



Novel Genome
>80% Complete, <10% MGO*
>90 Novelty Score

Known Genome
>80% Complete, <10% MGO*
<90 Novelty Score

*Marker Gene Overrepresentation

Cluster ID	Top Reference	Complete (%)	MGO (%)	Novelty Score	Abundance (%)	Contig N50	Genome Size	Num Contigs	GC (%)
cluster_1	<i>o__Clostridiales</i>	100.00	0.15	98.01	0.41	25,709	3,436,870	310	42.78
cluster_2	<i>Dialister_sp_CAG_486</i>	100.00	1.90	46.10	1.33	33,021	2,337,745	112	51.59
cluster_3	<i>Parabacteroides_merdae_CAG_48</i>	99.62	4.98	2.35	1.36	35,148	4,762,269	337	45.12
cluster_4	<i>c__Epsilonproteobacteria</i>	99.02	0.06	83.73	0.36	16,649	1,684,738	172	34.72
cluster_5	<i>Clostridium_sp_CAG_299</i>	98.73	2.77	15.78	0.41	22,077	3,186,923	279	49.15
cluster_6	<i>Clostridium_sp_CAG_58</i>	98.56	5.07	8.03	0.33	9,181	3,212,466	629	51.97
cluster_7	<i>o__Clostridiales</i>	97.99	0.22	95.58	0.61	80,133	1,900,650	43	36.36
cluster_8	<i>o__Clostridiales</i>	97.96	0.79	88.67	0.68	37,232	2,436,147	101	57.94
cluster_9	<i>f__Lachnospiraceae</i>	97.52	7.40	97.16	0.64	98,613	3,124,465	76	49.50
cluster_10	<i>o__Clostridiales</i>	97.32	0.17	95.16	0.56	42,421	2,508,671	139	56.02
cluster_11	<i>Collinsella_tanakaei_YIT12063</i>	97.18	3.70	30.60	0.51	6,996	2,792,247	615	60.69
cluster_12	<i>Bacteroides_vulgatus_str_3975_RP4</i>	96.93	3.08	2.39	10.45	8,367	6,201,921	1155	41.14
cluster_13	<i>Odoribacter_splanchnicus_CAG_14</i>	96.77	1.08	0.52	0.60	71,950	4,240,487	103	43.46
cluster_14	<i>Oscillibacter_sp_CAG_155</i>	96.64	0.19	79.45	0.52	35,843	2,660,018	163	59.28
cluster_15	<i>Bilophila_wadsworthia_3_1_6</i>	96.15	6.61	3.35	0.25	4,859	4,009,908	1095	59.36
cluster_16	<i>Alistipes_putredinis_CAG_67</i>	96.15	0.48	7.64	9.08	317,714	2,222,016	14	54.14
cluster_17	<i>o__Clostridiales</i>	95.75	1.85	97.93	0.34	20,312	2,581,704	231	55.62
cluster_18	<i>Clostridium_sp_CAG_505</i>	95.30	1.34	9.14	0.30	9,615	2,598,859	446	45.57
cluster_19	<i>Sutterella_wadsworthensis_2_1_59BFAA</i>	95.03	0.00	3.72	4.55	32,017	2,270,014	79	62.04
cluster_20	<i>Collinsella_stercoris_DSM_13279</i>	94.97	2.04	33.72	4.12	9,364	2,169,457	368	63.17
cluster_21	<i>Blautia_sp_CAG_257</i>	94.74	4.68	2.77	0.31	8,262	3,207,806	619	43.39
cluster_22	<i>Bacteroides_sp_D20</i>	93.19	4.65	24.09	0.78	16,674	4,348,210	460	46.21
cluster_23	<i>Azospirillum_sp_CAG_260</i>	92.47	2.69	1.15	2.40	54,012	1,804,931	91	47.19
cluster_24	<i>Parabacteroides_distasonis_ATCC_8503</i>	89.80	4.94	38.42	0.26	5,827	3,579,765	856	45.29
cluster_25	<i>o__Clostridiales</i>	89.68	0.00	94.75	0.61	26,646	2,444,153	111	61.63
cluster_26	<i>Bacteroides_coprophilus_CAG_333</i>	89.41	0.81	1.48	1.40	54,213	3,259,897	100	45.99
cluster_27	<i>o__Clostridiales</i>	89.15	1.81	97.78	0.22	3,148	2,413,933	904	56.46
cluster_28	<i>o__Clostridiales</i>	88.94	2.95	96.45	0.23	3,750	2,468,844	827	45.22
cluster_29	<i>Firmicutes_bacterium_CAG_424</i>	87.88	0.00	15.43	0.51	43,851	3,010,063	96	41.23
cluster_30	<i>o__Clostridiales</i>	87.64	3.66	94.20	0.25	4,389	2,920,334	860	43.34
cluster_31	<i>o__Clostridiales</i>	87.46	5.33	92.88	0.25	3,580	3,178,442	1139	60.20
cluster_32	<i>o__Clostridiales</i>	85.91	0.00	94.53	0.78	78,955	2,126,407	36	45.42
cluster_33	<i>Ruminococcus_gnavus_CAG_126</i>	85.38	0.00	77.39	0.66	81,677	2,282,817	32	43.47
cluster_34	<i>k__Bacteria</i>	84.83	2.81	98.59	0.26	8,793	1,819,722	311	33.24
cluster_35	<i>Collinsella_aerofaciens_ATCC_25986</i>	84.43	1.88	38.79	0.31	9,393	1,606,779	257	60.14
cluster_36	<i>_Clostridium_hiranonis_DSM_13275</i>	83.78	3.15	33.38	0.21	2,486	1,757,361	764	33.36
cluster_37	<i>p__Actinobacteria</i>	81.45	0.81	94.71	0.49	8,094	1,472,455	291	63.03
cluster_38	<i>o__Clostridiales</i>	80.69	5.15	87.27	0.41	22,791	1,841,237	151	26.81
cluster_39	<i>Oscillibacter_sp_KLE_1728</i>	76.71	0.69	1.63	0.59	13,466	2,245,680	208	61.63
cluster_40	<i>o__Clostridiales</i>	76.33	0.06	94.86	1.13	109,967	1,435,177	34	28.49
cluster_41	<i>o__Clostridiales</i>	74.33	0.47	94.73	0.78	26,312	2,014,059	89	60.59

Cluster ID	Top Reference	Complete (%)	MGO (%)	Novelty Score	Abundance (%)	Contig N50	Genome Size	Num Contigs	GC (%)
cluster_42	<i>Collinsella_intestinalis</i> _DSM_13280	70.96	3.93	74.20	0.32	5,484	1,606,747	397	62.98
cluster_43	<i>Bacteroides_stercoris</i> _CAG_120	68.58	4.38	6.77	7.06	4,740	3,591,651	962	44.46
cluster_44	<i>o__Clostridiales</i>	67.66	4.33	91.98	0.24	4,065	1,499,568	473	27.78
cluster_45	<i>Bacteroides_finegoldii</i> _DSM_17565	65.28	0.00	0.01	0.93	38,565	3,546,108	181	42.29
cluster_46	<i>c__Clostridia</i>	65.24	0.77	99.39	0.45	18,607	1,555,838	110	46.79
cluster_47	<i>Ruminococcaceae_bacterium</i> _D16	63.56	2.48	19.54	0.25	3,930	2,078,068	652	57.66
cluster_48	<i>Dorea_sp</i> _CAG_317	60.92	8.48	53.17	0.18	1,994	1,986,633	1034	44.54
cluster_49	<i>Lachnospiraceae_bacterium</i> _CAG_364	57.12	0.00	27.65	1.11	24,277	1,338,987	65	38.96
cluster_50	<i>o__Clostridiales</i>	55.11	3.16	91.57	0.21	2,273	2,144,549	998	42.96
cluster_51	<i>Blautia_hanseni</i> _DSM_20583	44.02	0.00	25.96	1.11	41,014	1,053,831	35	38.10
cluster_52	<i>Enterococcus_faecalis</i> _T11	42.46	8.80	19.90	0.17	2,032	1,346,274	681	42.96
cluster_53	<i>k__Bacteria</i>	32.71	5.26	83.95	0.18	1,802	1,348,456	732	46.94
cluster_54	<i>Prevotella_copri</i> _CAG_164	29.31	0.00	5.37	2.35	157,837	893,897	6	45.61
cluster_55	<i>f__Lachnospiraceae</i>	28.86	4.29	67.51	0.23	6,702	1,819,903	533	40.25
cluster_56	<i>Oscillibacter_sp</i> _KLE_1745	27.79	3.80	9.90	0.33	3,911	2,257,372	768	56.24
cluster_57	<i>Prevotella_copri</i> _CAG_164	26.69	0.34	13.21	2.35	58,510	879,496	15	45.68
cluster_58	<i>o__Clostridiales</i>	26.31	1.34	76.55	0.66	7,906	903,206	157	56.79
cluster_59	<i>Bacteroides_finegoldii</i> _DSM_17565	23.21	0.00	1.89	1.03	28,817	946,999	56	42.43
cluster_60	<i>p__Actinobacteria</i>	22.67	3.52	78.96	0.20	1,913	484,378	252	63.86
cluster_61	<i>k__Bacteria</i>	22.02	0.86	86.24	0.17	1,647	772,699	452	47.20
cluster_62	<i>o__Clostridiales</i>	21.88	0.00	96.39	0.16	1,497	641,441	417	44.85
cluster_63	<i>Collinsella_sp</i> _CAG_166	21.22	0.16	22.53	0.30	4,917	519,636	136	59.27
cluster_64	<i>Ruminococcaceae_bacterium</i> _D16	20.86	0.00	23.09	0.25	3,111	406,620	146	58.43
cluster_65	<i>k__Bacteria</i>	20.69	4.81	33.92	0.29	4,533	1,086,532	323	45.23
cluster_66	<i>k__Bacteria</i>	19.98	1.72	53.40	0.53	4,286	788,478	246	62.04
cluster_67	<i>c__Clostridia</i>	17.98	0.00	95.62	0.35	4,733	579,572	156	42.99
cluster_68	<i>k__Bacteria</i>	15.52	1.72	0.03	6.13	4,407	1,543,958	477	44.51
cluster_69	<i>k__Bacteria</i>	15.52	0.00	9.08	2.69	42,053	470,141	17	45.72
cluster_70	<i>k__Bacteria</i>	12.07	0.00	34.79	3.03	3,029	632,943	236	42.24
cluster_71	<i>p__Actinobacteria</i>	11.67	1.61	78.08	0.18	1,849	373,572	204	54.47
cluster_72	<i>k__Bacteria</i>	10.34	0.00	0.18	2.64	43,134	742,315	18	44.81
cluster_73	<i>k__Bacteria</i>	9.87	1.72	29.44	0.17	1,604	654,979	375	52.41
cluster_74	<i>k__Bacteria</i>	8.52	1.79	0.00	0.15	1,334	383,948	278	59.54
cluster_75	<i>root</i>	8.33	4.17	82.13	0.17	1,815	282,459	155	57.53
cluster_76	<i>root</i>	8.33	0.00	12.27	0.22	4,529	156,808	54	49.78
cluster_77	<i>o__Clostridiales</i>	8.33	0.13	18.06	0.53	6,321	511,463	121	38.96
cluster_78	<i>k__Bacteria</i>	7.89	0.00	45.78	0.17	1,783	283,687	160	47.78
cluster_79	<i>k__Bacteria</i>	6.90	0.00	0.09	2.43	17,694	455,959	40	42.74
cluster_80	<i>k__Bacteria</i>	6.58	0.00	14.78	1.75	4,499	536,994	153	44.97
cluster_81	<i>o__Lactobacillales</i>	5.86	0.37	3.64	0.18	2,303	199,101	101	45.28
cluster_82	<i>k__Bacteria</i>	5.17	0.00	14.13	0.70	7,859	527,671	128	48.93
cluster_83	<i>k__Bacteria</i>	5.17	0.00	0.00	2.81	5,559	733,076	204	55.04
cluster_84	<i>k__Bacteria</i>	4.94	0.00	54.27	0.18	2,073	358,702	161	57.59
cluster_85	<i>root</i>	4.17	0.00	82.15	0.16	1,729	113,468	67	51.06
cluster_86	<i>k__Bacteria</i>	2.07	0.00	42.36	0.17	1,892	96,427	53	53.50
cluster_87	<i>k__Bacteria</i>	1.72	0.00	0.00	1.32	20,588	725,307	84	54.58
cluster_88	<i>root</i>	0.00	0.00	0.00	0.60	3,704	479,881	163	44.27
cluster_89	<i>root</i>	0.00	0.00	0.00	0.23	85,227	92,422	6	61.60
cluster_90	<i>root</i>	0.00	0.00	0.00	0.18	2,214	60,099	28	48.32
cluster_91	<i>root</i>	0.00	0.00	0.00	0.17	2,125	82,451	39	52.86
cluster_92	<i>root</i>	0.00	0.00	0.00	0.66	2,366	150,201	75	61.15
cluster_93	<i>root</i>	0.00	0.00	0.00	0.16	1,852	141,031	70	54.58
cluster_94	<i>root</i>	0.00	0.00	0.00	0.17	1,234	25,510	18	55.55
cluster_95	<i>root</i>	0.00	0.00	0.00	0.18	1,622	106,507	60	53.32
cluster_96	<i>root</i>	0.00	0.00	0.00	0.16	1,392	76,668	50	46.10