



Name	Acidobacteria_Subdivision8_Amazon_FNV_2_1	Bacteroidetes_Amazon_FNV_2010_21_2	Methylothermobacteria_Amazon_FNV_2010_23_1	Acidobacteria_Amazon_FNV_2010_25_1	Acidobacteria_Subdivision8_Amazon_FNV_2_1	Proteobacteria_Amazon_FNV_2010_19_4	Proteobacteria_Amazon_FNV_2010_31_3	Acidobacteria_Amazon_FNV_2010_29_1_1
Analysis Project Type	MAG	MAG	MAG	MAG	MAG	MAG	MAG	MAG
Taxa ID approach	multi marker approach	multi marker approach	multi marker approach	multi marker approach	multi marker approach	multi marker approach	multi marker approach	multi marker approach
Taxa ID	Bacteria	Bacteria	Bacteria	Bacteria	Bacteria	Bacteria	Bacteria	Bacteria
Assembly software	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o
Annotation pipeline/tool	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST
Quality	medium-quality	medium-quality	medium-quality	medium-quality	medium-quality	medium-quality	medium-quality	medium-quality
Completion (%)	68.03	67.24	63.73	59.67	58.77	55.51	53.51	52.59
Contamination (%)	5.93	3.42	1.16	0.85	3.6	3.36	0.18	2.35
completeness software	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o
number of contigs	405	274	294	359	436	490	258	366
16S recovered	putative	putative	no	no	no	no	putative	no
16S recovery software	checkM	checkM	checkM	checkM	checkM	checkM	checkM	checkM
total # tRNAs	24	36	18	9	4	8	6	5
# of standard tRNAs extracted	13	16	11	8	3	6	4	5
tRNA detection software	Aragorn	tRNAscan-se	tRNAscan-se	tRNAscan-se	tRNAscan-se	tRNAscan-se	tRNAscan-se	tRNAscan-se
length (Mb)	7.44	4.43	3.04	2.6	3.57	3.34	2.13	3.04
GC content(%)	60.03	39.56	50.61	47.35	50.88	63.52	60.69	61.41
# CDS	6869	4119	2991	2630	3376	3545	2145	3065
NSO	24087	20381	11292	7198	8339	6628	8155	8548
completeness approach	marker gene based	marker gene based	marker gene based	marker gene based	marker gene based	marker gene based	marker gene based	marker gene based
decontamination software	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o
bin parameters	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage
binning software	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o
reassembly post binning	no	no	no	no	no	no	no	no
mag coverage software	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o	anvi'o

Name	Acidobacteria_Subdivision8_Amazon_FNV_20_2_3_8	Acidobacteria_Amazon_FNV_2010_17_8	Bacteroidetes_Amazon_FNV_2010_13_2	Chloroflexi_Amazon_FNV_2010_25_1
Analysis Project Type	MAG	MAG	MAG	MAG
Taxa ID approach	multi marker approach	multi marker approach	multi marker approach	multi marker approach
Taxa ID	Bacteria	Bacteria	Bacteria	Bacteria
Assembly software	anvi'o	anvi'o	anvi'o	anvi'o
Annotation pipeline/tool	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST	PATRIC/RAST
Quality	medium-quality	medium-quality	medium-quality	medium-quality
Completion (%)	51.96	51.59	51.39	51.38
Contamination (%)	0.81	1.57	0.81	2.47
completeness software	anvi'o	anvi'o	anvi'o	anvi'o
number of contigs	216	469	275	330
16S recovered	no	no	putative	no
16S recovery software	checkM	checkM	checkM	checkM
total # tRNAs	3	21	32	11
# of standard tRNAs extracted	2	10	14	8
tRNA detection software	tRNAscan-se	tRNAscan-se	tRNAscan-se	tRNAscan-se
length (Mb)	1.57	3.4	4.58	2.61
GC content(%)	51.8	55.46	42.76	58.44
# CDS	1582	3925	4733	2831
NSO	7154	6914	22057	7631
completeness approach	marker gene based	marker gene based	marker gene based	marker gene based
decontamination software	anvi'o	anvi'o	anvi'o	anvi'o
bin parameters	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage	kmer+coverage+codon usage
binning software	anvi'o	anvi'o	anvi'o	anvi'o
reassembly post binning	no	no	no	no
mag coverage software	anvi'o	anvi'o	anvi'o	anvi'o