



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	Slackia_piriformis_YIT_12062	100.00	8.53	60.79	0.27	148,569	2,519,994	166	52.01
cluster_2	Collinsella_tanakaei_YIT_12063	100.00	0.15	29.03	0.34	42,677	2,279,832	93	60.63
cluster_3	Firmicutes_bacterium_CAG_646	99.37	1.27	0.98	0.47	107,379	2,795,410	35	43.43
cluster_4	Clostridium_colicanis_209318	99.19	0.90	7.04	0.11	25,463	3,821,167	302	26.44
cluster_5	<i>o__Clostridiales</i>	98.31	1.27	97.98	0.48	48,387	3,325,221	108	39.81
cluster_6	Allobaculum_stercoricanis_DSM_13633	98.11	2.29	0.65	0.45	56,210	1,948,204	68	37.51
cluster_7	<i>c__Bacilli</i>	97.35	1.43	98.77	1.15	129,343	2,946,216	35	34.61
cluster_8	<i>o__Clostridiales</i>	97.32	0.17	96.35	0.22	25,766	2,922,812	164	42.53
cluster_9	<i>c__Bacilli</i>	97.13	1.60	98.77	0.17	90,168	2,929,229	66	37.86
cluster_10	<i>o__Clostridiales</i>	96.10	1.24	98.76	0.09	15,204	2,679,500	288	40.53
cluster_11	<i>o__Clostridiales</i>	95.82	0.84	98.34	0.17	61,332	2,639,948	102	48.05
cluster_12	Holdemanelia_biformis_DSM_3989	94.47	0.84	69.54	1.14	32,876	2,333,317	109	34.09
cluster_13	Lactobacillus_animalis_KCTC_3501_DSM_20602	93.91	0.26	0.04	0.43	36,172	1,663,082	57	41.30
cluster_14	Dorea_sp_CAG_317	92.40	2.92	50.00	0.63	42,587	2,449,813	101	40.49
cluster_15	Ruminococcus_gnavus_CAG_126	92.40	3.80	8.10	0.26	24,455	2,994,386	352	42.84
cluster_16	<i>o__Clostridiales</i>	91.73	8.11	96.13	0.09	3,799	2,818,766	921	29.37
cluster_17	<i>o__Clostridiales</i>	89.74	0.63	94.33	0.39	94,628	2,404,496	35	42.40
cluster_18	<i>o__Clostridiales</i>	89.66	0.00	96.04	0.45	127,644	2,570,915	28	42.43
cluster_19	<i>o__Clostridiales</i>	89.18	0.00	81.29	0.18	67,036	2,011,471	43	38.01
cluster_20	Clostridium_sp_CAG_299	88.61	0.00	1.37	0.27	152,015	2,822,839	25	49.03
cluster_21	<i>o__Clostridiales</i>	88.29	0.00	87.09	0.08	10,176	2,675,927	367	44.33
cluster_22	Eubacterium_dolichum_CAG_375	88.21	0.00	0.29	0.11	22,020	1,687,947	106	37.99
cluster_23	Lachnospiraceae_bacterium_6_1_63FAA	87.07	3.16	71.87	0.31	13,352	2,332,534	340	37.79
cluster_24	<i>o__Clostridiales</i>	82.19	3.38	85.31	0.20	10,581	2,820,863	448	39.05
cluster_25	Lachnospiraceae_bacterium_CAG_215	81.52	4.26	3.22	0.07	2,885	2,402,427	970	46.40
cluster_26	<i>o__Clostridiales</i>	74.19	0.90	86.70	0.27	46,645	2,417,179	77	27.91
cluster_27	<i>o__Clostridiales</i>	73.98	1.27	98.92	0.16	7,933	2,077,332	376	40.96
cluster_28	<i>o__Clostridiales</i>	73.46	6.15	96.77	0.08	10,810	2,155,983	337	58.82
cluster_29	<i>k__Bacteria</i>	62.07	1.72	98.72	0.79	726,927	1,184,736	2	27.23
cluster_30	<i>o__Clostridiales</i>	57.02	4.24	90.53	0.07	3,626	1,405,659	465	58.99
cluster_31	Collinsella_intestinalis_DSM_13280	55.99	2.79	21.87	2.80	3,443	1,004,206	348	61.48
cluster_32	<i>k__Bacteria</i>	55.17	0.00	98.56	1.71	125,122	2,051,362	17	37.54
cluster_33	_Clostridium_hiranonis_DSM_13275	54.35	9.27	28.61	0.75	7,733	1,789,419	344	30.74
cluster_34	Blautia_sp_CAG_257	51.32	2.29	7.68	0.70	4,750	1,920,987	515	43.33
cluster_35	_Clostridium_hiranonis_DSM_13275	51.08	7.34	30.24	3.30	10,300	1,106,839	153	31.05
cluster_36	<i>k__Bacteria</i>	50.88	0.00	97.66	0.18	134,423	1,120,217	10	36.45
cluster_37	<i>o__Clostridiales</i>	48.82	3.28	91.29	0.07	2,685	1,462,697	590	46.33
cluster_38	<i>o__Clostridiales</i>	48.73	0.00	95.96	1.23	39,960	1,188,535	39	41.54
cluster_39	_Clostridium_spiroforme_DSM_1552	48.11	0.00	42.35	0.11	39,992	1,223,857	64	28.70
cluster_40	<i>f__Lachnospiraceae</i>	46.72	0.06	97.46	0.09	20,676	1,018,831	65	43.81
cluster_41	<i>o__Clostridiales</i>	42.95	0.00	96.33	0.20	50,757	1,046,534	31	36.67

Cluster ID	Top Reference	Complete (%)	MGO (%)	Novelty Score	Abundance (%)	Contig N50	Genome Size	Num Contigs	GC (%)
cluster_42	_Clostridium_spiroforme_DSM_1552	40.35	0.00	51.31	0.10	16,577	1,081,309	115	29.12
cluster_43	<i>k__Bacteria</i>	40.00	0.00	97.03	0.09	27,041	1,022,556	55	42.85
cluster_44	<i>k__Bacteria</i>	39.95	0.00	93.17	0.64	3,794	1,430,495	469	42.92
cluster_45	Catenibacterium_sp_CAG_290	39.62	0.00	5.54	8.71	23,121	869,950	43	33.84
cluster_46	Collinsella_intestinalis_DSM_13280	39.50	0.00	2.83	1.35	3,724	929,398	309	62.29
cluster_47	<i>c__Bacilli</i>	38.19	0.00	96.89	1.66	50,593	1,170,738	52	36.99
cluster_48	Catenibacterium_sp_CAG_290	36.84	0.00	4.91	9.04	24,538	783,732	44	33.94
cluster_49	<i>k__Bacteria</i>	36.46	3.10	56.86	0.19	3,149	2,389,051	911	57.52
cluster_50	Collinsella_stercoris_DSM_13279	36.21	0.00	17.17	7.56	13,682	728,589	59	63.89
cluster_51	<i>o__Clostridiales</i>	34.97	4.44	56.88	1.11	10,045	1,943,205	439	44.21
cluster_52	Blautia_sp_CAG_257	34.71	7.38	29.64	0.32	5,067	3,152,725	908	41.26
cluster_53	_Clostridium_hiranonis_DSM_13275	34.01	0.00	49.38	0.83	19,637	1,091,576	94	30.77
cluster_54	Collinsella_stercoris_DSM_13279	31.50	1.72	13.52	7.80	4,846	807,272	191	63.71
cluster_55	Lachnospiraceae_bacterium_CAG_364	30.62	5.26	1.50	0.38	4,483	741,518	229	38.91
cluster_56	<i>c__Bacilli</i>	30.54	2.06	98.70	-	1,601	1,095,119	694	39.85
cluster_57	<i>k__Bacteria</i>	29.82	0.00	98.67	0.17	7,235	1,064,273	242	35.48
cluster_58	Firmicutes_bacterium_CAG_424	28.84	2.53	2.75	0.28	6,415	1,626,358	358	39.37
cluster_59	<i>k__Bacteria</i>	26.32	0.00	95.52	1.44	119,523	364,207	3	42.11
cluster_60	<i>c__Bacilli</i>	26.10	0.44	94.01	0.16	3,730	1,073,666	355	37.13
cluster_61	Clostridium_perfringens_JJC	25.00	0.00	12.28	0.52	4,008	791,471	226	28.02
cluster_62	Blautia_sp_CAG_257	24.56	0.00	3.68	0.63	9,183	682,507	102	43.80
cluster_63	Blautia_sp_CAG_257	23.81	0.00	12.33	0.57	9,480	640,512	76	43.73
cluster_64	<i>o__Clostridiales</i>	23.70	2.29	93.42	0.07	4,048	936,517	303	53.15
cluster_65	<i>o__Clostridiales</i>	23.10	0.90	77.87	0.24	2,701	1,056,514	425	41.01
cluster_66	Firmicutes_bacterium_CAG_424	23.01	1.75	6.94	0.11	3,256	647,747	230	40.60
cluster_67	Lachnospiraceae_bacterium_CAG_364	22.81	0.00	35.53	0.31	6,333	813,461	191	38.96
cluster_68	_Clostridium_hiranonis_DSM_13275	22.41	0.00	14.01	3.78	18,618	736,517	48	30.98
cluster_69	Clostridium_perfringens_ATCC_13124	22.21	0.00	6.49	1.08	4,819	947,233	226	27.84
cluster_70	Clostridium_perfringens	21.17	0.00	14.98	0.98	7,600	764,022	135	27.77
cluster_71	Firmicutes_bacterium_CAG_424	20.69	1.75	0.26	0.30	3,405	1,031,742	364	40.50
cluster_72	<i>o__Clostridiales</i>	20.59	0.00	96.17	1.34	5,667	403,619	91	41.99
cluster_73	Lachnospiraceae_bacterium_CAG_364	20.18	0.00	5.75	0.28	2,965	540,336	212	39.15
cluster_74	<i>k__Bacteria</i>	19.56	2.39	84.62	0.14	3,613	643,339	226	41.84
cluster_75	<i>k__Bacteria</i>	18.97	0.00	1.05	0.32	2,902	949,374	366	28.16
cluster_76	<i>k__Bacteria</i>	17.54	1.75	71.70	0.41	2,304	1,728,711	761	41.61
cluster_77	<i>k__Bacteria</i>	17.54	0.00	8.39	8.12	39,606	330,765	12	33.89
cluster_78	<i>k__Bacteria</i>	16.54	0.00	97.60	0.17	8,503	971,397	193	36.14
cluster_79	<i>k__Bacteria</i>	16.11	0.16	3.59	0.27	2,398	421,630	190	40.46
cluster_80	<i>k__Bacteria</i>	15.26	0.00	0.73	0.15	5,147	678,915	145	37.98
cluster_81	<i>k__Bacteria</i>	14.67	0.00	3.55	-	2,294	466,444	219	41.24
cluster_82	<i>k__Bacteria</i>	14.04	0.00	17.96	0.27	6,817	639,212	168	44.42
cluster_83	<i>k__Bacteria</i>	12.28	0.00	93.64	1.19	215,199	361,735	3	42.67
cluster_84	<i>k__Bacteria</i>	11.44	0.00	77.68	0.08	1,796	557,081	306	40.81
cluster_85	<i>k__Bacteria</i>	10.82	0.00	96.35	0.18	11,903	797,520	123	35.94
cluster_86	<i>k__Bacteria</i>	10.45	0.00	0.48	0.28	2,677	350,670	152	38.68
cluster_87	<i>k__Bacteria</i>	9.57	0.00	73.80	0.10	1,704	406,171	233	39.09
cluster_88	<i>k__Bacteria</i>	9.40	0.00	0.00	0.09	2,054	1,984,771	967	28.81
cluster_89	root	8.33	0.00	59.96	0.59	11,221	821,025	121	39.61
cluster_90	root	8.33	0.00	0.00	0.27	4,019	996,795	303	40.66
cluster_91	root	8.33	0.00	90.74	1.08	185,872	676,237	4	26.66
cluster_92	<i>o__Clostridiales</i>	6.55	0.02	88.33	1.63	2,878	271,947	113	41.88
cluster_93	<i>k__Bacteria</i>	5.58	0.00	0.00	0.34	2,565	827,537	353	41.22
cluster_94	<i>k__Bacteria</i>	5.26	0.00	56.48	-	1,647	305,560	172	40.63
cluster_95	<i>k__Bacteria</i>	5.26	0.00	14.75	0.44	5,075	570,207	162	39.32
cluster_96	<i>k__Bacteria</i>	5.18	0.00	12.50	0.26	6,205	307,985	64	38.25
cluster_97	root	4.17	0.00	0.00	0.09	3,735	556,134	180	39.04
cluster_98	root	4.17	0.00	53.72	0.33	109,772	743,745	7	27.89
cluster_100	root	0.00	0.00	0.00	0.41	2,970	1,009,687	379	41.65
cluster_101	root	0.00	0.00	0.00	0.32	2,345	400,568	188	39.10
cluster_102	root	0.00	0.00	0.00	1.38	51,113	140,582	11	38.20

Cluster ID	Top Reference	Complete (%)	MGO (%)	Novelty Score	Abundance (%)	Contig N50	Genome Size	Num Contigs	GC (%)
cluster_103	<i>root</i>	0.00	0.00	0.00	2.13	3,614	415,250	146	43.77
cluster_104	<i>root</i>	0.00	0.00	0.00	0.32	10,103	440,972	59	38.33
cluster_105	<i>root</i>	0.00	0.00	0.00	0.18	10,426	707,948	119	36.31
cluster_106	<i>root</i>	0.00	0.00	0.00	3.13	19,567	145,829	9	61.19
cluster_107	<i>root</i>	0.00	0.00	0.00	1.12	8,916	114,016	24	39.65
cluster_108	<i>root</i>	0.00	0.00	0.00	1.13	79,934	311,055	4	41.92