SUPPLEMENTAL TEXT.

Measurement of contact angle after aminosilanization. To measure the contact angle of polystyrene (PS) Petri dishes before and after silanization under mineral oil, Petri dishes were cut into 1 cm × 1 cm pieces, cleaned with ethanol and dried with nitrogen gas, and then immersed into mineral oil in a glass tank. 2 μL measured aqueous solution was carefully deposited on the surface. The contact angle of the droplet on the substrate was subsequently measured by using SL200B optical goniometer (SL200B, Shanghai, China). The same measurements were performed at least five times and the average contact angles were calculated.

Distortion-free imaging of sessile droplets. GFP-tagged *Pseudomonas aeruginosa* PAO1 was used to demonstrate the performance of sessile droplets on high resolution and distortion-free imaging. PAO1 was cultured in LB medium under 200 rpm/min at 37 ºC, adjusted to OD_{600}=1, and was diluted 200 times by LB medium as the cell suspension. Droplets (~6.9 nL) were generated from this sample and displayed onto APTES modified Petri dish. Sessile droplets on APTES modified surface had a slightly larger size and thinner thickness compare to those on untreated surface (Fig. S1D-E). The spherical shape of the droplets on untreated surface resulted in refraction and distortion of imaging by optical microscopes. In comparison, the APTES modified surface provides distortion-free imaging under an inverted microscope. This allowed us to obtain a higher cell count in the sessile

droplets (cell count: 23, Fig. S1E) than cell counted from the same volume droplet on untreated surface (cell count: 13, Fig. S1D) or in Teflon tubing (cell count: 11, Fig. S1C). It is notable that cells on the edge were clearly observed only in sessile droplets on the APTES modified surface.

Construction and operation of the dish drive for spiral streaking. The automated dish drive was composed of a microstepping spindle motor (Electric Rotary Actuator, Koganei, Tokyo, Japan) and a linear translation stage (Nanotec Electronic, Munich, Germany) (Fig. S2A). A 32-bit microcontroller (STM32F103, STMicroelectronics Geneva, Switzerland) with codes written in-house was used to control the spindle motor and the linear translation stage, and communicate with a laptop via USB interface. A program written in LabVIEW, setting and sending parameters to the microcontroller, to control the automated dish drive in accordance with constant linear velocity (CLV) model.

CLV model. To automatically streak droplets in closely packed spiral tracks with high capacity, the dish drive was programmed according to CLV scheme (Fig. S2B). Briefly, when the dish moved on the spiral tracks within the writing area from the inner diameter of R_1 to outer diameter of R_2, if the track spacing was set to Δr, the number of spiral tracks in the writing area was described as in (eq.1):

$$N(R_1, R_2) = \frac{R_2 - R_1}{\Delta r} \quad \text{(eq.1)}$$

The total number of droplets on the spiral tracks was the total length of tracks divided by spacing between adjacent droplets, as described in (eq.2):

$$\mathrm{n}(R_1, R_2) = \frac{\mathrm{L}(R_1, R_2)}{\Delta l} = \frac{2\pi \frac{R_1 + R_2}{2} \mathrm{N}(R_1, R_2)}{\Delta l} = \pi \frac{R_2^2 - R_1^2}{\Delta r \Delta l} \quad \text{(eq.2)}$$

As the platform was operated with a CLV of V, The velocity could be expressed as the total length of tracks $L(R_1, R_2)$ divided by the total time elapsed T, or the length of tracks $L(R_1, r)$ divided by time elapsed during a particular interval t:

$$V = \frac{L(R_1, R_2)}{T} = \frac{L(R_1, r)}{t}, \quad 0 \le t \le T \quad \text{(eq.3)}$$

Based on (eq.1) - (eq.3), the radial position at any time t could be derived as (eq.4):

$$r(t) = \sqrt{\frac{t}{t_{max}}(R_2^2 - r_1^2) + r_1^2} \quad \text{(eq.4)}$$

To operate with linear velocity of V, the rotational angular velocity (ω) of the spindle motor and the velocity of the linear translator (u) moving radially outwards could be expressed as (eq.5) and (eq.6):

$$\omega(t) = \frac{V}{r(t)} \quad \text{(eq.5)}$$

$$u(t) = \frac{dr}{dt} \quad \text{(eq.6)}$$

Depending on (eq.4) - (eq.6), we could get the rotational angular velocity (ω) and the velocity of the linear translator (u) if R_1, R_2, Δr and V are determined. The typical rotational angular velocity (ω) and the velocity of the linear translator (u) were plotted against time (Fig. S2C). Based on (eq.4), with a constant droplet generating frequency, the droplets

written on the dish could be easily addressed and indexed according to its radial position (Fig. S2D).

Fabrication and operation of droplet generating Device. There were two types of devices used in this research for microfluidic generating of mono-disperse droplets, the capillary-based device and the microfabricated PDMS device. The capillary-based device was fabricated by assembly of two 1.5-cm long fused-silica capillaries (40 μm I.D., 103 μm O.D.) with a Teflon tubing (15 to 30 cm long, 250 μm O.D., 200 μm I.D.) (Fig. S3A-B). The two capillaries were parallel inserted into the open end of the Teflon tubing and sealed with epoxy. The other end of the Teflon tubing extended to the streaking tip as described below.

PDMS devices were made by soft lithographic techniques (1) as described (2). Photolithorgraphy was performed with URE-2000/35 Mask Aligner (Institute of Optics and Electronics, Chinese Academy of Sciences, Chengdu, China). A Teflon tubing (15 to 30 cm long, 250 μm O.D., 200 μm I.D.), cut at an angle (~45°) to facilitate collecting of droplets, was inserted into the junction of the microchannels (200 μm in height, 200 μm in width) of the device through the outlet microchannel. Connections of Teflon tubing and PDMS devices were sealed with capillary wax (Hampton Research, Aliso Viejo, CA, USA).

Agilent gastight syringes with 30-gauge Teflon tubing were used to load aqueous solutions and carrier oil. Pump 11 Pico Plus elite syringe pumps controlled with LabVIEW

programs were used to drive flows. For capillary-based device, aqueous solutions and carrier oil were delivered via two fused-silica capillaries, and mono-disperse droplets were formed in the Teflon tubing. For PDMS-based device, the sample was mixed with another two aqueous reagents with constant mixing ratio or ramping programs, and co-flowed with carrier oil at the -junction to form droplets directly into the Teflon tubing (Fig. S3C).

Streaking tip fabrication and manual streaking operation. For manual streaking, 30-cm long Teflon tubing was used in the droplet generation devices. A pipette tip (200 μL size) was used as the conical sleeve surrounds the end of the Teflon tubing to reinforce the flexible Teflon tubing during manual streaking. The end of the tubing was leveled with the conical pipette tip outlet for easy streaking. For easy holding, the pipette tip was coupled with a plastic tube (5 cm in length, 3.5 mm O.D., 2 mm I.D.). To manually streak sessile droplet array, The device was connected with syringe pumps to forming droplet in the Teflon tubing, and the streaking tip was held by hand with a slightly angle (~5°) from vertical and touched the surface of Petri dish filled with mineral oil (10 mL). The streaking tip was dragged following a zig-zag pattern, with approximate line spacing of about 1.5 mm.

Tracking serial dilution using spiral droplet array. 0.5% (w/v) blue, yellow and red food dye solutions in Deionized water were used for evaluation of serial dilution in droplets.

Mineral oil was used as the carrier oil. The ramping program of flow rates was written in LabVIEW, which set the total flow rate to 3 μL/min, and ramped up or down flow rate of either blue, yellow or red dye solution to generate the rainbow color droplets. Pictures of the droplet array were taken with a compact camera (Nikon1 J1, Nikon, Tokyo, Japan) (Fig. 4D).

Determination of degradation rate of fluoranthene by isolated strains. The microbial isolates which could form transparent circles on MSM-fluoranthene agar plates and further grow on MSM-fluoranthene broth were characterized for capability of fluoranthene degradation. Three replicates were performed for each isolates. Fluoranthene in cultured samples after 9 days incubation were extracted with ethyl acetate for three times. All three extracts were pooled and concentrated by evaporation under nitrogen gas to 1 mL. Fluoranthene was quantified by a high performance liquid chromatography system (Agilent 1200 series, CA, USA) equipped with a ZORBAX Eclipse Plus C18 column (4.6 mm × 250 mm). The elute was performed by an acetonitrile-water (65:35) system at a flow rate of 1.2 mL/min and were detected at 254 nm. The degradation rate of fluoranthene was derived as (eq.7):

$$R_d = \frac{C_0 - C}{C_0} \times 100\% \qquad \text{(eq.7)}$$

where R_d (%) represents the degradation rate, C_0 (mg/L) represents the initial concentration of fluoranthene, and C (mg/L) represents the remained concentration of fluoranthene after incubation with the bacterial strain.

Metagenomic sequencing. Cells pooled from agar plates and MSPs using fluoranthene as the sole carbon source were used for metagenomic sequencing. Total DNAs were extracted with E.Z.N.A Mag-Bind Soil DNA Kit (Omega Bio-Tek, GA, USA) (3) by using a KingFisher Flex Magnetic Particle Processor (Thermo Scientific, MA, USA). Extractions were performed according to kit and instrument protocols. Eluted DNAs were used for 16S rRNA gene V4 region PCR amplification with the U515F (5'-GTGCCAGCMGCCGCGGTAA-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') (4) primers containing barcodes at the 5' end of the front primer (5). PCR reactions were performed in 50 μL volumes, each containing 1.5 μL of 10 μM forward and reverse primers respectively, 25 μL of 2× KAPA HiFi HotStart ReadyMix (Kapa Biosystems, Inc., MA, USA), and up to 23 μL of extracted DNA as a template. The PCRs were performed as follows: 32 cycles (98 °C, 20 s; 54 °C, 15 s; 72°C, 15 s) after an initial denaturation at 95 °C for 3 min, following a final extension at 72 °C for 60 s. Triplicate PCR products for each samples were purified using E.Z.N.A. Gel Extraction Kit (Omega Bio-Tek, Inc., GA, USA) and then quantified using Qubit dsDNA HS Assay Kits (Invitrogen, CA, USA). Equal amounts of PCR products were mixed to produce equivalent sequencing depth from all

samples. After purification by using Agencourt AMPure XP KIT, the pooled-PCR products were used to construct a DNA library using NEB E7370L DNA Library Preparation Kit according to instructions from Illumina (San Diego, California, USA). Finally, the single composite barcoded PCR product was sequenced on a MiSeq machine using PE250 protocol.

Sequence data processing and statistical analysis. Paired-end Illumina generated reads were subjected to the Skewer program (version 0.1.123) (6) with an error threshold of 0.2 for adapter trimming and de-multiplexing. The trimmed paired-reads were merged by the PEAR program (version 0.9.5) (7) with *p*-value of 0.01. Sequence reads were filtered (fastq_maxee = 0.5 and fastq_trunclen = 289), removed replication and discarded singletons followed the data handling procedure of Edgar and the website (http://drive5.com/usearch/manual/uparse_cmds.html, Edgar, R., UPARSE Commands, Date of access: 19/1/2015). On average, there were more than 30,000 raw sequences of each sample obtained for downstream data analysis. Operational taxonomic units (OTUs) were clustered at 97% similarity, checked for chimeras and abundance calculated with Uparse pipeline (8). Finally, qualified sequences were analyzed for relative abundance calculation (Table S1), and α-diversity indexes analysis with QIIME (9). Coverage was calculated using the equation:

$$C = (1 - \frac{n}{N}) \times 100\% \qquad \text{(eq.8)}$$

where *n* is the number of unique OTU and N is the total number of clones examined (10).

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SUPPLEMENTAL FIGURES:

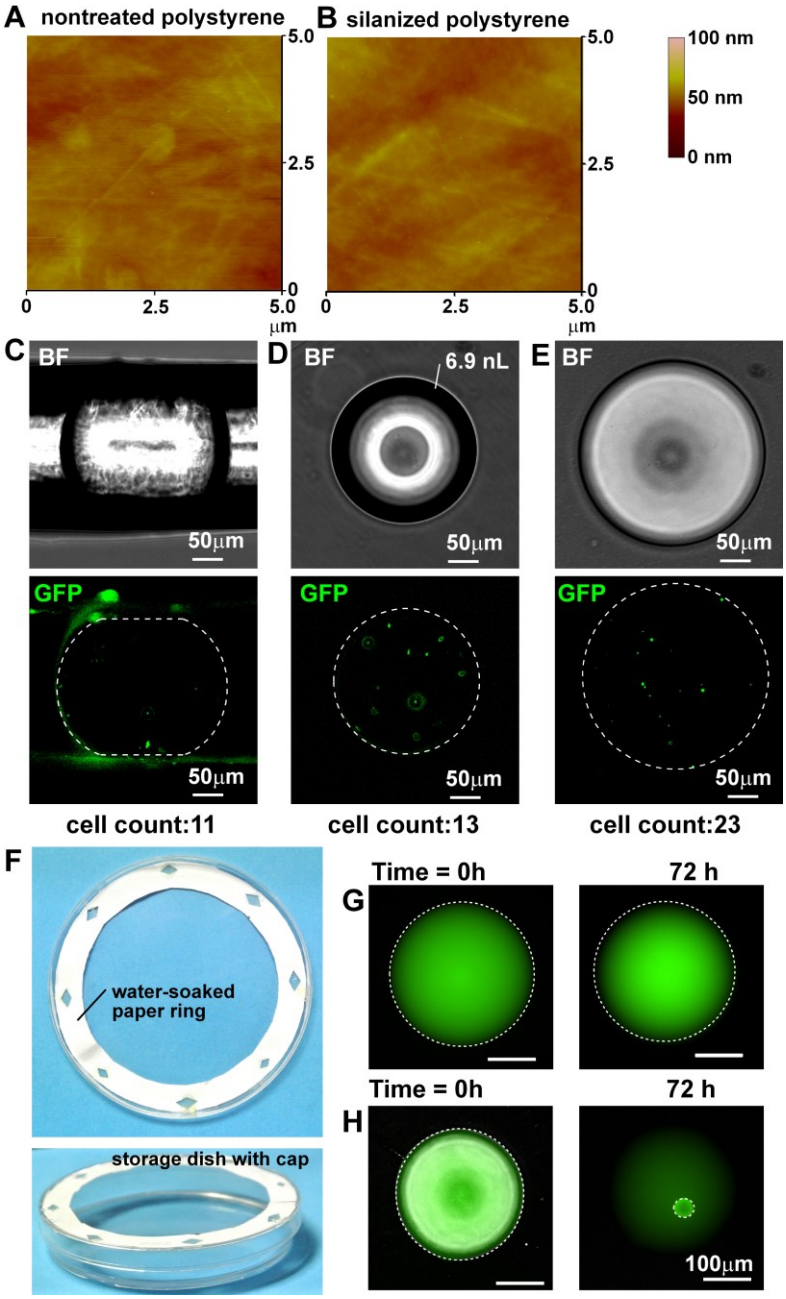

FIG S1. Modification and characterization of Polystyrene Petri dishes for droplet storage. (A-B) AFM images of untreated (A) and APTES-modified (B) surface. (C) Bright-field and green fluorescence images of 6.9 nL LB droplet containing GFP-tagged *Pseudomonas aeruginosa* PAO1 in a 200 µm I.D. Teflon tubing, on untreated Petri dish, and APTES-modified Petri dish. (D) Prevention of long-term evaporation during incubation by attaching a paper ring to the lid; Evaporation of droplets with fluorescein was monitored in 72 hours with (E) and without (F) wet paper ring.

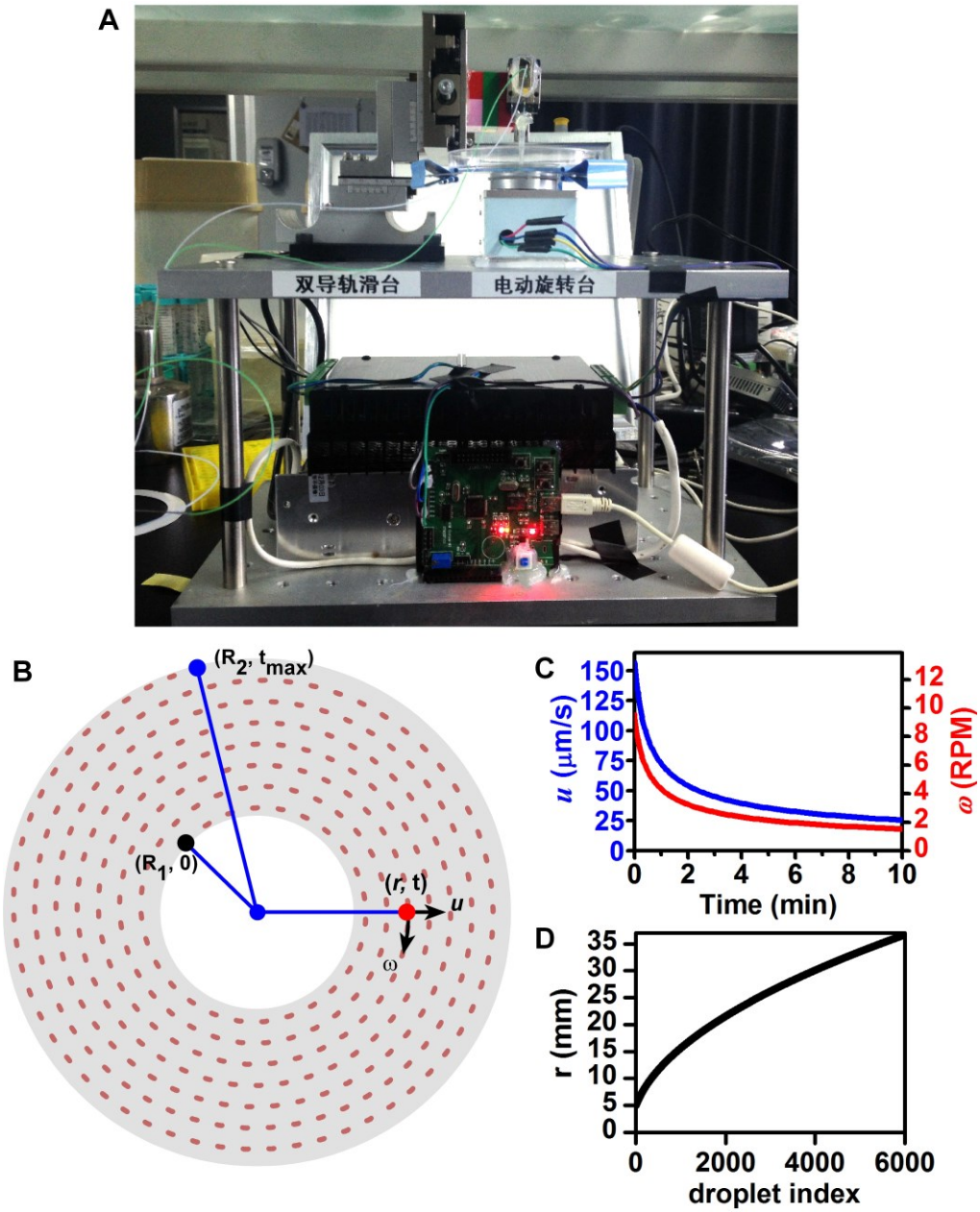

FIG S2. The constant linear velocity (CLV) model for streaking of sessile droplets on Petri dish. (A) A picture of the dish drive setup. (B) The typical spiral tracks generated by the CLV model. (C) Plots of the rotation angular velocity (ω) and the velocity of the linear translator (*u*) as a function of time. (D) A Plot of distance of droplets from the center as a function of the indexes of the droplets on the spiral tracks.

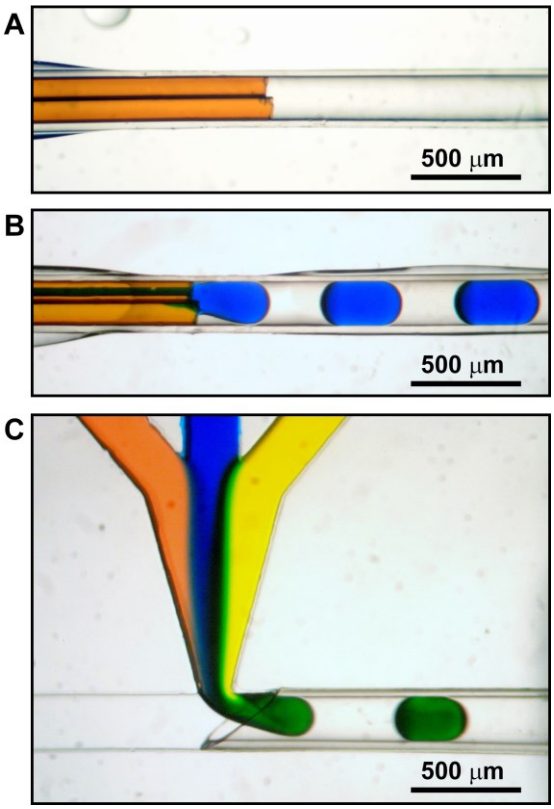

FIG S3. Microfluidic devices for forming droplets. (A) Micrograph of an empty capillary-based device with two inlets. (B) Micrograph of droplets of blue food dye solution forming directly into the Teflon tubing. (C) Micrograph of droplet formation in a four-inlet PDMS device with Teflon tubing inserted to the junction of microchannels.

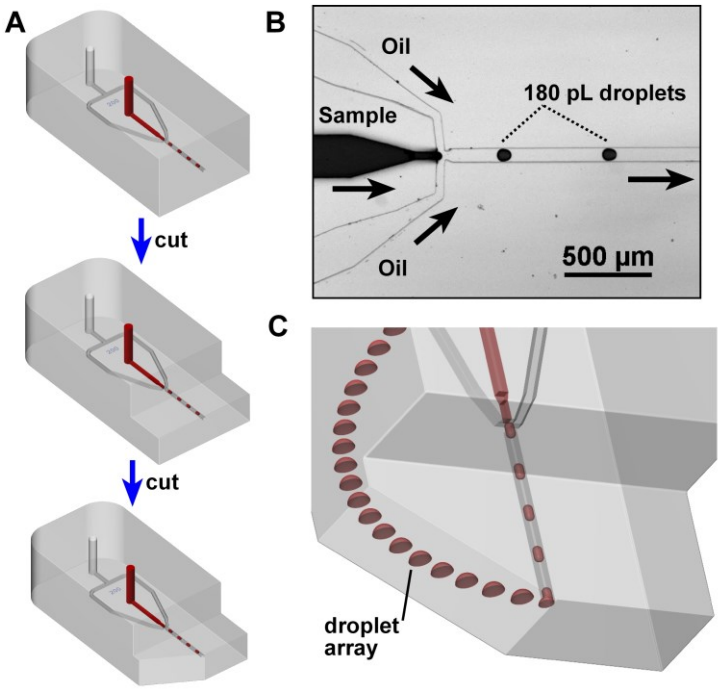

FIG S4. Fabrication of PDMS droplet-writing interface. (A) The cutting procedure of the droplet writing tip on a droplet generating device. (B) Microscopic photograph of the droplet-generation device producing 180 pL droplets. (C) 3D view from the Bottom of the writing tip during writing of droplet array on a flat transparent substrate covered by carrier oil.

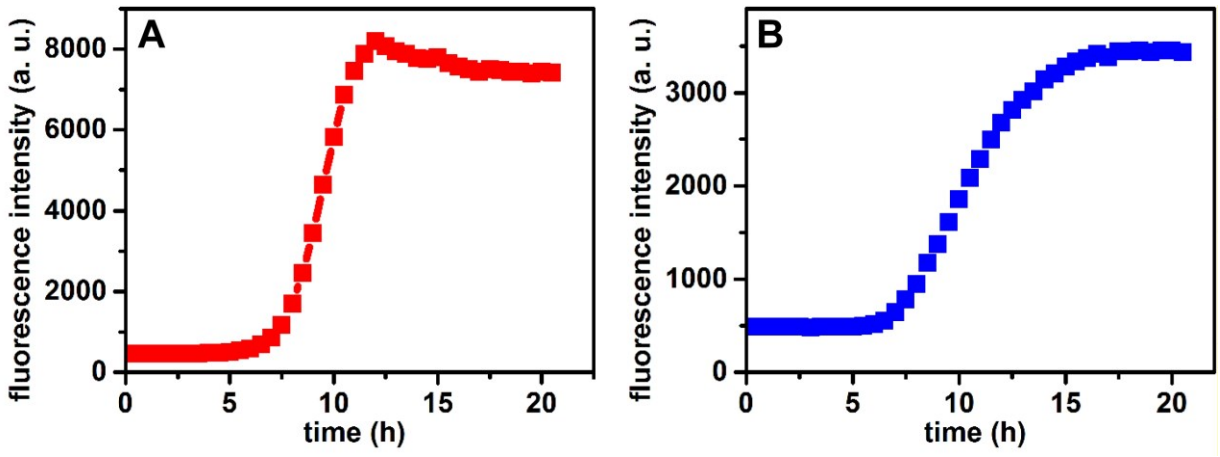

FIG S5. Typical growth curve from a single cell of RFP-tagged *E. coli* RP437 (A) and GFP-tagged *E. coli* RP1616 (B) based on integrated fluorescence intensity of droplets.

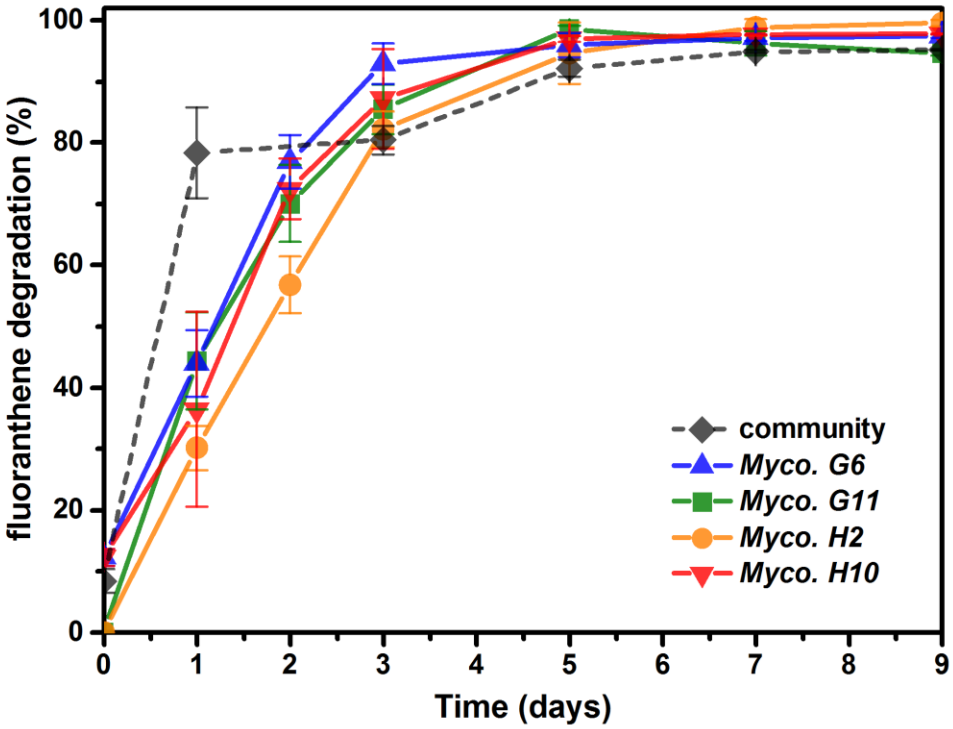

FIG S6. Efficiency of fluoranthene degradation for *Mycobacterium* strains obtained by the MSP method according to fluoranthene removal. The degradation of the original community is also plotted as the dotted gray line.

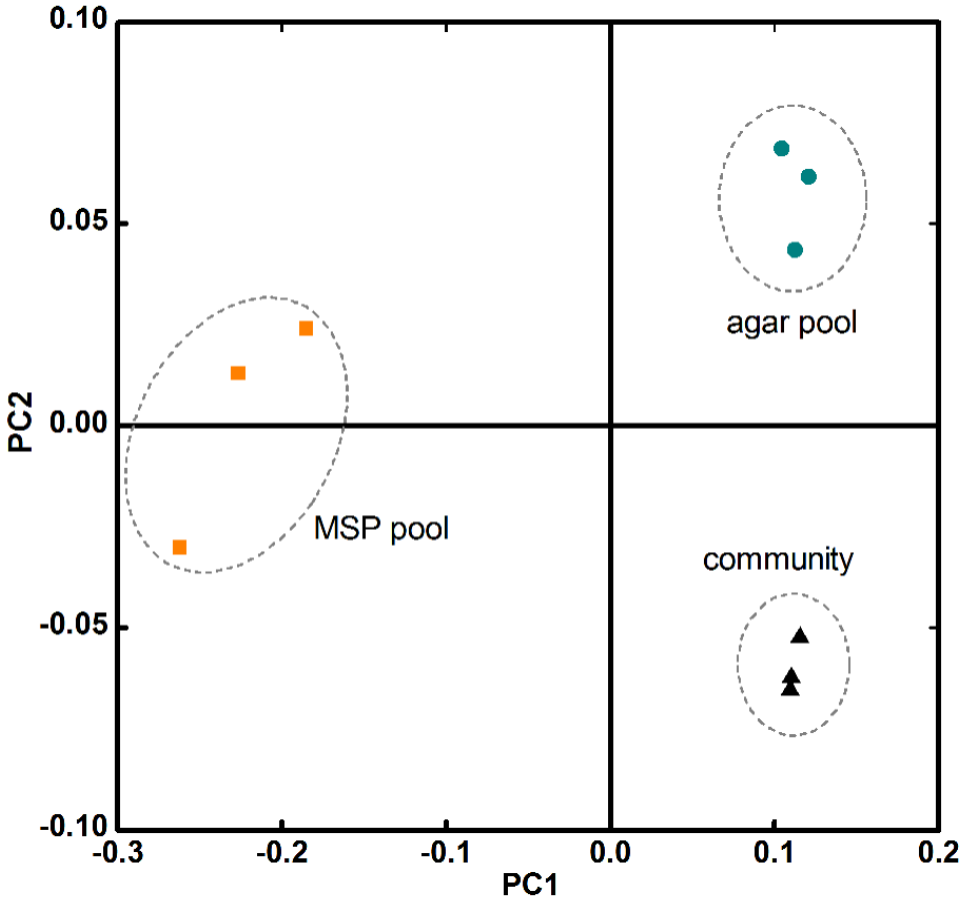

FIG S7. 2-dimentional principal coordinates analysis (PCoA) for characterizing the cluster of the three kinds of samples, including pooled cells from MSPs, pooled cells from agar plates, and the original community.

Table S1. Microbial isolates obtained from MSP method and agar plates using various culture media, and the corresponding relative abundances estimated by 16S rRNA sequencing of the original community.

Family	HTS abundance	Genus of isolates	Agar plate isolates	MSP isolates
Pseudomonadaceae	31.6659%	*Pseudomonas*	27	65
Mycobacteriaceae	20.4309%	*Mycobacterium*	0	13
Rhizobiaceae	5.4405%	*Shinella*	6	15
		Rhizobium	0	4
		Sinorhizobium	0	1
Comamonadaceae	3.7741%	*Diaphorobacter*	13	4
		Xenophilus	3	1
Xanthomonadaceae	2.3776%	*Pseudoxanthomonas*	14	4
Nocardioidaceae	1.4214%	*Nocardioides*	0	3
		Aeromicrobium	0	1
Alcaligenaceae	1.3238%	*Alcaligenes*	1	1
		Achromobacter	4	0
		Castellaniella	0	2
Sphingomonadaceae	0.3385%	*Sphingomonas*	13	1
Micrococcaceae	0.2315%	*Micrococcus*	1	14
		Kocuria	4	8
		Arthrobacter	1	4
Bradyrhizobiaceae	0.1599%	*Bosea*	0	1
		Nitrobacter	0	2
Microbacteriaceae	0.1505%	*Agrococcus*	0	1
		Curtobacterium	1	1
		Microbacterium	5	16
Enterobacteriaceae	0.1256%	*Proteus*	0	1
Moraxellaceae	0.0748%	*Acinetobacter*	4	4
		Moraxella	0	4
Planococcaceae	0.0208%	*Planomicrobium*	0	2
		Sporosarcina	0	1
		Planococcus	1	0
Flavobacteriaceae	0.0083%	*Flavobacterium*	1	0
		Myroides	0	1
Bacillaceae	0.0031%	*Bacillus*	0	8
		Lysinibacillus	0	1
		Oceanobacillus	0	2

Aerococcaceae	0.001%	*Aerococcus*	0	1
		Facklamia	0	1
Streptomycetaceae	0	*Streptomyces*	0	5
Staphylococcaceae	0	*Staphylococcus*	5	11
Pseudonocardiaceae	0	*Saccharothrix*	0	2
Paenibacillaceae	0	*Paenibacillus*	0	2
Brucellaceae	0	*Ochrobactrum*	0	1
Actinomycetales	0	*Gordonia*	0	1
Dietziaceae	0	*Dietzia*	0	1
Corynebacteriaceae	0	*Corynebacterium*	0	2
Dermabacteraceae	0	*Brachybacterium*	0	2
		Dermabacter	0	1
Nocardiaceae	0	*Rhodococcus*	1	1
Geodermatophilaceae	0	*Blastococcus*	0	1
Count of OTUs	/	47	18	44
Count of isolates			105	218

Table S2. Community profiling based on metagenomic sequencing of bacterial 16S rRNA genes. Average OTU abundances of three duplicates were given for original community, pooled cells from MSPs and pooled cells from agar plates. Fluoranthene was used as the sole carbon source.

Taxon	community	MSP pooled	agar plate pooled
Unassigned;Other;Other;Other;Other;Other	0.00435	0.003426	0.003977
p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__Acidobacteriaceae;g__	0	0	3.11E-05
p__Acidobacteria;c__Solibacteres;o__Solibacterales;f__Solibacteraceae;g__	3.11E-05	0	4.15E-05
p__Acidobacteria;c__[Chloracidobacteria];o__RB41;f__Ellin6075;g__	3.11E-05	0	0.000104
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Frankiaceae;g__	0.000166	0.000488	0.00053
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Intrasporangiaceae;g__Knoellia	0	5.19E-05	0
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Intrasporangiaceae;g__Phycicoccus	0	4.17E-05	0
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__	4.15E-05	2.08E-05	9.37E-05
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Microbacterium	0.001464	0.057873	0.002595

p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;Other	0.001163	0.003893	0.005201
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__	0.001153	0.003021	0.005326
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Microbispora	0	7.26E-05	0
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae;g__Mycobacterium	0.204309	0.012646	0.067206
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__	0.014214	0.001173	0.004859
p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium	3.11E-05	0.000488	2.07E-05
p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__;g__	0.000197	1.04E-05	0.000145
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1.04E-05	0.000426	0
p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__ML635J-40;g__	0	2.07E-05	0
p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium	2.07E-05	0.001568	2.08E-05
p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Myroides	6.23E-05	0.002886	2.08E-05
p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Chryseobacterium	0.0152	0.001256	0.001817
p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Wautersiella	0	8.3E-05	0
p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__;g__	1.04E-05	0.000249	1.04E-05
p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__	0.006811	0.000343	0.000478
p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium	1.04E-05	0.000156	0
p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__	0.00081	0.000197	0.003291
p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Chitinophaga	0.000291	0.000737	0.012189
p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolinaceae;g__T78	0	6.24E-05	0
p__Chloroflexi;c__Anaerolineae;o__envOPS12;f__;g__	0	1.04E-05	0
p__Cyanobacteria;c__Chloroplast;o__Streptophyta;f__;g__	0	6.24E-05	0
p__Firmicutes;c__Bacilli;o__Bacillales;f__Alicyclobacillaceae;g__	1.04E-05	0	2.08E-05
p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	3.11E-05	0.000125	0.000145
p__Firmicutes;c__Bacilli;o__Bacillales;f__Listeriaceae;g__Brochothrix	0.000301	0.013092	0.000426
p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;Other	9.36E-05	0.000104	0.000332

p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planococcus	7.26E-05	0.000208	8.32E-05
p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina	4.15E-05	4.15E-05	0.000104
p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus	0	0.000207	2.08E-05
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__	0	3.11E-05	0
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia	1.04E-05	0.000187	0
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Carnobacterium	0.000239	0.005929	0.000228
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	0.001018	0.001941	0.002159
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	4.15E-05	0.001433	4.15E-05
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc	0.000239	0.012542	0.000249
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus	0.01222	0.556622	0.008981
p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	0.000405	0.015771	0.000301
p__Firmicutes;c__Clostridia;o__Clostridiales;f__;g__	0	3.11E-05	0
p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Desulfosporosinus	9.35E-05	0.000197	6.24E-05
p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__Mogibacterium	1.04E-05	3.11E-05	1.04E-05
p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Finegoldia	0	1.04E-05	0
p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Helcococcus	0	4.15E-05	0
p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Peptoniphilus	1.04E-05	1.04E-05	0
p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Tissierella_Soehngenia	1.04E-05	0.000343	1.04E-05
p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	0	7.28E-05	0
p__Planctomycetes;c__OM190;o__CL500-15;f__;g__	0	1.04E-05	0
p__Planctomycetes;c__Planctomycetia;o__Gemmatales;f__Isosphaeraceae;g__	0.000322	4.15E-05	0.000758
p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__	0.010258	0.001952	0.006852
p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium	0.000519	3.11E-05	0.000291
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;Other;Other	5.2E-05	0.000997	7.28E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__;g__	0.001101	0.000197	0.000426

p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;Other	0.000841	0.006645	0.000862
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__	0.000758	0.007247	0.000903
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;Other	0.000177	0.000145	0.000197
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Devosia	0.000207	4.15E-05	0.000384
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium	0.009303	0.001132	0.005534
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__	0	2.07E-05	0
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium	4.15E-05	0.000425	2.07E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Aminobacter	0.000187	7.27E-05	2.07E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__	0.006967	0.001111	0.003447
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Agrobacterium	0.047438	0.006126	0.025728
p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;Other	3.11E-05	2.07E-05	1.04E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__	1.04E-05	4.17E-05	0
p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus	3.11E-05	0.000737	6.24E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__	0.004247	0.00054	0.002305
p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__Magnetospirillum	0.000259	1.04E-05	9.35E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__Phaeospirillum	0.000987	9.37E-05	0.00026
p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;Other	0.000114	1.04E-05	2.08E-05
p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium	5.19E-05	0.000218	0.000145
p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas	0.000716	0.003447	0.001495
p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingopyxis	0.002502	0.005679	0.059129

p__Proteobacteria;c__Betaproteobacteria;o__;f__;g__	0.000851	0.000135	0.00026
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__	0.005275	0.001392	0.006562
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Achromobacter	0.004786	0.001422	0.005939
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Denitrobacter	0.000363	9.35E-05	0.000145
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Pigmentiphaga	0.002813	0.000197	0.00163
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Burkholderia	0.000737	0.005181	0.000768
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;Other	0.019249	0.009427	0.016602
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__	0.003717	0.001973	0.002367
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Diaphorobacter	0.009012	0.005493	0.011203
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Hylemonella	0.005763	0.00055	0.002928
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;Other	0.000529	7.28E-05	6.24E-05
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__	2.07E-05	0.000498	0
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Janthinobacterium	2.07E-05	0.001204	0.000124
p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Ralstonia	5.19E-05	0.000312	5.19E-05
p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__	1.04E-05	0.000831	1.04E-05
p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__	5.2E-05	0.000436	3.11E-05
p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__	0.001256	0.008981	0.000831
p__Proteobacteria;c__Gammaproteobacteria;o__PYR10d3;f__;g__	0.000727	9.36E-05	0.000249
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;Other;Other	**0.250283**	**0.052131**	**0.226237**
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__	0.00028	0.008078	0.000176
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	0.000176	0.004849	0.000156

p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter	0.000166	0.010902	0.000177
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter	0.000125	0.003115	8.32E-05
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;Other	0.002056	0.021419	0.00136
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__	0.311841	0.05969	0.269781
p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	0.002762	0.0285	0.001973
p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Sinobacteraceae;g__	0.000104	8.32E-05	5.2E-05
p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Sinobacteraceae;g__Nevskia	0.000851	0.01167	0.001609
p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;Other	0	0.000249	0
p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter	0	0.000239	0
p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas	0.021056	0.023278	0.218014
p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Thermomonas	0.00272	0.00028	0.000467