

SUPPLEMENTARY MATERIAL

Diazotrophic Behaviour in a Non-sterile Bioreactor: the Effect of O₂-availability

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inqaba biotec metagenomic report

Sample Information

Index:	M13_bc1002_F--M13_bc1052
Sample Name:	A
Run Name:	210827_Cell2
Report Date:	Mon Aug 30 10:43:31 2021

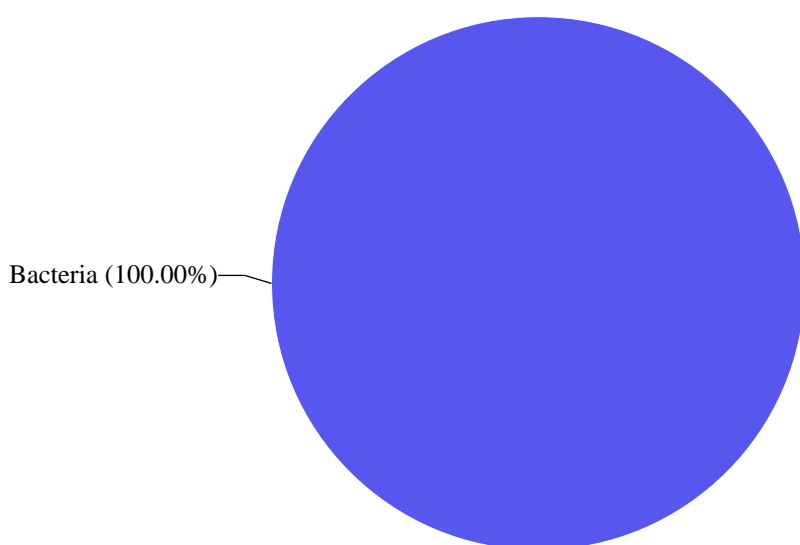
This report contains the summarized metagenomic analysis of full length 16s gene amplicons. Samples were sequenced on the Sequel system by PacBio (www.pacb.com). Raw subreads were processed through the SMRTlink (v9.0) Circular Consensus Sequences (CCS) algorithm to produce highly accurate reads (>QV40). These highly accurate reads were then processed through vsearch (<https://github.com/torognes/vsearch>) and taxonomic information was determined based on QIMME2. Report generation command used :`$create_vsearch_single_sample_pdf_report_pacbio.py create_vsearch_single_sample_pdf_report_pacbio.py demultiplex.M13_bc1002_F--M13_bc1052_R.hifi_reads_otu_table.tsv M13_bc1002_F--M13_bc1052 A 210827_Cell2 16s`

Taxonomical Classification

Kingdom Classification

Kingdom	Read Count	%
Bacteria	6985.0	100.00

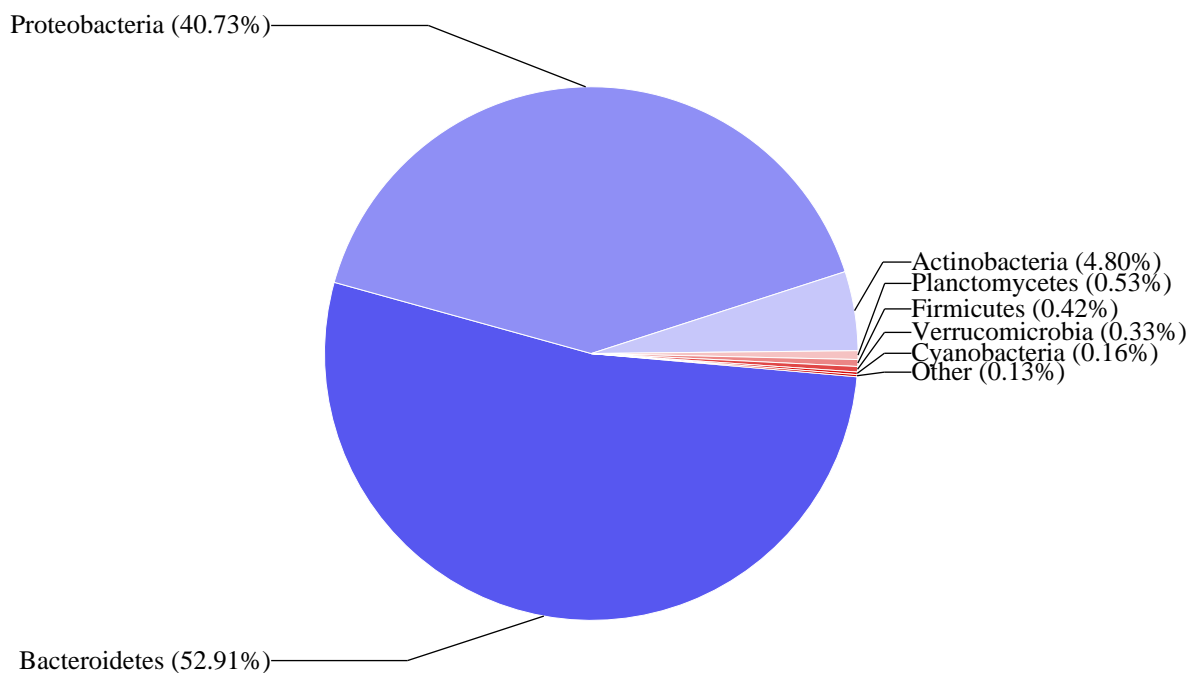
Top Kingdom Classification



Phylum Classification

Phyla Classification	Read Count	%
Bacteroidetes	3696.0	52.91
Proteobacteria	2845.0	40.73
Actinobacteria	335.0	4.80
Planctomycetes	37.0	0.53
Firmicutes	29.0	0.42
Verrucomicrobia	23.0	0.33
Cyanobacteria	11.0	0.16
Unknown	6.0	0.09
Acidobacteria	1.0	0.01
Armatimonadetes	1.0	0.01
Gemmatimonadetes	1.0	0.01

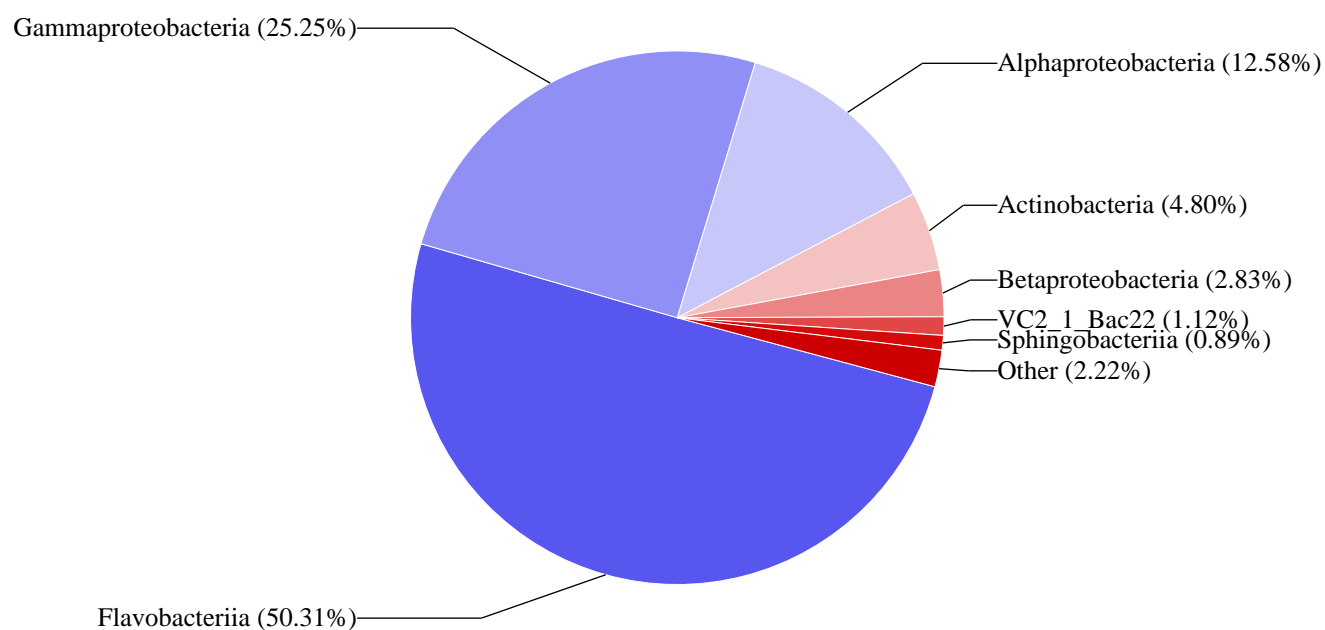
Top Phylum Classification



Class Classification

Class	Read Count	%
Flavobacteriia	3514.0	50.31
Gammaproteobacteria	1764.0	25.25
Alphaproteobacteria	879.0	12.58
Actinobacteria	335.0	4.80
Betaproteobacteria	198.0	2.83
VC2_1_Bac22	78.0	1.12
Sphingobacteriia	62.0	0.89
Planctomycetia	37.0	0.53
	25.0	0.36
Cytophagia	21.0	0.30
Clostridia	16.0	0.23
Verrucomicrobiae	15.0	0.21
Unknown	13.0	0.19
Bacilli	13.0	0.19
ML635J	11.0	0.16
Bacteroidia	1.0	0.01
Acidobacteria	1.0	0.01
Deltaproteobacteria	1.0	0.01
Gemmatimonadetes	1.0	0.01

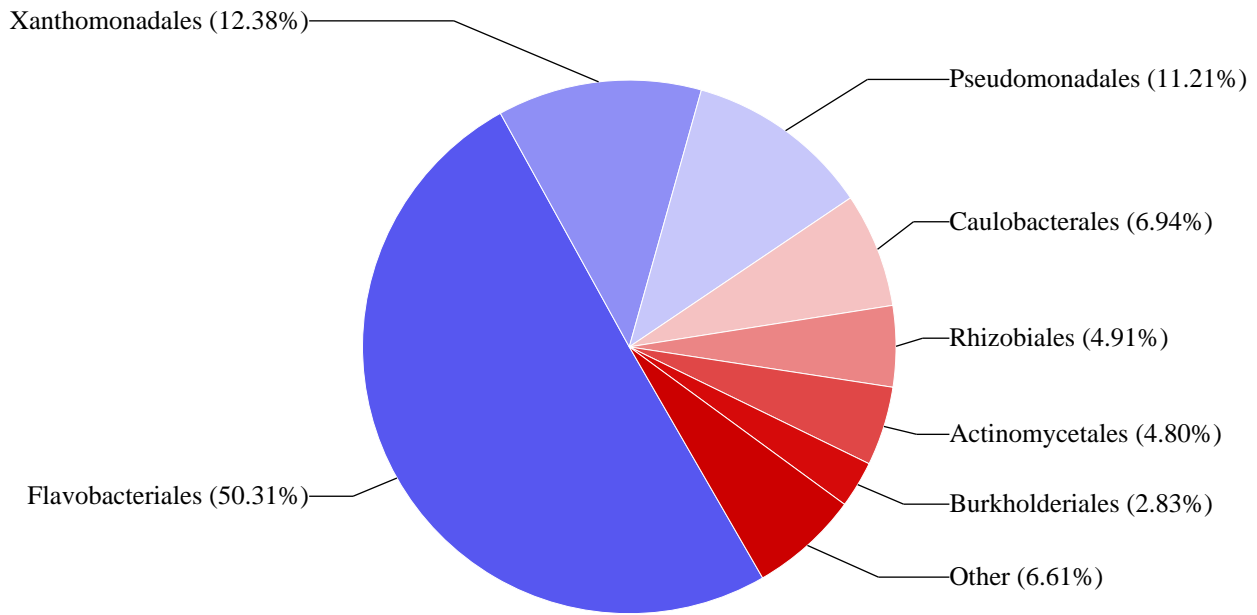
Top Class Classification



Order Classification

Order	Read Count	%
Flavobacteriales	3514.0	50.31
Xanthomonadales	865.0	12.38
Pseudomonadales	783.0	11.21
Caulobacterales	485.0	6.94
Rhizobiales	343.0	4.91
Actinomycetales	335.0	4.80
Burkholderiales	198.0	2.83
	114.0	1.63
Enterobacteriales	109.0	1.56
Sphingobacteriales	62.0	0.89
Gemmatales	37.0	0.53
Unknown	28.0	0.40
Sphingomonadales	25.0	0.36
Cytophagales	21.0	0.30
Clostridiales	16.0	0.23
Verrucomicrobiales	15.0	0.21
Rickettsiales	15.0	0.21
Lactobacillales	11.0	0.16
Rhodospirillales	4.0	0.06
Bacteroidales	1.0	0.01
iii1	1.0	0.01
Bacillales	1.0	0.01
Desulfuromonadales	1.0	0.01
Gemmatimonadales	1.0	0.01

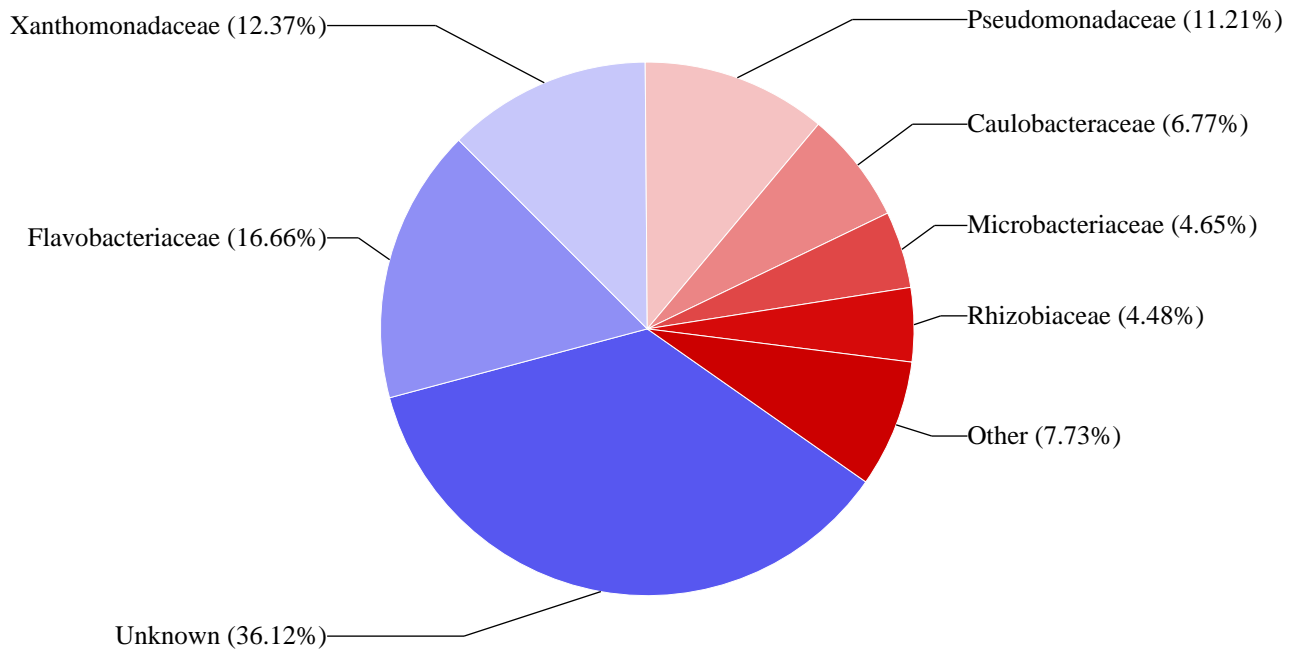
Top Order Classification



Family Classification

Family	Read Count	%
Unknown	2523.0	36.12
Flavobacteriaceae	1164.0	16.66
Xanthomonadaceae	864.0	12.37
Pseudomonadaceae	783.0	11.21
Caulobacteraceae	473.0	6.77
Microbacteriaceae	325.0	4.65
Rhizobiaceae	313.0	4.48
Comamonadaceae	193.0	2.76
Enterobacteriaceae	109.0	1.56
Sphingobacteriaceae	62.0	0.89
Isosphaeraceae	36.0	0.52
Sphingomonadaceae	24.0	0.34
Cytophagaceae	21.0	0.30
Clostridiaceae	16.0	0.23
Chitinophagaceae	16.0	0.23
Verrucomicrobiaceae	15.0	0.21
Hyphomicrobiaceae	12.0	0.17
Cellulomonadaceae	8.0	0.11
Streptococcaceae	8.0	0.11
Oxalobacteraceae	4.0	0.06
Rhodospirillaceae	3.0	0.04
Phyllobacteriaceae	3.0	0.04
Beijerinckiaceae	2.0	0.03
Sinobacteraceae	1.0	0.01
Paenibacillaceae	1.0	0.01
Desulfuromonadaceae	1.0	0.01
Gemmatimonadaceae	1.0	0.01
Acetobacteraceae	1.0	0.01
Gemmataceae	1.0	0.01
Alcaligenaceae	1.0	0.01
Enterococcaceae	1.0	0.01

Top Family Classification

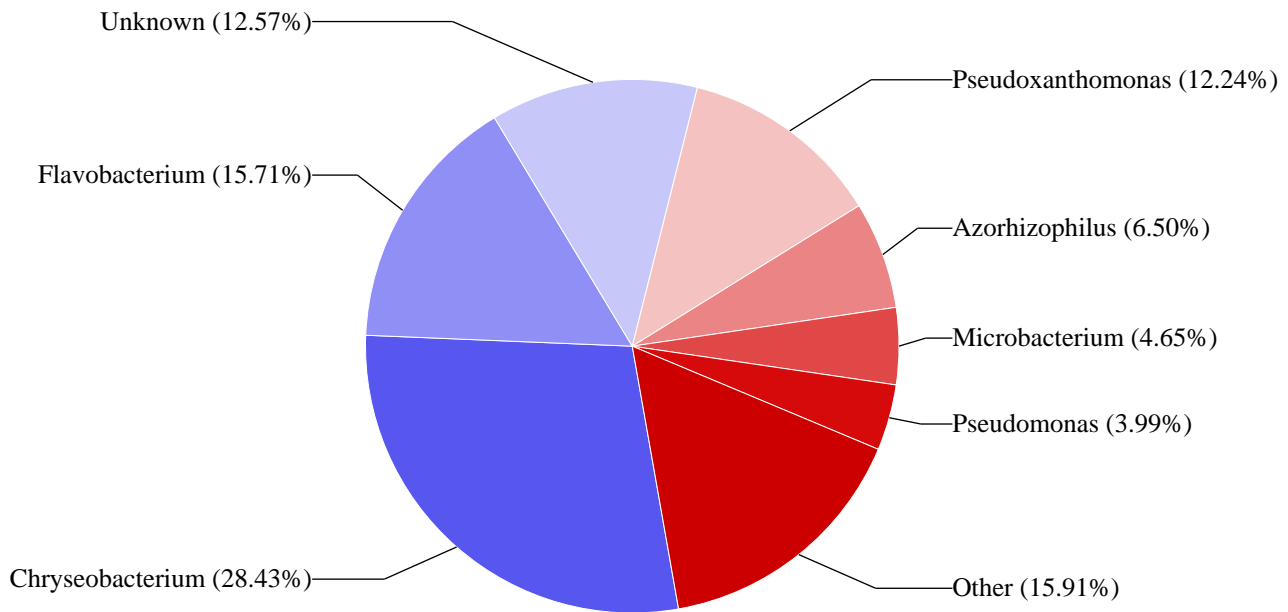


Genus Classification

Genus	Read Count	%
Chryseobacterium	1986.0	28.43
Flavobacterium	1097.0	15.71
Unknown	878.0	12.57
Pseudoxanthomonas	855.0	12.24
Azorhizophilus	454.0	6.50
Microbacterium	325.0	4.65
Pseudomonas	279.0	3.99
Agrobacterium	204.0	2.92
Caulobacter	162.0	2.32
Acidovorax	151.0	2.16
Brevundimonas	106.0	1.52
Elizabethkingia	83.0	1.19
Klebsiella	79.0	1.13
Mycoplana	53.0	0.76
Pedobacter	50.0	0.72
Riemerella	34.0	0.49
Flectobacillus	17.0	0.24
Clostridium	16.0	0.23
Sphingopyxis	14.0	0.20
Amorphomonas	11.0	0.16
Arthrospira	11.0	0.16
Azotobacter	10.0	0.14
Devosia	10.0	0.14
Cellulomonas	8.0	0.11
Candidatus	8.0	0.11
Shinella	7.0	0.10
Limnohabitans	7.0	0.10
Lactococcus	7.0	0.10
Kaistia	6.0	0.09
Imtechella	6.0	0.09
Salmonella	5.0	0.07
Novosphingobium	4.0	0.06
Sphingobium	4.0	0.06
Herbaspirillum	4.0	0.06
Azospirillum	3.0	0.04
Azomonas	3.0	0.04
Stenotrophomonas	3.0	0.04
Nitrobacteria	3.0	0.04
Variovorax	3.0	0.04
Xylophilus	2.0	0.03
Spirosoma	2.0	0.03

Pedomicrobium	2.0	0.03
Terrimonas	1.0	0.01
Mucilaginibacter	1.0	0.01
Hydrocarboniphaga	1.0	0.01
Dyella	1.0	0.01
Paenibacillus	1.0	0.01
Fimbriimonas	1.0	0.01
Gemmatimonas	1.0	0.01
Streptococcus	1.0	0.01
Gemmata	1.0	0.01
Phenylobacterium	1.0	0.01
Xenorhabdus	1.0	0.01
Vagococcus	1.0	0.01
Curvibacter	1.0	0.01

Top Genus Classification

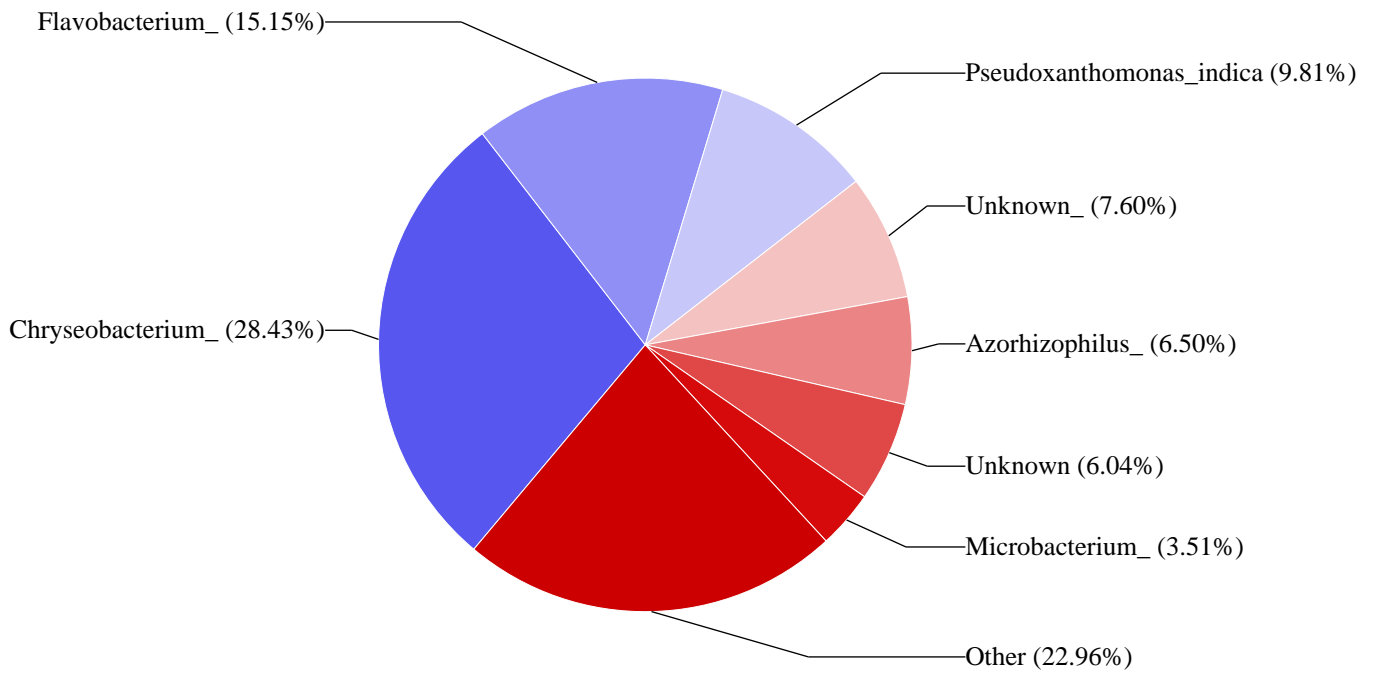


Species Classification

Species	Read Count	%
Chryseobacterium_	1986.0	28.43
Flavobacterium_	1058.0	15.15
Pseudoxanthomonas_indica	685.0	9.81
Unknown_	531.0	7.60
Azorhizophilus_	454.0	6.50
Unknown	422.0	6.04
Microbacterium_	245.0	3.51
Agrobacterium_	203.0	2.91
Pseudomonas_veronii	167.0	2.39
Pseudoxanthomonas_mexicana	161.0	2.30
Caulobacter_	161.0	2.30
Acidovorax_	137.0	1.96
Brevundimonas_poindexteriae	103.0	1.47
Elizabethkingia_	82.0	1.17
Klebsiella_	79.0	1.13
Pseudomonas_	76.0	1.09
Mycoplana_	53.0	0.76
Microbacterium_aurum	37.0	0.53
Pedobacter_	37.0	0.53
Riemerella_	34.0	0.49
Pseudomonas_umsongensis	23.0	0.33
Microbacterium_chocolatum	23.0	0.33
Flectobacillus_	17.0	0.24
Clostridium_pasteurianum	16.0	0.23
Flavobacterium_gelidilacus	15.0	0.21
Sphingopyxis_	14.0	0.20
Amorphomonas_oryzae	11.0	0.16
Arthrospira_	11.0	0.16
Azotobacter_armeniacus	10.0	0.14
Devosia_	10.0	0.14
Cellulomonas_	8.0	0.11
Acidovorax_delafieldii	8.0	0.11
Candidatus_	8.0	0.11
Limnohabitans_	7.0	0.10
Kaistia_	6.0	0.09
Shinella_	6.0	0.09
Imtechella_halotolerans	6.0	0.09
Pseudoxanthomonas_	5.0	0.07
Salmonella_	5.0	0.07

Herbaspirillum_	4.0	0.06
Lactococcus_garvieae	4.0	0.06
Flavobacterium_succinicans	4.0	0.06
Pseudomonas_thermotolerans	3.0	0.04
Acidovorax_wohlfahrtii	3.0	0.04
Novosphingobium_	3.0	0.04
Azospirillum_	3.0	0.04
Sphingobium_yanoikuyae	3.0	0.04
Nitrobacteria_hamadaniensis	3.0	0.04
Variovorax_	3.0	0.04
Lactococcus_	3.0	0.04
Xylophilus_ampelinus	2.0	0.03
Spirosoma_	2.0	0.03
Stenotrophomonas_acidaminiphila	2.0	0.03
Microbacterium_lacticum	2.0	0.03
Pedomicrobium_australicum	2.0	0.03
Sphingobium_	1.0	0.01
Agrobacterium_undicola	1.0	0.01
Hydrocarboniphaga_effusa	1.0	0.01
Azomonas_agilis	1.0	0.01
Stenotrophomonas_panacihumi	1.0	0.01
Microbacterium_maritypicum	1.0	0.01
Dyella_	1.0	0.01
Fimbriimonas_	1.0	0.01
Gemmatimonas_	1.0	0.01
Novosphingobium_stygium	1.0	0.01
Streptococcus_alactolyticus	1.0	0.01
Gemmata_obscuriglobus	1.0	0.01
Flavobacterium_frigidarium	1.0	0.01
Phenylobacterium_	1.0	0.01
Xenorhabdus_bovienii	1.0	0.01
Vagococcus_	1.0	0.01
Caulobacter_henricii	1.0	0.01
Azomonas_	1.0	0.01
Curvibacter_	1.0	0.01

Top Species Classification



----- End of report -----



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Sample Information

Index:	M13_bc1002_F--M13_bc1053
Sample Name:	B
Run Name:	210827_Cell2
Report Date:	Mon Aug 30 10:45:28 2021

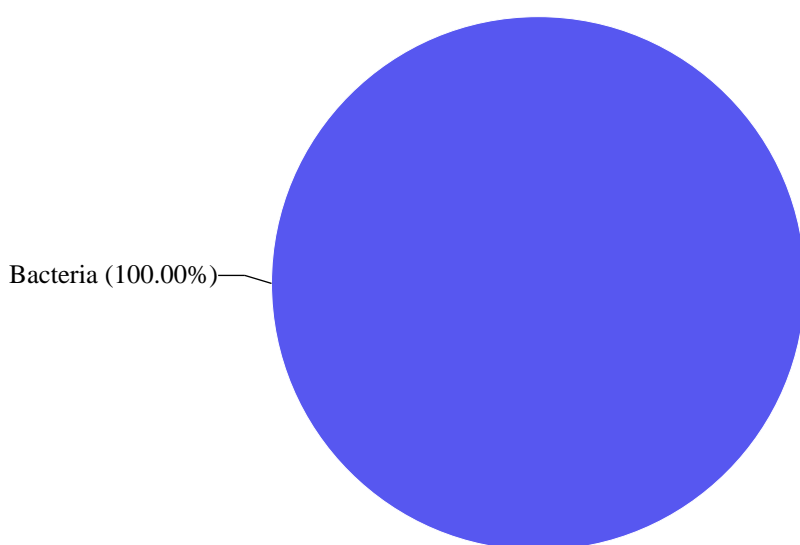
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Taxonomical Classification

Kingdom Classification

Kingdom	Read Count	%
Bacteria	8343.0	100.00

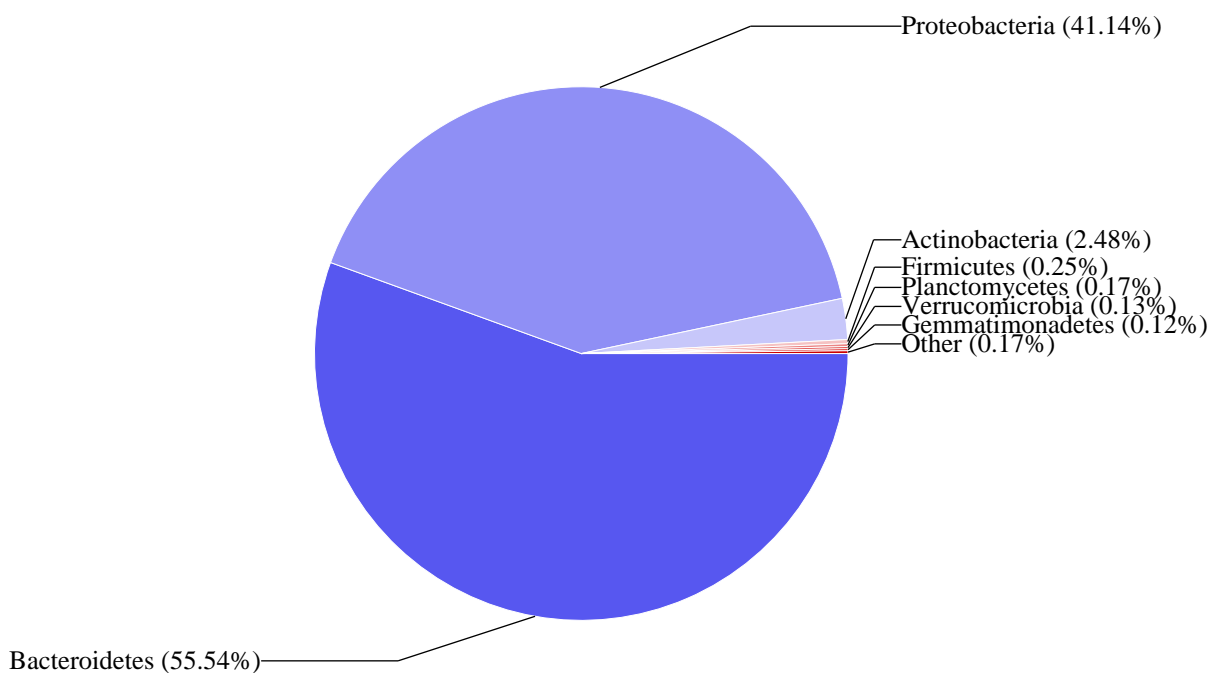
Top Kingdom Classification



Phylum Classification

Phyla Classification	Read Count	%
Bacteroidetes	4634.0	55.54
Proteobacteria	3432.0	41.14
Actinobacteria	207.0	2.48
Firmicutes	21.0	0.25
Planctomycetes	14.0	0.17
Verrucomicrobia	11.0	0.13
Gemmatimonadetes	10.0	0.12
Unknown	9.0	0.11
Chloroflexi	2.0	0.02
Acidobacteria	2.0	0.02
Cyanobacteria	1.0	0.01

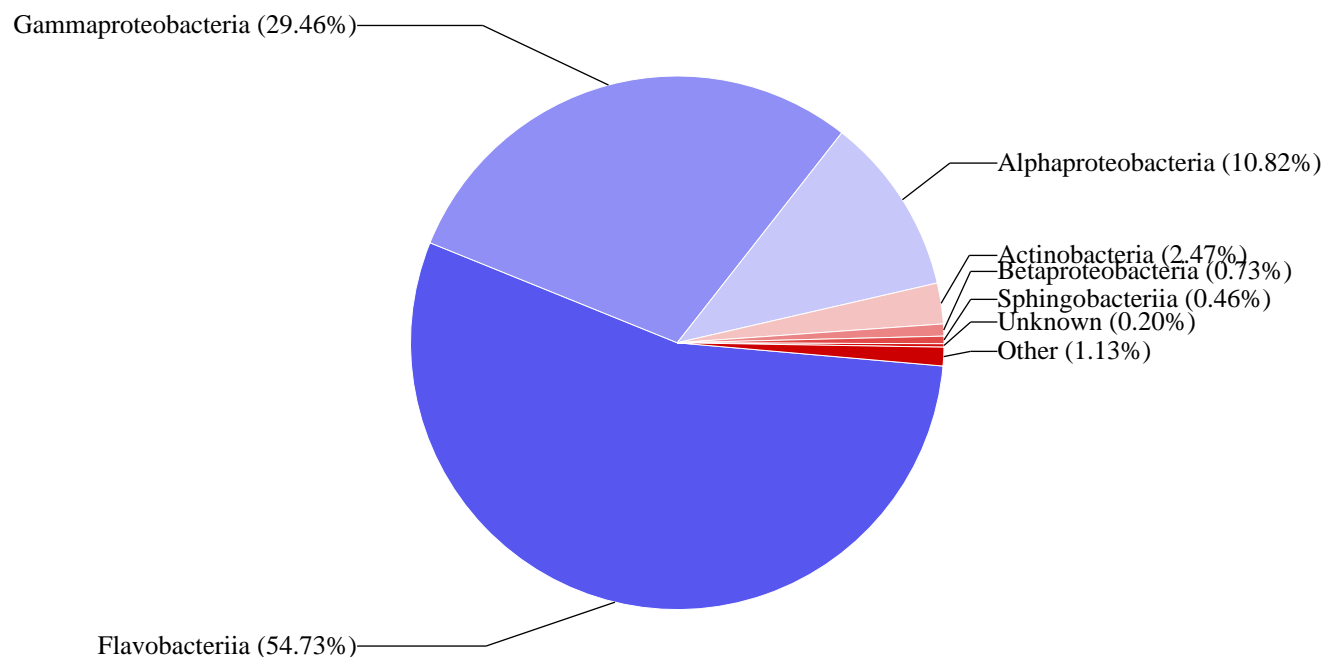
Top Phylum Classification



Class Classification

Class	Read Count	%
Flavobacteriia	4566.0	54.73
Gammaproteobacteria	2458.0	29.46
Alphaproteobacteria	903.0	10.82
Actinobacteria	206.0	2.47
Betaproteobacteria	61.0	0.73
Sphingobacteriia	38.0	0.46
Unknown	17.0	0.20
Bacilli	17.0	0.20
Planctomycetia	14.0	0.17
Cytophagia	13.0	0.16
	11.0	0.13
VC2_1_Bac22	11.0	0.13
Gemmatimonadetes	10.0	0.12
Verrucomicrobiae	6.0	0.07
Clostridia	4.0	0.05
Deltaproteobacteria	2.0	0.02
C0119	1.0	0.01
Ellin6529	1.0	0.01
Thermoleophilia	1.0	0.01
ML635J	1.0	0.01
Acidobacteriia	1.0	0.01
Acidobacteria	1.0	0.01

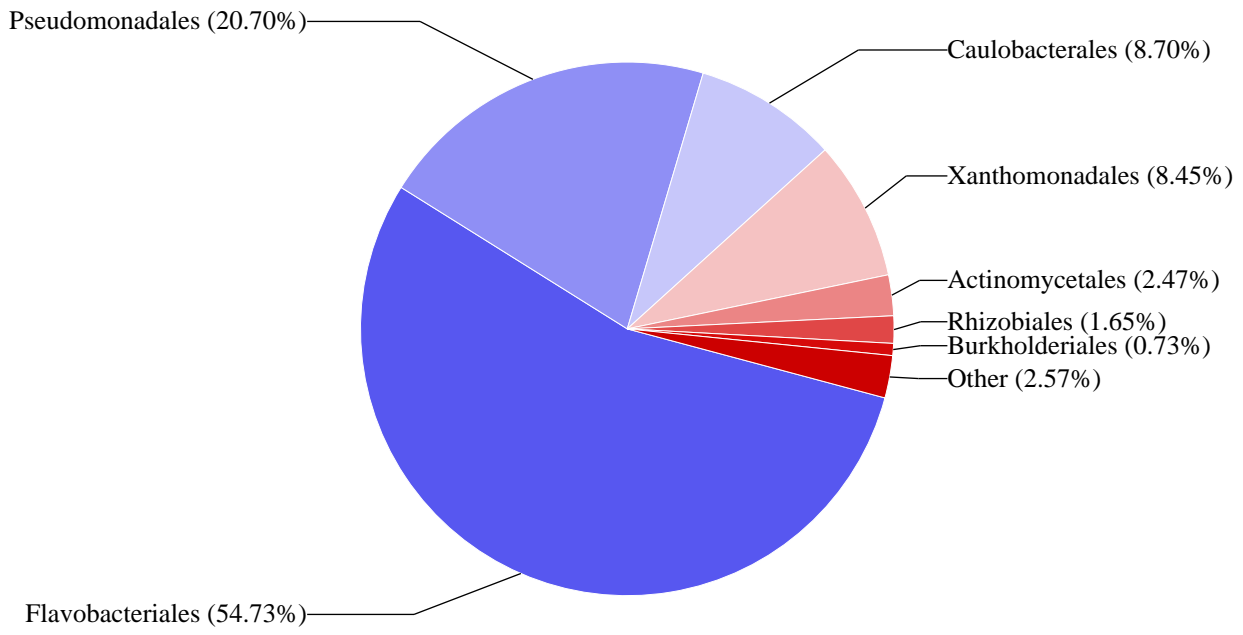
Top Class Classification



Order Classification

Order	Read Count	%
Flavobacteriales	4566.0	54.73
Pseudomonadales	1727.0	20.70
Caulobacterales	726.0	8.70
Xanthomonadales	705.0	8.45
Actinomycetales	206.0	2.47
Rhizobiales	138.0	1.65
Burkholderiales	61.0	0.73
Unknown	40.0	0.48
Sphingobacteriales	38.0	0.46
	25.0	0.30
Enterobacteriales	18.0	0.22
Lactobacillales	15.0	0.18
Sphingomonadales	15.0	0.18
Gemmatales	14.0	0.17
Cytophagales	13.0	0.16
Gemmatimonadales	10.0	0.12
Verrucomicrobiales	6.0	0.07
Rhodospirillales	5.0	0.06
Clostridiales	4.0	0.05
Rickettsiales	4.0	0.05
Bacillales	2.0	0.02
S	1.0	0.01
Gaiellales	1.0	0.01
Acidobacteriales	1.0	0.01
CCU21	1.0	0.01
Myxococcales	1.0	0.01

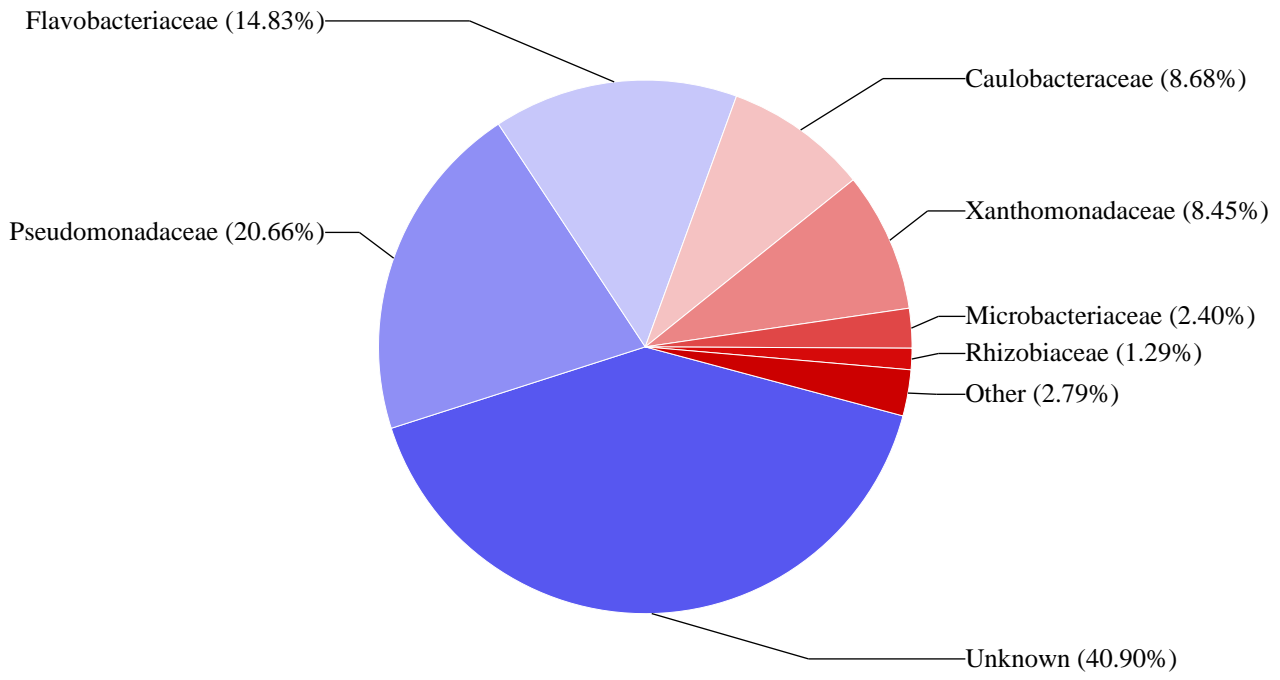
Top Order Classification



Family Classification

Family	Read Count	%
Unknown	3412.0	40.90
Pseudomonadaceae	1724.0	20.66
Flavobacteriaceae	1237.0	14.83
Caulobacteraceae	724.0	8.68
Xanthomonadaceae	705.0	8.45
Microbacteriaceae	200.0	2.40
Rhizobiaceae	108.0	1.29
Comamonadaceae	56.0	0.67
Sphingobacteriaceae	38.0	0.46
Enterobacteriaceae	18.0	0.22
Cytophagaceae	13.0	0.16
Sphingomonadaceae	13.0	0.16
Streptococcaceae	12.0	0.14
Isosphaeraceae	12.0	0.14
Hyphomicrobiaceae	11.0	0.13
Gemmatimonadaceae	8.0	0.10
Verrucomicrobiaceae	6.0	0.07
Chitinophagaceae	6.0	0.07
Cellulomonadaceae	5.0	0.06
Alcaligenaceae	5.0	0.06
Rhodospirillaceae	4.0	0.05
Clostridiaceae	4.0	0.05
Phyllobacteriaceae	4.0	0.05
Beijerinckiaceae	3.0	0.04
Moraxellaceae	3.0	0.04
Gemmataceae	2.0	0.02
Ellin5301	1.0	0.01
Gaiellaceae	1.0	0.01
Carnobacteriaceae	1.0	0.01
Acetobacteraceae	1.0	0.01
Acidobacteriaceae	1.0	0.01
Paenibacillaceae	1.0	0.01
Mycobacteriaceae	1.0	0.01
Erythrobacteraceae	1.0	0.01
Staphylococcaceae	1.0	0.01
Cystobacteraceae	1.0	0.01

Top Family Classification

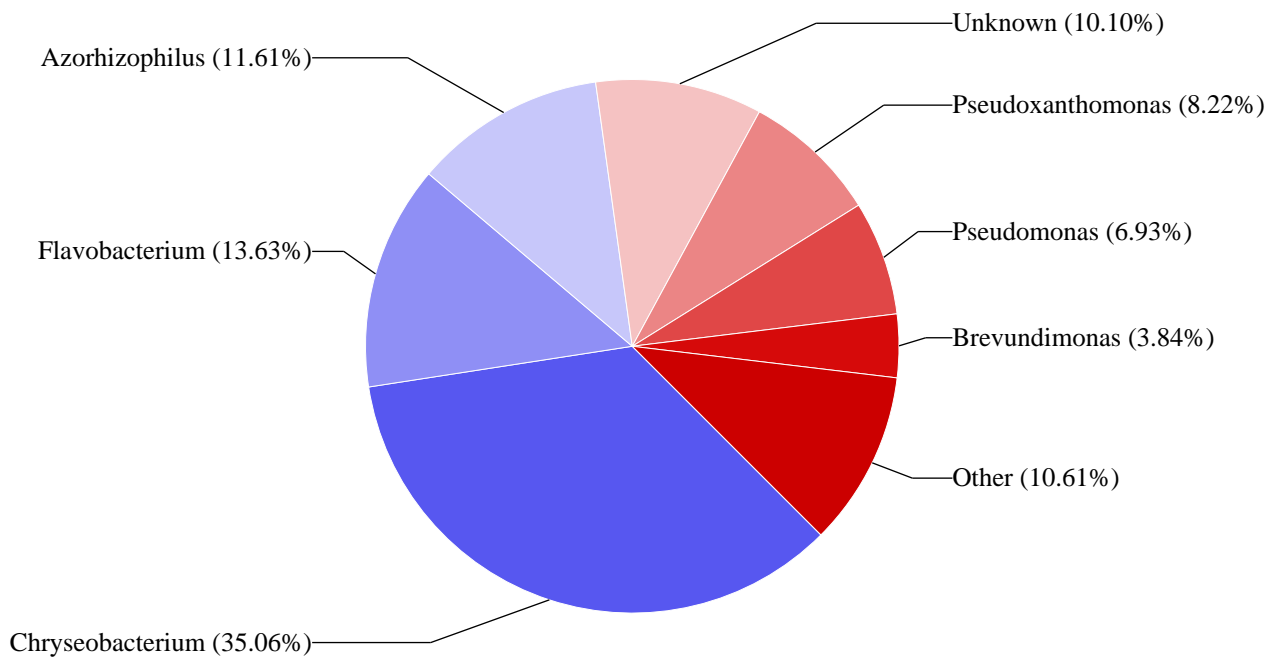


Genus Classification

Genus	Read Count	%
Chryseobacterium	2925.0	35.06
Flavobacterium	1137.0	13.63
Azorhizophilus	969.0	11.61
Unknown	843.0	10.10
Pseudoxanthomonas	686.0	8.22
Pseudomonas	578.0	6.93
Brevundimonas	320.0	3.84
Microbacterium	200.0	2.40
Mycoplana	153.0	1.83
Elizabethkingia	104.0	1.25
Agrobacterium	59.0	0.71
Riemerella	45.0	0.54
Caulobacter	40.0	0.48
Azotobacter	39.0	0.47
Pedobacter	36.0	0.43
Acidovorax	35.0	0.42
Azomonas	16.0	0.19
Stenotrophomonas	15.0	0.18
Flectobacillus	13.0	0.16
Lactococcus	12.0	0.14
Devosia	11.0	0.13
Shinella	10.0	0.12
Gemmatimonas	8.0	0.10
Amorphomonas	7.0	0.08
Novosphingobium	6.0	0.07
Kaistia	6.0	0.07
Cellulomonas	5.0	0.06
Arthrospira	5.0	0.06
Klebsiella	4.0	0.05
Achromobacter	4.0	0.05
Sphingopyxis	4.0	0.05
Candidatus	4.0	0.05
Variovorax	4.0	0.05
Clostridium	4.0	0.05
Xylophilus	3.0	0.04
Imtechella	3.0	0.04
Acinetobacter	3.0	0.04
Aminobacter	3.0	0.04
Enterobacter	2.0	0.02
Azospirillum	2.0	0.02
Nitrobacteria	2.0	0.02

Gemmata	1.0	0.01
Kerstersia	1.0	0.01
Chitinophaga	1.0	0.01
Limnohabitans	1.0	0.01
Chelatococcus	1.0	0.01
Sphingobium	1.0	0.01
Nostocoida	1.0	0.01
Curvibacter	1.0	0.01
Phaeospirillum	1.0	0.01
Luteimonas	1.0	0.01
Haloferula	1.0	0.01
Isobaculum	1.0	0.01
Paenibacillus	1.0	0.01
Mitsuaria	1.0	0.01
Mycobacterium	1.0	0.01
Erythromicrobium	1.0	0.01
Macrococcus	1.0	0.01
Salmonella	1.0	0.01

Top Genus Classification



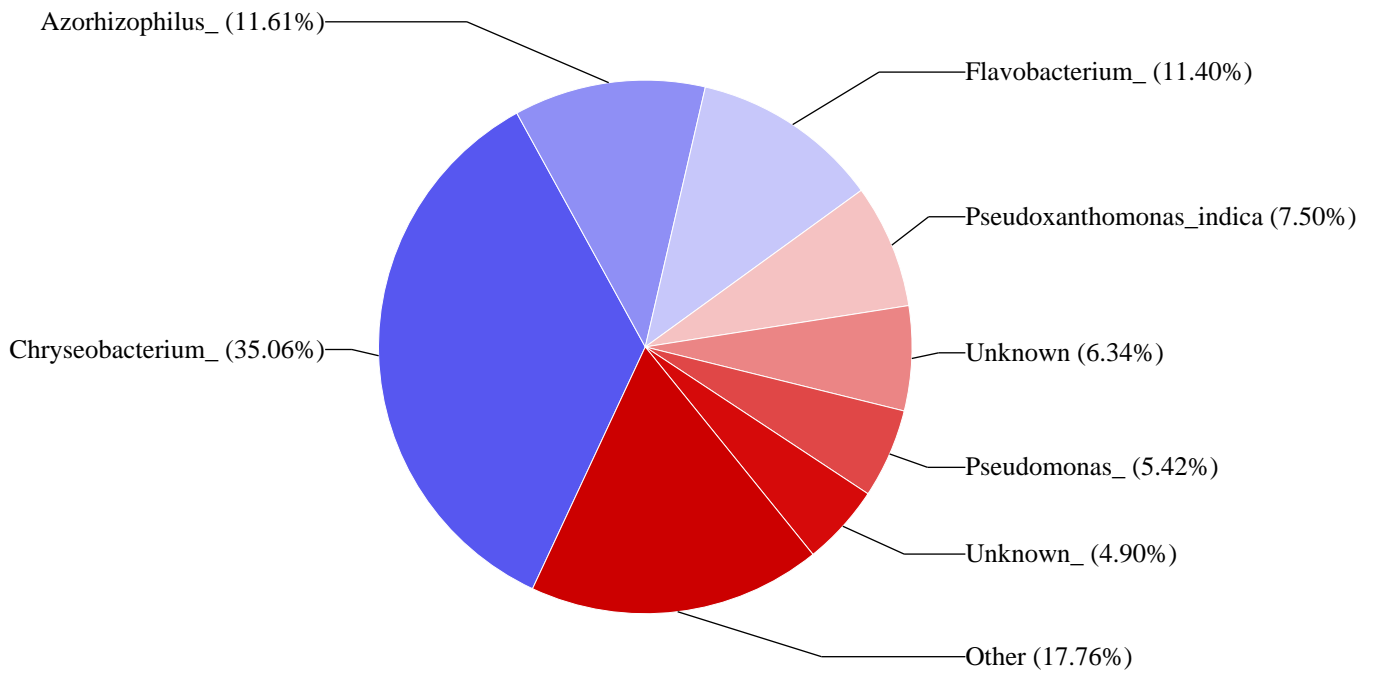
Species Classification

Species	Read Count	%
Chryseobacterium_	2925.0	35.06
Azorhizophilus_	969.0	11.61
Flavobacterium_	951.0	11.40
Pseudoxanthomonas_indica	626.0	7.50
Unknown	529.0	6.34
Pseudomonas_	452.0	5.42
Unknown_	409.0	4.90
Brevundimonas_poindexterae	312.0	3.74
Mycoplana_	153.0	1.83
Microbacterium_	145.0	1.74
Flavobacterium_succinicans	108.0	1.29
Elizabethkingia_	101.0	1.21
Pseudomonas_umsongensis	90.0	1.08
Agrobacterium_	58.0	0.70
Pseudoxanthomonas_mexicana	51.0	0.61
Riemerella_	45.0	0.54
Caulobacter_	40.0	0.48
Flavobacterium_gelidilacus	40.0	0.48
Azotobacter_armeniacus	39.0	0.47
Microbacterium_aurum	33.0	0.40
Pedobacter_	33.0	0.40
Acidovorax_	22.0	0.26
Microbacterium_chocolatum	14.0	0.17
Flectobacillus_	13.0	0.16
Devosia_	11.0	0.13
Azomonas_	9.0	0.11
Pseudomonas_viridiflava	9.0	0.11
Gemmatimonas_	8.0	0.10
Lactococcus_	8.0	0.10
Flavobacterium_frigidarium	7.0	0.08
Shinella_granuli	7.0	0.08
Amorphomonas_oryzae	7.0	0.08
Acidovorax_delafieldii	7.0	0.08
Stenotrophomonas_maltophilia	6.0	0.07
Kaistia_	6.0	0.07
Azomonas_agilis	5.0	0.06
Pseudoxanthomonas_	5.0	0.06
Arthrospira_	5.0	0.06
Stenotrophomonas_acidaminiphila	4.0	0.05

Lactococcus_garvieae	4.0	0.05
Klebsiella_	4.0	0.05
Cellulomonas_	4.0	0.05
Achromobacter_	4.0	0.05
Sphingopyxis_	4.0	0.05
Candidatus_	4.0	0.05
Variovorax_	4.0	0.05
Xylophilus_ampelinus	3.0	0.04
Novosphingobium_	3.0	0.04
Imtechella_halotolerans	3.0	0.04
Shinella_	3.0	0.04
Clostridium_pasteurianum	3.0	0.04
Aminobacter_	3.0	0.04
Stenotrophomonas_panacihumi	2.0	0.02
Acinetobacter_	2.0	0.02
Nitrobacteria_hamadaniensis	2.0	0.02
Acidovorax_wohlfahrtii	2.0	0.02
Enterobacter_cowanii	1.0	0.01
Gemmata_obscuriglobus	1.0	0.01
Kerstesia_gyiorum	1.0	0.01
Chitinophaga_	1.0	0.01
Limnohabitans_curvus	1.0	0.01
Chelatococcus_	1.0	0.01
Sphingobium_	1.0	0.01
Nostocoida_limicola	1.0	0.01
Curvibacter_	1.0	0.01
Microbacterium_maritypicum	1.0	0.01
Phaeospirillum_	1.0	0.01
Pseudomonas_thermotolerans	1.0	0.01
Pseudomonas_veronii	1.0	0.01
Azospirillum_	1.0	0.01
Novosphingobium_stygiun	1.0	0.01
Cellulomonas_uda	1.0	0.01
Luteimonas_mephitis	1.0	0.01
Stenotrophomonas_	1.0	0.01
Acinetobacter_venetianus	1.0	0.01
Isobaculum_melis	1.0	0.01
Paenibacillus_	1.0	0.01
Mitsuaria_chitosanitabida	1.0	0.01
Mycobacterium_	1.0	0.01
Brevundimonas_intermedia	1.0	0.01
Erythromicrobium_ramosum	1.0	0.01
Macrococcus_	1.0	0.01

Salmonella_	1.0	0.01
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Top Species Classification



----- End of report -----



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Africa's Genomics Company



inqaba biotec metagenomic report

Sample Information

Index:	M13_bc1002_F--M13_bc1054
Sample Name:	C
Run Name:	210827_Cell2
Report Date:	Mon Aug 30 10:45:56 2021

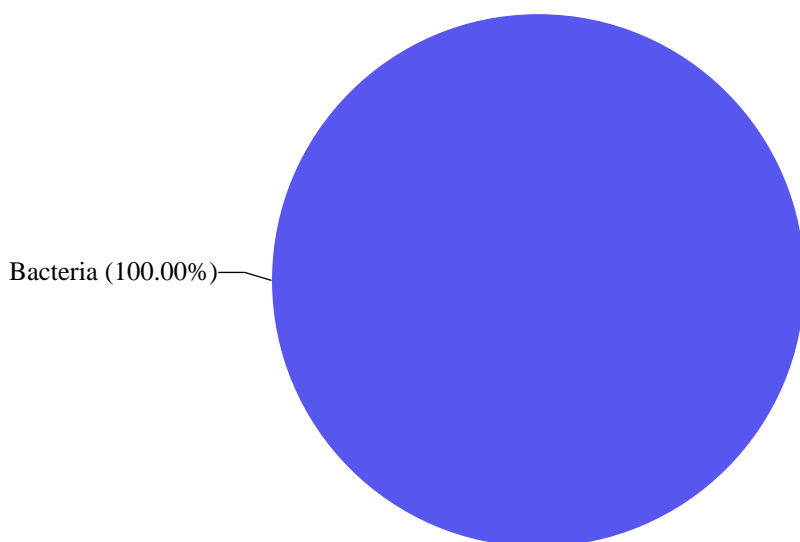
This report contains the summarized metagenomic analysis of full length 16s gene amplicons. Samples were sequenced on the Sequel system by PacBio (www.pacb.com). Raw subreads were processed through the SMRTlink (v9.0) Circular Consensus Sequences (CCS) algorithm to produce highly accurate reads (>QV40). These highly accurate reads were then processed through vsearch (<https://github.com/torognes/vsearch>) and taxonomic information was determined based on QIMME2. Report generation command used :
`$create_vsearch_single_sample_pdf_report_pacbio.py
create_vsearch_single_sample_pdf_report_pacbio.py
demultiplex.M13_bc1002_F--M13_bc1054_R.hifi_reads_otu_table.tsv M13_bc1002_F--M13_bc1054 C 210827_Cell2 16s`

Taxonomical Classification

Kingdom Classification

Kingdom	Read Count	%
Bacteria	303.0	100.00

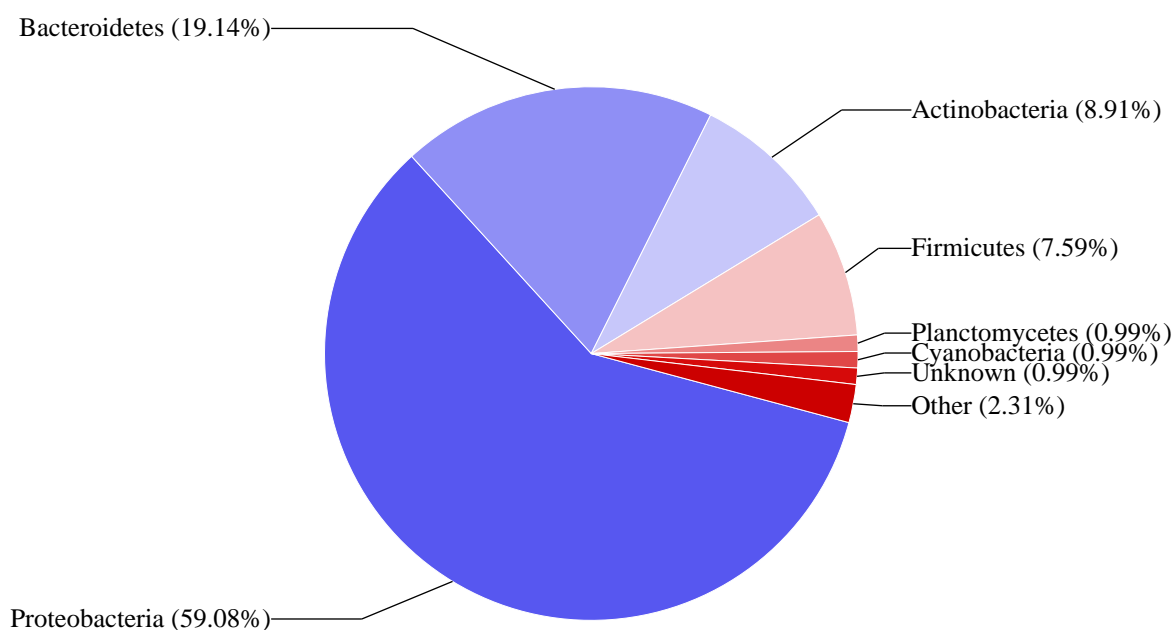
Top Kingdom Classification



Phylum Classification

Phyla Classification	Read Count	%
Proteobacteria	179.0	59.08
Bacteroidetes	58.0	19.14
Actinobacteria	27.0	8.91
Firmicutes	23.0	7.59
Planctomycetes	3.0	0.99
Cyanobacteria	3.0	0.99
Unknown	3.0	0.99
Acidobacteria	2.0	0.66
Verrucomicrobia	2.0	0.66
Chloroflexi	2.0	0.66
GAL15	1.0	0.33

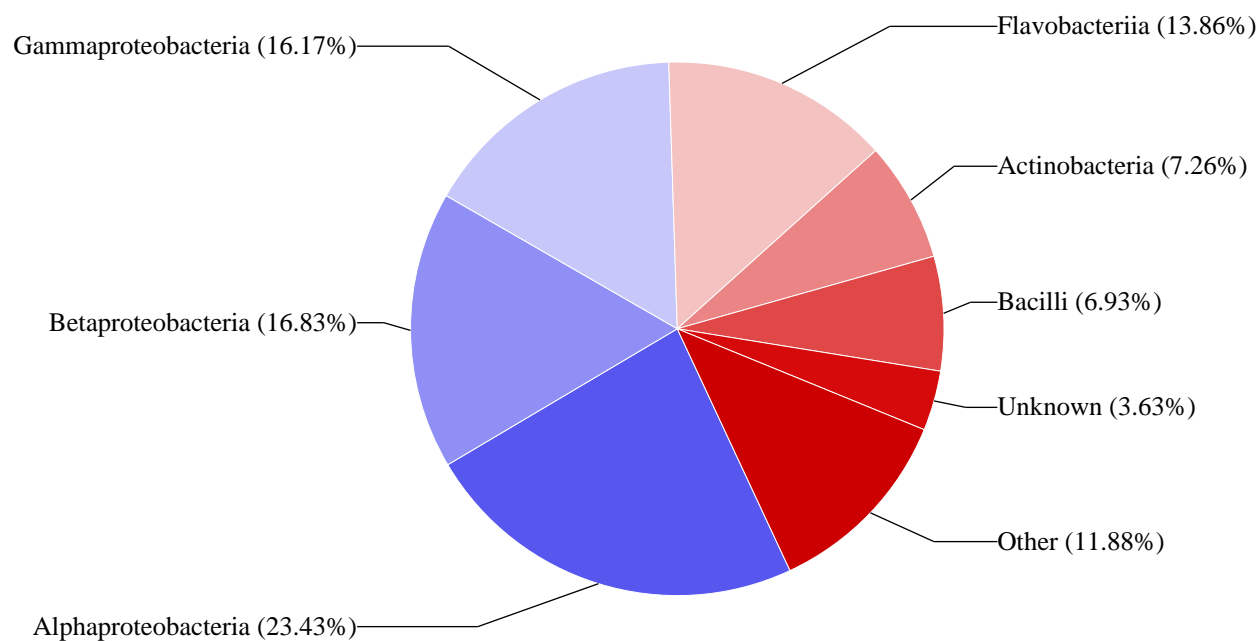
Top Phylum Classification



Class Classification

Class	Read Count	%
Alphaproteobacteria	71.0	23.43
Betaproteobacteria	51.0	16.83
Gammaproteobacteria	49.0	16.17
Flavobacteriia	42.0	13.86
Actinobacteria	22.0	7.26
Bacilli	21.0	6.93
Unknown	11.0	3.63
Sphingobacteriia	11.0	3.63
	4.0	1.32
Thermoleophilia	3.0	0.99
Planctomycetia	3.0	0.99
Deltaproteobacteria	2.0	0.66
Acidobacteria	2.0	0.66
Cytophagia	2.0	0.66
Clostridia	2.0	0.66
Verrucomicrobiae	1.0	0.33
Rubrobacteria	1.0	0.33
Oscillatoriothycideae	1.0	0.33
Chloroflexi	1.0	0.33
Anaerolineae	1.0	0.33
Chloroplast	1.0	0.33
VC2_1_Bac22	1.0	0.33

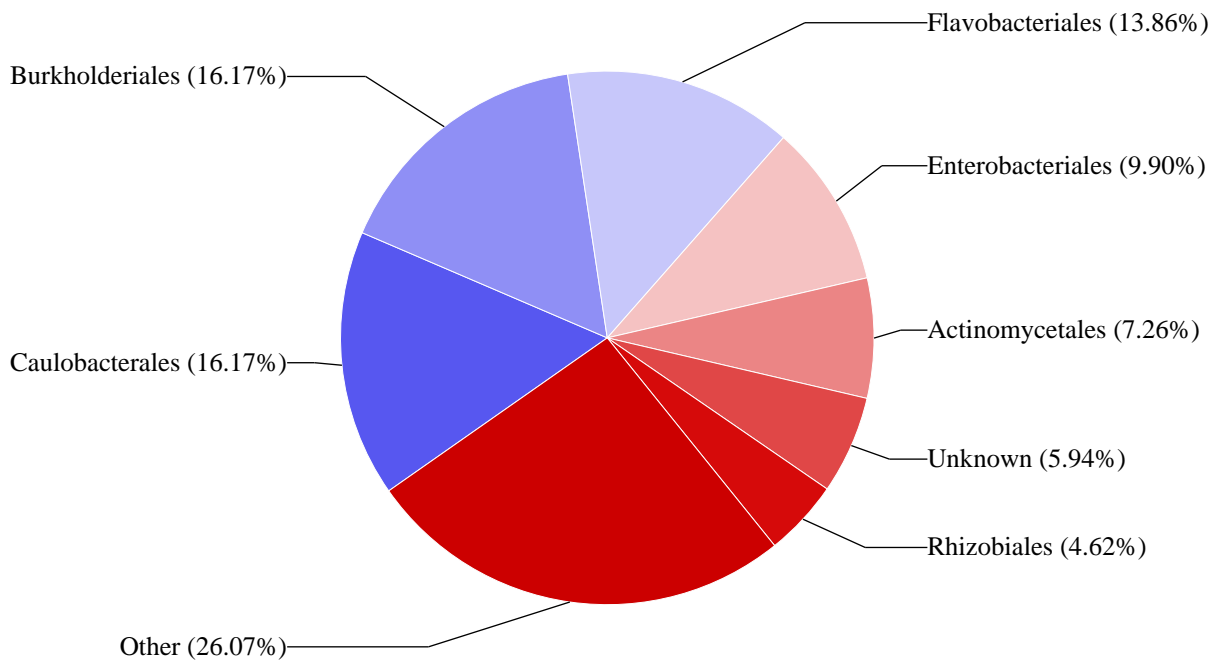
Top Class Classification



Order Classification

Order	Read Count	%
Caulobacteriales	49.0	16.17
Burkholderiales	49.0	16.17
Flavobacteriales	42.0	13.86
Enterobacteriales	30.0	9.90
Actinomycetales	22.0	7.26
Unknown	18.0	5.94
Rhizobiales	14.0	4.62
Xanthomonadales	13.0	4.29
Lactobacillales	12.0	3.96
Sphingobacteriales	11.0	3.63
Bacillales	8.0	2.64
	6.0	1.98
Pseudomonadales	5.0	1.65
Rhodospirillales	3.0	0.99
Sphingomonadales	3.0	0.99
Solirubrobacteriales	2.0	0.66
iii1	2.0	0.66
Gemmatales	2.0	0.66
Cytophagales	2.0	0.66
Clostridiales	2.0	0.66
Myxococcales	1.0	0.33
Legionellales	1.0	0.33
Verrucomicrobiales	1.0	0.33
Rubrobacteriales	1.0	0.33
Gaiellales	1.0	0.33
SBR1031	1.0	0.33
Stramenopiles	1.0	0.33
MKC10	1.0	0.33

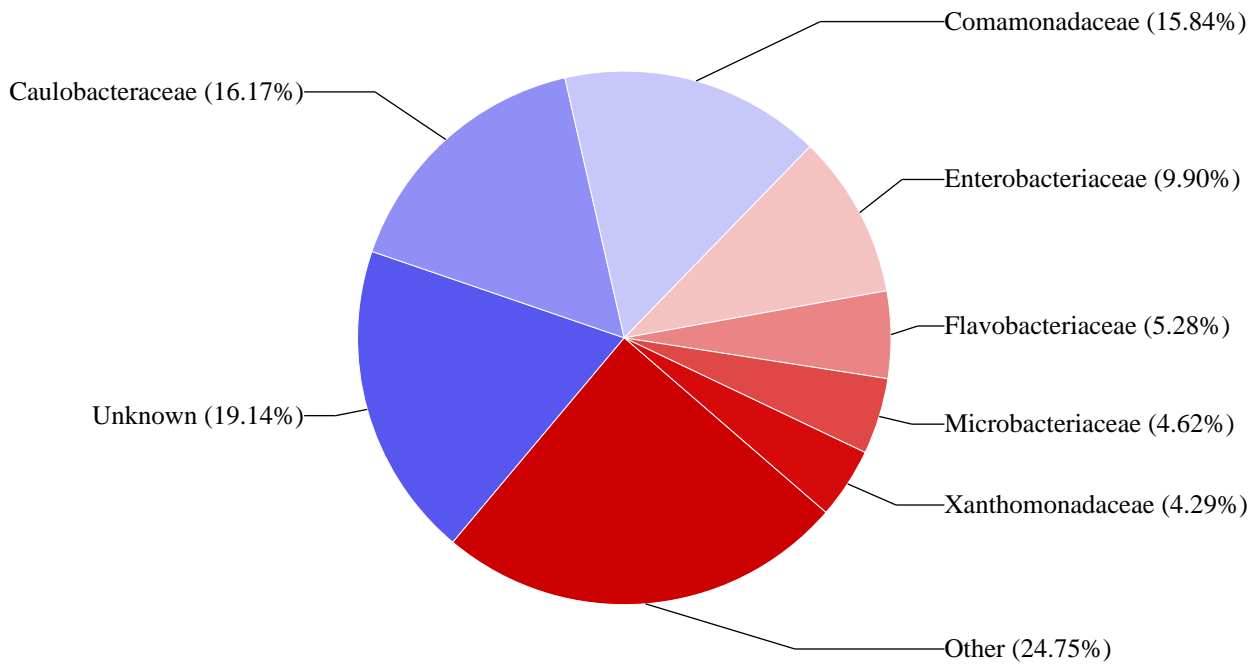
Top Order Classification



Family Classification

Family	Read Count	%
Unknown	58.0	19.14
Caulobacteraceae	49.0	16.17
Comamonadaceae	48.0	15.84
Enterobacteriaceae	30.0	9.90
Flavobacteriaceae	16.0	5.28
Microbacteriaceae	14.0	4.62
Xanthomonadaceae	13.0	4.29
Sphingobacteriaceae	11.0	3.63
Rhizobiaceae	10.0	3.30
Streptococcaceae	10.0	3.30
Staphylococcaceae	4.0	1.32
Pseudomonadaceae	4.0	1.32
Paenibacillaceae	3.0	0.99
Sphingomonadaceae	3.0	0.99
Rhodospirillaceae	2.0	0.66
Leuconostocaceae	2.0	0.66
Chitinophagaceae	2.0	0.66
Cytophagaceae	2.0	0.66
Geodermatophilaceae	2.0	0.66
Clostridiaceae	2.0	0.66
Alcaligenaceae	1.0	0.33
Polyangiaceae	1.0	0.33
Legionellaceae	1.0	0.33
Verrucomicrobiaceae	1.0	0.33
Streptomycetaceae	1.0	0.33
Isosphaeraceae	1.0	0.33
Rubrobacteraceae	1.0	0.33
Acetobacteraceae	1.0	0.33
Hyphomicrobiaceae	1.0	0.33
Gaiellaceae	1.0	0.33
Bradyrhizobiaceae	1.0	0.33
A4b	1.0	0.33
Bacillaceae	1.0	0.33
Gemmataceae	1.0	0.33
Cellulomonadaceae	1.0	0.33
Nocardiodaceae	1.0	0.33
Micromonosporaceae	1.0	0.33
Moraxellaceae	1.0	0.33

Top Family Classification

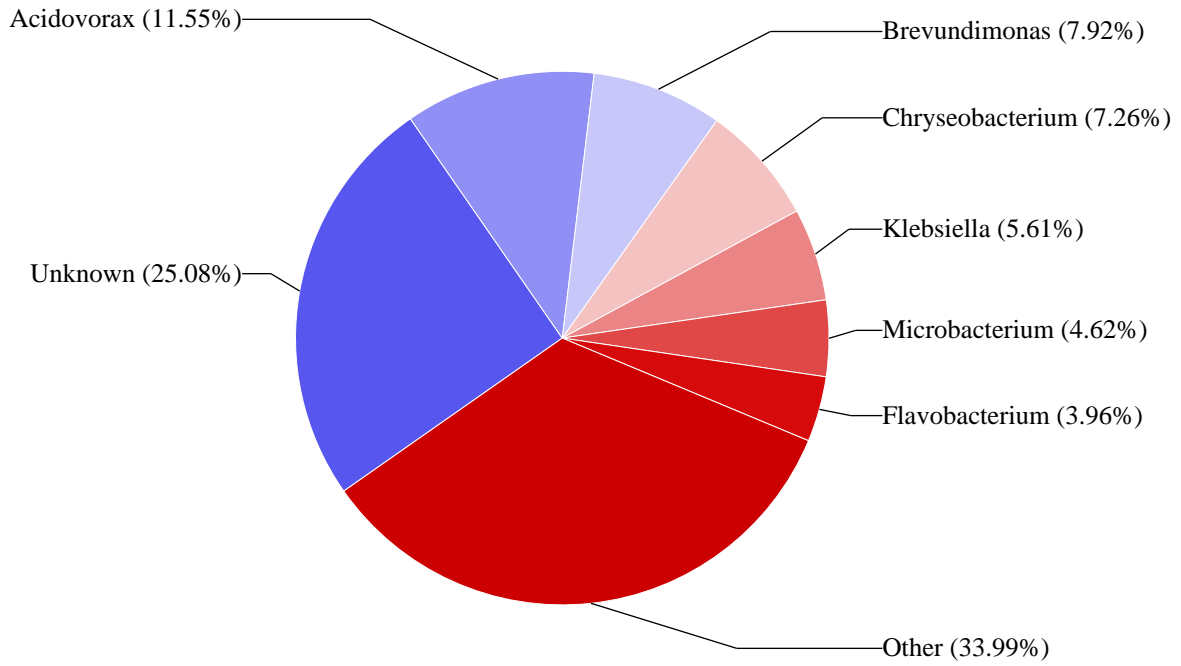


Genus Classification

Genus	Read Count	%
Unknown	76.0	25.08
Acidovorax	35.0	11.55
Brevundimonas	24.0	7.92
Chryseobacterium	22.0	7.26
Klebsiella	17.0	5.61
Microbacterium	14.0	4.62
Flavobacterium	12.0	3.96
Pseudoxanthomonas	10.0	3.30
Pedobacter	10.0	3.30
Mycoplana	10.0	3.30
Lactococcus	8.0	2.64
Variovorax	6.0	1.98
Agrobacterium	6.0	1.98
Salmonella	4.0	1.32
Macrococcus	4.0	1.32
Stenotrophomonas	3.0	0.99
Limnohabitans	3.0	0.99
Enterobacter	2.0	0.66
Paenibacillus	2.0	0.66
Azorhizophilus	2.0	0.66
Pseudomonas	2.0	0.66
Flectobacillus	2.0	0.66
Clostridium	2.0	0.66
Legionella	1.0	0.33
Phaeospirillum	1.0	0.33
Terrimonas	1.0	0.33
Azospirillum	1.0	0.33
Streptomyces	1.0	0.33
Singulisphaera	1.0	0.33
Rubrobacter	1.0	0.33
Ammoniphilus	1.0	0.33
Hydrogenophaga	1.0	0.33
Schlegelella	1.0	0.33
Amorphomonas	1.0	0.33
Modestobacter	1.0	0.33
Novosphingobium	1.0	0.33
Craurococcus	1.0	0.33
Pedomicrobium	1.0	0.33
Blastococcus	1.0	0.33
Streptococcus	1.0	0.33
Bacillus	1.0	0.33

Parasegitibacter	1.0	0.33
Leptothrix	1.0	0.33
Sphingosinicella	1.0	0.33
Caulobacter	1.0	0.33
Mucilaginibacter	1.0	0.33
Cellulomonas	1.0	0.33
Nocardioides	1.0	0.33
Imtechella	1.0	0.33
Agitococcus	1.0	0.33

Top Genus Classification

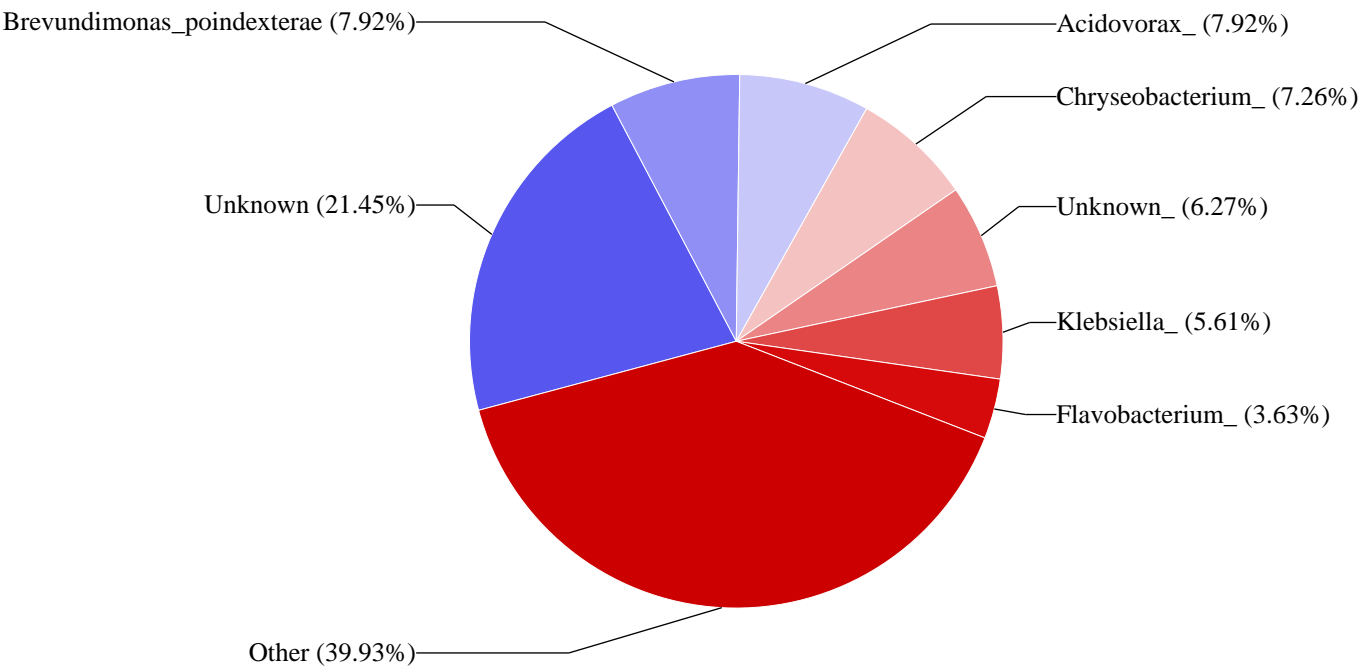


Species Classification

Species	Read Count	%
Unknown	65.0	21.45
Brevundimonas_poindexterae	24.0	7.92
Acidovorax_	24.0	7.92
Chryseobacterium_	22.0	7.26
Unknown_	19.0	6.27
Klebsiella_	17.0	5.61
Flavobacterium_	11.0	3.63
Acidovorax_delafieldii	10.0	3.30
Pseudoxanthomonas_indica	10.0	3.30
Mycoplana_	10.0	3.30
Microbacterium_	9.0	2.97
Pedobacter_	9.0	2.97
Variovorax_	6.0	1.98
Agrobacterium_	6.0	1.98
Lactococcus_	5.0	1.65
Microbacterium_aurum	4.0	1.32
Salmonella_	4.0	1.32
Lactococcus_garvieae	3.0	0.99
Macrococcus_caseolyticus	2.0	0.66
Azorhizophilus_	2.0	0.66
Macrococcus_	2.0	0.66
Flectobacillus_	2.0	0.66
Limnohabitans_	2.0	0.66
Clostridium_pasteurianum	2.0	0.66
Paenibacillus_illinoisensis	1.0	0.33
Legionella_	1.0	0.33
Phaeospirillum_	1.0	0.33
Terrimonas_ferruginea	1.0	0.33
Azospirillum_	1.0	0.33
Pseudomonas_umsongensis	1.0	0.33
Singulisphaera_rosea	1.0	0.33
Rubrobacter_	1.0	0.33
Paenibacillus_	1.0	0.33
Ammoniphilus_oxalaticus	1.0	0.33
Hydrogenophaga_palleronii	1.0	0.33
Schlegelella_	1.0	0.33
Amorphomonas_oryzae	1.0	0.33
Modestobacter_	1.0	0.33
Stenotrophomonas_maltophilia	1.0	0.33

Novosphingobium_stygium	1.0	0.33
Craurococcus_roseus	1.0	0.33
Pedomicrobium_	1.0	0.33
Blastococcus_aggregatus	1.0	0.33
Pseudomonas_carboxydohydrogena	1.0	0.33
Streptococcus_alactolyticus	1.0	0.33
Bacillus_badius	1.0	0.33
Parasegitibacter_luojiensis	1.0	0.33
Leptothrix_	1.0	0.33
Limnohabitans_curvus	1.0	0.33
Stenotrophomonas_	1.0	0.33
Sphingosinicella_microcystinivorans	1.0	0.33
Caulobacter_	1.0	0.33
Cellulomonas_	1.0	0.33
Imtechella_halotolerans	1.0	0.33
Flavobacterium_gelidilacus	1.0	0.33
Acidovorax_konjaci	1.0	0.33
Agitococcus_lubricus	1.0	0.33

Top Species Classification



----- End of report -----