

Table S1 List of the group specific probes.

Probe	Sequence (5' – 3')	Target	References
EUB338	GCTGCCTCCCGTAGGAGT		
EUB338 II	GCAGCCACCCGTAGGTGT	Bacteria	[1][2]
EUB338 III	GCTGCCACCCGTAGGTGT		
Delta495a	AGTTAGCCGGTGCTTCTT		
Delta495b	AGTTAGCCGGCGCTTCCT	<i>Deltaproteobacteria</i>	[3,4]
Delta495c	AATTAGCCGGTGCTTCCT		
Lgc354a	TGGAAGATTCCCTACTGC	<i>Firmicutes</i> ^{[1][2]} (Gram ⁺	
Lgc354b	CGGAAGATTCCCTACTGC	bacteria with low GC	[5]
Lgc354c	CCGAAGATTCCCTACTGC	content)	
Gnsb941	AAACCACACGCTCCGCT	<i>Chloroflexi</i> (green nonsulfur bacteria)	[6]
Alf968	GGTAAGGTTCTGCGCGTT	<i>Alphaproteobacteria</i> (except Rickettsiales)	[7]
Bet42a	GCCTTCCCACTTCGTTT	<i>Betaproteobacteria</i>	[8]
Gam2a	GCCTTCCCACATCGTTT	<i>Gammaproteobacteria</i>	[8]
Hgc69a	TATAGTTACCACCGCCGT	<i>Actinobacteria</i> (high GC Gram ⁺ bacteria)	[9]
Pla46	GACTTGCATGCCTAATCC	<i>Planctomycetales</i>	[10]
Cf319a	TGGTCCGTGTCTCAGTAC	<i>Flavobacteria</i> , <i>Bacteroidetes</i> , <i>Sphingobacteria</i>	[11]
Arc915	GTGCTCCCCCGCCAATTCCT	<i>Archaea</i> ^{[1][2]}	[12]
TM7905	CCGTCAATTCCTTTATGTTTTA	Candidate division TM7	[13]
DF988*	GATACGACGCCCATGTCAAGGG	<i>Defluvicoccus</i>	[14]
DF1020*	CCGGCCGAACCGACTCCC		
TFO-DF218	GAAGCCTTTGCCCTCAG	<i>Defluvicoccus</i> related	[15]
TFO-DF618	GCCTCACTTGTCTAACCG	TFO	
SBR9-1a	AAGCGCAAGTTCCAGGTTG	<i>Sphingomonas</i>	[16]
THAU646	TCTGCCGTACTCTAGCCTT	<i>Thauera</i> sp.	[17]
AZO644	GCCGTACTCTAGCCGTGC	<i>Azoarcus</i> sp.	[18]
PAR651	ACCTCTCTCGAACTCCAG	<i>Paracoccus</i>	[19]
AMAR839	CCGAACGGCAAGCCACAGCGTC	<i>Amaricoccus</i> sp.	[20]
ACI145	TTTCGCTTCGTTATCCCC	<i>Acidovorax</i> spp.	[21]

Table S2 Primers used in PCR and Sequencing.

	Primers	Sequence (5' – 3')
PCR	27f	AGAGTTTGATCMTGGCTCAG
	1492r	TACGGYTACCTTGTTACGACTT
	T7f	TAATACGACTCACTATAGGG
	U19r	GTTTTCCCAGTCACGACGT
	M13r	TCACACAGGAAACAGCTATGAC
Sequencing	530f	GTGCCAGCMGCCGCGG
	926f	AAACTYAAAKGAATTGACGG
	907r	CCGTCAATTCMTTTRAGTTT
	519r	GWATTACCGCGGCKGCTG

M = C:A; Y = C:T; K = G:T; R = A:G; W = A:T; all 1:1

Table S3 Clone library results

Microrganism	Sequence name	Clone number	% of similarity between sequences	Affiliation at group level
<i>Acidovorax</i>	Catarina_0	1	≥ 97%	<i>Betaproteobacteria</i>
	Catarina_0	5		
	Catarina_0	21		
	Catarina_1	39		
	Catarina_1	41		
	Catarina_1	46		
	Catarina_1	51		
	Catarina_2	85		
	Catarina_3	87		
	Catarina_3	92		
	Catarina_3	102		
	Catarina_3	104		
	Catarina_3	107		
	Catarina_4	126		
Catarina_5	132			
<i>Acidovorax "like"</i>	Catarina_5	141	94 - 96%	
	Catarina_5	145		
	Catarina_6	149		
	Catarina_6	155		
<i>Comomonas</i>	Catarina_6	157	100%	<i>Betaproteobacteria</i>
	Catarina_0	2		
<i>Leadbetterella</i>	Catarina_2	75	94%	<i>Cytophagia</i>
	Catarina_0	12		
<i>Catellibacterium</i>	Catarina_3	105		
<i>Ramlibacter</i>	Catarina_0	39		<i>Alphaproteobacteria</i>
	Catarina_1	40	96%	<i>Betaproteobacteria</i>
<i>Giesbergeria</i>	Catarina_1	43		<i>Betaproteobacteria</i>
	Catarina_1	57		<i>Flavobacteria</i>
<i>Salinirepens</i>	Catarina_1	60		
	Catarina_2	66	92 - 96%	<i>Alphaproteobacteria</i>
	Catarina_2	72		
Catarina_3	90			
<i>Paracoccus "like"</i>	Catarina_3	100	≥ 98%	
	Catarina_4	113		
	Catarina_6	158		
<i>Paracoccus</i>	Catarina_2	67	100%	<i>Alphaproteobacteria</i>
	Catarina_4	117		
<i>Agrobacterium</i>	Catarina_2	68	≥ 99%	<i>Betaproteobacteria</i>
	Catarina_2	86		
<i>Rhodoferax</i>	Catarina_5	83		
	Catarina_2	70		
	Catarina_2	76		
<i>Simplicispira</i>	Catarina_4	118	≥ 97%	<i>Betaproteobacteria</i>
	Catarina_5	133		
	Catarina_5	136		
	Catarina_5	147		
	Catarina_6	148		
<i>Shinella</i>	Catarina_6	164	99%	<i>Alphaproteobacteria</i>
	Catarina_3	101		
	Catarina_5	139		
<i>Novosphingobium</i>	Catarina_4	108		<i>Alphaproteobacteria</i>
<i>Hydrogenophaga</i>	Catarina_4	123	100%	<i>Betaproteobacteria</i>
	Catarina_4	125		
<i>Albidiferax</i>	Catarina_4	131		<i>Betaproteobacteria</i>
<i>Thauera</i>	Catarina_5	134		<i>Betaproteobacteria</i>
<i>Pseudoxanthomonas</i>	Catarina_5	146		<i>Gammaproteobacteria</i>

<i>Limnohabitans</i>	Catarina_6	152	98%	<i>Betaproteobacteria</i>
	Catarina_6	154		
<i>Variovorax</i>	Catarina_6	163		<i>Betaproteobacteria</i>

Table S4 Results of the complete sequencing.

Sequence name	Highest Similarity	% Identity	Acession number
CR1	<i>Acidovorax caeni</i>	94%	KT262954
CR2	<i>Acidovorax wautersii</i>	98%	KT262955
CR3	<i>Fluviicola taffensis</i>	92%	KT262951
CR4	<i>Leadbetterella byssophila</i>	95%	KT262956
CR5	<i>Comamonas testosteroni</i>	90%	KT262952
CR6	<i>Paracoccus siganidrum</i>	98%	KT262957
CR7	<i>Agrobacterium tumefaciens</i>	99%	KT262958
CR8	<i>Acidovorax radialis</i>	98%	KT262959
CR9	<i>Simplicispira metamorpha</i>	98%	KT262960
CR10	<i>Comamonas testosteroni</i>	99%	KT262961
CR11	<i>Alcaligenes aquatilis</i>	94%	KT262962
CR12	<i>Shinella zoogloeoides</i>	99%	KT262953
CR13	<i>Pseudoxanthomonas kaohsiungensis</i>	99%	KT262963
CR14	<i>Acidovorax delafieldii</i>	98%	KT262964
CR15	<i>Simplicispira metamorpha</i>	97%	KT262965

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