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The metabolic and genetic diversity of soil bacterial communities depends on the soil management system and C/N dynamics: The case of sustainable and conventional olive groves

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ABSTRACT

Under Mediterranean type climates, a sustainable soil management aimed at increasing soil organic carbon and microbiological diversity is of key importance. The aim of this study was to characterize and compare soils from a mature Mediterranean olive (*Olea europaea* L.) orchard subjected to two different soil management systems (sustainable, S_{mng}, and conventional, C_{mng}) for 18 years. Composite soil samples were analyzed qualitatively (pedological determinations) and quantitatively (soil C, N and pH). Bacterial metabolic activity and diversity were evaluated spectrophometrically by the Biolog® assay, while 16S-based metagenomics analysis was used to analyse the abundance of N-cycling bacteria. From the general analysis of the data obtained by the study of soil profiles and litter, C and N dynamics, and the genetic and functional diversity of soil bacteria, it emerged that the S_{mng} system caused an improvement in soil organic matter in the topsoil layers, compared to the C_{mng} system, with consequent increases in the abundance of soil N-cycling bacteria but without affecting the indices related to total bacterial metabolic activity and diversity. The results obtained could promote the development of new approaches for optimizing soil carbon cycling, managing nutrient transport, and sustaining and improving olive yield and quality.

1. Introduction

In Mediterranean orchards, a sustainable soil management (S_{mng}) aimed at increasing soil organic carbon (SOC) stocks (e.g., by no-tillage, increased C and N inputs, recycling of pruning residuals, cover crops) can affect many soil parameters, such as physical characteristics (Palese et al., 2014), chemical parameters (Sofo et al., 2010; Montanaro et al., 2010), water content (Celano et al., 2011), and CO_2 fluxes (Montanaro et al., 2012). Soil management, if not well planned and conducted, can provoke decreases in soil organic matter (SOM), mainly due to SOM mineralization (Montanaro et al., 2010). In Mediterranean olive orchards, semi-arid climates, via stimulated microbial metabolism and respiration, cause decreases of SOC and other nutrients (primarily soil N; Pascazio et al., 2018). In these agrosystems, a S_{mng} that includes a localized and evapotranspiration-based irrigation can improve plant physiological status, olives and oil production and quality in the mid-term (Palese et al., 2009; Sofo et al., 2010). In olive groves, the S_{mng} also gives considerable economic advantages to the farmers (Pergola et al., 2013) and provides efficient ecosystemic and sociocultural services (Montanaro et al., 2017). In addition, the S_{mng} applied to olive orchards can reduce the negative repercussions on the environment linked to nutrient leaching/runoff, particularly weighty for nitrates (Palese et al., 2015).

Soil microorganisms' dynamics (e.g., mobility, growth, nutrient absorption and respiration), major responsible of soil fertility and quality (Bünemann et al., 2018), are strongly affected both by the type of soil management and irrigation (Enwall et al., 2007; Jeanbille et al., 2016), and this has been widely demonstrated in fruit crops (Palese et al., 2009; Sofo et al., 2014a,b; Pascazio et al., 2018). The functionality and metabolism of soil microorganisms are related to soil quality

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and fertility, as they influence and at the same time are influenced by the soil C and N contents, being bacteria an essential part of C and, even more, of N cycling processes (de Vries and Shade, 2013; de Vries and Wallenstein, 2017; Mooshammer et al., 2014; Zhang et al., 2014; Li et al., 2018).

In the case of olive orchards, that are a conspicuous part of the Mediterranean agricultural landscape (about 9.5 Mha in 2010, according to Pergola et al., 2013) and are often characterized by lowe levels of soil organic matter, knowing if the agronomic practices adopted are beneficial or not for soil microbial communities assumes a key importance (Sofo et al., 2014b; Pascazio et al., 2018). One of the easiest and reliable techniques for defining soil microbiological status is the determination of bacterial metabolic diversity by the Biolog® method, having a high discriminating power between bacterial soil communities from different soil environments and from soils subjected to various agronomic treatments (Zhang et al., 2014). Culture-based and genetic techniques have been used successfully in olive orchards to ascertain the presence of N-cycling functional bacteria and better characterize the portion of soil microbiota involved in soil N metabolism (Sofo et al., 2010). This is particularly important for olive orchards, where N is often a limiting factor, even when soils are managed sustainably and have high organic C inputs (Montanaro et al., 2010; Celano et al., 2011). Besides microbiological and genetic analysis, nowadays, next-generation sequencing (NGS), coupled with bioinformatic tools and metagenomic approaches, have made it easier to comprehensively analyze microbial communities on any type of matrix, including soils (Lakshmanan et al., 2014; Jansson and Hofmockel, 2018).

From the opposite side, qualitative soil profile descriptions, and the analysis of C/N ratios and pH values both in topsoil and subsoil can be very useful when interpreting soil C and N data for understanding the general context of the environment soil microorganisms live in (FAO, 2006; Mooshammer et al., 2014). Particularly, the characteristics of the litter layer are a very informative addition to the soil profile description, as they reflect the equilibrium between litter production, litter microbial decomposition and interaction with the mineral soil (Zanella et al., 2018a).

Because of the complexity and site-specificity of soils, defining soil quality is not an easy task (Bünemann et al., 2018). The study of the soil N-cycling bacteria and of the N dynamics could help to understand how soil management can affect soil status (Pascazio et al., 2018; Li et al., 2018). On this basis, the aim of this study was to characterize and compare soils from a Mediterranean olive orchard subjected to two different soil management systems (sustainable, S_{mng}, and locally conventional management, C_{mng}) for 18 years. Considering the higher C and N inputs in the S_{mng}, compared to the C_{mng}, bacterial diversity, particularly of N-cycling bacteria, was analyzed and discussed in relation to soil properties, in order to understand how eventual C/N and pH imbalances can regulate soil C dynamics and N cycling.

2. Materials and methods

2.1. Experimental site, orchard management and soil sampling

The trial was done in a 2-ha olive orchard (*Olea europaea* L., cv. 'Maiatica'; 70-year.old plants with a distance of 8 × 8 m; NE orientation) located in Ferrandina (Southern Italy, Basilicata region; N 40°29′; E 16°28′). The area has a semi-arid climate, with an annual rainfall of 565 mm (mean 1995–2015), concentrated mostly in the winter, and a mean annual temperature of 16.1 °C. The soil is a sandy loam, a Haplic Calcisol, according to the World Reference Base for Soil Resources, with a mean bulk density of 1.30 g cm^{-3} and sediment as parental material. The major landform is plain, the slope form is classified as convex-straight and the slope gradient class as gently sloping (2–5%) (FAO, 2006). The depth of the groundwater at the moment of the analysis was > 1.5 m.

Half of the orchard (1 ha) has been managed using organic agricultural practices for 17 years (2000–2017) (sustainable management, S_{mng}) (Table S1). Trees were drip-irrigated from March to October (2800 m^3 ha^{-1} $year^{-1}$) with urban wastewater. The average values of organic C, N, P and K contained in the treated wastewater were 124, 54, 3 and 50 kg ha^{-1} $year^{-1}$, respectively (mean 2000–2016). Six drip emitters (8 L h^{-1}) over a 1-m radius were placed around each plant. A light pruning was carried out every year during winter. The soil was permanently covered by spontaneous self-seeding weeds, that were mowed twice a year. Cover crop residues and prunings were shredded and left along the row as mulch. An integrative amount of 40 kg ha^{-1} $year^{-1}$ of $N\text{-}NO_3^-$ was distributed by fertigation once per year, during the fruit set and pit hardening phase (early spring), in order to entirely satisfy olive nutrient needs.

The other half of the orchard (1 ha) was kept as 'control' plot. It was rainfed and conducted with a locally conventional management (C_{mng}) for 17 years (2000–2017), according to the practices usually adopted by farmers in the region (Table S1). The C_{mng} was managed by tillage (milling at 10 cm depth) performed 2–3 times per year to control weeds. Intensive pruning was carried out every two years, but pruned residues were removed from the olive orchard. A mineral fertilization was carried out once per year, during the fruit set and pit hardening phase (early spring), using ternary compounds (NPK 20-10-10 fertilizer at doses ranging from 300 to 500 kg ha^{-1} $year^{-1}$).

In March 2017, soil samplings was performed in both the treatments (S_{mng} and C_{mng}) in the non-irrigated inter-row area, in order to avoid interferences due to water regime between the two treatments. Soil subsamples were picked in 10 points over a 1-m radius area around each olive tree, at different soil depths (0, 5, 10, 20, 30, 60 and 90 cm) for chemical analysis, and from the topsoil layer (0–30 cm) for bacterial communities' analysis (Biolog® assay and 16S-based metagenomics analysis). The 10 sub-samples were pooled on site to constitute a composite soil sample of about 1 kg. For both the soil management systems (S_{mng} and C_{mng}), three composite samples ($n = 3$), each composed of 10 different sub-samples, were prepared. This sampling techniques allowed to minimize spatial variability, according to Bacon and Hudson (2001) and Tian et al. (2004). After removing visible crop residues, the soil composite samples were immediately stored in sterilized plastic bags at 4 °C for chemical and microbiological analysis, and at −20 °C for DNA extraction, and subsequently analysed within 10 days.

2.2. Soil and litter layer description

Before soil description analysis, the litter layer in the S_{mng} spot was removed and ground vegetation was cut. Excavation was made with an auger at a soil depth of 1.5 m. The chips from the auger were carefully laid out on a black piece of plastic, next to a meter, in order to check depth regularly. This procedure was done three times for each soil treatment (S_{mng} and C_{mng}). Soil changes, such as compacted or heavier layers, shiny surface of chips from the auger, indicative for a higher clay content, were observed. Master horizons were identified and named, according to FAO (2006). FAO guidelines were used for soil profile description of both S_{mng} and C_{mng}. At the end, the holes were closed and the surface trumped for avoiding damages to humans or animals.

For litter layer description, the litter layer was carefully observed and described using the reference guidelines of Zanella et al. (2018b). In brief, a 'micro-pit' (30–50 cm wide and 20 cm deep) was dug for describing the boundary between litter layer and mineral soil, and the structure of the A-horizon. A straight, clean cut with the spade at one side of the profile was done, disturbing soil and litter layer as little as possible. A loupe was used to examine zoogenic pellets. For the sake of consistency with the soil description analysis described above, the same FAO protocol (2006) was used to describe the structure of the A horizon and its lower boundary in both S_{mng} and C_{mng}.

2.3. Soil chemical analysis

All the chemical reagents were purchased from Sigma-Aldrich (Saint Louis, MI, USA) unless differently reported. On soil composite samples (soil depths of 0, 5, 10, 20, 30, 60 and 90 cm), total organic carbon (TOC), total N (TN) and pH were determined. All the soil samples were air-dried at approximately 25 °C and then sieved through a 2-mm stainless steel sieve. The size fraction smaller than 2 mm was used for soil chemical analyses. Soil pH was measured by a glass electrode (Basic 20®; Crison Instruments SA, Barcelona, Spain) both in distilled water and $CaCl_2$ using a suspension 1:2.5 soil to liquid phase ratio (Pansu and Gautheyrou, 2006). Total organic carbon (TOC) was determined by Walkley and Black method by oxidation at 170 °C with potassium dichromate ($K_2Cr_2O_7$) in presence of sulfuric acid (H_2SO_4), and the excess $K_2Cr_2O_7$ was measured by Möhr salt titration (Pansu and Gautheyrou, 2006). Total nitrogen (TN) was measured by Kjeldahl method (Pansu and Gautheyrou, 2006)

2.4. Soil biolog® analysis

Three replicates of 10 g-subsamples (dry weight equivalent) of each soil composite sample (0–30 cm) were suspended in Ringer solution and sonicated for 2 min to disperse microbial cell, according to (Sofo et al., 2018), till having a final value of 10^4 CFU (colony-forming units) mL^{-1}.

Sole carbon source utilization patterns of soil microbial communities were assessed using the Biolog® 96-well Eco-Microplates™ (AES Laboratoire, France), containing 31 different carbon sources. An aliquot of 100 µl of the soil dilution at 10^{-3} dilution was used for the assay. The microplates were incubated at 25 °C in darkness and the substrate-utilization profiles were analyzed on well-absorbance values at the 96-h observation period using a Microplate E-Max Reader (Bio-Rad; Hercules, CA USA) with 590- (primary) and 750-mm (secondary) wavelength filters.

Data were analyzed to determine the metabolic diversity indices accurately described by Sofo et al. (2018). The indices examined were the following: average well color development (*AWCD*), a measure of total bacterial metabolic activity, Shannon's diversity index (*H'*), Shannon's evenness index (*E*), i.e. the equitability of activities across all the utilized substrates, McIntosh's diversity index (*U*), and McIntosh's evenness index (*Z*). In addition to total *AWCD*, the carbon substrates of the Biolog® plates were divided into eight main groups of compounds, respectively, and the *AWCD* value for each group was calculated.

2.5. Extraction of soil total DNA and identification of specific bacterial taxa

DNA was extracted from an amount of 0.5 g of soil using the method described by Pascazio et al. (2018). The quality and concentration of the extracted DNA extracts were determined spectrophometrically at 260, 280 and 230 nm using a NanoDrop®ND-1000 UV–Vis spectrophotometer (Thermo Fisher Scientific, Inc., Waltham, MA, USA).

For each sample of soil DNA, the taxonomic characterization up to the species level of bacterial communities were carried out through a 16S-based metagenomics approach. 16S library preparation and sequencing were performed by IGA Technology Services S.r.L. (Udine, Italy). Bacterial 16S library preparation workflow included two PCR amplifications. An initial PCR amplification was performed on genomic DNA to amplify the variable V3-V4 region of 16S ribosomal RNA gene. Gene-specific primers with overhang adapters for compatibility with Illumina index and sequencing adapters were used. The primer sequences, without the adapters, were: 16S-341F 5′-CCTACGGGNGGCWGCAG-3′ and 16S-805R 5′-GACTACHVGGGTATCTAATCC-3′ (Klindworth et al., 2013). The PCR products were purified and used as target for a limited cycle amplification to add Illumina flow-cell binding domains and dual index adapters using NexteraXT Index Kit (FC-131-1001/FC-131-1002). The resulting libraries were purified, quantified and normalized. Up to 96 libraries were pooled and sequenced from both ends on an Illumina MiSeq and more than 100,000 reads of about 300 bp were generated.

2.6. Statistical analysis

The statistical analysis of the soil chemical data was performed using Sigmastat 3.1 SPSS Inc. software (SPSS Inc., Quarry Bay, Hong Kong). The means of all the measured parameters were treated by one-way analysis of variance (ANOVA) with the orchard management type (S_{mng} and C_{mng}) as factor. Means were separated according to Fisher's LSD test at $p \leq 0.05$. In this experiment, three analytical replicates for each treatment from the three independent composite soil samples ($n = 3$) were considered.

Regarding the metagenomic analysis, the most abundant and long reads in each OTU (operational taxonomic unit) were selected as representative sequences. These sequences were then used for the taxonomy assignments using the GreenGene database, version 2013_8 (http://greengenes.secondgenome.com/) as a reference database. Rarefaction curves end-points and normalization of counts for diversity analysis were set to 50% of the target sequencing coverage. Samples not satisfying the count threshold were not included. The results were compared using a nonparametric two-sample *t*-test and the *p* values were calculated through 999 Monte Carlo permutations. Only the OTUs of the bacteria involved in N-cycling processes (see references in the discussion) and significantly different between S_{mng} and C_{mng} at $p \leq 0.05$ were considered and here discussed. The OTUs belonging to the same bacterial taxon were grouped.

3. Results

3.1. Soil, litter and humus description

The soil profile and description reported in Table 1 indicates in both the treatments an A horizon of 0–45 cm, a B horizon of 45–90 cm and a C horizon < 90 cm. The mineral nature is mainly carbonatic. Soil plasticity was defined as 'plastic' in the A horizons, 'slightly plastic' in the B horizons and 'non-plastic' in the C horizons. Soil consistence was defined as 'firm' in the A horizons and 'friable' in the B horizons of both the management systems. The A horizon of the S_{mng} was 'sticky', compared to the C_{mng}, that was 'slightly sticky'. Differences in the degree of soil stickiness between the two management systems were observed also in the B horizon.

The different soil management in the two agricultural systems caused the lack of organic horizons in the C_{mng}, while S_{mng} presented defined OL and OH horizons (Table 2). With reference to Agro humus systems and forms (Zanella et al., 2018c), the topsoil of C_{mng} was attributed to a 'massive Agro Mull' (absence of OH horizon and presence of massive, poorly zoogenic A horizon) while S_{mng} was attributed to a 'biomacro Agro Amphi' (presence of biomacrostructured A and OH horizons). Only the S_{mng} topsoil can be classified even with reference to Terrestrial *natural* humus systems and forms (Zanella et al. 2018b). The presence of zoogenic A and OH horizons allows to assign the profile to an Amphi system; more precisely, the transition (OH/A < 5 mm) and OH thickness (OH ≥ 1 cm) corresponded to the ones of an Eumesoamphi form. The classification of C_{mng} is impossible if reference is made to Terrestrial *natural* humus systems and forms because the A horizon does not show signs of macro- or mesofauna activity. Not having organic horizons, it would end up in a Mull system; not showing biological activity in A horizon, it would be located in a Mor system. This is a typical situation in stressed agricultural soils (Zanella et al., 2018c). Intensive agriculture pushes an original Mull system to another poor of pedofauna system that resembles a natural Mor, a system that develops in very difficult conditions of cold climate and/or strong acidity of the substratum.

Table 1
Soil profile and classification in the sustainable (S_{mng}) and the conventional (C_{mng}) systems, according to FAO guidelines for profile description (2006).

Soil management	Soil horizon	Depth (cm)	Field texture	Color matrix (Munsell)	Nature of mineral concentrations	Carbonate reaction (HCl)	Plasticity	Consistence when moist	Stickiness	Observations
Sustainable (S_{mng})	A1	0–30	Sandy Loam	10.0YR-2/2	Carbonates	Moderately calcareous	Plastic	Firm	Sticky	Presence of roots (herbaceous)
	A2	30–45	Sandy Loam	10.0YR-3/2	Carbonates	Moderately calcareous	Plastic	Firm	Sticky	Presence of roots (herbaceous)
	Bk	45–90	Sandy Loam	5.0Y-3/2	Carbonates	Moderately calcareous	Slightly plastic	Friable	Slightly sticky	–
	Ck	< 90	Sandy Loam	5.0Y-4/4	Carbonates-silica	Strongly calcareous	Non-plastic	Friable	Non-sticky	–
Conventional (C_{mng})	Ap1	0–30	Sandy Loam	10.0YR-2/2	Carbonates	Moderately calcareous	Plastic	Firm	Slightly sticky	–
	Ap2	30–45	Sandy Loam	10.0YR-3/2	Carbonates	Moderately calcareous	Plastic	Firm	Slightly sticky	–
	Bk	45–90	Sandy Loam	5.0Y-3/2	Carbonates	Moderately calcareous	Slightly plastic	Friable	Non-sticky	–
	Ck	< 90	Sandy Loam	5.0Y-4/4	Carbonates-silica	Strongly calcareous	Non-plastic	Friable	Non-sticky	–

3.2. Soil chemical parameters

The profiles of TOC and TN levels in the two management systems, and particularly in the topsoil (0–5 cm), were considerably different (Fig. 1). In the first 5 cm of soils, TOC was significantly higher ($p \leq 0.05$) in the S_{mng}, compared to the C_{mng}, while the trend was reversed at 10, 20 and 30 cm, and became not statistically different between the two treatments at 60 and 90 cm. Regarding TN, its levels were significantly higher in the S_{mng} at 0 and 5 cm, while the differences in the remaining soil depths were not statistically significant. The C/N ratios in the S_{mng} were significantly lower at 5, 10, 20, 30 and 60 cm, and not significantly different at 0 and 90 cm, compared to the respective values of the C_{mng}. In the litter of the S_{mng}, the values of TOC, TN and C/N were 443.90 ± 17.93 (SD) g kg^{-1}, 5.60 ± 0.58 g kg^{-1}, and 79.27 ± 8.91, respectively.

In the S_{mng}, the values of soil pH measured both in water and $CaCl_2$ increased with rising soil depth from 0 to 10 cm, then remained relatively stable, and increased again at 90 cm, whereas soil pH in the C_{mng} increased constantly from 0 to 90 cm in water (excepting for the value at 60 cm), in $CaCl_2$ the trend was similar but with a slight decrease at 90 cm (Fig. 2).

The values of TOC, TN and pH cumulated for the soil depths 0–30, 30–60 and 60–90 cm are reported in Table 3.

3.3. Soil metabolic diversity of soil bacteria

The Biolog® analysis showed that total *AWCD* and *S* were not significantly different between the S_{mng} and C_{mng} (Table 4). No significant differences between the two management systems were found for the two indices of bacterial community diversity here used (*H'* and *U*) nor for evenness indices (*E* and *Z*) (Table 4). As for total *AWCD*, the *AWCD* calculated for the principal classes of bacterial carbon substrates were not significantly different between the S_{mng} and C_{mng} (Fig. S1).

3.4. Identification of N-cycling bacteria

The abundance of the bacterial taxa involved in N transformations statistically different ($p \leq 0.05$) between S_{mng} and C_{mng} are reported in Fig. 3. In the C_{mng} system, the total abundance of free-living N-fixing Proteobacteria, Actinobacteria and Cyanobacteria was statistically higher than in the S_{mng} system. Differently, N-fixing symbiont Proteobacteria belonging to the Rhizobiales order were more abundant in the S_{mng}. The abundance of two OTUs of denitrifying bacteria (*Denitrobacter* spp. and *Pseudomonas* spp.) was different between the two soil management systems, being higher in the S_{mng}. The abundance of the three bacterial taxa involved in nitrogen oxidation from ammonia to nitrates (two Bacteria OTUs belonging to *Nitrospira* spp. and *Nitrosovibrio* spp., and the Archea OTU *Nitrosospherae* spp.) was higher in the S_{mng}, compared to C_{mng}.

Overall raw results of the metagenomic analysis, with relative abundance of a) all the total OTUs and, specifically, b) of the OTUs belonging to N-cycling bacteria and statistically different ($p \leq 0.05$) between the two management systems are presented in Supplementary Tables S2 and S3, respectively.

4. Discussion

The description of the different soil layers (horizons) gives a good general idea of what is going on in a soil profile in terms of soil genesis, leaching, bioturbation and water table dynamics. This is particularly important for agro-ecosystems, that originate from natural or semi-natural environments successively disturbed by original vegetation change and agronomic practices (Zanella et al., 2018c). Despite the conversion of a soil from natural to agronomic causes a certain level of disturbance in the activity of many soil invertebrates, such as earthworms and enchytraeids, microorganisms are less affected by the

Table 2
Little layer and humus description in the sustainable (S_{mng}) and the conventional (C_{mng}) systems using the classification of Zanella et al. (2018b).

Soil management		Sustainable (S_{mng})	Conventional (C_{mng})
Is there a litter layer present?		Yes	No
Is there an OL layer present (layer characterised by the accumulation of leaves and needles. Although possibly discolored and slightly fragmented, the leaves or needles are still easily discernible to the naked eye)?		Yes	No
Average thickness (cm)		3	–
Is it an nOL layer (litter age < 1 year)?		Yes	No
Is it an vOL layer (leaves or needles are slightly altered: i.e. slightly discolored, bleached, matted, skeletonized, or slightly fragmented)?		Discontinuous	No
Average thickness (cm)		1	–
Is there an OF layer present (layer characterised by the accumulation of partly decomposed litter, i.e. clearly fragmented and bleached, skeletonized leaves or needles)?		No	No
Is the material mainly fragmented by soil fauna (zoOF - e.g., mite pellets visible) or by fungi (nozOF - layer is matted and permeated by hyphae)?		Intermediate	No
Is there an OH layer present (layer characterised by black, grey-brown or reddish-brown, well decomposed litter. Individual leaves or needles are no longer visible)?		Yes	No
Average thickness (cm)		1	–
Dig a micro-pit ca 20 cm deep and note the transition of the litter layer to the mineral soil. How is this transition?		sharp (< 5mm)	–
How deep is the A horizon? (cm)		45	45
What is the structure of the mineral A horizon?		Grade: moderate Type: granular Size: medium	Grade: moderate Type: granular Size: medium
How is the transition between the mineral A horizon and the underlying soil (E or B horizon)?		Distinctness: gradual Topography: wavy	Distinctness: gradual Topography: wavy
Are there any droppings of earthworms identifiable in the A horizon?		Yes	No
Are there any droppings of other soil fauna (enchytraeids and arthropods) identifiable in the A-horizon?		Yes	No
Humus classification according to Zanella et al. (2018b)	System	AMPHI	–
	Form	Eumacroamphi	–
Humus classification according to Zanella et al. (2018c)	System	AGRO AMPHI	AGRO MULL
	Form	Biomacro Agro Amphi	Massive Agro Mull

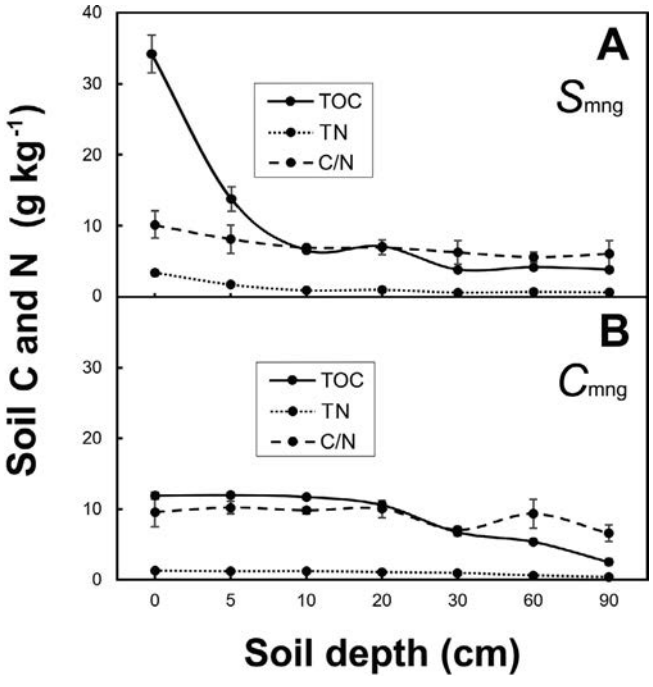

Fig. 1. Soil total organic carbon (TOC; continuous line), total nitrogen (TN; dotted line) and C/N ratio (dashed line) of soils from (A) the sustainable (S_{mng}) and (B) the conventional (C_{mng}) systems measured at different soil depths. Each value represents the mean (± SD) from composite soil samples (n = 3).

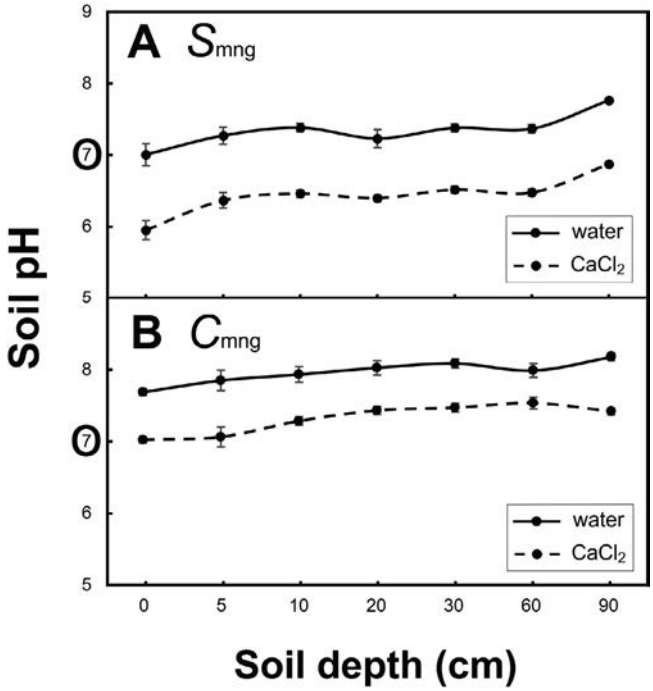

Fig. 2. pH measured in water (continuous line) and in $CaCl_2$ (dashed line) of soils from (A) the sustainable (S_{mng}) and (B) the conventional (C_{mng}) systems measured at different soil depths. Each value represents the mean (± SD) from composite soil samples (n = 3).

agronomic practices adopted and continue to play a key role in the maintenance of soil fertility (Bünemann et al., 2018). This trend was confirmed by our results, where in both the soil management systems a high bacterial metabolic activity in the topsoil (0–30 cm) (Table 4 and Fig. 3) was observed, while only the A horizon of the S_{mng} system there was the presence of droppings of earthworms and of other soil fauna identifiable (Tables 1 and 2).

In the case the agriculture techniques adopted are not sustainable, changes in land use towards agriculture are often accompanied by changes in soil structure, reduced edaphic biodiversity, soil erosion, nutrients runoff, ground and surface-water use, and soil contamination (Celano et al., 2011; Palese et al., 2014; Zanella et al., 2018c). In this

Table 3
Soil total organic carbon (TOC), total nitrogen (TN), C/N ratio. pH measured in water and pH measured in $CaCl_2$ of soils from the sustainable (S_{mng}) and the conventional (C_{mng}) systems measured at different soil depths. Each value represents the mean (± SD) from composite soil samples (n = 3). Average values were cumulated from the values of Tables 1 and 2, and refereed to grouped soil depths (0–30, 30–60 and 60–90 cm). Values followed by different letters are statistically different ($p \leq 0.05$) within columns.

Soil system	Soil depth (cm)	TOC (g kg^{-1})	TN (g kg^{-1})	C/N	pH_{water}	pH_{CaCl2}
Sustainable (S_{mng})	0–30	13.18 ± 0.22 a	1.56 ± 0.20 a	7.69 ± 0.37 b	7.23 ± 0.09 c	6.34 ± 0.08 d
	30–60	4.02 ± 0.08 d	0.70 ± 0.11 c	5.94 ± 0.17c	7.37 ± 0.06 bc	6.50 ± 0.05 cd
	60–90	4.03 ± 0.12 d	0.71 ± 0.13 c	5.84 ± 0.26c	7.57 ± 0.05b	6.68 ± 0.04 c
Conventional (C_{mng})	0–30	10.59 ± 0.32 b	1.13 ± 0.09 b	9.33 ± 0.10 a	7.91 ± 0.09 a	7.26 ± 0.07 b
	30–60	6.04 ± 0.43 c	0.77 ± 0.05 c	8.21 ± 0.23 ab	8.02 ± 0.08 a	7.50 ± 0.07 a
	60–90	3.94 ± 0.29 d	0.49 ± 0.08 d	7.96 ± 0.61 b	8.07 ± 0.07 a	7.47 ± 0.06 a

perspective, the need of sustainable agricultural techniques and soil management systems, like the high C-input set of practices used in this experiment (i.e., the S_{mng} system described in the Materials and Methods section), becomes urgent for soil preservation and conservation, especially in Mediterranean soils (Sofo et al., 2014a,b).

From the soil qualitative analyses (Table 1), it appears that the presence of roots from spontaneous cover crops was observed only in the A horizon of the S_{mng}. This resulted in increases in soil stickiness, that was higher in the A and Bk horizons of the S_{mng}, where the suffix 'k' indicates the accumulation of pedogenic carbonates. This effect was likely due to the higher levels of water (held by the roots of grasses), root exudates and organic acids, whose synergic action on soil structure is able to modify soil stickiness (Palese et al., 2015; Zanella et al., 2018b). Another clear aspect emerging from the comparison of the two management systems was the absence of litter in the C_{mng} system (Table 2).

The litter layer refers to all the dead organic debris (such as leaves, needles, branches and twigs, either still recognizable or significantly altered) on top of the mineral soil surface, and is an important visual clue for characterizing the rate of recycling of organic matter, that enters the A horizon through the litter. The sustainable practices of the S_{mng} system, especially no-tillage, allowed to maintain a well-developed little layer (OL) with an average thickness of 3 cm (including 1 cm of new litter, nOL, and 2 cm of old litter, vOL) and tracks of the activity of soil fauna (zoOF) and fungal hyphae (nozOF) (specific terms and diagnostic horizons according to Zanella et al., 2018a). Due to its high content of organic matter deriving from crop and pruning residues, litter provided S_{mng} topsoil (0–5 cm) with higher TOC and TN contents, compared to the C_{mng} (Fig. 1). In both the soil management systems, the trends of TOC and TN generally decreased with increasing soil depth (Fig. 1). The higher content of organic matter, likely transported in the deeper soil layers in a dissolved form by soil solution, caused lower soil pH in the S_{mng} system (Fig. 2), whose values ranged from 7.68 to 8.16 (in water) due to the carbonatic nature of the soil (Table 1). The average difference of topsoil (0–5 cm) pH measured in water and $CaCl_2$ was higher in S_{mng} (0.98) than in C_{mng} (0.71) (Fig. 2), so demonstrating that the soil exchangeable H^+ in S_{mng} mainly derived from organic matter functional groups (Fig. 1).

The topsoil, the outermost layer of soil (0–30 cm), is known to have the highest concentration of organic matter and microorganisms, with consequent high biological soil activity. For this reason, in this soil layer, bacterial metabolic diversity indices were estimated by Biolog® (Table 4) and the relative abundances of the bacterial (OTUs) were measured by 16S-based metagenomic analysis (Tables S1 and S2, and Fig. 3).

Biolog® indices are related to the metabolic activity, number, variety and diversity of bacteria, including diversity within and between functional groups (Sofo et al., 2018), being affected by agricultural practices and C-inputs in the agro-ecosystem (Sofo et al., 2014a,b). From the results (Table 4 and Fig. S1), it did not appear a significant metabolic inhibition of bacterial metabolism in the soil managed conventionally (C_{mng}), compared to the S_{mng} system. The long-term application of sustainable management did not lead to a significantly higher total bacterial metabolic activity (*AWCD* and *S*) and diversity (*H'* and *U*), nor to the predominance of few metabolic groups of bacteria (*E* and *Z*). The same trend was found within the main groups of bacterial carbon substrates (Fig. S1). This suggests that the difference between the C_{mng} and S_{mng} systems likely resides in the abundance of bacterial taxonomic groups having specific functions (qualitative differences) more than in parameters based on total bacterial metabolic activity (quantitative differences).

Contrary to soil C, whose reactions are overlapped and difficult to attribute to specific soil microorganisms, transformations among N forms are mostly mediated by bacteria (Robertson and Groffman, 2015; Van Groenigen et al., 2015). As an example, nitrification, denitrification and fixation, are carried out by a relatively restricted number of bacterial genera (de Vries and Shade, 2013; Mooshammer et al., 2014), whose genes are good markers for N availability for plants and indices of soil fertility, as they can be unequivocally interpreted and reference values are available (see Pascazio et al., 2018, for a study in olive). Our results depicted a scenario where N-cycling was generally up-regulated in the S_{mng}, compared to C_{mng} (Table S2 and Fig. 3). This is in accordance with a previous culture-based analysis carried out in the same system by Sofo et al. (2010), who found that the number of ammonifying bacteria, proteolytic bacteria, and *Azotobacter* spp. under a sustainable management system was significantly higher, compared to a conventional one. The increase in soil TN, with the consequent reduced C/N, in the topsoil (0–30 cm) of the S_{mng} (Table 3 and Fig. 1) likely had a priming effect on N-cycling bacteria, as also recently highlighted by Pascazio et al. (2018). Interestingly, even if the total abundance of N-fixing bacteria was comparable in the two systems (610 in the S_{mng} and 567 in the C_{mng}), significant differences were found in the abundance of

Table 4
Bacterial community indices, identified by Biolog® 96-well Eco-Microplates™, of soils from the sustainable (S_{mng}) and the conventional (C_{mng}) systems. Each value represents the mean (± SD) from composite soil samples (n = 3). Values followed by different letters are statistically different ($p \leq 0.05$) within columns. *AWCD* = average well colour development; *S* = richness; *H'* = Shannon's diversity index; *E* = Shannon's evenness index; *U* = McIntosh's diversity index; *Z* = McIntosh's evenness index.

Soil management	*AWCD*	*S*	*H'*	*E*	*U*	*Z*
Sustainable (S_{mng})	0.720 ± 0.039 a	15.111 ± 0.928 a	3.179 ± 0.085 a	2.661 ± 0.130 a	4.692 ± 0.300 a	0.963 ± 0.014 a
Conventional (C_{mng})	0.852 ± 0.076 a	16.778 ± 2.386 a	3.228 ± 0.175 a	2.629 ± 0.086 a	5.557 ± 0.358 a	0.964 ± 0.012 a

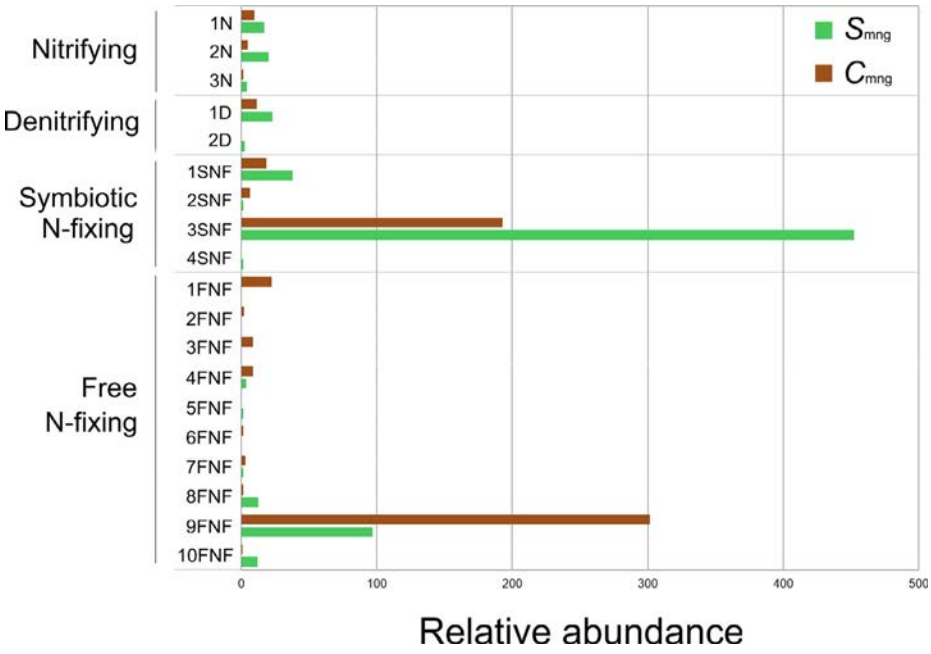

Fig. 3. Relative abundances of the operational taxonomical units (OTUs) of N-cycling bacteria that were statistically different in soils from the sustainable (S_{mng}) and the conventional (C_{mng}) systems. Only the OTUs with a statistical difference ($p \leq 0.05$) between S_{mng} and C_{mng} were considered. k: kingdom; p: phylum; c: class; o: order; f: family; g: genus; s: species. *Legend*: Nitrifying – 1N: k: Bacteria; p: Nitrospirae; c: Nitrospira; o: Nitrospirales; f: Nitrospiraceae; g: Nitrospira; 2N: k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Nitrosomonadales; f: Nitrosomonadaceae; g: Nitrosovibrio; s: tenuis; 3N: k: Archaea; p: Crenarchaeota; c: Thaumarchaeota; o: Nitrososphaerales; f: Nitrososphaeraceae; g: Nitrososphaera. Denitryfing – 1D: k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: corrugata; 2D: k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae; g: Denitrobacter. Symbiontic N-fixing – 1SNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Mesorhizobium; 2SNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhizobiaceae; g: Sinorhizobium; s: meliloti; 3SNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: elkanii; 4SNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: pachyrhizi. Free N-fixing – (Cyanobacteria) 1FNF: k: Bacteria; p: Cyanobacteria; c: Oscillatoriophycideae; o: Chroococcales; f: Phormidiaceae; g: Microcoleus; s: vaginatus; 2FNF: k: Bacteria; p: Cyanobacteria; c: Synechococcophycideae; o: Synechococcales; f: Acaryochloridaceae; g: Acaryochloris; 3FNF: k: Bacteria; p: Cyanobacteria; c: Nostocophycideae; o: Nostocales; f: Nostocaceae; g: Nostoc; (Other bacteria) 4FNF: k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Frankiaceae; g: Frankia; 5FNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Azospirillum; 6FNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Phaeospirillum; s: fulvum; 7FNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; 8FNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Acidisphaera; 9FNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; 10FNF: k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae.

free N-fixing bacteria (higher in the C_{mng}) and symbiont N-fixing bacteria (higher in the S_{mng}) (Table S2 and Fig. 3). This discrepancy between the two systems was likely due to the presence of the dense root systems of cover crops in the S_{mng} (Palese et al., 2014), including many spontaneous Fabaceae, whose root nodules host Rhizobiales N-fixing bacteria (Robertson and Groffman, 2015). On the other side, the C_{mng} relies on a N-fixation mainly carried out by free N-fixing bacteria, including Cyanobacteria, as the continuous mechanical disturbance of this plot did not allow the presence of spontaneous Fabaceae, with their root-associated N-fixing bacteria. In the C_{mng}, soil TN in the 0–30 cm soil layer was significantly lower and the C/N higher than in the S_{mng} (Table 3). Considering that the average C/N value of the biomass of N-cycling bacteria calculated from the literature (de Vries and Shade, 2013, 2018; Van Groenigen et al., 2015; and references within) is 7.86, the soil C/N in the S_{mng} (7.69) was very close to the optimum for bacterial growth and can be the cause of the enhanced N-turnover observed in this system (Table S2 and Fig. 3).

From the general analysis of the data obtained by the study of soil profiles, C and N dynamics, and the genetic and functional diversity of soil bacteria, it emerged that a sustainable orchard management caused an improvement in soil organic matter, whose positive effects were reflected on soil N-cycling bacteria, without affecting total bacterial metabolic activity and diversity. Even if there is substantial diversity regarding olive orchard management among the Mediterranean countries (Pergola et al., 2013), the determination of set of standards and common operating principles based on scientific knowledge is urgent, and they should be adopted to design and adjust the local soil management practices in order to increase microbiological diversity. The results obtained could be important for prediction of the impacts of environmental perturbations on key functions carried out by the soil microbiome and will promote the development of new approaches for optimizing soil carbon cycling, managing nutrient transport, and sustaining and improving crop yield and product quality.

Finally, the benefits we have recorded in the soil have significant and functional consequences on human health (de Vries and Wallenstein, 2017; Zanella et al., 2018d) and also positive effects on climate warming (Caitlin et al., 2017; Ferrarini et al., 2018; Minasny et al., 2018). We really hope that this article could help to understand how important is the soil as a living matrix capable of recycling biological structures and transforming them into future biodiversity. We would like to have a 'more biological' soil, the only basis for a healthier world.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.apsoil.2018.12.022.

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Supplementary Table 1. Agricultural practices adopted in the sustainable (S_{mng}) and in the conventional (C_{mng}) systems.

Practice	S_{mng}		C_{mng}
Soil tillage	• No tillage. Spontaneous weeds and grasses mowed at least twice a year.		• Tillage (milling at 10 cm soil depth) performed 2-3 times per year in order to keep the soil bare.
Fertilization	• Guided fertilization: fertigation based on a nutrient balance approach which takes into account nutrient input (by wastewater), output (by yield), and recycling/immobilisation in the grove system (by pruned material, senescent leaves, cover crops). The average values of organic C, N, P and K contained in the treated wastewater were 124, 54, 3 and 50 kg ha^{-1} $year^{-1}$. An integrative amount of 40 kg ha^{-1} $year^{-1}$ of $N\text{-}NO_3^-$ was distributed in the early spring.		• Mineral fertilization carried out empirically once per year in early spring by using granular product applied to the soil (NPK 20-10-10 fertilizer at doses ranging from 300 to 500 kg ha^{-1} $year^{-1}$).
Irrigation	• Guided drip irrigation with treated municipal wastewater based on crop evapotranspiration calculated according to FAO equation: $ET_c = K_r \times K_c \times ET_o$ (K_r = reduction coefficient; K_c = crop coefficient; ET_o = potential evapotranspiration) - (6 self-compensating drippers per tree delivering 8 L h^{-1}).		• No irrigation (about 35 m^3 rainfall $plant^{-1}$ $year^{-1}$).
Pruning	• Light winter pruning performed each year in order to reach vegetative-reproductive balance of trees. Pruning material cut and left on the ground as mulch.		• Heavy pruning carried out every two years. Pruned residues burned out of the olive grove.

Supplementary Table 2. Relative abundances of the bacterial operational taxonomical units (OTUs) that were statistically different in soils from the sustainable (S_{mng}) and the conventional (C_{mng}) systems. Only the OTUs with a statistical difference ($p \leq 0.05$) between S_{mng} and C_{mng} were considered. k: kingdom; p: phylum; c: class; o: order; f: family; g: genus; s: species.

OTU ID	*p* level	Relative abundance S_{mng}	Relative abundance C_{mng}	Taxonomic group
EF516597.1	0.025	1.00	0.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
HQ844545.1	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylocystaceae; g: Methylosinus; s:
AB240329.1	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
JQ655798.1	0.025	3.00	0.00	k: Bacteria; p: Acidobacteria; c: Acidobacteria; o: Acidobacteriales; f: Koribacteraceae; g: Candidatus Koribacter; s:
JF181356.1	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
AM941213.2	0.025	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
HQ597923.1	0.025	1.00	0.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.ReferenceOTU65	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Devosia; s:
New.ReferenceOTU29	0.025	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Olivibacter; s: soli
New.CleanUp.ReferenceOTU66	0.025	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Segetibacter; s:
New.CleanUp.ReferenceOTU634	0.025	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU2429	0.025	0.00	1.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera; s:
New.CleanUp.ReferenceOTU4188	0.025	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae
New.CleanUp.ReferenceOTU5145	0.025	0.00	1.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU5541	0.025	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter; s:
New.CleanUp.ReferenceOTU5679	0.025	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Microlunatus
New.CleanUp.ReferenceOTU9350	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU14286	0.025	1.00	0.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU16147	0.025	1.00	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU18925	0.025	1.00	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU21213	0.025	1.00	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU21366	0.025	0.00	2.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU23047	0.025	0.00	1.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU23469	0.025	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU24937	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae
New.CleanUp.ReferenceOTU25112	0.025	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae; g: Chondromyces; s:
New.CleanUp.ReferenceOTU25350	0.025	0.00	1.00	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU26743	0.025	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Catellatospora; s:
New.CleanUp.ReferenceOTU28757	0.025	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
New.CleanUp.ReferenceOTU29438	0.025	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
NR_025797.1	0.034	2.33	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Agromyces; s: salentinus
HM835307.1	0.034	2.33	0.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Solibacillus; s:
DQ490438.1	0.034	16.33	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium; s:
JF417842.1	0.034	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
HM319694.1	0.034	1.00	2.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Dyadobacter; s:
GQ418041.1	0.034	7.67	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae; g: Pigmentiphaga
GQ402805.1	0.034	0.00	2.67	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
AB425063.1	0.034	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Brevundimonas; s:
EU881291.1	0.034	0.00	1.67	k: Bacteria; p: Acidobacteria; c: Acidobacteria; o: Acidobacteriales; f: Koribacteraceae; g: Candidatus Koribacter; s:
EF540401.1	0.034	0.00	3.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium; s:
HQ386386.1	0.034	0.00	2.33	k: Bacteria; p: Cyanobacteria; c: Nostocophycideae; o: Nostocales; f: Nostocaceae; g: Nostoc; s:
HM156138.1	0.034	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
JF178945.1	0.034	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
FM882233.1	0.034	0.00	2.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
JF185563.1	0.034	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Thermomonas; s:
NR_027534.1	0.034	0.00	2.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s: tataouinensis
CP000301.1	0.034	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: pachyrhizi
AY328705.1	0.034	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Phaeospirillum; s: fulvum
JF041026.1	0.034	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: wittichii
EU022308.1	0.034	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Mesorhizobium
DQ297946.1	0.034	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Novosphingobium; s:
JF084320.1	0.034	0.00	1.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.ReferenceOTU67	0.034	11.33	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.ReferenceOTU47	0.034	0.00	2.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.ReferenceOTU46	0.034	1.33	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Methylibium; s:
New.CleanUp.ReferenceOTU0	0.034	0.00	2.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU458	0.034	3.00	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU820	0.034	2.00	0.00	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.CleanUp.ReferenceOTU1412	0.034	4.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU2048	0.034	2.00	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU2101	0.034	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
New.CleanUp.ReferenceOTU2291	0.034	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Azospirillum
New.CleanUp.ReferenceOTU2580	0.034	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Virgisporangium; s: ochraceum
New.CleanUp.ReferenceOTU3110	0.034	0.00	1.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
New.CleanUp.ReferenceOTU3563	0.034	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Inquilinus; s: limosus
New.CleanUp.ReferenceOTU4185	0.034	2.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU5653	0.034	0.00	3.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae
New.CleanUp.ReferenceOTU5786	0.034	0.00	1.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU5800	0.034	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Myxococcaceae; g: Anaeromyxobacter; s:
New.CleanUp.ReferenceOTU5993	0.034	1.33	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
New.CleanUp.ReferenceOTU6160	0.034	0.00	2.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU6630	0.034	1.33	0.00	k: Bacteria; p: Chloroflexi; c: Chloroflexi; o: Roseiflexales; f: Kouleothrixaceae; g: Kouleothrix
New.CleanUp.ReferenceOTU6979	0.034	0.00	1.67	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU7039	0.034	0.00	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
New.CleanUp.ReferenceOTU7098	0.034	0.00	5.33	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s: aurantiaca
New.CleanUp.ReferenceOTU7342	0.034	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
New.CleanUp.ReferenceOTU7515	0.034	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
New.CleanUp.ReferenceOTU8127	0.034	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
New.CleanUp.ReferenceOTU8957	0.034	0.00	2.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU9846	0.034	0.00	1.67	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia
New.CleanUp.ReferenceOTU10065	0.034	1.67	0.00	k: Bacteria; p: Verrucomicrobia; c: Opitutae; o: Opitutales; f: Opitutaceae; g: Opitutus; s:
New.CleanUp.ReferenceOTU10543	0.034	0.00	1.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU10898	0.034	0.00	2.00	k: Bacteria; p: Cyanobacteria; c: Synechococcophycideae; o: Synechococcales; f: Acaryochloridaceae; g: Acaryochloris
New.CleanUp.ReferenceOTU11935	0.034	0.00	1.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU11986	0.034	0.00	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU12181	0.034	0.00	1.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s:
New.CleanUp.ReferenceOTU12688	0.034	1.33	0.00	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s:
New.CleanUp.ReferenceOTU13500	0.034	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Chelatococcus; s: daeguensis
New.CleanUp.ReferenceOTU14373	0.034	0.00	5.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU14620	0.034	0.67	2.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU15025	0.034	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria
New.CleanUp.ReferenceOTU15050	0.034	2.67	1.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.CleanUp.ReferenceOTU15222	0.034	0.00	5.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU15324	0.034	0.67	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU15403	0.034	0.00	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
New.CleanUp.ReferenceOTU15926	0.034	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae
New.CleanUp.ReferenceOTU15967	0.034	0.00	2.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.CleanUp.ReferenceOTU16034	0.034	1.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU16112	0.034	1.33	0.00	k: Bacteria; p: Firmicutes; c: Erysipelotrichi; o: Erysipelotrichales; f: Coprobacillaceae; g: Coprobacillus; s: cateniformis
New.CleanUp.ReferenceOTU16421	0.034	0.67	3.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU16902	0.034	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
New.CleanUp.ReferenceOTU17433	0.034	2.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Coxiellaceae; g: Aquicella; s:
New.CleanUp.ReferenceOTU17797	0.034	0.00	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU18018	0.034	1.33	0.00	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s:
New.CleanUp.ReferenceOTU18922	0.034	1.00	2.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU19070	0.034	3.00	1.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:

New.CleanUp.ReferenceOTU19328	0.034	1.67	0.00 k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Cystobacteraceae; g: Cystobacter
New.CleanUp.ReferenceOTU19624	0.034	1.33	0.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Thermomonosporaceae; g: Actinomadura
New.CleanUp.ReferenceOTU21331	0.034	1.67	0.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Chitinophaga
New.CleanUp.ReferenceOTU21837	0.034	0.00	1.67 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU22087	0.034	1.33	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU22662	0.034	3.00	5.33 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU22815	0.034	0.00	1.33 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU23130	0.034	0.00	1.33 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU23426	0.034	1.67	0.00 k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Flavobacterium; s:
New.CleanUp.ReferenceOTU23694	0.034	0.00	1.33 k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.CleanUp.ReferenceOTU23915	0.034	2.67	0.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU23948	0.034	0.00	1.33 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU24204	0.034	0.00	1.67 k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU24460	0.034	0.00	1.67 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU24989	0.034	0.00	1.33 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU26383	0.034	2.00	0.00 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU27178	0.034	1.33	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Caulobacter
New.CleanUp.ReferenceOTU27609	0.034	0.33	2.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU27701	0.034	1.67	0.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.CleanUp.ReferenceOTU28302	0.034	1.33	0.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter; s:
New.CleanUp.ReferenceOTU28479	0.034	2.33	0.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae; g: Denitrobacter; s:
New.CleanUp.ReferenceOTU28606	0.034	2.33	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Amaricoccus; s:
New.CleanUp.ReferenceOTU28898	0.034	1.67	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae
New.CleanUp.ReferenceOTU29415	0.034	1.00	3.00 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU29484	0.034	0.00	1.33 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU29864	0.034	0.00	1.33 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Azohydromonas; s:
New.CleanUp.ReferenceOTU29935	0.034	0.00	1.67 k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae
New.CleanUp.ReferenceOTU30507	0.034	2.00	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Beijerinckia
New.CleanUp.ReferenceOTU30512	0.034	1.33	0.00 k: Bacteria; p: Tenericutes; c: Mollicutes; o: Anaeroplasmatales; f: Anaeroplasmataceae; g: Asteroleplasma; s:
HM329116.1	0.037	2.33	0.00 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
FJ592871.1	0.037	0.00	6.33 k: Bacteria; p: Cyanobacteria; c: Nostocophycideae; o: Nostocales; f: Nostocaceae; g: Nostoc; s:
FN662904.1	0.037	4.33	1.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
JF135666.1	0.037	0.00	6.00 k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
JQ798496.1	0.037	0.00	4.67 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Promicromonosporaceae; g: Promicromonospora; s:
JF081353.1	0.037	0.00	2.67 k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
GQ264384.1	0.037	2.00	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Hyphomicrobium; s:
JF079373.1	0.037	8.33	0.00 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Thermomonas; s:
DQ532142.1	0.037	0.00	4.67 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium; s:
DQ125771.1	0.037	3.67	0.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Salinibacterium; s:
AF237815.1	0.037	2.67	0.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Actinopolymorpha; s: singaporensis
HM309204.1	0.037	2.67	0.00 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
FJ889351.1	0.037	11.33	0.00 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Rhodanobacter; s:
GQ261279.1	0.037	0.00	4.33 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Pontibacter; s:
HM814595.1	0.037	8.67	0.00 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
FJ895033.1	0.037	2.00	4.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Janthinobacterium; s: lividum
HQ397161.1	0.037	2.00	6.00 k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
HM340458.1	0.037	0.00	2.00 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Enterobacteriales; f: Enterobacteriaceae; g: Erwinia
AJ581625.1	0.037	0.00	2.33 k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.ReferenceOTU42	0.037	0.00	22.33 k: Bacteria; p: Cyanobacteria; c: Oscillatoriophycideae; o: Chroococcales; f: Phormidiaceae; g: Microcoleus; s: vaginatus
New.CleanUp.ReferenceOTU1875	0.037	2.67	0.00 k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU1887	0.037	5.67	0.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Burkholderiaceae; g: Burkholderia; s: glathei
New.CleanUp.ReferenceOTU1934	0.037	0.00	2.33 k: Bacteria; p: Tenericutes; c: Mollicutes; o: Anaeroplasmatales; f: Anaeroplasmataceae; g: Asteroleplasma; s:
New.CleanUp.ReferenceOTU4290	0.037	0.00	2.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU5424	0.037	0.00	3.33 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae
New.CleanUp.ReferenceOTU5438	0.037	0.00	3.00 k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU5674	0.037	0.00	2.33 k: Bacteria; p: Chloroflexi; c: Chloroflexi; o: Chloroflexales; f: Oscillochloridaceae; g: Oscillochloris; s: trichoides
New.CleanUp.ReferenceOTU7226	0.037	0.00	2.00 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU7366	0.037	0.00	2.00 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU7783	0.037	0.00	3.67 k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s: aurantiaca
New.CleanUp.ReferenceOTU7959	0.037	3.00	0.00 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Alicyclobacillaceae; g: Alicyclobacillus; s:
New.CleanUp.ReferenceOTU8114	0.037	2.00	0.00 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Xylella; s:
New.CleanUp.ReferenceOTU8161	0.037	0.00	2.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s: rhombi
New.CleanUp.ReferenceOTU8205	0.037	10.00	0.00 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
New.CleanUp.ReferenceOTU8771	0.037	7.33	0.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU8828	0.037	2.67	0.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU9134	0.037	22.67	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s: aerolata
New.CleanUp.ReferenceOTU9437	0.037	10.33	3.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU10093	0.037	2.00	0.00 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter; s:
New.CleanUp.ReferenceOTU12008	0.037	0.00	2.00 k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Cystobacteraceae; g: Cystobacter
New.CleanUp.ReferenceOTU13063	0.037	5.67	0.00 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU13100	0.037	0.00	3.33 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Coxiellaceae; g: Aquicella; s:
New.CleanUp.ReferenceOTU13253	0.037	2.00	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Phyllobacterium; s:
New.CleanUp.ReferenceOTU13292	0.037	0.00	3.00 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU13770	0.037	3.00	1.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Hyphomicrobium; s: vulgare
New.CleanUp.ReferenceOTU14068	0.037	0.00	2.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
New.CleanUp.ReferenceOTU15201	0.037	2.67	0.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae
New.CleanUp.ReferenceOTU16050	0.037	0.00	3.00 k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU16252	0.037	2.67	0.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
New.CleanUp.ReferenceOTU17017	0.037	5.00	0.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Burkholderiaceae; g: Burkholderia
New.CleanUp.ReferenceOTU17899	0.037	0.00	2.33 k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.CleanUp.ReferenceOTU18603	0.037	0.00	4.00 k: Bacteria; p: Armatimonadetes; c: Chthonomonadetes; o: Chthonomonadales; f: Chthonomonadaceae; g: Chthonomonas; s:
New.CleanUp.ReferenceOTU19122	0.037	3.00	0.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU19235	0.037	5.67	0.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.CleanUp.ReferenceOTU19421	0.037	6.67	0.00 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.CleanUp.ReferenceOTU19561	0.037	13.33	0.00 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niastella
New.CleanUp.ReferenceOTU20810	0.037	10.00	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU21693	0.037	2.67	0.00 k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s:
New.CleanUp.ReferenceOTU22216	0.037	1.00	7.67 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU23081	0.037	4.33	0.00 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU24409	0.037	11.33	0.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s: aerolata
New.CleanUp.ReferenceOTU24590	0.037	2.67	0.00 k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Legionellaceae; g: Legionella; s:
New.CleanUp.ReferenceOTU27880	0.037	6.00	2.00 k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.CleanUp.ReferenceOTU28834	0.037	0.00	2.00 k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
FN811231.1	0.043	1.67	8.67 k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
AY328628.1	0.043	3.33	0.33 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s:
FJ490527.1	0.043	7.33	1.67 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia; s: kongjuensis
EF516512.1	0.043	29.33	17.00 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
FJ625382.1	0.043	2.67	0.33 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HM269222.1	0.043	3.67	1.33 k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
DQ017944.1	0.043	2.33	0.33 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HM270504.1	0.043	2.67	0.67 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Actinomycetospora; s:
HM839194.1	0.043	2.33	0.33 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Brevibacillus; s: brevis
FJ820400.1	0.043	0.67	3.00 k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Rubrivivax; s:
HM267225.1	0.043	5.67	0.33 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
JF049227.1	0.043	2.33	6.67 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia; s:
JF224943.1	0.043	0.33	2.67 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Salinibacterium; s:
HM844564.1	0.043	14.00	0.33 k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
JF232065.1	0.043	0.67	3.33 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Phenylobacterium; s:
AF423289.1	0.043	1.33	6.33 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
AJ311174.1	0.043	0.33	3.33 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Actinosynnemataceae; g: Kibdelosporangium; s:
NZ_ABVL01000001.1	0.043	4.67	0.67 k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s:
FJ152869.1	0.043	3.00	0.67 k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
New.ReferenceOTU156	0.043	1.33	5.33 k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.ReferenceOTU85	0.043	8.33	16.33 k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.ReferenceOTU106	0.043	1.00	5.33 k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:

New.CleanUp.ReferenceOTU1288	0.043	0.67	2.67	k: Bacteria; p: Verrucomicrobia; c: Opitutae; o: Opitutales; f: Opitutaceae; g: Opitutus; s:
New.CleanUp.ReferenceOTU1436	0.043	3.67	8.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU1468	0.043	1.33	4.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU1972	0.043	6.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
New.CleanUp.ReferenceOTU2154	0.043	1.67	8.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU3315	0.043	2.33	0.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Actinosynnemataceae; g: Actinokineospora
New.CleanUp.ReferenceOTU3503	0.043	1.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae
New.CleanUp.ReferenceOTU4087	0.043	3.33	12.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU4621	0.043	0.33	2.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU6404	0.043	1.67	4.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
New.CleanUp.ReferenceOTU6865	0.043	9.00	2.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Candidatus Xiphinematobacter; s:
New.CleanUp.ReferenceOTU7112	0.043	4.33	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Erythrobacteraceae; g: Erythromicrobium
New.CleanUp.ReferenceOTU8349	0.043	0.67	3.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU9074	0.043	0.33	3.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU9276	0.043	5.33	2.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Patulibacteraceae; g: Patulibacter; s: americanus
New.CleanUp.ReferenceOTU12374	0.043	0.33	3.67	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU12424	0.043	2.67	0.67	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s: amoebophila
New.CleanUp.ReferenceOTU14745	0.043	4.33	1.33	k: Archaea; p: Crenarchaeota; c: Thaumarchaeota; o: Nitrososphaerales; f: Nitrososphaeraceae; g: Candidatus Nitrososphaera; s:
New.CleanUp.ReferenceOTU17783	0.043	0.33	4.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU18059	0.043	3.00	11.67	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.CleanUp.ReferenceOTU18377	0.043	0.33	3.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter
New.CleanUp.ReferenceOTU19435	0.043	0.33	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s: tataouinensis
New.CleanUp.ReferenceOTU20390	0.043	42.00	28.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Kribbella; s:
New.CleanUp.ReferenceOTU20555	0.043	0.67	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU22278	0.043	4.67	0.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter; s:
New.CleanUp.ReferenceOTU23085	0.043	0.67	3.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU23165	0.043	3.00	6.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae; g: Chondromyces; s: crocatus
New.CleanUp.ReferenceOTU24324	0.043	0.67	3.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU24920	0.043	0.33	2.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingobium
New.CleanUp.ReferenceOTU25397	0.043	3.33	0.33	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s: amoebophila
New.CleanUp.ReferenceOTU25551	0.043	0.33	7.00	k: Bacteria; p: Verrucomicrobia; c: Verrucomicrobiae; o: Verrucomicrobiales; f: Verrucomicrobiaceae; g: Luteolibacter; s:
New.CleanUp.ReferenceOTU25833	0.043	0.67	5.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU25934	0.043	0.33	3.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
New.CleanUp.ReferenceOTU26578	0.043	0.33	2.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU26701	0.043	0.67	2.33	k: Bacteria; p: Actinobacteria; c: Nitriliruptoria; o: Euzebyales; f: Euzebyaceae; g: Euzebya; s:
New.CleanUp.ReferenceOTU26772	0.043	0.33	3.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU27244	0.043	0.67	2.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU27896	0.043	2.33	0.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae
New.CleanUp.ReferenceOTU29757	0.043	13.00	8.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU30004	0.043	3.33	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niabella
New.CleanUp.ReferenceOTU30495	0.043	0.33	3.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
HQ910327.1	0.046	1.00	9.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium; s:
DQ125578.1	0.046	3.00	8.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
HM330580.1	0.046	14.33	1.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
EU449609.1	0.046	5.33	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
DQ304805.1	0.046	2.67	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Inquilinus; s: limosus
JF178952.1	0.046	5.00	0.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: glycanilyticus
EF050430.1	0.046	45.33	26.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
L40612.1	0.046	3.67	8.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Frankiaceae; g: Frankia; s:
HQ132468.1	0.046	3.67	9.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Micromonospora
JF180348.1	0.046	5.00	1.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Pseudoxanthomonas; s:
DQ129304.1	0.046	1.00	7.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
DQ129585.1	0.046	2.33	9.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
FR687520.1	0.046	7.00	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
DQ248234.1	0.046	6.00	22.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
AY395335.1	0.046	7.33	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Microlunatus; s:
HM274399.1	0.046	6.67	12.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Actinoplanes; s:
JF048456.1	0.046	8.67	4.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s:
HM328008.1	0.046	0.67	8.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Yonghaparkia; s:
HM334145.1	0.046	7.33	26.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter; s:
EU335236.1	0.046	6.33	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
AM935954.1	0.046	4.00	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
JF123892.1	0.046	9.67	18.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Catellatospora; s:
HM277682.1	0.046	5.33	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhodobiaceae; g: Afifella; s:
AY328725.1	0.046	1.67	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
HM274453.1	0.046	6.00	13.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s:
GQ396897.1	0.046	7.67	14.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
HM269081.1	0.046	14.33	3.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s:
DQ125847.1	0.046	5.33	8.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s:
HQ114093.1	0.046	1.33	6.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s:
EU181492.1	0.046	1.00	5.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter; s:
EU873545.1	0.046	5.67	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: xanthophaeus
JQ428716.1	0.046	2.67	11.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
AM935081.1	0.046	13.33	5.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardiaceae; g: Nocardia; s: farcinica
DQ906897.1	0.046	1.67	8.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas; s:
JN023141.1	0.046	0.33	3.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s:
JF145531.1	0.046	11.00	5.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s:
JQ861340.1	0.046	3.00	7.33	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
DQ532236.1	0.046	1.00	16.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium; s:
HM459620.1	0.046	11.67	1.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: agarexedens
AY395351.1	0.046	42.00	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HM317272.1	0.046	10.00	1.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Variovorax; s: soli
AF290484.1	0.046	9.33	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Phyllobacterium; s:
AM697325.1	0.046	5.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
HM278456.1	0.046	0.67	4.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae
FJ529981.1	0.046	20.33	4.67	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Nitrosomonadales; f: Nitrosomonadaceae; g: Nitrosovibrio; s: tenuis
JF180336.1	0.046	1.33	5.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Arenimonas; s:
HM366507.1	0.046	8.33	15.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s: obscurus
AJ582029.1	0.046	12.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
EU335162.1	0.046	6.00	13.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
HM278783.1	0.046	1.67	9.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia; s:
FJ790625.1	0.046	3.67	8.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas; s:
JF077978.1	0.046	1.33	15.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s: rhombi
JF211276.1	0.046	18.33	27.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Iamiaceae; g: Iamia; s:
AJ292612.1	0.046	4.67	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: mesophilicum
FN436186.1	0.046	0.33	3.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
JF178808.1	0.046	5.00	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Bacillaceae; g: Bacillus; s: lentus
FN811266.1	0.046	18.33	71.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
HM445223.1	0.046	3.00	7.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium; s:
HM845753.1	0.046	41.33	34.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s:
JF085268.1	0.046	4.33	1.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Thermoactinomycetaceae; g: Shimazuella; s:
HM241105.1	0.046	5.67	0.33	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
JF203279.1	0.046	1.00	3.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
HM339185.1	0.046	2.33	8.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.ReferenceOTU2	0.046	4.00	16.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.ReferenceOTU16	0.046	1.67	7.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.ReferenceOTU89	0.046	29.00	47.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Pedomicrobium
New.ReferenceOTU36	0.046	1.00	6.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
New.CleanUp.ReferenceOTU98	0.046	3.67	0.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Micromonospora
New.CleanUp.ReferenceOTU813	0.046	26.67	10.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s:
New.CleanUp.ReferenceOTU827	0.046	0.67	3.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU2196	0.046	12.33	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Acidisphaera; s:
New.CleanUp.ReferenceOTU2273	0.046	4.33	0.33	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Flavobacterium; s:
New.CleanUp.ReferenceOTU2460	0.046	3.67	9.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU2924	0.046	4.67	12.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae

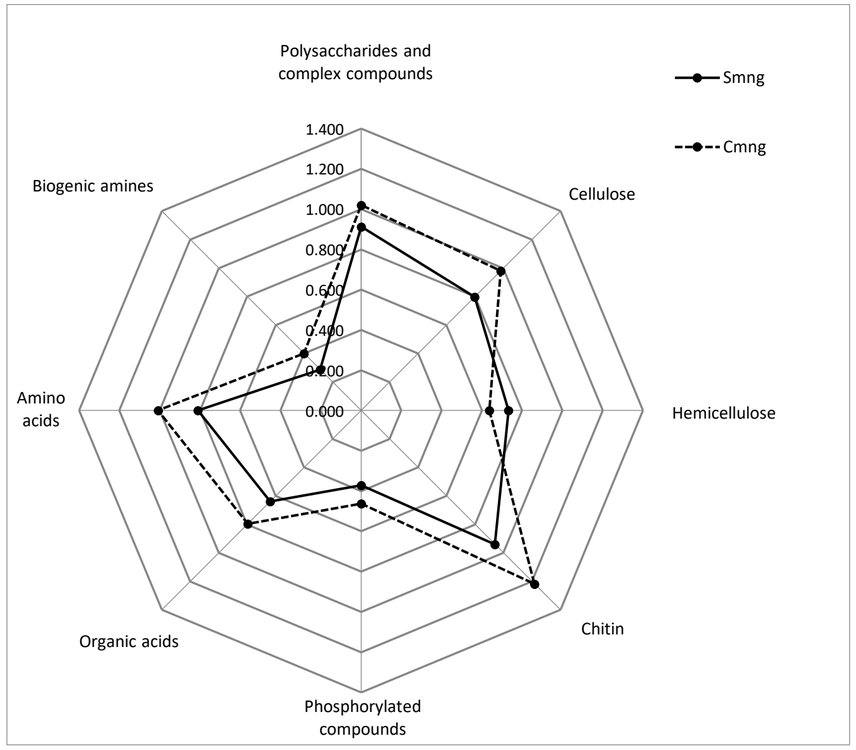
New.CleanUp.ReferenceOTU3038	0.046	0.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Saccharopolyspora; s: erythraea
New.CleanUp.ReferenceOTU4559	0.046	12.67	36.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas; s:
New.CleanUp.ReferenceOTU4812	0.046	1.33	13.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Xanthobacteraceae; g: Ancylobacter; s:
New.CleanUp.ReferenceOTU5168	0.046	10.00	0.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU5176	0.046	0.67	5.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU5563	0.046	1.67	7.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
New.CleanUp.ReferenceOTU6816	0.046	4.33	9.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU7223	0.046	0.67	11.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU7606	0.046	3.00	0.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU8919	0.046	0.33	5.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU9380	0.046	11.00	2.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU9490	0.046	2.33	9.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niastella
New.CleanUp.ReferenceOTU9758	0.046	7.67	2.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera; s:
New.CleanUp.ReferenceOTU10076	0.046	11.00	0.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: sepulcri
New.CleanUp.ReferenceOTU10150	0.046	7.33	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Bacillaceae; g: Bacillus
New.CleanUp.ReferenceOTU10465	0.046	0.67	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales
New.CleanUp.ReferenceOTU10579	0.046	3.33	8.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Entotheonellales; f: Entotheonellaceae; g: Candidatus Entotheonella; s:
New.CleanUp.ReferenceOTU10965	0.046	0.33	5.67	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea; s:
New.CleanUp.ReferenceOTU11047	0.046	1.33	5.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Myxococcaceae; g: Myxococcus
New.CleanUp.ReferenceOTU11306	0.046	0.33	3.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Azorhizophilus; s:
New.CleanUp.ReferenceOTU11359	0.046	16.67	9.67	k: Bacteria; p: Nitrospirae; c: Nitrospira; o: Nitrospirales; f: Nitrospiraceae; g: Nitrospira; s:
New.CleanUp.ReferenceOTU11543	0.046	4.67	1.00	k: Bacteria; p: Chloroflexi; c: Chloroflexi; o: Roseiflexales; f: Kouleothrixaceae; g: Kouleothrix; s:
New.CleanUp.ReferenceOTU11728	0.046	0.33	3.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU12425	0.046	2.33	9.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU12575	0.046	0.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU12732	0.046	1.67	5.67	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.CleanUp.ReferenceOTU13106	0.046	2.33	8.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niastella; s:
New.CleanUp.ReferenceOTU13277	0.046	14.00	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Aeromicrobium
New.CleanUp.ReferenceOTU13476	0.046	3.33	9.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Amaricoccus; s:
New.CleanUp.ReferenceOTU14621	0.046	1.33	4.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s:
New.CleanUp.ReferenceOTU14682	0.046	1.33	5.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae
New.CleanUp.ReferenceOTU15383	0.046	0.67	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae
New.CleanUp.ReferenceOTU15620	0.046	4.33	11.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU16488	0.046	2.33	6.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU17399	0.046	0.67	3.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU18679	0.046	1.00	3.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU18696	0.046	7.67	3.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU19105	0.046	8.67	14.33	k: Bacteria; p: Actinobacteria
New.CleanUp.ReferenceOTU19268	0.046	0.33	4.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU20513	0.046	3.67	9.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU22183	0.046	1.33	4.67	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea; s:
New.CleanUp.ReferenceOTU22330	0.046	2.33	9.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU22527	0.046	5.33	11.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU23159	0.046	7.00	20.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter; s: denitrificans
New.CleanUp.ReferenceOTU23463	0.046	5.67	13.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU23513	0.046	1.67	6.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter; s:
New.CleanUp.ReferenceOTU23541	0.046	14.33	9.67	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU24410	0.046	0.33	7.33	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Flavobacterium; s: succinicans
New.CleanUp.ReferenceOTU24424	0.046	5.33	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Catellatospora; s:
New.CleanUp.ReferenceOTU24452	0.046	1.00	8.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Haliangiaceae; g: Haliangium; s:
New.CleanUp.ReferenceOTU24926	0.046	5.33	11.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Erythrobacteraceae; g: Lutibacterium; s:
New.CleanUp.ReferenceOTU24975	0.046	15.33	6.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Intrasporangiaceae
New.CleanUp.ReferenceOTU26158	0.046	0.67	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
New.CleanUp.ReferenceOTU27776	0.046	0.33	3.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU27973	0.046	4.33	14.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU28001	0.046	1.00	9.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU28397	0.046	4.33	8.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU28708	0.046	7.33	13.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU28967	0.046	1.67	8.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Nannocystaceae; g: Plesiocystis; s:
New.CleanUp.ReferenceOTU29328	0.046	1.67	13.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU29422	0.046	12.67	6.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
New.CleanUp.ReferenceOTU29458	0.046	3.33	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU30151	0.046	1.00	10.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Cystobacteraceae; g: Cystobacter; s: fuscus
New.CleanUp.ReferenceOTU30192	0.046	3.33	16.67	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Iamiaceae; g: Iamia; s:
New.CleanUp.ReferenceOTU30330	0.046	2.33	10.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU30553	0.046	4.00	1.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
AB374371.1	0.050	2.67	8.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhodobiaceae; g: Afifella; s:
AJ292603.1	0.050	452.00	193.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: elkanii
AY395348.1	0.050	109.67	58.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
AJ968702.1	0.050	1.00	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
AY425763.1	0.050	68.67	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HM269229.1	0.050	10.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Microlunatus; s:
JF021408.1	0.050	7.00	16.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
EF516107.1	0.050	9.67	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium; s:
FJ889257.1	0.050	87.67	66.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Verrucosispora; s: gifhornensis
AB496412.1	0.050	9.00	2.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
JF092073.1	0.050	7.67	18.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Alicyclobacillaceae; g: Alicyclobacillus; s:
JF089694.1	0.050	10.33	41.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
JF174754.1	0.050	14.00	29.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia; s:
HM263278.1	0.050	29.33	43.67	k: Bacteria; p: Verrucomicrobia; c: Opitutae; o: Opitutales; f: Opitutaceae; g: Opitutus; s:
DQ125909.1	0.050	22.33	11.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Micromonospora
DQ129615.1	0.050	3.00	21.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
GQ263362.1	0.050	28.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: albireticuli
FM209311.1	0.050	1.67	12.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter; s:
HM341158.1	0.050	3.00	7.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s:
JF033767.1	0.050	161.33	246.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s:
FJ479456.1	0.050	19.00	11.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Kribbella; s:
AF377867.1	0.050	1.67	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhizobiaceae; g: Sinorhizobium; s: meliloti
AJ863369.1	0.050	88.33	31.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
DQ129563.1	0.050	5.67	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Williamsiaceae; g: Williamsia; s:
JF042953.1	0.050	6.00	68.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter
GU968460.1	0.050	2.00	16.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s: rhombi
FJ152735.1	0.050	3.33	10.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
HM845809.1	0.050	43.67	19.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Actinomycetospora; s:
HM186185.1	0.050	2.00	13.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s:
HM829036.1	0.050	13.33	4.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: chondroitinus
FJ889339.1	0.050	16.00	32.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Thermomonas; s:
JF098858.1	0.050	40.67	97.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
HM438548.1	0.050	11.00	29.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter; s:
AF423260.1	0.050	74.00	35.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: mirabilis
AY395414.1	0.050	31.00	10.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HQ538687.1	0.050	8.00	19.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
AF292996.1	0.050	37.67	24.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
AB257630.1	0.050	3.00	8.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhodobiaceae; g: Afifella; s:
FJ791174.1	0.050	4.67	28.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Cellulomonadaceae; g: Cellulomonas; s:
HM240903.1	0.050	4.00	11.67	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
HM278777.1	0.050	18.33	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium; s:
DQ453806.1	0.050	25.67	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HM557519.1	0.050	1.67	8.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s:
FJ849551.1	0.050	17.00	34.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
HM330072.1	0.050	6.67	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
U48996.1	0.050	55.00	13.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptosporangiaceae; g: Streptosporangium; s:
FJ891056.1	0.050	50.67	100.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
AY425768.1	0.050	14.00	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
HM306204.1	0.050	40.00	10.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Coxiellaceae; g: Rickettsiella; s:

HM438620.1	0.050	14.00	42.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter; s:
DQ248308.1	0.050	39.00	87.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas; s:
HM152696.1	0.050	23.00	11.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: corrugata
JF066170.1	0.050	12.33	24.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula; s:
HM275474.1	0.050	22.67	7.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Alicyclobacillaceae; g: Alicyclobacillus; s:
JF031109.1	0.050	8.33	21.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s: obscurus
HM274365.1	0.050	48.67	1.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina; s:
EU589316.1	0.050	16.33	56.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
AY133099.1	0.050	57.00	109.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s:
EU135879.1	0.050	10.33	19.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: tendae
EF682982.1	0.050	19.33	49.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas; s:
JF129033.1	0.050	4.67	10.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
HM334837.1	0.050	175.00	397.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter; s:
New.ReferenceOTU73	0.050	1.00	8.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.ReferenceOTU133	0.050	12.00	4.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.ReferenceOTU61	0.050	45.33	76.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s:
New.ReferenceOTU128	0.050	10.67	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.ReferenceOTU18	0.050	111.33	25.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.ReferenceOTU15	0.050	7.00	24.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.ReferenceOTU93	0.050	9.00	18.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae; g: Chondromyces; s:
New.ReferenceOTU34	0.050	43.67	20.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae
New.ReferenceOTU35	0.050	46.33	27.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.ReferenceOTU37	0.050	2.00	5.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Promicromonosporaceae; g: Cellulosimicrobium; s:
New.ReferenceOTU6	0.050	15.33	30.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Haliangiaceae; g: Haliangium; s: ochraceum
New.ReferenceOTU26	0.050	128.33	233.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas; s:
New.ReferenceOTU25	0.050	41.33	30.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s:
New.ReferenceOTU169	0.050	204.33	114.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium; s:
New.ReferenceOTU168	0.050	448.67	628.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.ReferenceOTU160	0.050	165.67	82.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.ReferenceOTU163	0.050	60.33	116.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s:
New.ReferenceOTU165	0.050	7.67	19.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.ReferenceOTU55	0.050	33.33	9.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.ReferenceOTU58	0.050	1.33	5.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.ReferenceOTU48	0.050	29.33	50.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.ReferenceOTU105	0.050	46.00	24.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
New.CleanUp.ReferenceOTU874	0.050	14.00	49.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU940	0.050	7.33	17.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata; s:
New.CleanUp.ReferenceOTU1319	0.050	7.33	26.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU2922	0.050	8.00	1.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera; s:
New.CleanUp.ReferenceOTU3415	0.050	2.33	18.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s:
New.CleanUp.ReferenceOTU3429	0.050	108.00	64.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s: aerolata
New.CleanUp.ReferenceOTU3818	0.050	3.67	19.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU3913	0.050	27.67	18.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae
New.CleanUp.ReferenceOTU4233	0.050	3.67	8.67	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Nannocystaceae; g: Plesiocystis; s:
New.CleanUp.ReferenceOTU5445	0.050	18.67	7.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU5602	0.050	3.00	14.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU6066	0.050	4.67	19.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s:
New.CleanUp.ReferenceOTU6432	0.050	7.33	22.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU6533	0.050	2.00	7.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU7276	0.050	1.33	5.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU8084	0.050	14.33	44.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter; s:
New.CleanUp.ReferenceOTU8125	0.050	15.00	6.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU8809	0.050	19.33	53.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU9301	0.050	1.67	9.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU10319	0.050	4.33	9.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU10323	0.050	4.00	13.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU10652	0.050	26.33	41.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU10720	0.050	6.33	17.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter; s:
New.CleanUp.ReferenceOTU10949	0.050	10.00	4.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes; s:
New.CleanUp.ReferenceOTU12002	0.050	2.67	22.00	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU13252	0.050	17.33	4.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae
New.CleanUp.ReferenceOTU14007	0.050	7.33	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU14515	0.050	1.00	9.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU14655	0.050	2.33	7.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Chelatococcus; s: daeguensis
New.CleanUp.ReferenceOTU15439	0.050	2.00	24.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Cellulomonadaceae; g: Cellulomonas; s:
New.CleanUp.ReferenceOTU15717	0.050	3.00	10.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
New.CleanUp.ReferenceOTU15725	0.050	4.67	11.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU17130	0.050	10.67	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae
New.CleanUp.ReferenceOTU17264	0.050	1.00	7.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
New.CleanUp.ReferenceOTU17577	0.050	2.33	8.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
New.CleanUp.ReferenceOTU17820	0.050	5.33	31.33	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea; s:
New.CleanUp.ReferenceOTU19164	0.050	19.67	10.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
New.CleanUp.ReferenceOTU19964	0.050	37.00	68.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
New.CleanUp.ReferenceOTU20126	0.050	14.67	29.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU20510	0.050	31.67	2.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU21506	0.050	5.33	17.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU22832	0.050	1.00	10.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter; s:
New.CleanUp.ReferenceOTU23556	0.050	4.00	12.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera; s:
New.CleanUp.ReferenceOTU23640	0.050	3.00	10.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU23751	0.050	4.67	24.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU23862	0.050	11.00	32.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Acidimicrobiaceae
New.CleanUp.ReferenceOTU24528	0.050	19.33	34.67	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU24794	0.050	1.00	7.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU24864	0.050	2.33	13.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU24894	0.050	8.33	46.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU25542	0.050	2.67	11.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces; s:
New.CleanUp.ReferenceOTU26246	0.050	31.67	3.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
New.CleanUp.ReferenceOTU26274	0.050	1.67	6.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Chromatiales; f: Ectothiorhodospiraceae; g: Methylonatrum; s: kenyense
New.CleanUp.ReferenceOTU26425	0.050	19.33	58.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s:
New.CleanUp.ReferenceOTU26611	0.050	2.33	14.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas; s:
New.CleanUp.ReferenceOTU26710	0.050	36.33	18.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Mesorhizobium
New.CleanUp.ReferenceOTU27209	0.050	17.67	48.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides; s:
New.CleanUp.ReferenceOTU27313	0.050	3.00	7.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylocystaceae
New.CleanUp.ReferenceOTU28138	0.050	45.00	19.67	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Acidimicrobiaceae; g: Acidimicrobium
New.CleanUp.ReferenceOTU28529	0.050	24.33	6.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Aeromicrobium
New.CleanUp.ReferenceOTU28751	0.050	15.67	5.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera; s:
New.CleanUp.ReferenceOTU28788	0.050	6.67	30.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter; s:
New.CleanUp.ReferenceOTU28803	0.050	2.33	8.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
New.CleanUp.ReferenceOTU28855	0.050	2.00	7.33	k: Bacteria; p: Armatimonadetes; c: Armatimonadia; o: Armatimonadales; f: Armatimonadaceae; g: Armatimonas; s:
New.CleanUp.ReferenceOTU29140	0.050	2.00	11.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter; s:
New.CleanUp.ReferenceOTU30047	0.050	70.00	27.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Hyphomicrobium; s:
New.CleanUp.ReferenceOTU30562	0.050	6.00	12.00	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Acidimicrobiaceae

Supplementary Table 3. Relative abundances of the bacterial operational taxonomical units (OTUs) of N-ciclying bacteria that were statistically different in soils from the sustainable (S_{mng}) and the conventional (C_{mng}) systems. Only the OTUs with a statistical difference ($p \leq 0.05$) between S_{mng} and C_{mng} were considered. k: kingdom; p: phylum; c: class; o: order; f: family; g: genus; s: species.

Type	Taxonomy	Relative abundance	
		S_{mng}	C_{mng}
Free N-fixing	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae	11.67	1.00
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas	97.00	301.33
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Acidisphaera	12.33	1.67
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae	1.67	3.33
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Phaeospirillum; s: fulvum	0.00	1.67
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Azospirillum	1.67	0.00
	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Frankiaceae; g: Frankia	3.67	8.33
	k: Bacteria; p: Cyanobacteria; c: Nostocophycideae; o: Nostocales; f: Nostocaceae; g: Nostoc	0.00	8.67
	k: Bacteria; p: Cyanobacteria; c: Synechococcophycideae; o: Synechococcales; f: Acaryochloridaceae; g: Acaryochloris	0.00	2.00
	k: Bacteria; p: Cyanobacteria; c: Oscillatoriophycideae; o: Chroococcales; f: Phormidiaceae; g: Microcoleus; s: vaginatus	0.00	22.33
	Total free N-fixing	**116.33**	**349.33**
Symbiotic N-fixing	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: pachyrhizi	1.67	0.00
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: elkanii	452.00	193.00
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhizobiaceae; g: Sinorhizobium; s: meliloti	1.67	6.67
	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Mesorhizobium	38.00	18.33
	Total symbiotic N-fixing	**493.33**	**218.00**
	Total N-fixing	**609.67**	**567.33**
Denitrifying	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae; g: Denitrobacter	2.33	0.00
	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: corrugata	23.00	11.33
	Total denitrifying	**25.33**	**11.33**
Nitrifying	k: Archaea; p: Crenarchaeota; c: Thaumarchaeota; o: Nitrososphaerales; f: Nitrososphaeraceae; g: Nitrososphaera	4.33	1.33
	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Nitrosomonadales; f: Nitrosomonadaceae; g: Nitrosovibrio; s: tenuis	20.33	4.67
	k: Bacteria; p: Nitrospirae; c: Nitrospira; o: Nitrospirales; f: Nitrospiraceae; g: Nitrospira	16.67	9.67
	Total nitrifying	**41.33**	**15.67**

Supplementary Figure S1. Radar diagrams of bacterial *AWCD* calculated for all the principal classes of carbon substrates, identified by Biolog® 96-well Eco-Microplates™, in soils from the sustainable (S_{mng}, continuous line) and the conventional (C_{mng}, dashed line) systems. Means (n = 3) with the * are statistically different ($p \leq 0.05$).



Classes of carbon substrates	S_{mng} *AWCD*	S_{mng} SD	C_{mng} *AWCD*	C_{mng} SD
Polysaccharides and complex compounds	0.913	0.130	1.020	0.156
Cellulose	0.797	0.212	0.982	0.192
Hemicellulose	0.733	0.167	0.636	0.084
Chitin	0.940	0.338	1.217	0.091
Phosphorylated compounds	0.371	0.294	0.463	0.196
Organic acids	0.638	0.113	0.797	0.096
Amino acids	0.810	0.130	1.008	0.110
Biogenic amines	0.287	0.145	0.400	0.130