	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;GZKB75;unclassified;unclassified	0	0.01	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Rs-H88_termite_group	0.02	0	0	0	0.03	0.01	0.02	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;uncultured_3	0.05	0.14	0.01	0.11	0.05	0.1	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;PL-11B10;unclassified	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Hodotermes_mossambicus_cluster	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;M2PT2-76_termite_group	0.04	0	0	0.01	0.13	0.12	0.03	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Kalotermitidae_Cluster	0.51	0	0	0	0.11	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_I	0.06	0	0	0	0	0.01	0	0	0.01	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Lower_Termite_Cluster_II	0.14	0.01	0.01	0	0.24	0.01	0.02	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Qadd_Reticulitermes_Cluster	0	0.02	0	0.01	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Rhinotermitidae_Cluster_Qadd	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_1	0.08	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_2	0.12	0.13	0.11	0.13	0.13	0.16	0.17	0	0.07	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta_sp_Kalotermes	0	0	0	0	0	0.01	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I	0.05	0.02	0.29	0.16	0	0.03	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Nasutite	0.52	0.01	0.08	0	7.32	5.7	5.57	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Soil_Fee	0.03	1.15	0.2	2.17	0.03	0.22	0.29	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Higher_Termite_Cluster-Trinervit	0.15	0	0.02	0	0.3	0.25	1.21	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster	6.41	0.24	2.06	0.02	0.86	0.96	1.14	0	0	0	0.01
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Kaloterm	0.46	0.01	0	0	0.35	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Mastote	0.31	0	0.13	0	0.78	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Reticulit	0	0.02	0	0	0.3	0.02	0.01	0.01	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0	0.01	0	0	0.11	0.01	0.02	0.01	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0.39	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Lower_Termite_Cluster-Trepone	0.19	0	0.07	0	0.38	0.02	0.01	0	0.02	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Microcerotermes_Cluster	5.71	0	0.24	0.07	0	0	0.02	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ia-Mixed_Higher_Termite_Cluster	0.07	0.29	0.14	0.22	0.24	0.51	1.96	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster	0.08	0	0	0	0.03	0.04	0.25	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster	16.83	0	0.07	0	1.54	0.3	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0.02	0	0	0	0.08	0.36	0.07	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0.03	0	0	0	0.22	0.14	0.69	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	2.92	0.01	0	0	22.84	39.97	0.14	0.02	0.01	0	0

Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0.93	0.01	0.47	0.08	5.62	1.52	4.2	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0	0	0	0	0	0.08	7.64	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Higher_Termite_Cluster-	0.06	0.02	0.21	0	0	0.02	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Microcerotermes_Cluste	1.52	0.02	0.16	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster	0.29	0	0	0	0.11	0.04	0.02	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Macroterr	0.01	0	0.03	0.07	0.11	0.01	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Microcero	13.63	0.25	0.08	0	7.29	0.42	1.21	0.02	0.01	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0.01	0	0	0	0.05	0	0.01	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0.94	0.04	0.06	0.08	12.01	3.88	1.42	0.01	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0.1	0.03	0.05	0.11	16.12	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-PCHT_Cluster-Nasutiterr	0	0	0	0	0	0.02	0.02	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0.02	0	0.01	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Termite_Treponema_I-Termite_Treponema_Ib_Cluster-Rhinotermitidae_Cluster	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Treponema_2	0.02	0.01	0.01	0	0.46	0.01	0.02	0	0.03	0	0.01
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Trinervitermes_cluster_a	0.27	0	0.01	0	0.35	1.39	0.36	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;unclassified	11.44	2.57	8.73	5.25	5.43	11.5	5.65	0.01	0.01	0.02	0.01
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured_4	0.16	0	0.03	0	0	1.05	0.22	0	0	0	0
Spirochaetes;Spirochaetes;Spirochaetales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes;Spirochaetes;unclassified;unclassified;unclassified	0	0.02	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Candidatus_Tammella	0.01	0	0	0.01	0	0	0.05	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Cloacibacillus	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Jonquetella	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;Synergistes_jonesii	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;unclassified	0	0	0.05	0	0.08	0	0.02	0.01	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_1	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_4	0	0	0	0	0	0	0	0	0	0	0
Synergistetes;Synergistia;Synergistales;Synergistaceae;uncultured_6	0.7	1.08	5.05	5.58	0.65	0.09	0.83	0	0.48	0	0
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_I	0.66	0	0.45	0	3.56	5.1	1.59	0	0	0	0
TG3;TG3;TG3_sp1;Termite_Cluster;Termite_Cluster_II	4.45	0.06	1.54	0	0	0.06	0	0	0	0	0
TG3;TG3;TG3_sp1;Termite_Cluster;unclassified	0.05	0	0.36	0	0	0.22	0.04	0	0	0	0
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;Nasutitermes_Cluster	0.61	0.01	0.03	0	0.49	1.12	0.39	0	0	0	0
TG3;TG3;TG3_sp2;Termite_Cockroach_Cluster;unclassified	0	0	0	0	0	0	0	0	0	0	0
TG3;TG3;unclassified;unclassified;unclassified	0	0	0	0	0	0.02	0	0	0	0	0
unclassified;unclassified;unclassified;unclassified;unclassified	0.85	0.25	2.21	0.28	0.97	1.13	0.21	0.43	0.15	0.23	0.07
Verrucomicrobia;Acidimethylosilex;Termite_group_A;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Acidimethylosilex;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;OPB35_soil_group;unclassified;unclassified;unclassified	0	0.04	0.04	0.02	0	0	0	0	0.01	0	0
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0.01	0.11	0.07	0.42	0.08	0.01	0.02	0	0.15	0	0
Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Cerasicoccus	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;unclassified	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Opitutae;vadinHA64;unclassified;unclassified	0.01	0	0.01	0.02	0.03	0	0	0	0.01	0	0
Verrucomicrobia;Spartobacteria;Candidatus_Xiphinematobacter;Candidatus_Xiphinematobacter;Candidatus_Xiphinematobacter	0	0.02	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;Chthoniobacter;unclassified;unclassified	0	0.27	0	0.15	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;DA101_soil_group;unclassified;unclassified	0	0.01	0	0.09	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;FukuN18_freshwater_group;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;unclassified;unclassified;unclassified	0	0.01	0	0.04	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;uncultured_1;unclassified;unclassified	0	0	0	0.01	0	0	0	0	0	0	0
Verrucomicrobia;Spartobacteria;zEL20;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0.03
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0.07	0.2
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Akkermansia	0	0	0	0	0.03	0	0	0	0	0.42	0.4
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;unclassified	0	0	0	0	0	0	0	0	0	0.02	0.03
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_1;uncultured_2	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;Prosthecobacter	0	0	0	0	0	0	0	0	0	0	0
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae_2;uncultured_2	0	0	0	0	0	0	0	0	0.05	0	0
WCHB1-60;unclassified;unclassified;unclassified;unclassified	0	0	0	0	0	0	0	0	0	0	0