



**Novel Genome**  
 >70% Complete, <10% MGO\*  
 >90 Novelty Score

**Known Genome**  
 >70% Complete, <10% MGO\*  
 <90 Novelty Score

\*Marker Gene Overrepresentation

Cluster ID	Top Reference	Complete (%)	MGO (%)	Novelty Score	Abundance <sup>1</sup>	Contig N50	Genome Size	Num Contigs	GC (%)
bin_7	<i>o__Clostridiales (UID1226)</i>	100.00	0.15	98.01	4.24	17,843	3,300,702	255	42.82
bin_23	<i>Alistipes_putredinis_CAG_67</i>	99.52	0.48	8.06	0.21	402,853	2,229,858	18	54.25
bin_9	<i>f__Lachnospiraceae (UID1256)</i>	99.42	1.17	81.70	1.73	161,002	2,923,309	99	43.15
bin_21	<i>Dialister_sp_CAG_486</i>	99.37	1.90	45.85	4.15	41,635	2,348,463	144	51.67
bin_8	<i>o__Clostridiales (UID1212)</i>	99.33	4.72	95.64	3.69	38,859	2,935,896	201	59.51
bin_5	<i>Prevotella_copri_CAG_164</i>	98.99	1.69	20.97	6.31	205,415	3,486,797	115	45.02
bin_10	<i>Clostridium_sp_CAG_299</i>	98.73	0.95	13.58	2.25	68,258	2,878,419	175	49.38
bin_18	<i>o__Clostridiales (UID1212)</i>	98.66	0.00	95.22	2.57	13,180	2,454,410	52	45.53
bin_4	<i>Firmicutes_bacterium_CAG_424</i>	98.48	0.13	20.15	4.64	120,288	3,506,315	181	41.08
bin_6	<i>Bacteroides_coprophilus_CAG_333</i>	98.14	0.81	2.05	0.53	5,611	3,303,708	102	46.15
bin_15	<i>Sutterella_wadsworthensis_2_1_59BFAA</i>	98.14	0.62	2.94	1.80	24,615	2,643,152	142	61.76
bin_29	<i>o__Clostridiales (UID1212)</i>	97.99	0.22	95.58	0.78	5,244	1,795,742	39	36.01
bin_19	<i>o__Clostridiales (UID1212)</i>	97.96	0.79	87.19	2.12	33,963	2,389,594	115	57.87
bin_32	<i>c__Epsilonproteobacteria (UID3066)</i>	97.56	0.00	82.79	0.15	11,350	1,559,558	121	35.04
bin_20	<i>o__Clostridiales (UID1212)</i>	97.32	0.17	95.95	1.58	134,461	2,374,013	92	56.10
bin_2	<i>Parabacteroides_merdae_CAG_48</i>	97.21	0.52	1.12	0.53	102,291	4,017,742	149	45.51
bin_13	<i>f__Lachnospiraceae (UID1286)</i>	96.94	0.98	97.95	1.73	49,126	2,722,281	48	50.52
bin_16	<i>Oscillibacter_sp_CAG_155</i>	96.64	0.19	78.07	1.74	44,243	2,636,302	134	59.41
bin_17	<i>Oscillibacter_sp_KLE_1728</i>	95.78	4.83	3.25	1.91	6,724	2,495,600	274	61.83
bin_14	<i>o__Clostridiales (UID1212)</i>	94.57	0.00	93.40	1.42	24,953	2,699,365	161	61.31
bin_22	<i>o__Clostridiales (UID1212)</i>	94.41	1.85	99.16	0.41	30,738	2,309,471	151	56.18
bin_12	<i>Lachnospiraceae_bacterium_6_1_63FAA</i>	94.24	0.53	33.58	6.46	44,630	2,722,520	224	38.82
bin_1	<i>Bacteroides_finegoldii_DSM_17565</i>	92.66	5.33	1.02	0.33	33,380	4,448,137	245	42.12
bin_24	<i>Clostridium_sp_CAG_58</i>	91.40	2.22	5.04	0.72	22,217	2,229,716	259	53.82
bin_25	<i>Collinsella_stercoris_DSM_13279</i>	90.55	2.40	32.27	10.38	5,659	2,205,993	366	63.15
bin_26	<i>Clostridium_sp_CAG_505</i>	89.14	0.67	7.37	0.75	19,203	2,034,211	232	46.06
bin_3	<i>Bacteroides_vulgatus_str_3975_RP4</i>	88.69	1.49	2.26	4.31	9,200	4,013,095	558	41.61
bin_11	<i>Bilophila_wadsworthia_ATCC_49260</i>	83.14	0.59	3.38	0.50	2,990	2,723,688	472	61.09
bin_35	<i>o__Clostridiales (UID1212)</i>	76.33	0.40	94.86	0.71	109,967	1,476,765	36	28.31
bin_27	<i>Collinsella_tanakaei_YIT_12063</i>	76.26	3.04	22.05	1.83	9,385	1,819,892	248	60.81
bin_30	<i>Collinsella_aerofaciens_ATCC_25986</i>	75.77	1.88	31.74	0.48	15,638	1,622,044	203	60.25
bin_31	<i>o__Clostridiales (UID1212)</i>	63.44	0.00	95.05	0.58	3,815	1,620,235	334	62.33
bin_33	<i>o__Clostridiales (UID1226)</i>	61.23	0.95	98.70	0.86	3,050	1,503,828	315	45.86
bin_38	<i>k__Bacteria (UID203)</i>	55.39	0.86	71.81	0.18	2,938	1,195,001	201	63.71
bin_40	<i>o__Clostridiales (UID1212)</i>	52.90	0.67	84.37	0.14	88,574	1,086,364	33	27.11
bin_28	<i>k__Bacteria (UID203)</i>	49.01	5.26	86.10	0.25	4,874	1,812,694	321	43.81
bin_37	<i>c__Clostridia (UID1085)</i>	43.48	0.51	99.08	0.58	7,616	1,254,951	91	47.75
bin_34	<i>k__Bacteria (UID203)</i>	41.90	0.00	84.73	0.51	3,235	1,499,044	323	57.91
bin_43	<i>k__Bacteria (UID203)</i>	40.52	0.00	94.21	0.71	14,248	582,679	54	62.29
bin_39	<i>Ruminococcaceae_bacterium_D16</i>	38.79	1.72	9.25	0.45	4,982	1,193,777	254	59.98
bin_36	<i>Blautia_sp_CAG_257</i>	26.48	0.00	0.00	0.44	26,390	1,343,331	121	44.20

Cluster ID	Top Reference	Complete (%)	MGO (%)	Novelty Score	Abundance	Contig N50	Genome Size	Num Contigs	GC (%)
bin_51	<i>k__Bacteria (UID203)</i>	25.86	0.00	98.46	0.07	8,859	275,347	40	43.59
bin_48	<i>_Clostridium_hiranonis_DSM_13275</i>	21.55	0.00	20.22	0.15	2,661	411,612	110	31.78
bin_53	<i>k__Bacteria (UID203)</i>	17.24	0.00	31.74	0.13	5,690	226,425	46	33.27
bin_55	<i>k__Bacteria (UID203)</i>	17.24	0.00	95.44	0.03	4,745	192,572	28	40.34
bin_44	<i>k__Bacteria (UID203)</i>	13.95	0.00	81.39	0.59	4,476	502,159	99	64.99
bin_45	<i>o__Bacteroidales (UID2657)</i>	13.21	0.00	1.24	0.44	2,128	488,793	77	45.60
bin_50	<i>o__Lactobacillales (UID544)</i>	13.08	0.00	1.78	0.02	6,249	299,062	72	38.92
bin_46	<i>k__Bacteria (UID203)</i>	12.93	0.00	1.04	0.33	5,283	445,606	98	47.55
bin_54	<i>k__Bacteria (UID203)</i>	10.34	0.00	36.55	0.01	119,075	207,839	3	46.54
bin_60	<i>k__Bacteria (UID203)</i>	10.34	0.00	96.19	0.05	16,587	144,516	21	45.91
bin_58	<i>k__Bacteria (UID203)</i>	9.01	0.00	83.39	0.12	17,507	151,856	23	63.58
bin_41	<i>root (UID1)</i>	4.17	0.00	0.00	0.00	335,313	635,469	3	43.18
bin_42	<i>root (UID1)</i>	4.17	0.00	0.00	0.44	9,662	603,875	137	42.29
bin_57	<i>k__Bacteria (UID203)</i>	0.69	0.00	53.46	0.14	54,615	159,058	4	41.89
bin_47	<i>root (UID1)</i>	0.00	0.00	0.00	0.16	24,386	443,212	75	38.78
bin_49	<i>root (UID1)</i>	0.00	0.00	0.00	0.06	7,527	383,763	52	35.01
bin_52	<i>root (UID1)</i>	0.00	0.00	0.00	0.13	46,140	233,305	22	44.41
bin_56	<i>root (UID1)</i>	0.00	0.00	0.00	0.03	2,655	176,518	26	37.56
bin_59	<i>root (UID1)</i>	0.00	0.00	0.00	0.01	2,910	146,640	23	33.04
bin_61	<i>root (UID1)</i>	0.00	0.00	0.00	0.13	7,404	109,340	15	61.86
bin_62	<i>root (UID1)</i>	0.00	0.00	0.00	0.02	18,212	108,749	12	39.95
bin_63	<i>root (UID1)</i>	0.00	0.00	0.00	0.03	16,971	102,988	13	41.40
bin_64	<i>root (UID1)</i>	0.00	0.00	0.00	0.01	3,405	101,851	27	43.30

1) For samples processed after December 2, 2020 abundance will show the average read depth for each bin by length. Older samples will show an estimated relative abundance percentage.