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Evaluation of the possible persistence of potential human pathogenic bacteria in olive orchards irrigated with treated urban wastewater

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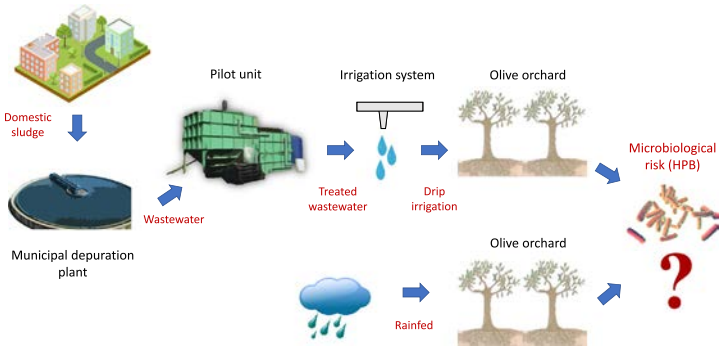
HIGHLIGHTS

- Treated urban wastewater (TWW) can contain human pathogenic bacteria (HPB).
- A TWW-irrigated (*WW*tr) and a rainfed (*RF*tr) olive orchard were compared.
- 16S-rRNA-microbiological analyses on soil, xylem sap, and phyllosphere were done.
- *WW*tr soil contained more potential HPB than xylem sap and phyllosphere.
- Urban TWW, if adequately-treated and applied, does not constitute health risks.

GRAPHICAL ABSTRACT



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ABSTRACT

Under suitable conditions, low-quality, treated urban wastewater (TWW) is an additional water resource for irrigation in water-scarce environments but its use in agriculture requires a careful monitoring of a range of hygiene parameters, including human pathogenic bacteria (HPB). DNA-based microbiological analyses on soil, xylem sap, and leaves surface (phyllosphere) were carried out in an olive (*Olea europaea* L.) grove located in Southern Italy (Basilicata region). The experimental grove has been managed in two plots for 18 years. The experimental plot (WW_{tr}) was drip irrigated daily with TWW (2800 m^3 ha^{-1} $year^{-1}$), while the control plot (RF_{tr}) was rainfed. The results of the 16S-rRNA-based metagenomic analysis demonstrated that the phyllosphere had the lowest number of potential HPB (6), compared to soil (22) and xylem (26) compartments. Gammaproteobacteria, including potential HPB, like *Pseudomonas* and *Acinetobacter* spp., were significantly higher in WW_{tr} soil and xylem sap, compared to RF_{tr}. A similar trend was observed for *Burkholderia* spp. (Betaproteobacteria) and *Mycobacterium* spp. (Actinobacteria). The Firmicutes *Enterococcus*, *Staphylococcus* and *Streptococcus* spp. were more abundant in WW_{tr} xylem sap. The pathogenic *Clostridium perfringens* was found higher on WW_{tr} leaves (relative abundance 7.17 in WW_{tr} and 1.33 in RF_{tr}) and *Enterococcus faecalis* in WW_{tr} xylem sap (93.22 in WW_{tr} and 7.08 in RF_{tr}). On the basis of the results obtained, the irrigation with TWW can be considered a realistic and safe agronomic practice in Mediterranean orchards, and an opportunity for farmers and consumers.

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1. Introduction

Olive trees (*Olea europaea* L.) represent one of the most important oil crops world-wide, which have characterized the Mediterranean landscape since ancient times. In 2018, on an area of 10.65 Mha, an amount of 19.27 Mt of olives was harvested world-wide (FAOSTAT, 2018). Considering the olive orchards are mainly located in areas characterized by water scarcity, the need for a sustainable approach in irrigation management has become evident in order to improve or maintain soil quality, health and fertility (Sofo et al., 2014; Pascazio et al., 2015). As a good example Bedbabis et al. (2015) successfully adopted treated urban wastewater (TWW) for irrigating olive trees grown under a semi-arid climate, so obtaining several benefits in terms of increased yield and soil organic matter, and faster olive ripening, with consequent high levels of phenols, tocopherols and pigments in fruits. Thus, under suitable conditions, TWW can be an additional water resource in agriculture.

On the other side, the use of TWW can cause an increase in the genetic and functional and metabolic diversity of soil bacterial communities, as demonstrated by Becerra-Castro et al. (2015) and Lüneberg et al. (2018), and more specifically in olive groves by Sofo et al. (2010), with evident benefits to soil quality and crop production. On the other hand, the adoption of WW_{tr} in agriculture requires a careful monitoring of a range of hygiene parameters, including the presence of potential human pathogenic bacteria (HPB) (Palese et al., 2009; Becerra-Castro et al., 2015). The advantages of using TWW for irrigation has been extensively studied in olive groves but not always the potential consequences for public health and environmental quality have been taken into account (Qadir et al., 2010; Courault et al., 2017). In leafy green production, the use of irrigation water deriving from drainage ditches causes significantly increases in *E. coli* (Allende et al., 2018). In soils irrigated with untreated urban WW, HPB can be a serious threat, as recently pointed out by Lüneberg et al. (2018), who found soil contaminations of potentially active and harmful *Acinetobacter*, *Bacillus* and *Nocardia* spp.

Palese et al. (2009) already studied the effects of TWW on the microbiological quality of soil and olive fruits adopting a traditional culture-based method. Here, in the same system, we adopted a metagenomic analysis based on 16S-rRNA gene sequencing with the aim of identifying potential HPB in soil, xylem sap and leaf surface (phyllosphere), that might be a source of fruit contamination and a health risk for the population. On the basis of other authors' work and point of view, previous research from our research group, and original data, we here present our opinions on this argument, based on experimental data.

2. Materials and methods

2.1. Experimental site and olive grove management

The trial was carried out in a 2-ha mature olive grove (*Olea europaea* L., cv. 'Maiatica'; plants with an age of approximately 70 years, trained to vase at 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, annual precipitation of 565 mm (mean 1995–2015), falling mostly in the winter, and mean annual temperature ranging from 15 to 17 °C.

In the experimental plot (WW_{tr}), olive plants were drip-irrigated from March to October (2800 m^3 ha^{-1} $year^{-1}$) with TWW. Six drip emitters discharging 8 L h^{-1} over a 1-m radius were placed for each plant. The distribution pipes and emitters were placed 1.5 m above the ground, in order to facilitate soil tillage. A pilot unit (Fig. S1) was used to treat urban wastewater (about 50 m^3 day^{-1}) according to the simplified scheme described in Palese et al. (2009). In brief, sewer water was collected in the municipal depuration plant, that included grilling, desalting, primary sedimentation, biological oxidation with activated sludge, denitrification, and secondary sedimentation. Successively, wastewater was pumped to the pilot unit taking it from three different points of the depuration plant (sewer water, water before the denitrification unit, and water from the final sedimentation plant, at a proportion of 1:2:2, v/v). Here, it was subjected to clariflocculation, further sedimentation and bland disinfection with peracetic acid 2.5 mg L^{-1} for 60 min. The scheme partially excluded the biological processes for the removal of organic carbon (C) and nitrogen (N) from the wastewater, in order to recover them and use them as fertilizing substances. The flow squeeze from the pre-denitrification unit allowed to use water subjected to a reduction of only the rapidly biodegradable organic matter fraction, that is often cause of soil anoxic conditions. In WW_{tr}, the average annual amounts of organic C, N, P and K distributed by the treated wastewater were 124, 54, 3 and 50 kg ha^{-1} $year^{-1}$, respectively (mean 2000–2016). An integrative amount of 40 kg ha^{-1} of N-NO_3^- per year was distributed by fertigation during fruit set and pit hardening phase, in order to entirely satisfy olive nutrient needs. The composition of TWW is shown in Table 1. According to earlier published data (Palese et al., 2009) obtained using culture-based techniques, *Escherichia coli* concentration in the TWW varied considerably from 0 to 78,000 CFU 100 mL^{-1}, *Salmonella* was never detected in the TWW, and variable levels of enterococci (from 0 to 28,000 CFU 100 mL^{-1}) and sulphite-reducing *Clostridium* spores (from 10 to 31,000 CFU 100 mL^{-1}) were observed.

An adjacent plot, characterized by soil and trees having similar features, was taken as control. This plot was naturally rainfed (RF_{tr}) (about 35 m^3 water $plant^{-1}$ $year^{-1}$) and a mineral fertilization was carried out once per year, during fruit set and pit hardening phase, using ternary compounds (NPK 20-10-10 fertilizer at doses ranging from 300 to 500 kg ha^{-1} $year^{-1}$; mean 2000–2016).

2.2. Soil and plant tissue sampling

In May 2017, soil sub-samples for both the treatments (WW_{tr} and RF_{tr}) were picked at 0–30 cm depth in ten different points around (over a 1-m radius) each plant ($n = 3$, three plants per plot) and pooled on site to constitute a composite soil sample of about 2 kg. In order to avoid border interferences, plants located in the central part of each plot and far 24 m each other were randomly chosen. Three composite soil samples ($n = 3$) for each treatment were collected and stored at −20 °C for DNA extraction.

Leaves were collected for both WW_{tr} and RF_{tr}. For each treatment, three composite leaf samples were randomly collected in the upper part of the canopy using sterile gloves and equipment from the same plants used for collecting the soil. The same plants used for collecting the soil were selected. Leaf samples were stored immediately at 4 °C in sterile plastic bags and brought to the laboratory, where they were stored at −20 °C without any further processing. Bacteria from the phyllosphere were desorbed from a mix of 50 leaves per plant by the method of Redford and Fierer (2009). Leaves were washed with 50 mL of detergent solution (Tris-HCl 20 mM, EDTA 10 mM and Triton

Table 1
Chemical parameters (±standard error) of the treated urban wastewater applied in the olive orchard ($n = 10$, one per month). Period of sampling: March–October 2016 and March–May 2017. COD: chemical oxygen demand.

Parameter	Unit of measure	Value
pH	–	7.6 ± 0.3
Conductivity	(μS cm^{-1})	884.0 ± 43.4
Organic C	(mg L^{-1})	20.4 ± 5.5
N (NO_3^- + NH_4^+)	(mg L^{-1})	18.3 ± 4.7
Na	(mg L^{-1})	121.3 ± 32.1
Mg	(mg L^{-1})	13.8 ± 2.5
Ca	(mg L^{-1})	67.8 ± 8.1
B	(mg L^{-1})	0.7 ± 0.1
K	(mg L^{-1})	17.2 ± 3.6
P	(mg L^{-1})	1.4 ± 0.4
COD	(mg L^{-1})	180.4 ± 29.0

0.024) by mechanical agitation at 100 rpm for 15 min on a rotary shaker (Thomas Scientific, Inc., Swedesboro NJ, USA). The washing solution was centrifuged at 5000 ×*g* for 10 min at 4 °C, the supernatant was discarded, and the resulting pellet was air dried for 2 h under laminar flow fan and then stored at −20 °C.

The xylem sap was extracted from shoots of olive trees of both WW_{tr} and RF_{tr} using Scholander-type hand-made chambers pressurized with N_2 (Fig. S2). The same plants used for collecting the soil and the leaves were selected. Two shoots, approximately 15–20 cm in length, were taken from each of the four cardinal points per plant using sterile cutting shears and a pool of plant material was collected, put in plastic bags, transported to the laboratory, and stored under at −20 °C before the use. For each shoot, a 1-cm wide bark strip was removed in the proximal part with a sharp knife sterilized with 75% ethanol in order to exclude the phloem sap and to prevent external contamination. The cut end of the stem was placed, through the hole with a gasket, in the Scholander pressure chamber lid with approximately 3 cm of the cut end facing out; this part of the stem was connected to a thin plastic tube through which the liquid was let flow into a 1.5-mL microcentrifuge tube. The foliage of the shoot was placed in the pressure chamber and the lid was locked down. The foliage of the cutting was placed in the pressure chamber. High pressure was applied (approximately from 50 to 70 bar) to force xylem sap from the tissue at the proximal end of the cutting. After, discarding the first drops, xylem sap was collected into 1.5-mL microcentrifuge tubes (the procedure took about 15–20 min per shoot) and stored at −20 °C before analysis.

2.3. DNA extraction

Total bacterial DNA was extracted from 0.5 g of each soil and phyllosphere pellet sample according to the protocol of the FastDNA® SPIN Kit for soil in combination with the Thermo Savant FastPrep® System homogenizer (MP Biomedicals LLC, Cleveland, OH, USA). Sap samples were centrifuged at 12,000 ×*g* for 10 min at 4 °C. The pellet and the respective supernatant were stored at −20 °C separately. The pellet was used for total DNA extraction using the "DNeasy Blood Tissue" Qiagen kit.

The quality and concentration of DNA extracts were determined at 260, 280 and 230 nm using a NanoDrop®ND-1000 UV–Vis spectrophotometer (Thermo Fisher Scientific, Inc., Waltham, MA, USA). The fragmentation of the DNA was checked by agarose gel electrophoresis (0.7% w/v agarose-0.5× Tris-Borate-EDTA) and UV visualization of the gels stained with Gel RedTM (Biotium, Inc., Hayward, CA, USA).

2.4. Library preparation, sequencing and bioinformatics analysis

DNA samples isolated from soil, phyllosphere and xylem sap were characterized up to the species level of bacterial communities. Two amplification steps in the library workflow were performed: an initial PCR amplification using locus specific 16S PCR primers and a subsequent amplification that integrated relevant Illumina flow-cell binding domains and unique indices (NexteraXT Index Kit, FC-131-1001/FC-131-1002). In particular, the variable V3 and V4 regions of the 16S rRNA gene were amplified to determine bacterial community compositions. For the 16S locus, the target sequences were those reported by Klindworth et al. (2013). Libraries were sequenced in a MiSeq run in paired end with 300-bp reads producing about 100,000 sequences per sample by IGA Technology Services S.r.l. (Udine, Italy).

The bioinformatic pipeline QIIME2 (https://view.qiime2.org/) was used to process and analyze the obtained 16S amplicon sequences. The preliminary processing of the data included de-multiplexing and quality filtering with a minimum length of 200 bp. Following the QIIME2, the USEARCH algorithm (version 8.1.1756) allowed to perform the following steps: chimera filtering, grouping of replicate sequences, sorting sequences per decreasing abundance and operational taxonomical units (OTUs) identification. For OTUs' picking, the open reference protocol was used. Reads were aligned against reference database, a modified version of GreenGene (version 2013_8). Only matches with a minimum identity of 94% were retained and clustered representing the centroid. Query sequences not sharing similarity with the centroid constituted a novel OTU and the most abundant and long reads in each OTU were selected as representative sequences. In this step, the clustering threshold was set at 97% and OTUs were generated with a minimum of two sequenced fragments. The RDP classifier and GreenGene database were used to assign taxonomy with a minimum confidence threshold of 0.50. Rarefaction curves end-points and normalization of counts for diversity analysis were set to 50% of the target sequencing coverage. Due to different size of the samples, a cutoff of 20,000 high-quality reads was selected. Samples not satisfying the count threshold were not included in standard alpha-and beta-diversity estimators. The total count was retained for taxonomic abundances estimation and used accordingly for ad-hoc statistical testing of

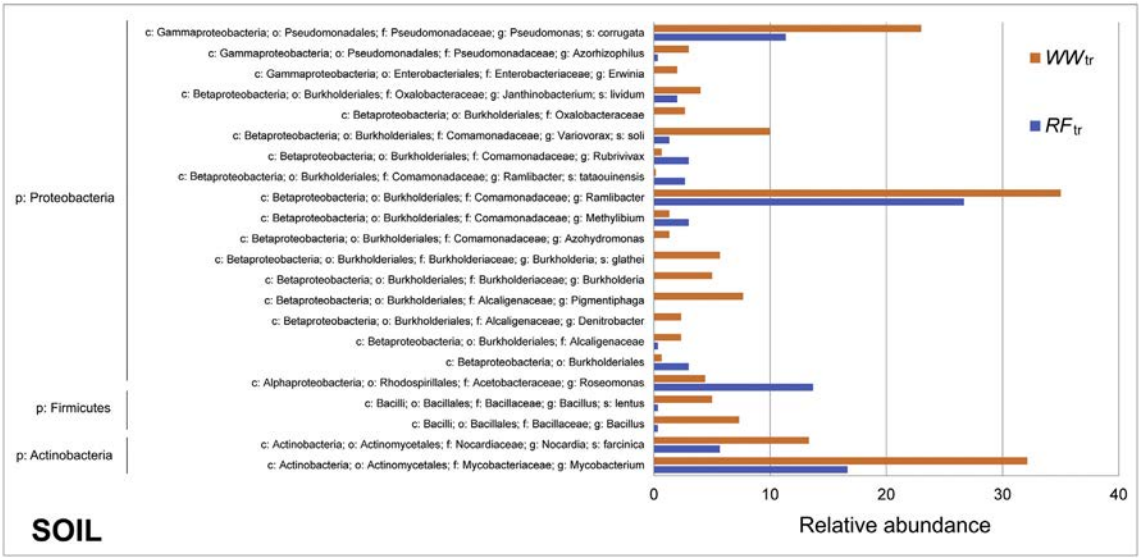

Fig. 1. Relative abundances of the bacterial operational taxonomical units (OTUs) of potential human pathogenic bacteria (HPB) that were statistically different in soils of the olive orchard irrigated with treated urban wastewater (WW_{tr}) and the rainfed olive orchard (RF_{tr}). Only the OTUs with a statistical difference ($p < 0.05$) between WW_{tr} and RF_{tr} were considered. p, phylum; c, class; o, order; f, family; g, genus; s, species.

taxonomic abundance. Overall raw results of the analysis are presented in Tables S1–S3.

The potential HPB were chosen on the basis of the 'Inventory list of human pathogenic microorganisms in plant production systems' (https://docs.google.com/spreadsheets/d/13qDivF5Hi8GrhTWalubfd18NVlFINAwENbVTMSbxwls/edit?usp=sharing) (COST HUPLANT control, 2018) and of the bibliography consulted (see References section). Only the HPBMs with an abundance significantly different at $p < 0.05$ between WW_{tr} and RF_{tr} were reported.

3. Results and discussion

The metagenomic analysis (showed in Fig. 1 for soil, and in Fig. 2A, B for xylem sap and phyllosphere, respectively) revealed statistically higher abundance ($p < 0.05$) of some potential HPB belonging to the phyla Actinobacteria, Firmicutes and Proteobacteria in the soil and xylem sap, and to Firmicutes and Proteobacteria in the phyllosphere. Leaf surface had the lowest number of potential HPB (6), compared to soil (22) and xylem (26) compartments. This suggests that olive phyllosphere, more subjected to environmental variables and also for this reason far for having constant conditions (Whipps et al., 2008), is not a habitat suitable for HPB, whereas xylem, being more stable, could be a reservoir of HPB. The richness in HPB in soil is surely due to the fact that most of the wastewater ends up directly in the soil and only a minimal part to the canopy by aerosol (drip emitters are 1.5-m high and canopy tops are on average 4.5 m high; Fig. S3). Thus, roots are the main entrance to the xylem for microorganisms and so the transmission of bacteria to the phyllosphere is internal. On the other side, this could also likely be due to the fact that the colonization of internal tissues normally occurs from the soil to aerial plant parts through xylem vessels but also vice versa through the stomata (Compant et al., 2005), making xylem a compartment with a higher microbial diversity.

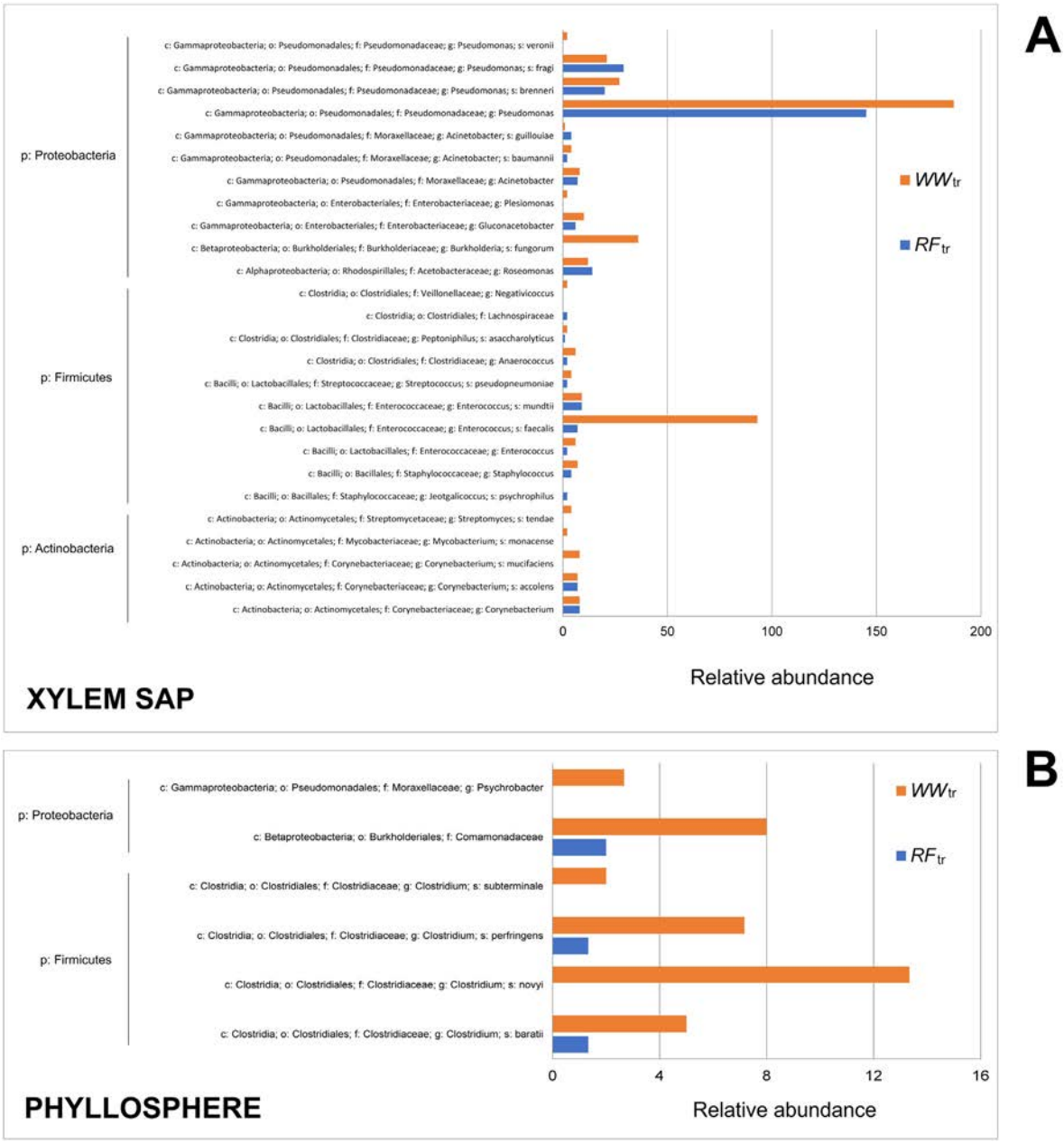

Fig. 2. Relative abundances of the bacterial operational taxonomical units (OTUs) that were statistically different in (A) the xylem sap and (B) phyllosphere (leaf surface) of olive plants irrigated with treated urban wastewater (WW_{tr}) or rainfed (RF_{tr}). Only the OTUs with a statistical difference ($p < 0.05$) between WW_{tr} and RF_{tr} were considered. p, phylum; c, class; o, order; f, family; g, genus; s, species.

This is particularly true for Firmicutes, where at the class level xylem sap contained both Bacilli and Clostridia, the former likely coming from the soil and the latter from the phyllosphere.

Gammaproteobacteria, including potential pathogenic like *Pseudomonas* and *Acinetobacter* spp., were found significantly higher in WW_{tr} soil and xylem sap. Among Betaproteobacteria, Burkhorderiales order was over-represented in WW_{tr}, with the presence of OTUs (2 in soil and 1 in xylem sap) belonging to *Burkholderia* spp., a genus potentially pathogenic for humans (Becerra-Castro et al., 2015). Among Firmicutes, *Enterococcus*, *Staphylococcus* and *Streptococcus* spp. (3, 1 and 1 OTUs, respectively) were found to be significantly higher in WW_{tr} xylem sap. These latter groups probably came from the soil, where they found harshest conditions compared to xylem and have a high competition with other microorganisms (Lakshmanan et al., 2014), so being not detected here. *Mycobacterium* spp., belonging to Actinobacteria, were more abundant in both WW_{tr} soil and xylem sap. Regarding the certain and harmful HPB, *Clostridium perfringens* was found higher on WW_{tr} leaves (relative abundance 7.17 in WW_{tr} and 1.33 in RF_{tr}) and *Enterococcus faecalis* more abundant in WW_{tr} xylem sap (93.22 in WW_{tr} and 7.08 in RF_{tr}). Considering the strict relationship between leaf surface (phyllosphere) and fruit surface (carposphere) (examined in olive by Pascazio et al., 2015) and the close contact between xylem sap and fruit pulp, the presence of these two HPB could be taken into account for TWW irrigation practices.

In conclusion, the results confirmed that, excepting for two cases (*Clostridium* and *Enterococcus*) that should be ascertained with more sampling throughout the year and in different years, fertigation with urban TWW did not cause a substantial and significant increase in HPB. In the same system, Palese et al. (2009) found *Escherichia coli*, *Enterococcus* spp. and *Clostridium* spp. in the TWW used but not in topsoil (10-cm depth). The same authors did not detect any microbial contamination on olive fruits harvested directly from the canopy. Considering a) the discontinuity of the urban TWW composition and distribution, often concentrated in the hot and dry period (Becerra-Castro et al., 2015), b) the culture-based data previously obtained by Palese et al. (2009) in olive, c) the fact that in a DNA-based analysis we have data on bacterial presence more than on vitality and persistence, as recently reviewed by Morgan et al. (2017) in TWW-irrigated grapevine, and d) taking into account the HPB mortality and inactivation due to soil resilience and competition with endogenous bacteria (Whipps et al., 2008; Lakshmanan et al., 2014), we can assert that the irrigation with adequately-treated and applied urban wastewater can be considered a realistic and safe agronomic practice in Mediterranean orchards, and an opportunity for farmers and consumers.

Author contributions

AS conceived the conceptual idea for the study. CX, BD and CC designed the study, and CF and MS carried out the field work. ANM, CF and AS carried out the data analysis with help from MS and CC. The first draft of the manuscript was written by AS, with all authors contributing substantially to revisions.

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Conflict of interest statement

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.scitotenv.2018.12.264.

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Supplementary Table 1. Relative abundances of the bacterial operational taxonomical units (OTUs) that were statistically different in soils of the olive orchard irrigated with treated urban wastewater (WW_{tr}) and the rainfed olive orchard (RF_{tr}). Only the OTUs with a statistical difference ($p < 0.05$) between WW_{tr} and RF_{tr} were considered. k, kingdom; p, phylum; c, class; o, order; f, family; g, genus; s, species.

SOIL

OTU ID	*p* level	Relative abundance		Taxonomic group
		WW_{tr}	RF_{tr}	
EF516597.1	0.0253	1.00	0.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
HQ844545.1	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylocystaceae; g: Methylosinus
AB240329.1	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
JQ655798.1	0.0253	3.00	0.00	k: Bacteria; p: Acidobacteria; c: Acidobacteria; o: Acidobacteriales; f: Koribacteraceae; g: Candidatus Koribacter
JF181356.1	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
AM941213.2	0.0253	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
HQ597923.1	0.0253	1.00	0.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.ReferenceOTU65	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Devosia
New.ReferenceOTU29	0.0253	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Olivibacter; s: soli
New.CleanUp.ReferenceOTU66	0.0253	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Segetibacter
New.CleanUp.ReferenceOTU634	0.0253	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU2429	0.0253	0.00	1.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera
New.CleanUp.ReferenceOTU4188	0.0253	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae
New.CleanUp.ReferenceOTU5145	0.0253	0.00	1.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU5541	0.0253	0.00	1.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
New.CleanUp.ReferenceOTU5679	0.0253	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Microlunatus
New.CleanUp.ReferenceOTU9350	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU14286	0.0253	1.00	0.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU16147	0.0253	1.00	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU18925	0.0253	1.00	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU21213	0.0253	1.00	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU21366	0.0253	0.00	2.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU23047	0.0253	0.00	1.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU23469	0.0253	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU24937	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae
New.CleanUp.ReferenceOTU25112	0.0253	0.00	1.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae; g: Chondromyces
New.CleanUp.ReferenceOTU25350	0.0253	0.00	1.00	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU26743	0.0253	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Catellatospora
New.CleanUp.ReferenceOTU28757	0.0253	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
New.CleanUp.ReferenceOTU29438	0.0253	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
NR_025797.1	0.0339	2.33	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Agromyces; s: salentinus
HM835307.1	0.0339	2.33	0.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Solibacillus
DQ490438.1	0.0339	16.33	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
JF417842.1	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
HM319694.1	0.0339	1.00	2.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Dyadobacter
GQ418041.1	0.0339	7.67	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae; g: Pigmentiphaga
GQ402805.1	0.0339	0.00	2.67	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
AB425063.1	0.0339	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Brevundimonas
EU881291.1	0.0339	0.00	1.67	k: Bacteria; p: Acidobacteria; c: Acidobacteria; o: Acidobacteriales; f: Koribacteraceae; g: Candidatus Koribacter
EF540401.1	0.0339	0.00	3.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium
HQ386386.1	0.0339	0.00	2.33	k: Bacteria; p: Cyanobacteria; c: Nostocophycideae; o: Nostocales; f: Nostocaceae; g: Nostoc
HM156138.1	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
JF178945.1	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
FM882233.1	0.0339	0.00	2.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
JF185563.1	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Thermomonas
NR_027534.1	0.0339	0.00	2.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s: tataouinensis
CP000301.1	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: pachyrhizi
AY328705.1	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Phaeospirillum; s: fulvum
JF041026.1	0.0339	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: wittichii
EU022308.1	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Mesorhizobium
DQ297946.1	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Novosphingobium
JF084320.1	0.0339	0.00	1.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.ReferenceOTU67	0.0339	11.33	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.ReferenceOTU47	0.0339	0.00	2.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.ReferenceOTU46	0.0339	1.33	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Methylibium
New.CleanUp.ReferenceOTU0	0.0339	0.00	2.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU458	0.0339	3.00	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU820	0.0339	2.00	0.00	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.CleanUp.ReferenceOTU1412	0.0339	4.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU2048	0.0339	2.00	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU2101	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
New.CleanUp.ReferenceOTU2291	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Azospirillum
New.CleanUp.ReferenceOTU2580	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Virgisporangium; s: ochraceum
New.CleanUp.ReferenceOTU3110	0.0339	0.00	1.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
New.CleanUp.ReferenceOTU3563	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Inquilinus; s: limosus
New.CleanUp.ReferenceOTU4185	0.0339	2.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU5653	0.0339	0.00	3.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae
New.CleanUp.ReferenceOTU5786	0.0339	0.00	1.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU5800	0.0339	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Myxococcaceae; g: Anaeromyxobacter
New.CleanUp.ReferenceOTU5993	0.0339	1.33	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
New.CleanUp.ReferenceOTU6160	0.0339	0.00	2.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU6630	0.0339	1.33	0.00	k: Bacteria; p: Chloroflexi; c: Chloroflexi; o: Roseiflexales; f: Kouleothrixaceae; g: Kouleothrix
New.CleanUp.ReferenceOTU6979	0.0339	0.00	1.67	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU7039	0.0339	0.00	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
New.CleanUp.ReferenceOTU7098	0.0339	0.00	5.33	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s: aurantiaca
New.CleanUp.ReferenceOTU7342	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
New.CleanUp.ReferenceOTU7515	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
New.CleanUp.ReferenceOTU8127	0.0339	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
New.CleanUp.ReferenceOTU8957	0.0339	0.00	2.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU9846	0.0339	0.00	1.67	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia
New.CleanUp.ReferenceOTU10065	0.0339	1.67	0.00	k: Bacteria; p: Verrucomicrobia; c: Opitutae; o: Opitutales; f: Opitutaceae; g: Opitutus
New.CleanUp.ReferenceOTU10543	0.0339	0.00	1.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU10898	0.0339	0.00	2.00	k: Bacteria; p: Cyanobacteria; c: Synechococcophycideae; o: Synechococcales; f: Acaryochloridaceae; g: Acaryochloris
New.CleanUp.ReferenceOTU11935	0.0339	0.00	1.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU11986	0.0339	0.00	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU12181	0.0339	0.00	1.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter
New.CleanUp.ReferenceOTU12688	0.0339	1.33	0.00	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia
New.CleanUp.ReferenceOTU13500	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Chelatococcus; s: daeguensis
New.CleanUp.ReferenceOTU14373	0.0339	0.00	5.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU14620	0.0339	0.67	2.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU15025	0.0339	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria
New.CleanUp.ReferenceOTU15050	0.0339	2.67	1.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.CleanUp.ReferenceOTU15222	0.0339	0.00	5.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU15324	0.0339	0.67	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU15403	0.0339	0.00	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
New.CleanUp.ReferenceOTU15926	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae
New.CleanUp.ReferenceOTU15967	0.0339	0.00	2.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.CleanUp.ReferenceOTU16034	0.0339	1.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU16112	0.0339	1.33	0.00	k: Bacteria; p: Firmicutes; c: Erysipelotrichi; o: Erysipelotrichales; f: Coprobacillaceae; g: Coprobacillus; s: cateniformis
New.CleanUp.ReferenceOTU16421	0.0339	0.67	3.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU16902	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
New.CleanUp.ReferenceOTU17433	0.0339	2.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Coxiellaceae; g: Aquicella
New.CleanUp.ReferenceOTU17797	0.0339	0.00	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU18018	0.0339	1.33	0.00	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia
New.CleanUp.ReferenceOTU18922	0.0339	1.00	2.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU19070	0.0339	3.00	1.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU19328	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Cystobacteraceae; g: Cystobacter
New.CleanUp.ReferenceOTU19624	0.0339	1.33	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Thermomonosporaceae; g: Actinomadura
New.CleanUp.ReferenceOTU21331	0.0339	1.67	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Chitinophaga
New.CleanUp.ReferenceOTU21837	0.0339	0.00	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU22087	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU22662	0.0339	3.00	5.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU22815	0.0339	0.00	1.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU23130	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU23426	0.0339	1.67	0.00	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Flavobacterium
New.CleanUp.ReferenceOTU23694	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales

New.CleanUp.ReferenceOTU23915	0.0339	2.67	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU23948	0.0339	0.00	1.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU24204	0.0339	0.00	1.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU24460	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU24989	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU26383	0.0339	2.00	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU27178	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Caulobacter
New.CleanUp.ReferenceOTU27609	0.0339	0.33	2.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU27701	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.CleanUp.ReferenceOTU28302	0.0339	1.33	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU28479	0.0339	2.33	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae; g: Denitrobacter
New.CleanUp.ReferenceOTU28606	0.0339	2.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Amaricoccus
New.CleanUp.ReferenceOTU28898	0.0339	1.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae
New.CleanUp.ReferenceOTU29415	0.0339	1.00	3.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU29484	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU29864	0.0339	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Azohydromonas
New.CleanUp.ReferenceOTU29935	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae
New.CleanUp.ReferenceOTU30507	0.0339	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Beijerinckia
New.CleanUp.ReferenceOTU30512	0.0339	1.33	0.00	k: Bacteria; p: Tenericutes; c: Mollicutes; o: Anaeroplasmatales; f: Anaeroplasmataceae; g: Asteroleplasma
HM329116.1	0.0369	2.33	0.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
FJ592871.1	0.0369	0.00	6.33	k: Bacteria; p: Cyanobacteria; c: Nostocophycideae; o: Nostocales; f: Nostocaceae; g: Nostoc
FN662904.1	0.0369	4.33	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
JF135666.1	0.0369	0.00	6.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
JQ798496.1	0.0369	0.00	4.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Promicromonosporaceae; g: Promicromonospora
JF081353.1	0.0369	0.00	2.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
GQ264384.1	0.0369	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Hyphomicrobium
JF079373.1	0.0369	8.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Thermomonas
DQ532142.1	0.0369	0.00	4.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium
DQ125771.1	0.0369	3.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Salinibacterium
AF237815.1	0.0369	2.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Actinopolymorpha; s: singaporensis
HM309204.1	0.0369	2.67	0.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
FJ889351.1	0.0369	11.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Rhodanobacter
GQ261279.1	0.0369	0.00	4.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Pontibacter
HM814595.1	0.0369	8.67	0.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
FJ895033.1	0.0369	2.00	4.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Janthinobacterium; s: lividum
HQ397161.1	0.0369	2.00	6.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
HM340458.1	0.0369	0.00	2.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Enterobacteriales; f: Enterobacteriaceae; g: Erwinia
AJ581625.1	0.0369	0.00	2.33	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.ReferenceOTU42	0.0369	0.00	22.33	k: Bacteria; p: Cyanobacteria; c: Oscillatoriophycideae; o: Chroococcales; f: Phormidiaceae; g: Microcoleus; s: vaginatus
New.CleanUp.ReferenceOTU1875	0.0369	2.67	0.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU1887	0.0369	5.67	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Burkholderiaceae; g: Burkholderia; s: glathei
New.CleanUp.ReferenceOTU1934	0.0369	0.00	2.33	k: Bacteria; p: Tenericutes; c: Mollicutes; o: Anaeroplasmatales; f: Anaeroplasmataceae; g: Asteroleplasma
New.CleanUp.ReferenceOTU4290	0.0369	0.00	2.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU5424	0.0369	0.00	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae
New.CleanUp.ReferenceOTU5438	0.0369	0.00	3.00	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU5674	0.0369	0.00	2.33	k: Bacteria; p: Chloroflexi; c: Chloroflexi; o: Chloroflexales; f: Oscillochloridaceae; g: Oscillochloris; s: trichoides
New.CleanUp.ReferenceOTU7226	0.0369	0.00	2.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU7366	0.0369	0.00	2.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU7783	0.0369	0.00	3.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas; s: aurantiaca
New.CleanUp.ReferenceOTU7959	0.0369	3.00	0.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Alicyclobacillaceae; g: Alicyclobacillus
New.CleanUp.ReferenceOTU8114	0.0369	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Xylella
New.CleanUp.ReferenceOTU8161	0.0369	0.00	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s: rhombi
New.CleanUp.ReferenceOTU8205	0.0369	10.00	0.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales
New.CleanUp.ReferenceOTU8771	0.0369	7.33	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU8828	0.0369	2.67	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU9134	0.0369	22.67	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s: aerolata
New.CleanUp.ReferenceOTU9437	0.0369	10.33	3.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU10093	0.0369	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter
New.CleanUp.ReferenceOTU12008	0.0369	0.00	2.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Cystobacteraceae; g: Cystobacter
New.CleanUp.ReferenceOTU13063	0.0369	5.67	0.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU13100	0.0369	0.00	3.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Coxiellaceae; g: Aquicella
New.CleanUp.ReferenceOTU13253	0.0369	2.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Phyllobacterium
New.CleanUp.ReferenceOTU13292	0.0369	0.00	3.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU13770	0.0369	3.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Hyphomicrobium; s: vulgare
New.CleanUp.ReferenceOTU14068	0.0369	0.00	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
New.CleanUp.ReferenceOTU15201	0.0369	2.67	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae
New.CleanUp.ReferenceOTU16050	0.0369	0.00	3.00	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU16252	0.0369	2.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
New.CleanUp.ReferenceOTU17017	0.0369	5.00	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Burkholderiaceae; g: Burkholderia
New.CleanUp.ReferenceOTU17899	0.0369	0.00	2.33	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.CleanUp.ReferenceOTU18603	0.0369	0.00	4.00	k: Bacteria; p: Armatimonadetes; c: Chthonomonadetes; o: Chthonomonadales; f: Chthonomonadaceae; g: Chthonomonas
New.CleanUp.ReferenceOTU19122	0.0369	3.00	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU19235	0.0369	5.67	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.CleanUp.ReferenceOTU19421	0.0369	6.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.CleanUp.ReferenceOTU19561	0.0369	13.33	0.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niastella
New.CleanUp.ReferenceOTU20810	0.0369	10.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU21693	0.0369	2.67	0.00	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia
New.CleanUp.ReferenceOTU22216	0.0369	1.00	7.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU23081	0.0369	4.33	0.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU24409	0.0369	11.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s: aerolata
New.CleanUp.ReferenceOTU24590	0.0369	2.67	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Legionellaceae; g: Legionella
New.CleanUp.ReferenceOTU27880	0.0369	6.00	2.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.CleanUp.ReferenceOTU28834	0.0369	0.00	2.00	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
FN811231.1	0.0431	1.67	8.67	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
AY328628.1	0.0431	3.33	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
FJ490527.1	0.0431	7.33	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia; s: kongjuensis
EF516512.1	0.0431	29.33	17.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
FJ625382.1	0.0431	2.67	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HM269222.1	0.0431	3.67	1.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
DQ017944.1	0.0431	2.33	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HM270504.1	0.0431	2.67	0.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Actinomycetospora
HM839194.1	0.0431	2.33	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Brevibacillus; s: brevis
FJ820400.1	0.0431	0.67	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Rubrivivax
HM267225.1	0.0431	5.67	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
JF049227.1	0.0431	2.33	6.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
JF224943.1	0.0431	0.33	2.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Salinibacterium
HM844564.1	0.0431	14.00	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
JF232065.1	0.0431	0.67	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Phenylobacterium
AF423289.1	0.0431	1.33	6.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
AJ311174.1	0.0431	0.33	3.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Actinosynnemataceae; g: Kibdelosporangium
NZ_ABVL01000001.1	0.0431	4.67	0.67	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter
FJ152869.1	0.0431	3.00	0.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
New.ReferenceOTU156	0.0431	1.33	5.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.ReferenceOTU85	0.0431	8.33	16.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.ReferenceOTU106	0.0431	1.00	5.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU1288	0.0431	0.67	2.67	k: Bacteria; p: Verrucomicrobia; c: Opitutae; o: Opitutales; f: Opitutaceae; g: Opitutus
New.CleanUp.ReferenceOTU1436	0.0431	3.67	8.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU1468	0.0431	1.33	4.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU1972	0.0431	6.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
New.CleanUp.ReferenceOTU2154	0.0431	1.67	8.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU3315	0.0431	2.33	0.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Actinosynnemataceae; g: Actinokineospora
New.CleanUp.ReferenceOTU3503	0.0431	1.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae
New.CleanUp.ReferenceOTU4087	0.0431	3.33	12.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU4621	0.0431	0.33	2.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU6404	0.0431	1.67	4.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
New.CleanUp.ReferenceOTU6865	0.0431	9.00	2.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Candidatus Xiphinematobacter
New.CleanUp.ReferenceOTU7112	0.0431	4.33	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Erythrobacteraceae; g: Erythromicrobium
New.CleanUp.ReferenceOTU8349	0.0431	0.67	3.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU9074	0.0431	0.33	3.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU9276	0.0431	5.33	2.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Patulibacteraceae; g: Patulibacter; s: americanus
New.CleanUp.ReferenceOTU12374	0.0431	0.33	3.67	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU12424	0.0431	2.67	0.67	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s: amoebophila
New.CleanUp.ReferenceOTU14745	0.0431	4.33	1.33	k: Archaea; p: Crenarchaeota; c: Thaumarchaeota; o: Nitrososphaerales; f: Nitrososphaeraceae; g: Candidatus Nitrososphaera
New.CleanUp.ReferenceOTU17783	0.0431	0.33	4.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU18059	0.0431	3.00	11.67	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.CleanUp.ReferenceOTU18377	0.0431	0.33	3.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter

New.CleanUp.ReferenceOTU19435	0.0431	0.33	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter; s: tataouinensis
New.CleanUp.ReferenceOTU20390	0.0431	42.00	28.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Kribbella
New.CleanUp.ReferenceOTU20555	0.0431	0.67	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU22278	0.0431	4.67	0.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
New.CleanUp.ReferenceOTU23085	0.0431	0.67	3.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU23165	0.0431	3.00	6.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae; g: Chondromyces; s: crocatus
New.CleanUp.ReferenceOTU24324	0.0431	0.67	3.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU24920	0.0431	0.33	2.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingobium
New.CleanUp.ReferenceOTU25397	0.0431	3.33	0.33	k: Bacteria; p: Chlamydiae; c: Chlamydiia; o: Chlamydiales; f: Parachlamydiaceae; g: Candidatus Protochlamydia; s: amoebophila
New.CleanUp.ReferenceOTU25551	0.0431	0.33	7.00	k: Bacteria; p: Verrucomicrobia; c: Verrucomicrobiae; o: Verrucomicrobiales; f: Verrucomicrobiaceae; g: Luteolibacter
New.CleanUp.ReferenceOTU25833	0.0431	0.67	5.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU25934	0.0431	0.33	3.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
New.CleanUp.ReferenceOTU26578	0.0431	0.33	2.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU26701	0.0431	0.67	2.33	k: Bacteria; p: Actinobacteria; c: Nitriliruptoria; o: Euzebyales; f: Euzebyaceae; g: Euzebya
New.CleanUp.ReferenceOTU26772	0.0431	0.33	3.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU27244	0.0431	0.67	2.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU27896	0.0431	2.33	0.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Alcaligenaceae
New.CleanUp.ReferenceOTU29757	0.0431	13.00	8.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU30004	0.0431	3.33	1.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niabella
New.CleanUp.ReferenceOTU30495	0.0431	0.33	3.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
HQ910327.1	0.0463	1.00	9.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium
DQ125578.1	0.0463	3.00	8.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
HM330580.1	0.0463	14.33	1.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
EU449609.1	0.0463	5.33	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
DQ304805.1	0.0463	2.67	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Inquilinus; s: limosus
JF178952.1	0.0463	5.00	0.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: glycanilyticus
EF050430.1	0.0463	45.33	26.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
L40612.1	0.0463	3.67	8.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Frankiaceae; g: Frankia
HQ132468.1	0.0463	3.67	9.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Micromonospora
JF180348.1	0.0463	5.00	1.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Pseudoxanthomonas
DQ129304.1	0.0463	1.00	7.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
DQ129585.1	0.0463	2.33	9.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
FR687520.1	0.0463	7.00	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
DQ248234.1	0.0463	6.00	22.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
AY395335.1	0.0463	7.33	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Microlunatus
HM274399.1	0.0463	6.67	12.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Actinoplanes
JF048456.1	0.0463	8.67	4.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter
HM328008.1	0.0463	0.67	8.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Yonghaparkia
HM334145.1	0.0463	7.33	26.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
EU335236.1	0.0463	6.33	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
AM935954.1	0.0463	4.00	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
JF123892.1	0.0463	9.67	18.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Catellatospora
HM277682.1	0.0463	5.33	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhodobiaceae; g: Afifella
AY328725.1	0.0463	1.67	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
HM274453.1	0.0463	6.00	13.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus
GQ396897.1	0.0463	7.67	14.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
HM269081.1	0.0463	14.33	3.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus
DQ125847.1	0.0463	5.33	8.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter
HQ114093.1	0.0463	1.33	6.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter
EU181492.1	0.0463	1.00	5.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
EU873545.1	0.0463	5.67	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: xanthophaeus
JQ428716.1	0.0463	2.67	11.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
AM935081.1	0.0463	13.33	5.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardiaceae; g: Nocardia; s: farcinica
DQ906897.1	0.0463	1.67	8.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas
JN023141.1	0.0463	0.33	3.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
JF145531.1	0.0463	11.00	5.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter
JQ861340.1	0.0463	3.00	7.33	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
DQ532236.1	0.0463	1.00	16.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium
HM459620.1	0.0463	11.67	1.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: agarexedens
AY395351.1	0.0463	42.00	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HM317272.1	0.0463	10.00	1.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Variovorax; s: soli
AF290484.1	0.0463	9.33	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Phyllobacterium
AM697325.1	0.0463	5.00	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
HM278456.1	0.0463	0.67	4.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae
FJ529981.1	0.0463	20.33	4.67	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Nitrosomonadales; f: Nitrosomonadaceae; g: Nitrosovibrio; s: tenuis
JF180336.1	0.0463	1.33	5.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Arenimonas
HM366507.1	0.0463	8.33	15.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s: obscurus
AJ582029.1	0.0463	12.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
EU335162.1	0.0463	6.00	13.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
HM278783.1	0.0463	1.67	9.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
FJ790625.1	0.0463	3.67	8.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas
JF077978.1	0.0463	1.33	15.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s: rhombi
JF211276.1	0.0463	18.33	27.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Iamiaceae; g: Iamia
AJ292612.1	0.0463	4.67	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: mesophilicum
FN436186.1	0.0463	0.33	3.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
JF178808.1	0.0463	5.00	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Bacillaceae; g: Bacillus; s: lentus
FN811266.1	0.0463	18.33	71.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
HM445223.1	0.0463	3.00	7.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
HM845753.1	0.0463	41.33	34.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
JF085268.1	0.0463	4.33	1.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Thermoactinomycetaceae; g: Shimazuella
HM241105.1	0.0463	5.67	0.33	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
JF203279.1	0.0463	1.00	3.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
HM339185.1	0.0463	2.33	8.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.ReferenceOTU2	0.0463	4.00	16.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.ReferenceOTU16	0.0463	1.67	7.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.ReferenceOTU89	0.0463	29.00	47.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Pedomicrobium
New.ReferenceOTU36	0.0463	1.00	6.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
New.CleanUp.ReferenceOTU98	0.0463	3.67	0.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Micromonospora
New.CleanUp.ReferenceOTU813	0.0463	26.67	10.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus
New.CleanUp.ReferenceOTU827	0.0463	0.67	3.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU2196	0.0463	12.33	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Acidisphaera
New.CleanUp.ReferenceOTU2273	0.0463	4.33	0.33	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Flavobacterium
New.CleanUp.ReferenceOTU2460	0.0463	3.67	9.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU2924	0.0463	4.67	12.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae
New.CleanUp.ReferenceOTU3038	0.0463	0.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Saccharopolyspora; s: erythraea
New.CleanUp.ReferenceOTU4559	0.0463	12.67	36.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas
New.CleanUp.ReferenceOTU4812	0.0463	1.33	13.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Xanthobacteraceae; g: Ancylobacter
New.CleanUp.ReferenceOTU5168	0.0463	10.00	0.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU5176	0.0463	0.67	5.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU5563	0.0463	1.67	7.67	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
New.CleanUp.ReferenceOTU6816	0.0463	4.33	9.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU7223	0.0463	0.67	11.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU7606	0.0463	3.00	0.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU8919	0.0463	0.33	5.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU9380	0.0463	11.00	2.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU9490	0.0463	2.33	9.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niastella
New.CleanUp.ReferenceOTU9758	0.0463	7.67	2.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera
New.CleanUp.ReferenceOTU10076	0.0463	11.00	0.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: sepulcri
New.CleanUp.ReferenceOTU10150	0.0463	7.33	0.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Bacillaceae; g: Bacillus
New.CleanUp.ReferenceOTU10465	0.0463	0.67	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales
New.CleanUp.ReferenceOTU10579	0.0463	3.33	8.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Entotheonellales; f: Entotheonellaceae; g: Candidatus Entotheonella
New.CleanUp.ReferenceOTU10965	0.0463	0.33	5.67	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU11047	0.0463	1.33	5.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Myxococcaceae; g: Myxococcus
New.CleanUp.ReferenceOTU11306	0.0463	0.33	3.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Azorhizophilus
New.CleanUp.ReferenceOTU11359	0.0463	16.67	9.67	k: Bacteria; p: Nitrospirae; c: Nitrospira; o: Nitrospirales; f: Nitrospiraceae; g: Nitrospira
New.CleanUp.ReferenceOTU11543	0.0463	4.67	1.00	k: Bacteria; p: Chloroflexi; c: Chloroflexi; o: Roseiflexales; f: Kouleothrixaceae; g: Kouleothrix
New.CleanUp.ReferenceOTU11728	0.0463	0.33	3.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU12425	0.0463	2.33	9.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU12575	0.0463	0.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU12732	0.0463	1.67	5.67	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.CleanUp.ReferenceOTU13106	0.0463	2.33	8.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Niastella
New.CleanUp.ReferenceOTU13277	0.0463	14.00	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Aeromicrobium
New.CleanUp.ReferenceOTU13476	0.0463	3.33	9.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Amaricoccus
New.CleanUp.ReferenceOTU14621	0.0463	1.33	4.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
New.CleanUp.ReferenceOTU14682	0.0463	1.33	5.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae
New.CleanUp.ReferenceOTU15383	0.0463	0.67	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae

New.CleanUp.ReferenceOTU15620	0.0463	4.33	11.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU16488	0.0463	2.33	6.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU17399	0.0463	0.67	3.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU18679	0.0463	1.00	3.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU18696	0.0463	7.67	3.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU19105	0.0463	8.67	14.33	k: Bacteria; p: Actinobacteria
New.CleanUp.ReferenceOTU19268	0.0463	0.33	4.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU20513	0.0463	3.67	9.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU22183	0.0463	1.33	4.67	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU22330	0.0463	2.33	9.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU22527	0.0463	5.33	11.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU23159	0.0463	7.00	20.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter; s: denitrificans
New.CleanUp.ReferenceOTU23463	0.0463	5.67	13.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU23513	0.0463	1.67	6.00	k: Bacteria; p: Acidobacteria; c: Solibacteres; o: Solibacterales; f: Solibacteraceae; g: Candidatus Solibacter
New.CleanUp.ReferenceOTU23541	0.0463	14.33	9.67	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Rhodocyclales; f: Rhodocyclaceae
New.CleanUp.ReferenceOTU24410	0.0463	0.33	7.33	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Flavobacterium; s: succinicans
New.CleanUp.ReferenceOTU24424	0.0463	5.33	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Catellatospora
New.CleanUp.ReferenceOTU24452	0.0463	1.00	8.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Haliangiaceae; g: Haliangium
New.CleanUp.ReferenceOTU24926	0.0463	5.33	11.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Erythrobacteraceae; g: Lutibacterium
New.CleanUp.ReferenceOTU24975	0.0463	15.33	6.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Intrasporangiaceae
New.CleanUp.ReferenceOTU26158	0.0463	0.67	3.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
New.CleanUp.ReferenceOTU27776	0.0463	0.33	3.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU27973	0.0463	4.33	14.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU28001	0.0463	1.00	9.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU28397	0.0463	4.33	8.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU28708	0.0463	7.33	13.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU28967	0.0463	1.67	8.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Nannocystaceae; g: Plesiocystis
New.CleanUp.ReferenceOTU29328	0.0463	1.67	13.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU29422	0.0463	12.67	6.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
New.CleanUp.ReferenceOTU29458	0.0463	3.33	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU30151	0.0463	1.00	10.00	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Cystobacteraceae; g: Cystobacter; s: fuscus
New.CleanUp.ReferenceOTU30192	0.0463	3.33	16.67	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Iamiaceae; g: Iamia
New.CleanUp.ReferenceOTU30330	0.0463	2.33	10.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU30553	0.0463	4.00	1.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
AB374371.1	0.0495	2.67	8.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhodobiaceae; g: Afifella
AJ292603.1	0.0495	452.00	193.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium; s: elkanii
AY395348.1	0.0495	109.67	58.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
AJ968702.1	0.0495	1.00	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
AY425763.1	0.0495	68.67	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HM269229.1	0.0495	10.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Microlunatus
JF021408.1	0.0495	7.00	16.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
EF516107.1	0.0495	9.67	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
FJ889257.1	0.0495	87.67	66.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Verrucosispora; s: gifhornensis
AB496412.1	0.0495	9.00	2.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
JF092073.1	0.0495	7.67	18.67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Alicyclobacillaceae; g: Alicyclobacillus
JF089694.1	0.0495	10.33	41.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
JF174754.1	0.0495	14.00	29.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Pseudonocardia
HM263278.1	0.0495	29.33	43.67	k: Bacteria; p: Verrucomicrobia; c: Opitutae; o: Opitutales; f: Opitutaceae; g: Opitutus
DQ125909.1	0.0495	22.33	11.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Micromonospora
DQ129615.1	0.0495	3.00	21.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
GQ263362.1	0.0495	28.33	4.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: albireticuli
FM209311.1	0.0495	1.67	12.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Adhaeribacter
HM341158.1	0.0495	3.00	7.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter
JF033767.1	0.0495	161.33	246.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
FJ479456.1	0.0495	19.00	11.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Kribbella
AF377867.1	0.0495	1.67	6.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhizobiaceae; g: Sinorhizobium; s: meliloti
AJ863369.1	0.0495	88.33	31.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
DQ129563.1	0.0495	5.67	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Williamsiaceae; g: Williamsia
JF042953.1	0.0495	6.00	68.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter
GU968460.1	0.0495	2.00	16.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter; s: rhombi
FJ152735.1	0.0495	3.33	10.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
HM845809.1	0.0495	43.67	19.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Pseudonocardiaceae; g: Actinomycetospora
HM186185.1	0.0495	2.00	13.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter
HM829036.1	0.0495	13.33	4.00	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Paenibacillaceae; g: Paenibacillus; s: chondroitinus
FJ889339.1	0.0495	16.00	32.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Thermomonas
JF098858.1	0.0495	40.67	97.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
HM438548.1	0.0495	11.00	29.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Lysobacter
AF423260.1	0.0495	74.00	35.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: mirabilis
AY395414.1	0.0495	31.00	10.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HQ538687.1	0.0495	8.00	19.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
AF292996.1	0.0495	37.67	24.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
AB257630.1	0.0495	3.00	8.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhodobiaceae; g: Afifella
FJ791174.1	0.0495	4.67	28.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Cellulomonadaceae; g: Cellulomonas
HM240903.1	0.0495	4.00	11.67	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
HM278777.1	0.0495	18.33	1.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
DQ453806.1	0.0495	25.67	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HM557519.1	0.0495	1.67	8.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter
FJ849551.1	0.0495	17.00	34.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
HM330072.1	0.0495	6.67	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
U48996.1	0.0495	55.00	13.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptosporangiaceae; g: Streptosporangium
FJ891056.1	0.0495	50.67	100.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
AY425768.1	0.0495	14.00	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
HM306204.1	0.0495	40.00	10.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Legionellales; f: Coxiellaceae; g: Rickettsiella
HM438620.1	0.0495	14.00	42.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Kaistobacter
DQ248308.1	0.0495	39.00	87.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas
HM152696.1	0.0495	23.00	11.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: corrugata
JF066170.1	0.0495	12.33	24.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Pirellulales; f: Pirellulaceae; g: Pirellula
HM275474.1	0.0495	22.67	7.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Alicyclobacillaceae; g: Alicyclobacillus
JF031109.1	0.0495	8.33	21.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus; s: obscurus
HM274365.1	0.0495	48.67	1.33	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Planococcaceae; g: Sporosarcina
EU589316.1	0.0495	16.33	56.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
AY133099.1	0.0495	57.00	109.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella
EU135879.1	0.0495	10.33	19.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: tendae
EF682982.1	0.0495	19.33	49.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas
JF129033.1	0.0495	4.67	10.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
HM334837.1	0.0495	175.00	397.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
New.ReferenceOTU73	0.0495	1.00	8.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.ReferenceOTU133	0.0495	12.00	4.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.ReferenceOTU61	0.0495	45.33	76.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.ReferenceOTU128	0.0495	10.67	3.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria
New.ReferenceOTU18	0.0495	111.33	25.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.ReferenceOTU15	0.0495	7.00	24.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.ReferenceOTU93	0.0495	9.00	18.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Polyangiaceae; g: Chondromyces
New.ReferenceOTU34	0.0495	43.67	20.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae
New.ReferenceOTU35	0.0495	46.33	27.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales
New.ReferenceOTU37	0.0495	2.00	5.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Promicromonosporaceae; g: Cellulosimicrobium
New.ReferenceOTU6	0.0495	15.33	30.33	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Haliangiaceae; g: Haliangium; s: ochraceum
New.ReferenceOTU26	0.0495	128.33	233.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Balneimonas
New.ReferenceOTU25	0.0495	41.33	30.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Ramlibacter
New.ReferenceOTU169	0.0495	204.33	114.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium
New.ReferenceOTU168	0.0495	448.67	628.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.ReferenceOTU160	0.0495	165.67	82.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces
New.ReferenceOTU163	0.0495	60.33	116.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella
New.ReferenceOTU165	0.0495	7.67	19.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.ReferenceOTU55	0.0495	33.33	9.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.ReferenceOTU58	0.0495	1.33	5.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.ReferenceOTU48	0.0495	29.33	50.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.ReferenceOTU105	0.0495	46.00	24.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
New.CleanUp.ReferenceOTU874	0.0495	14.00	49.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU940	0.0495	7.33	17.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
New.CleanUp.ReferenceOTU1319	0.0495	7.33	26.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU2922	0.0495	8.00	1.00	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera
New.CleanUp.ReferenceOTU3415	0.0495	2.33	18.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU3429	0.0495	108.00	64.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Rhodospirillaceae; g: Skermanella; s: aerolata
New.CleanUp.ReferenceOTU3818	0.0495	3.67	19.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU3913	0.0495	27.67	18.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae

New.CleanUp.ReferenceOTU4233	0.0495	3.67	8.67	k: Bacteria; p: Proteobacteria; c: Deltaproteobacteria; o: Myxococcales; f: Nannocystaceae; g: Plesiocystis
New.CleanUp.ReferenceOTU5445	0.0495	18.67	7.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU5602	0.0495	3.00	14.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU6066	0.0495	4.67	19.67	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
New.CleanUp.ReferenceOTU6432	0.0495	7.33	22.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU6533	0.0495	2.00	7.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU7276	0.0495	1.33	5.00	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU8084	0.0495	14.33	44.33	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Sinobacteraceae; g: Steroidobacter
New.CleanUp.ReferenceOTU8125	0.0495	15.00	6.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU8809	0.0495	19.33	53.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter; s: soli
New.CleanUp.ReferenceOTU9301	0.0495	1.67	9.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU10319	0.0495	4.33	9.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU10323	0.0495	4.00	13.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobactersoli
New.CleanUp.ReferenceOTU10652	0.0495	26.33	41.00	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU10720	0.0495	6.33	17.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
New.CleanUp.ReferenceOTU10949	0.0495	10.00	4.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Rhodoplanes
New.CleanUp.ReferenceOTU12002	0.0495	2.67	22.00	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU13252	0.0495	17.33	4.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae
New.CleanUp.ReferenceOTU14007	0.0495	7.33	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU14515	0.0495	1.00	9.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU14655	0.0495	2.33	7.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Chelatococcus; s: daeguensis
New.CleanUp.ReferenceOTU15439	0.0495	2.00	24.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Cellulomonadaceae; g: Cellulomonas
New.CleanUp.ReferenceOTU15717	0.0495	3.00	10.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
New.CleanUp.ReferenceOTU15725	0.0495	4.67	11.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU17130	0.0495	10.67	1.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae
New.CleanUp.ReferenceOTU17264	0.0495	1.00	7.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
New.CleanUp.ReferenceOTU17577	0.0495	2.33	8.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
New.CleanUp.ReferenceOTU17820	0.0495	5.33	31.33	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU19164	0.0495	19.67	10.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
New.CleanUp.ReferenceOTU19964	0.0495	37.00	68.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
New.CleanUp.ReferenceOTU20126	0.0495	14.67	29.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU20510	0.0495	31.67	2.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU21506	0.0495	5.33	17.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU22832	0.0495	1.00	10.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae; g: Flavisolibacter
New.CleanUp.ReferenceOTU23556	0.0495	4.00	12.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera
New.CleanUp.ReferenceOTU23640	0.0495	3.00	10.33	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Solirubrobacteraceae; g: Solirubrobacter
New.CleanUp.ReferenceOTU23751	0.0495	4.67	24.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU23862	0.0495	11.00	32.33	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Acidimicrobiaceae
New.CleanUp.ReferenceOTU24528	0.0495	19.33	34.67	k: Bacteria; p: Chloroflexi; c: Anaerolineae; o: Caldilineales; f: Caldilineaceae; g: Caldilinea
New.CleanUp.ReferenceOTU24794	0.0495	1.00	7.33	k: Bacteria; p: Verrucomicrobia; c: Spartobacteria; o: Chthoniobacterales; f: Chthoniobacteraceae; g: Chthoniobacter; s: flavus
New.CleanUp.ReferenceOTU24864	0.0495	2.33	13.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU24894	0.0495	8.33	46.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU25542	0.0495	2.67	11.67	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Planctomycetales; f: Planctomycetaceae; g: Planctomyces
New.CleanUp.ReferenceOTU26246	0.0495	31.67	3.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae
New.CleanUp.ReferenceOTU26274	0.0495	1.67	6.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Chromatiales; f: Ectothiorhodospiraceae; g: Methylonatrum; s: kenyense
New.CleanUp.ReferenceOTU26425	0.0495	19.33	58.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Geodermatophilus
New.CleanUp.ReferenceOTU26611	0.0495	2.33	14.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
New.CleanUp.ReferenceOTU26710	0.0495	36.33	18.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Phyllobacteriaceae; g: Mesorhizobium
New.CleanUp.ReferenceOTU27209	0.0495	17.67	48.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Nocardioides
New.CleanUp.ReferenceOTU27313	0.0495	3.00	7.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylocystaceae
New.CleanUp.ReferenceOTU28138	0.0495	45.00	19.67	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Acidimicrobiaceae; g: Acidimicrobium
New.CleanUp.ReferenceOTU28529	0.0495	24.33	6.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Aeromicrobium
New.CleanUp.ReferenceOTU28751	0.0495	15.67	5.33	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Isosphaeraceae; g: Singulisphaera
New.CleanUp.ReferenceOTU28788	0.0495	6.67	30.00	k: Bacteria; p: Actinobacteria; c: Rubrobacteria; o: Rubrobacterales; f: Rubrobacteraceae; g: Rubrobacter
New.CleanUp.ReferenceOTU28803	0.0495	2.33	8.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Blastococcus; s: aggregatus
New.CleanUp.ReferenceOTU28855	0.0495	2.00	7.33	k: Bacteria; p: Armatimonadetes; c: Armatimonadia; o: Armatimonadales; f: Armatimonadaceae; g: Armatimonas
New.CleanUp.ReferenceOTU29140	0.0495	2.00	11.67	k: Bacteria; p: Actinobacteria; c: Thermoleophilia; o: Solirubrobacterales; f: Conexibacteraceae; g: Conexibacter
New.CleanUp.ReferenceOTU30047	0.0495	70.00	27.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Hyphomicrobiaceae; g: Hyphomicrobium
New.CleanUp.ReferenceOTU30562	0.0495	6.00	12.00	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Acidimicrobiaceae

Supplementary Table 2. Relative abundances of the bacterial operational taxonomical units (OTUs) that were statistically different in the xylem sap of olive plants irrigated with treated urban wastewater (WW_{tr}) or rainfed (RF_{tr}). Only the OTUs with a statistical difference ($p < 0.05$) between WW_{tr} and RF_{tr} were considered. k, kingdom; p, phylum; c, class; o, order; f, family; g, genus; s, species.

XYLEM SAP

OTU ID	*p* level	Relative abundance		Taxonomic group
		WW_{tr}	RF_{tr}	
HM316131.1	0.0253	1	1	k: Bacteria; p: Acidobacteria; c: Acidobacteria; o: Acidobacteriales; f: Acidobacteriaceae; g: Terriglobus
JF145398.1	0.0253	2	0	k: Bacteria; p: Actinobacteria; c: Acidimicrobiia; o: Acidimicrobiales; f: Iamiaceae; g: Iamia
HQ843744.1	0.0253	0	2	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
EU431701.1	0.0253	2	0	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Bogoriellaceae; g: Georgenia
AF407716.1	0.0253	0	2	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Brevibacteriaceae; g: Brevibacterium
EU431717.1	0.0253	8	8	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Corynebacteriaceae; g: Corynebacterium
EU937846.1	0.0253	7	7	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Corynebacteriaceae; g: Corynebacterium; s: accolens
HM332256.1	0.0253	8	0	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Corynebacteriaceae; g: Corynebacterium; s: mucifaciens
AB601635.1	0.0253	1	1	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Cryptosporangiaceae; g: Cryptosporangium
AY662018.1	0.0253	7	6	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
FR691455.1	0.0253	10	15	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
FJ193407.1	0.0253	2	0	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Gordoniaceae; g: Gordonia
AY493923.1	0.0253	3	1	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Kineosporiaceae
HQ684738.1	0.0253	40	62	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Kineosporiaceae; g: Kineococcus
AJ315073.1	0.0253	5	14	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Kineosporiaceae; g: Kineosporia
AY145582.1	0.0253	8	6	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae
HM371092.1	0.0253	4	11	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Curtobacterium
JF182271.1	0.0253	7	9	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Frigoribacterium
HQ645197.1	0.0253	60	56	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Yonghaparkia
AB179516.1	0.0253	11	4	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Yonghaparkia
HQ445848.1	0.0253	2	1	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Microbacteriaceae; g: Yonghaparkia; s: alkaliphila
EF516103.1	0.0253	2	3	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae
FJ348430.1	0.0253	1	2	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter
HQ267976.1	0.0253	0	2	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Kocuria
FJ152699.1	0.0253	0	2	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Kocuria; s: palustris
FJ936960.1	0.0253	0	5	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Kocuria; s: rhizophila
AB294335.1	0.0253	2	2	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Micrococcus; s: luteus
AB301910.1	0.0253	2	0	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Mycobacteriaceae; g: Mycobacterium; s: monacense
FR667329.1	0.0253	2	0	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardiaceae; g: Rhodococcus; s: fascians
AB240360.1	0.0253	7	7	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Nocardioidaceae; g: Friedmanniella
JF093085.1	0.0339	1	8	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Propionibacteriaceae; g: Propionibacterium; s: acnes
JF016593.1	0.0339	4	0	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Streptomycetaceae; g: Streptomyces; s: tendae
EU202833.1	0.0339	2	2	k: Bacteria; p: Bacteroidetes; c: Bacteroidia; o: Bacteroidales; f: Prevotellaceae; g: Prevotella; s: copri
JQ428483.1	0.0339	1	2	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Chryseobacterium
AM935727.1	0.0339	2	0	k: Bacteria; p: Bacteroidetes; c: Flavobacteriia; o: Flavobacteriales; f: Flavobacteriaceae; g: Elizabethkingia; s: meningoseptica
HM156146.1	0.0339	6	1	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Chitinophagaceae
HQ674922.1	0.0339	317	388	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
GU294699.1	0.0339	5	4	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Spirosoma
CP000769.1	0.0339	59	61	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Pedobacter
HM063954.1	0.0339	2	1	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Sphingobacteriaceae; g: Sphingobacterium; s: multivorum
GQ264514.1	0.0339	2	0	k: Bacteria; p: Cyanobacteria; c: Synechococcophycideae; o: Pseudanabaenales; f: Pseudanabaenaceae; g: Leptolyngbya
DQ228401.1	0.0339	1	2	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Bacillaceae; g: Bacillus; s: aryabhattai
GQ389111.1	0.0339	0	2	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Bacillaceae; g: Bacillus; s: korlensis
JF145317.1	0.0339	0	2	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Staphylococcaceae; g: Jeotgalicoccus; s: psychrophilus
HM341045.1	0.0339	1	1	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Staphylococcaceae; g: Staphylococcus
HM270691.1	0.0339	13	6	k: Bacteria; p: Firmicutes; c: Bacilli; o: Bacillales; f: Staphylococcaceae; g: Staphylococcus
AB037007.1	0.0339	1	1	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales
AB015565.1	0.0339	6	2	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Enterococcaceae; g: Enterococcus
JF086626.1	0.0339	93	67	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Enterococcaceae; g: Enterococcus; s: faecalis
AF052390.1	0.0339	9	9	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Enterococcaceae; g: Enterococcus; s: mundtii
AB562921.1	0.0339	13	9	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae
HM330921.1	0.0339	1116	878	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Lactobacillus
HM153789.1	0.0339	32	23	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Lactobacillus; s: brantae
EF612398.1	0.0339	39	40	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Lactobacillus; s: fabifermentans
GU187034.1	0.0339	2	0	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Lactobacillus; s: lindneri
HM256350.1	0.0339	68	64	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Lactobacillus; s: plantarum
JF030520.1	0.0339	3	11	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Lactobacillus; s: sanfranciscensis
NR_036804.1	0.0339	5	6	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Pediococcus
X77959.1	0.0339	5	2	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Lactobacillaceae; g: Pediococcus
FJ790553.1	0.0339	7	4	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Leuconostocaceae; g: Fructobacillus
HM841333.1	0.0339	2029	1339	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Leuconostocaceae; g: Fructobacillus
HM808192.1	0.0339	257	193	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Leuconostocaceae; g: Fructobacillus; s: fructosus
HQ183918.1	0.0339	2	0	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Leuconostocaceae; g: Leuconostoc
AF234703.1	0.0339	197	180	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Leuconostocaceae; g: Leuconostoc; s: citreum
FJ193299.1	0.0339	357	355	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Streptococcaceae; g: Lactococcus
JN628302.1	0.0339	1	1	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Streptococcaceae; g: Lactococcus; s: garvieae
HM249181.1	0.0339	4	2	k: Bacteria; p: Firmicutes; c: Bacilli; o: Lactobacillales; f: Streptococcaceae; g: Streptococcus; s: pseudopneumoniae
FJ193402.1	0.0339	6	2	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Anaerococcus
FJ492839.1	0.0339	2	1	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Peptoniphilus; s: asaccharolyticus
GU983352.1	0.0339	0	2	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Lachnospiraceae
JF016881.1	0.0339	2	0	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Veillonellaceae; g: Negativicoccus
HM278638.1	0.0339	0	3	k: Bacteria; p: Gemmatimonadetes; c: Gemmatimonadetes; o: Gemmatimonadales; f: Gemmatimonadaceae; g: Gemmatimonas
HM329568.1	0.0339	1	1	k: Bacteria; p: Planctomycetes; c: Planctomycetia; o: Gemmatales; f: Gemmataceae; g: Gemmata
FJ984675.1	0.0339	3	5	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Brevundimonas; s: bullata
AY724055.2	0.0339	1	1	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Caulobacterales; f: Caulobacteraceae; g: Caulobacter
HM366479.1	0.0339	174	126	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
AM930301.1	0.0339	5	6	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae
HM185843.1	0.0339	1	1	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Methylocella
HM328188.1	0.0339	7	5	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Bradyrhizobiaceae; g: Bradyrhizobium
EU665096.1	0.0431	2	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
JF040770.1	0.0431	14	16	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium
AJ581615.1	0.0431	181	103	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: adhaesivum
JF226743.1	0.0431	4	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: komagatae
EU665164.1	0.0431	5	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: marchantiae
DQ125837.1	0.0431	108	42	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: mesophilicum
JF001031.1	0.0431	8	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: organophilum
GQ157429.1	0.0431	0	3	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Rhizobiaceae; g: Agrobacterium
AB255063.1	0.0431	0	2	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Paracoccus
HM438305.1	0.0431	5	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Paracoccus; s: marcusii
JF034188.1	0.0431	0	4	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodobacterales; f: Rhodobacteraceae; g: Rubellimicrobium
DQ302728.1	0.0431	20	53	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae
HM272255.1	0.0431	21	22	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Acidisoma
HQ114030.1	0.0431	12	14	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Roseomonas
HQ183837.1	0.0431	0	6	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Erythrobacteraceae; g: Lutibacterium
HM278333.1	0.0431	2	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae
EU332828.1	0.0431	3	6	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Novosphingobium
New.ReferenceOTU0	0.0463	57	12	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Novosphingobium
New.ReferenceOTU100	0.0463	47	9	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
New.CleanUp.ReferenceOTU7	0.0463	155	184	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
New.CleanUp.ReferenceOTU101	0.0463	44	39	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: asaccharolytica
New.CleanUp.ReferenceOTU148	0.0463	2	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: aurantiaca
New.CleanUp.ReferenceOTU236	0.0463	59	25	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: azotifigens
New.CleanUp.ReferenceOTU275	0.0463	2	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: dokdonensis
New.CleanUp.ReferenceOTU521	0.0463	1	1	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: panni
New.CleanUp.ReferenceOTU577	0.0463	22	13	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: wittichii
New.CleanUp.ReferenceOTU616	0.0463	11	3	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: yabuuchiae
New.CleanUp.ReferenceOTU619	0.0463	2	0	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: yunnanensis
New.CleanUp.ReferenceOTU667	0.0463	0	36	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Burkholderiaceae; g: Burkholderia; s: fungorum
New.CleanUp.ReferenceOTU668	0.0463	1	11	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae
New.CleanUp.ReferenceOTU810	0.0463	2	1	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Comamonas
New.CleanUp.ReferenceOTU922	0.0463	6	4	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Delftia; s: acidovorans
New.CleanUp.ReferenceOTU976	0.0463	1	1	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Delftia; s: lacustris

New.CleanUp.ReferenceOTU1122	0.0495	11	8	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Cupriavidus; s: pauculus
New.CleanUp.ReferenceOTU1187	0.0495	3	2	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Janthinobacterium
New.CleanUp.ReferenceOTU1238	0.0495	2	2	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Janthinobacterium
New.CleanUp.ReferenceOTU1348	0.0495	10	16	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Janthinobacterium; s: agaricidamnosum
New.CleanUp.ReferenceOTU1433	0.0495	203	176	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Oxalobacteraceae; g: Janthinobacterium; s: lividum
New.CleanUp.ReferenceOTU1471	0.0495	1	1	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Alteromonadales; f: Chromatiaceae; g: Alishewanella
New.CleanUp.ReferenceOTU1502	0.0495	3	9	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Alteromonadales; f: Shewanellaceae; g: Shewanella; s: baltica
New.CleanUp.ReferenceOTU1584	0.0495	10	6	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Enterobacteriales; f: Enterobacteriaceae; g: Gluconacetobacter
New.CleanUp.ReferenceOTU1585	0.0495	2	0	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Enterobacteriales; f: Enterobacteriaceae; g: Plesiomonas
New.CleanUp.ReferenceOTU1591	0.0495	8	7	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Moraxellaceae; g: Acinetobacter
New.CleanUp.ReferenceOTU1610	0.0495	4	2	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Moraxellaceae; g: Acinetobacter; s: baumannii
New.CleanUp.ReferenceOTU1762	0.0495	1	4	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Moraxellaceae; g: Acinetobacter; s: guillouiae
New.CleanUp.ReferenceOTU2091	0.0495	2	0	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Moraxellaceae; g: Enhydrobacter
New.CleanUp.ReferenceOTU2135	0.0495	187	145	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas
New.CleanUp.ReferenceOTU2340	0.0495	27	20	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: brenneri
New.CleanUp.ReferenceOTU2400	0.0495	21	29	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: fragi
New.CleanUp.ReferenceOTU2435	0.0495	2	0	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Pseudomonadaceae; g: Pseudomonas; s: veronii
New.CleanUp.ReferenceOTU2454	0.0495	12	9	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Stenotrophomonas; s: geniculata
New.CleanUp.ReferenceOTU2482	0.0495	0	4	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae; g: Xanthomonas
New.CleanUp.ReferenceOTU2535	0.0495	8	5	k: Bacteria; p: Thermi; c: Deinococci; o: Deinococcales; f: Deinococcaceae; g: Deinococcus
New.CleanUp.ReferenceOTU2582	0.0495	5	1	k: Bacteria; p: Thermi; c: Deinococci; o: Thermales; f: Thermaceae; g: Meiothermus; s: silvanus

Supplementary Table 3. Relative abundances of the bacterial operational taxonomical units (OTUs) that were statistically different in the phyllosphere (leaf surface) of olive plants irrigated with treaed urban wastewater (WW_{tr}) or rainfed (RF_{tr}). Only the OTUs with a statistical difference ($p < 0.05$) between WW_{tr} and RF_{tr} were considered. k, kingdom; p, phylum; c, class; o, order; f, family; g, genus; s, species.

PHYLLOSPHERE

OTU ID	*p* level	Relative abundance		Taxonomic group
		WW_{tr}	RF_{tr}	
JN559538.1	0.0253	2.00	0.00	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Clostridium; s: subterminale
HM315314.1	0.0253	1.00	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: adhaesivum
FM873458.1	0.0253	0.00	1.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Kocuria;
HM272697.1	0.0339	0.00	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Geodermatophilaceae; g: Modestobacter
HM278382.1	0.0339	2.33	0.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae; g: Variovorax; s: paradoxus
JF020944.1	0.0339	0.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: adhaesivum
JF049593.1	0.0339	0.33	2.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: adhaesivum
New.CleanUp.ReferenceOTU542	0.0339	2.00	0.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
New.CleanUp.ReferenceOTU1744	0.0339	0.00	1.67	k: Bacteria; p: Cyanobacteria; c: Oscillatoriophycideae; o: Chroococcales; f: Phormidiaceae; g: Microcoleus; s: vaginatus
New.CleanUp.ReferenceOTU2054	0.0339	0.00	1.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.CleanUp.ReferenceOTU4091	0.0339	1.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Kineosporiaceae; g: Kineococcus
New.CleanUp.ReferenceOTU9499	0.0339	2.67	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Pseudomonadales; f: Moraxellaceae; g: Psychrobacter
New.CleanUp.ReferenceOTU12968	0.0339	1.33	0.00	k: Bacteria; p: Proteobacteria; c: Gammaproteobacteria; o: Xanthomonadales; f: Xanthomonadaceae
New.CleanUp.ReferenceOTU14372	0.0339	1.33	0.00	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Clostridium; s: perfringens
New.CleanUp.ReferenceOTU15461	0.0339	2.67	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Couchioplanes
AY558587.1	0.0369	13.33	0.00	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Clostridium; s: novyi
AJ576423.1	0.0369	0.00	2.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Arthrobacter
AB478676.1	0.0369	8.00	2.00	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae
New.CleanUp.ReferenceOTU3788	0.0369	2.33	0.00	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales
New.CleanUp.ReferenceOTU5257	0.0369	2.33	0.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae; g: Acidisphaera
AF371840.1	0.0431	5.00	1.33	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Clostridium; s: baratii
New.CleanUp.ReferenceOTU13625	0.0431	1.67	3.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
AF385532.1	0.0463	3.67	0.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micrococcaceae; g: Kocuria; s: rhizophila
AF371845.1	0.0463	13.00	2.67	k: Bacteria; p: Firmicutes; c: Clostridia; o: Clostridiales; f: Clostridiaceae; g: Clostridium; s: perfringens
EU071484.1	0.0463	8.00	1.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
AJ555244.1	0.0463	2.67	6.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Beijerinckiaceae; g: Methylocella
DQ071104.1	0.0463	3.00	0.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas; s: asaccharolytica
New.ReferenceOTU9	0.0463	7.67	16.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
New.CleanUp.ReferenceOTU8413	0.0463	2.33	9.67	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Kineosporiaceae; g: Kineococcus
New.CleanUp.ReferenceOTU15290	0.0463	2.33	9.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
HM335388.1	0.0495	98.67	25.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
DQ129612.1	0.0495	124.33	29.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Sphingomonadales; f: Sphingomonadaceae; g: Sphingomonas
HM322346.1	0.0495	92.67	68.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
HQ115548.1	0.0495	38.33	18.33	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Comamonadaceae
HM312958.1	0.0495	26.67	42.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
AB015566.1	0.0495	573.00	837.67	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales; f: Methylobacteriaceae; g: Methylobacterium; s: adhaesivum
JF077740.1	0.0495	874.67	509.67	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
HM270012.1	0.0495	20.67	1.33	k: Bacteria; p: Actinobacteria; c: Actinobacteria; o: Actinomycetales; f: Micromonosporaceae; g: Couchioplanes
New.ReferenceOTU0	0.0495	1714.00	3023.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhizobiales
New.ReferenceOTU4	0.0495	201.00	449.00	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae
New.ReferenceOTU16	0.0495	15.33	33.67	k: Bacteria; p: Proteobacteria; c: Betaproteobacteria; o: Burkholderiales; f: Burkholderiaceae; g: Burkholderia
New.ReferenceOTU44	0.0495	389.67	760.00	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
New.ReferenceOTU22	0.0495	55.33	9.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
New.CleanUp.ReferenceOTU5149	0.0495	36.67	5.33	k: Bacteria; p: Bacteroidetes; c: Sphingobacteriia; o: Sphingobacteriales; f: Flexibacteraceae; g: Hymenobacter
New.CleanUp.ReferenceOTU11231	0.0495	1.00	6.33	k: Bacteria; p: Proteobacteria; c: Alphaproteobacteria; o: Rhodospirillales; f: Acetobacteraceae

Supplementary Figure 1
Pilot unit for urban wastewater treatment

Irrigation with urban wastewater treated by a pilot unit.

Secondary treatment (excepting sand filtration as a tertiary treatment).

Treated urban wastewater distributed from May to October by drip irrigation.

Amount of treated urban wastewater applied = 2800 $m^3\ ha^{-1}\ year^{-1}$ (mean 2000-2016).

Supplementary Figure 2
Xylem sap extraction method

- **Equipment:** Scholander chambers with N_2.
- **Pressure applied:** 50-70 bar for 15-20 minutes per shoot.

Catia Fausto, one of the authors, while is extracting xylem sap.

Analysis of sap samples

- DNA extraction
- 16S rRNA gene amplified by PCR
- Metagenomic analysis of bacterial communities: DNA sequencing (Illumina MiSeq platform), and OTU (Operational Taxonomic Unit) identification.

Supplementary Figure 3
Drip irrigation system

- Six **drip emitters** discharging 8 L h^{-1} over a 1-m radius for each plant.
- **Canopies** approximately 4.5 m high.
- The **distribution pipes and emitters** were placed approximately 1.5 m above the ground.