

SUPPLEMENTARY MATERIAL

Aerobic polishing of liquid digestate for preparation of hydroponic fertiliser

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inqaba biotec metagenomic report

Sample Information

Index:	M13_bc1010_F--M13_bc1066_R
Sample Name:	JM-Biofilm-16S
Run Name:	231127_Cell1
Report Date:	Tue Nov 28 11:22:22 2023

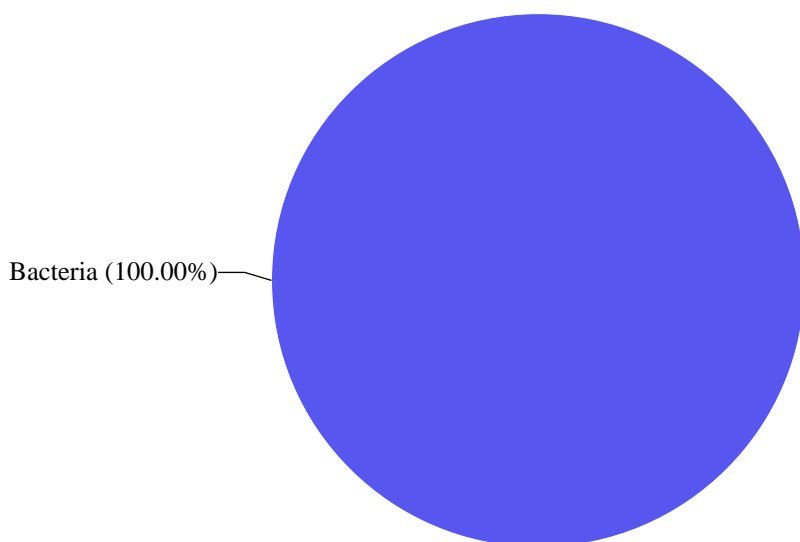
This report contains the summarized metagenomic analysis of full length 16s gene amplicons. Samples were sequenced on the Sequel IIe system by PacBio (www.pacb.com). Raw sub-reads were processed through the SMRTlink (v11.0) Circular Consensus Sequences (CCS) algorithm to produce highly accurate reads (>QV40). These highly accurate reads were then processed through vsearch (<https://github.com/torognes/vsearch>) and taxonomic information was determined based on QIIME2. Report generation command used :
`$create_vsearch_single_sample_pdf_report_pacbio.py
create_vsearch_single_sample_pdf_report_pacbio.py
JM-Biofilm-16S_M13_bc1010_F--M13_bc1066_R.hifi_reads-filtered-feature-table-asv.tsv M13_bc1010_F--M13_bc1066_R
JM-Biofilm-16S 231127_Cell1 16S`

Taxonomical Classification

Kingdom Classification

Kingdom	Read Count	%
Bacteria	44840.0	100.00

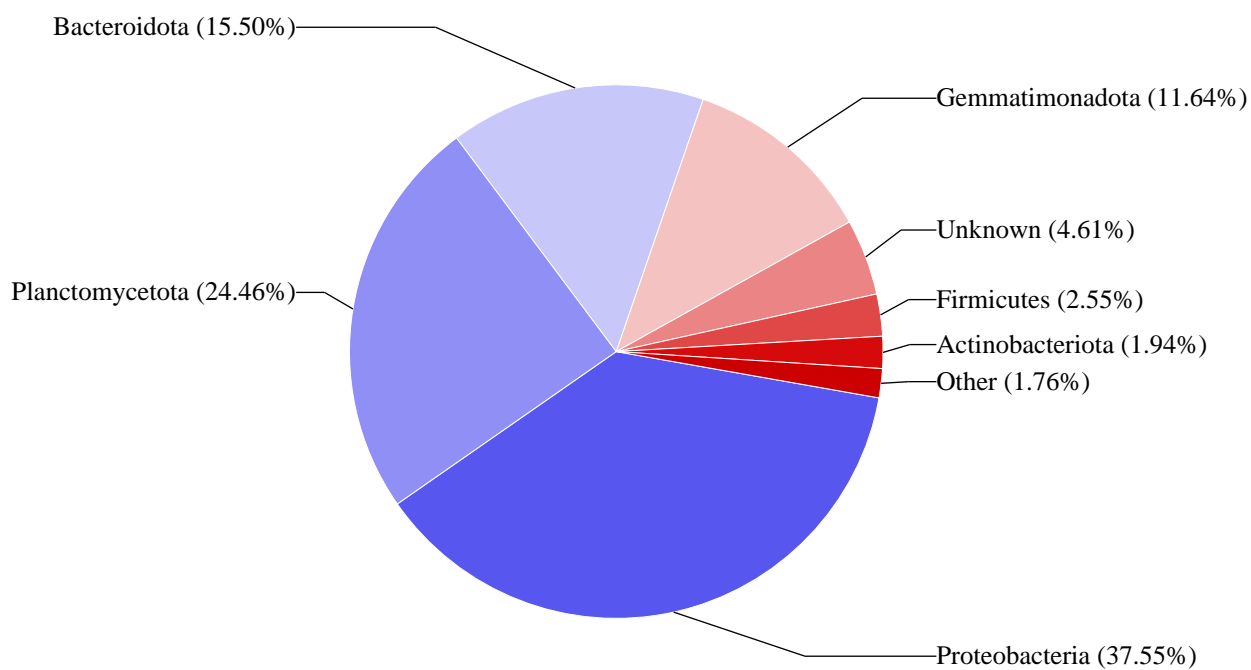
Top Kingdom Classification



Phylum Classification

Phyla Classification	Read Count	%
Proteobacteria	16835.0	37.55
Planctomycetota	10969.0	24.46
Bacteroidota	6949.0	15.50
Gemmatimonadota	5220.0	11.64
Unknown	2066.0	4.61
Firmicutes	1143.0	2.55
Actinobacteriota	868.0	1.94
Chloroflexi	606.0	1.35
Myxococcota	95.0	0.21
Patescibacteria	54.0	0.12
SAR324_clade	24.0	0.05
Desulfobacterota	10.0	0.02

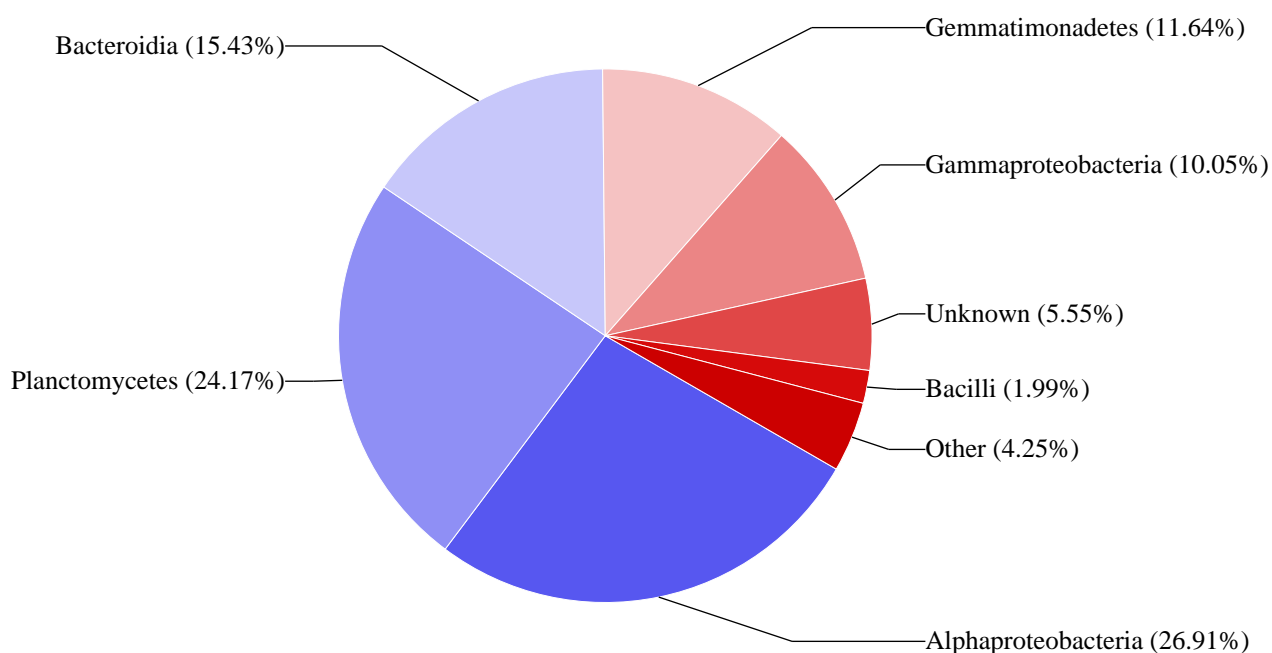
Top Phylum Classification



Class Classification

Class	Read Count	%
Alphaproteobacteria	12066.0	26.91
Planctomycetes	10835.0	24.17
Bacteroidia	6918.0	15.43
Gemmatimonadetes	5220.0	11.64
Gammaproteobacteria	4507.0	10.05
Unknown	2489.0	5.55
Bacilli	894.0	1.99
Anaerolineae	413.0	0.92
Acidimicrobiia	397.0	0.89
Actinobacteria	379.0	0.85
Clostridia	194.0	0.43
Chloroflexia	184.0	0.41
Polyangia	90.0	0.20
Thermoleophilia	86.0	0.19
Saccharimonadia	54.0	0.12
Limnochordia	45.0	0.10
SJA	31.0	0.07
SAR324_clade	24.0	0.05
Desulfovibrionia	10.0	0.02

Top Class Classification

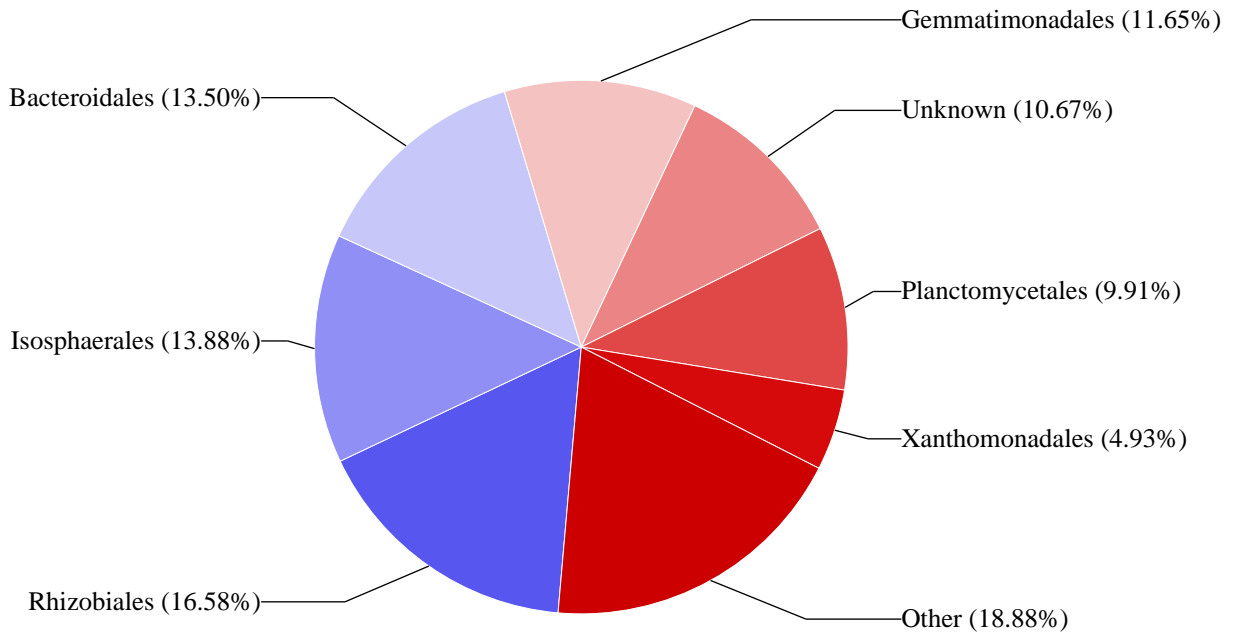


Order Classification

Order	Read Count	%
Rhizobiales	7427.0	16.58
Isosphaerales	6218.0	13.88
Bacteroidales	6048.0	13.50
Gemmatimonadales	5220.0	11.65
Unknown	4781.0	10.67
Planctomycetales	4438.0	9.91
Xanthomonadales	2208.0	4.93
Burkholderiales	1902.0	4.25
Reyranellales	819.0	1.83
Chitinophagales	740.0	1.65
Sphingomonadales	698.0	1.56
Paenibacillales	693.0	1.55
Caulobacterales	442.0	0.99
SBR1031	388.0	0.87
Microtrichales	373.0	0.83
Acetobacterales	246.0	0.55
Corynebacteriales	245.0	0.55
Legionellales	190.0	0.42
Rhodospirillales	170.0	0.38
Bacillales	155.0	0.35
Thermomicrobiales	143.0	0.32
Pseudomonadales	142.0	0.32
Peptostreptococcales	139.0	0.31
Micrococcales	108.0	0.24
Rhodobacterales	99.0	0.22
mle1	88.0	0.20
Solirubrobacterales	82.0	0.18
Azospirillales	74.0	0.17
Ferrovibrionales	68.0	0.15
uncultured	56.0	0.13
Saccharimonadales	54.0	0.12
Sphingobacteriales	44.0	0.10
Kallotenuales	41.0	0.09
MBA03	37.0	0.08
SJA	31.0	0.07
Bacteroidetes_VC2	31.0	0.07
SAR324_clade	24.0	0.05
Puniceispirillales	19.0	0.04
Anaerolineales	19.0	0.04

Christensenellales	15.0	0.03
Izemoplasmatales	13.0	0.03
Oscillospirales	13.0	0.03
Defluviicoccales	12.0	0.03
Propionibacteriales	12.0	0.03
Clostridia	11.0	0.02
Desulfovibrionales	10.0	0.02
Lachnospirales	7.0	0.02
Micropepsales	6.0	0.01

Top Order Classification

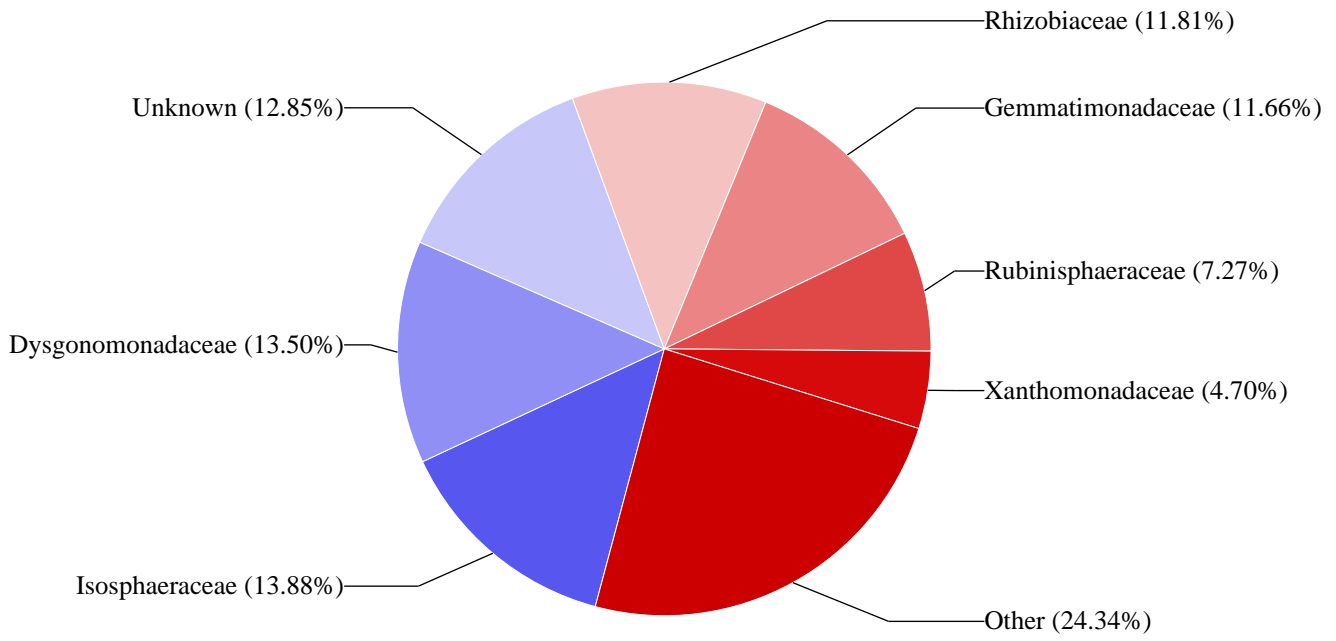


Family Classification

Family	Read Count	%
Isosphaeraceae	6218.0	13.88
Dysgonomonadaceae	6047.0	13.50
Unknown	5757.0	12.85
Rhizobiaceae	5288.0	11.81
Gemmatimonadaceae	5220.0	11.66
Rubinisphaeraceae	3254.0	7.27
Xanthomonadaceae	2103.0	4.70
Comamonadaceae	1719.0	3.84
Xanthobacteraceae	1044.0	2.33
Reyranellaceae	819.0	1.83
Sphingomonadaceae	698.0	1.56
Paenibacillaceae	693.0	1.55
Chitinophagaceae	676.0	1.51
uncultured	476.0	1.06
Schlesneriaceae	466.0	1.04
Caulobacteraceae	442.0	0.99
A4b	359.0	0.80
Microtrichaceae	276.0	0.62
Acetobacteraceae	246.0	0.55
Devosiaceae	244.0	0.54
Beijerinckiaceae	236.0	0.53
Nocardiaceae	235.0	0.52
Legionellaceae	190.0	0.42
Rhodospirillaceae	158.0	0.35
Hyphomicrobiaceae	149.0	0.33
JG30	144.0	0.32
Bacillaceae	121.0	0.27
Alcaligenaceae	119.0	0.27
Moraxellaceae	104.0	0.23
Rhodobacteraceae	99.0	0.22
Microbacteriaceae	96.0	0.21
Rhodanobacteraceae	90.0	0.20
Proteiniboraceae	88.0	0.20
mle1	88.0	0.20
Solirubrobacteraceae	77.0	0.17
Ferrovibrionaceae	68.0	0.15
Azospirillaceae	66.0	0.15
Ilumatobacteraceae	47.0	0.10
Sphingobacteriaceae	44.0	0.10

AKIW781	41.0	0.09
Saccharimonadales	40.0	0.09
Pseudomonadaceae	38.0	0.08
Rhodocyclaceae	38.0	0.08
MBA03	37.0	0.08
Rhizobiales_Incertae_Sedis	32.0	0.07
Planococcaceae	32.0	0.07
SJA	31.0	0.07
Bacteroidetes_VC2	31.0	0.07
Sedimentibacteraceae	25.0	0.06
SAR324_clade	24.0	0.05
Anaerolineaceae	19.0	0.04
Kaistiaceae	15.0	0.03
Christensenellaceae	15.0	0.03
Izemoplasmatales	13.0	0.03
Propionibacteriaceae	12.0	0.03
Anaerovoracaceae	11.0	0.02
Desulfovibrionaceae	10.0	0.02
Peptostreptococcales	9.0	0.02
UCG	8.0	0.02
Azospirillales_Incertae_Sedis	8.0	0.02
Gracilibacteraceae	7.0	0.02
Micropepsaceae	6.0	0.01
Lachnospiraceae	6.0	0.01
SBR1031	5.0	0.01
Burkholderiaceae	5.0	0.01
Mycobacteriaceae	5.0	0.01

Top Family Classification



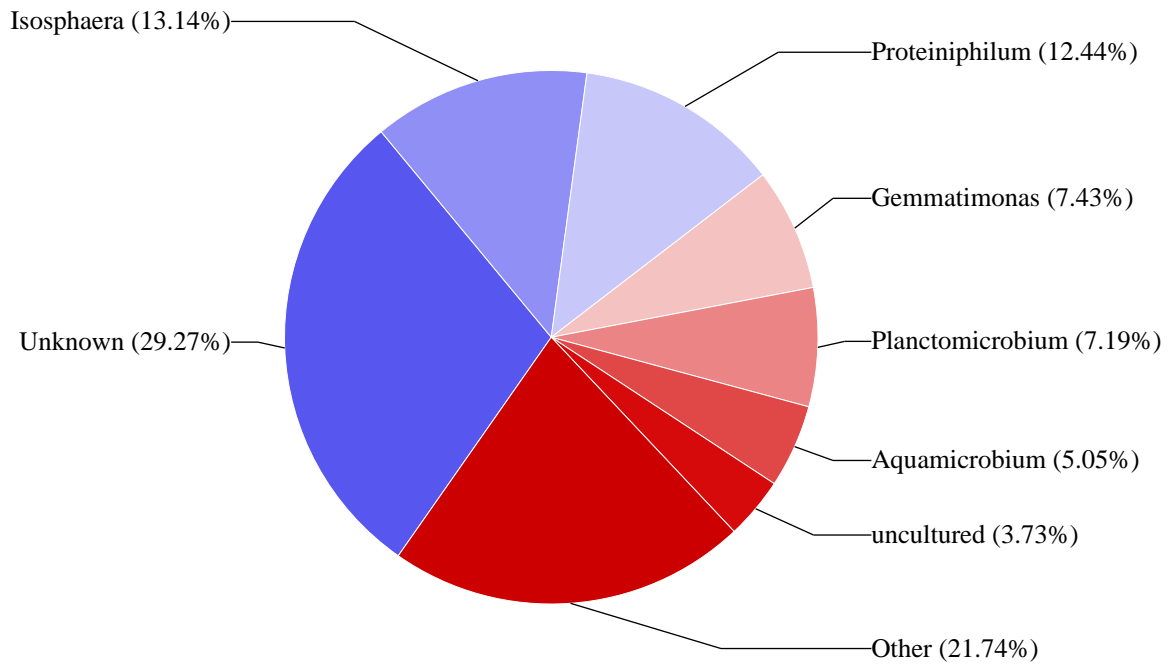
Genus Classification

Genus	Read Count	%
Unknown	13099.0	29.27
Isosphaera	5881.0	13.14
Proteiniphilum	5568.0	12.44
Gemmatimonas	3323.0	7.43
Planctomicrobium	3218.0	7.19
Aquamicrobium	2258.0	5.05
uncultured	1670.0	3.73
Luteimonas	1320.0	2.95
Reyranella	814.0	1.82
Paenibacillus	636.0	1.42
Hydrogenophaga	552.0	1.23
Planctopirus	466.0	1.04
Terrimonas	446.0	1.00
A4b	359.0	0.80
Sphingopyxis	351.0	0.78
Phenylobacterium	310.0	0.69
IMCC26207	275.0	0.61
Roseomonas	229.0	0.51
Shinella	221.0	0.49
Acidovorax	216.0	0.48
Petrimonas	207.0	0.46
Legionella	190.0	0.42
Caenispirillum	157.0	0.35
Bosea	147.0	0.33
JG30	144.0	0.32
Devosia	139.0	0.31
Fermentimonas	126.0	0.28
Rhodococcus	104.0	0.23
Acinetobacter	102.0	0.23
Proteiniborus	88.0	0.20
mle1	88.0	0.20
Stenotrophomonas	81.0	0.18
Bacillus	80.0	0.18
Tahibacter	77.0	0.17
Mesorhizobium	77.0	0.17
Edaphobaculum	76.0	0.17
Pseudorhodoplanes	75.0	0.17
Xanthobacter	74.0	0.17
Hyphomicrobium	70.0	0.16
Ferrovibrio	68.0	0.15
Pseudaminobacter	68.0	0.15

Azospirillum	66.0	0.15
Paracoccus	63.0	0.14
Altererythrobacter	55.0	0.12
Ochrobactrum	47.0	0.11
Microbacterium	47.0	0.11
AKIW781	41.0	0.09
Saccharimonadales	40.0	0.09
Pseudomonas	38.0	0.08
Youhaiella	38.0	0.08
Pedobacter	38.0	0.08
MBA03	37.0	0.08
Brevundimonas	35.0	0.08
SH	33.0	0.07
SJA	31.0	0.07
Comamonas	31.0	0.07
Bacteroidetes_VC2	31.0	0.07
Novosphingobium	30.0	0.07
Pseudolabrys	25.0	0.06
Bradyrhizobium	25.0	0.06
Azospira	25.0	0.06
Sedimentibacter	25.0	0.06
Anoxybacillus	24.0	0.05
Lysinibacillus	24.0	0.05
SAR324_clade	24.0	0.05
Pedomicrobium	24.0	0.05
Pseudorhodoferax	23.0	0.05
Nitratireductor	23.0	0.05
Alicyclophilus	23.0	0.05
Leucobacter	21.0	0.05
Bauldia	19.0	0.04
Lysobacter	19.0	0.04
Pseudoxanthobacter	18.0	0.04
JCM_18997	18.0	0.04
Cohnella	16.0	0.04
Kaistia	15.0	0.03
Xanthobacteraceae	15.0	0.03
alpha_cluster	14.0	0.03
Christensenellaceae_R	14.0	0.03
Izemoplasmatales	13.0	0.03
Phreatobacter	13.0	0.03
UCG	11.0	0.02
Pseudoxanthomonas	11.0	0.02
Allorhizobium	11.0	0.02

Desulfovibrio	10.0	0.02
Delftia	8.0	0.02
Stella	8.0	0.02
Sphingaurantiacus	7.0	0.02
Afipia	7.0	0.02
Lutispora	7.0	0.02
Alcaligenes	7.0	0.02
Thauera	6.0	0.01
Sphingomonas	6.0	0.01
Anaerolinea	6.0	0.01
Extensimonas	6.0	0.01
Tepidimonas	5.0	0.01
Amnipila	5.0	0.01
Pseudoflavitalea	5.0	0.01
SBR1031	5.0	0.01
Mycobacterium	5.0	0.01

Top Genus Classification



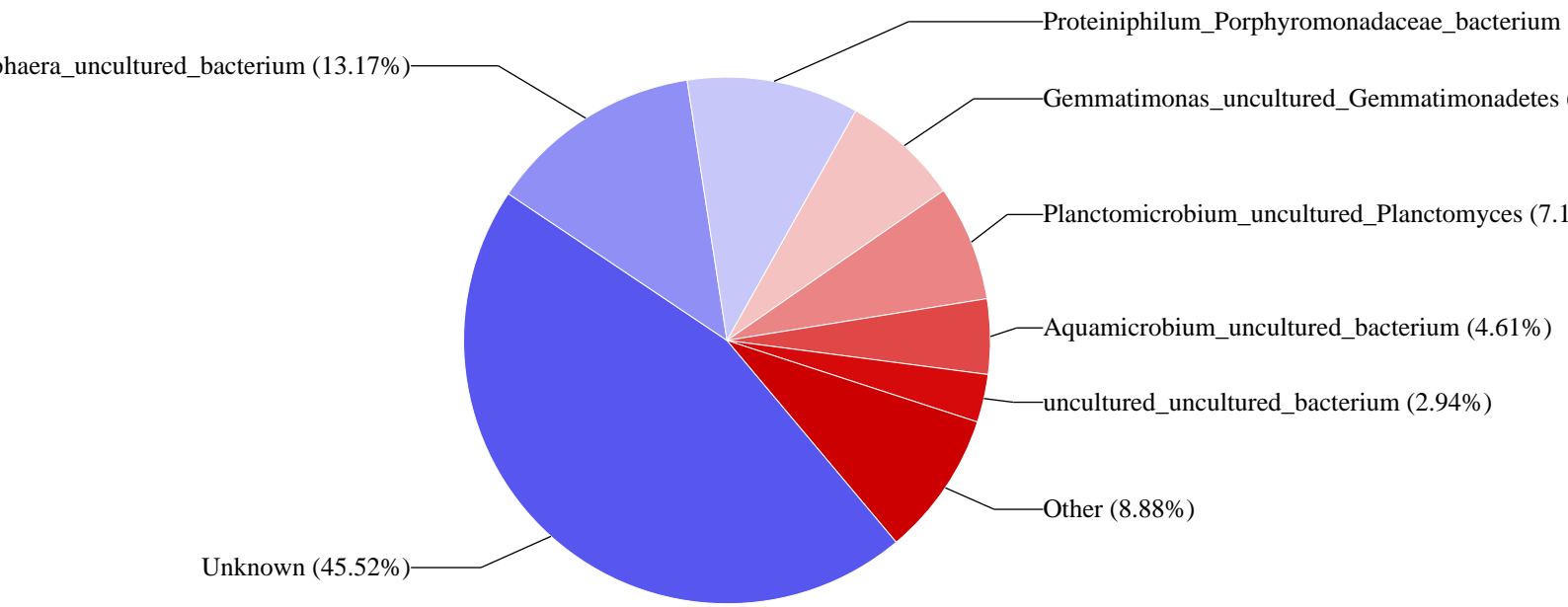
Species Classification

Species	Read Count	%
Unknown	20327.0	45.52
Isosphaera_uncultured_bacterium	5881.0	13.17
Proteiniphilum_Porphyrimonadaceae_bacterium	4716.0	10.56
Gemmatimonas_uncultured_Gemmatimonadetes	3224.0	7.22
Planctomicrobium_uncultured_Planctomyces	3172.0	7.10
Aquamicrobium_uncultured_bacterium	2058.0	4.61
uncultured_uncultured_bacterium	1314.0	2.94
Luteimonas_uncultured_bacterium	1040.0	2.33
Proteiniphilum_Proteiniphilum_saccharofermentans	557.0	1.25
Hydrogenophaga_uncultured_bacterium	402.0	0.90
Petrimonas_Petrimonas_mucosa	196.0	0.44
Caenispirillum_uncultured_Caenispirillum	153.0	0.34
Paenibacillus_uncultured_Firmicutes	118.0	0.26
A4b_uncultured_bacterium	98.0	0.22
mle1_uncultured_bacterium	85.0	0.19
Legionella_Legionella_pneumophila	82.0	0.18
Tahibacter_uncultured_bacterium	77.0	0.17
JG30_uncultured_Chloroflexi	73.0	0.16
uncultured_metagenome	55.0	0.12
Paenibacillus_uncultured_bacterium	49.0	0.11
Stenotrophomonas_Stenotrophomonas_acidaminiphila	49.0	0.11
Luteimonas_Luteimonas_terricola	44.0	0.10
Terrimonas_Hypsibius_dujardini	44.0	0.10
Phenylobacterium_uncultured_bacterium	40.0	0.09
Saccharimonadales_uncultured_bacterium	39.0	0.09
Sphingopyxis_Sphingopyxis_terrae	37.0	0.08
AKIW781_uncultured_Kouleothrix	37.0	0.08
Acinetobacter_Acinetobacter_junii	33.0	0.07
Ferrovibrio_uncultured_bacterium	32.0	0.07
SJA_uncultured_bacterium	31.0	0.07
Proteiniborus_uncultured_bacterium	31.0	0.07
IMCC26207_uncultured_actinobacterium	28.0	0.06
Hyphomicrobium_uncultured_Hyphomicrobiaceae	24.0	0.05
JG30_uncultured_bacterium	21.0	0.05
Fermentimonas_Fermentimonas_caenicola	20.0	0.04
Paracoccus_Paracoccus_versutus	19.0	0.04
Devosia_uncultured_bacterium	19.0	0.04
MBA03_uncultured_bacterium	19.0	0.04
Nitratireductor_Nitratireductor_indicus	19.0	0.04

uncultured_Afipia_sp	18.0	0.04
Pseudorhodoplanes_uncultured_Rhizobiales	18.0	0.04
JG30_uncultured_soil	17.0	0.04
Pseudoxanthobacter_Pseudoxanthobacter_liyangensis	16.0	0.04
Azospirillum_Azospirillum_brasilense	15.0	0.03
Bauldia_metagenome	15.0	0.03
Comamonas_Comamonas_testosteroni	15.0	0.03
Altererythrobacter_uncultured_bacterium	13.0	0.03
Xanthobacteraceae_uncultured_bacterium	13.0	0.03
SAR324_clade_uncultured_bacterium	13.0	0.03
Phenylobacterium_uncultured_Alphaproteobacteria	13.0	0.03
Altererythrobacter_Sphingomonas_sp	12.0	0.03
Desulfovibrio_Desulfovibrio_putialis	10.0	0.02
Anoxybacillus_Anoxybacillus_geothermalis	9.0	0.02
MBA03_uncultured_Clostridiales	9.0	0.02
Sphingopyxis_uncultured_bacterium	9.0	0.02
Pseudolabrys_metagenome	9.0	0.02
Anoxybacillus_Anoxybacillus_sp	9.0	0.02
Pseudomonas_Pseudomonas_aeruginosa	9.0	0.02
SH_uncultured_bacterium	8.0	0.02
Rhodococcus_Rhodococcus_ruber	8.0	0.02
Stella_metagenome	8.0	0.02
Ferrovibrio_metagenome	7.0	0.02
Bosea_uncultured_bacterium	7.0	0.02
Pseudaminobacter_uncultured_bacterium	7.0	0.02
Pseudorhodoplanes_uncultured_Alphaproteobacteria	7.0	0.02
Rhodococcus_Rhodococcus_hoagii	6.0	0.01
Izemoplasmatales_uncultured_bacterium	6.0	0.01
Lysobacter_uncultured_bacterium	6.0	0.01
Acidovorax_uncultured_bacterium	6.0	0.01
Sedimentibacter_iron	6.0	0.01
Sedimentibacter_uncultured_bacterium	6.0	0.01
Reyranella_metagenome	6.0	0.01
Hyphomicrobium_Hyphomicrobium_zavarzinii	6.0	0.01
JCM_18997_Conexibacter_sp	6.0	0.01
Amnipila_uncultured_Anaerovorax	5.0	0.01
Azospirillum_uncultured_Azospirillum	5.0	0.01
UCG_uncultured_bacterium	5.0	0.01
Brevundimonas_uncultured_Caulobacteraceae	5.0	0.01
Leucobacter_Leucobacter_chironomi	5.0	0.01
Christensenellaceae_R_uncultured_bacterium	5.0	0.01
Acinetobacter_uncultured_bacterium	5.0	0.01
Pseudolabrys_Pseudolabrys_taiwanensis	5.0	0.01

Extensimonas_Brachymonas_petroleovorans	5.0	0.01
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Top Species Classification



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