



Bins that were identified in the **merged** profile database '**merged 2**' and stored in the database as "**MAXBIN2**" collection, describe **69** bins accounting for **134,385,101** nucleotides, which represent **92.25%** of all nucleotides stored in the contigs database, and **92.25%** of nucleotides stored in the profile database.

Basics

The merged profile database that was generated with the minimum contig length of **1,000** contained **57,414** contigs, which correspond to **100%** of all contigs, and **100%** of all nucleotides found in the contigs database.

Profile DB (**merged 2** w/ 3 samples).

Key	Value
Created on	2024-01-09 14:32:31
Version	38
Number of contigs	57,414
Number of splits	57,725
Contig length cutoff min	1,000
Contig length cutoff max	9,223,372,036,854,775,807
Samples in profile	BGR_130305_bam_sorted, BGR_130527_bam_sorted, BGR_130708_bam_sorted
Total nucleotides	145.68 Mb
SNVs profiled	True
SCVs profiled	False
IN/DEls profiled	True
Report variability full	False
Min coverage for variability	10.00

Contigs DB (**biol217**)

Key	Value
Project name	biol217
Created on	2024-01-03 11:47:37
Version	21
Total nucleotides	145.68 Mb
Number of contigs	57,414
Number of splits	57,725
Genes are called	True
External gene calls	False
External amino acid sequences	False
K-mer size	4
Split length	20,000
Splits consider gene calls	True
SCG taxonomy was run	True
Gene function sources	None :(
Summary reformatted contig names	False

Profile DB description

No description is provided

Summary of Bins (69)

Summary of each bin. You can download the information below also as a TAB-delimited file (bins_summary.txt). Here is another TAB-delimited file that reports data for each single profile (such as number of reads mapped, etc) ().

Bin	Source	Taxonomy	Total Size	Num Contigs	N50	GC Content	Compl.	Red.	SCG Domain
MAXBIN__010	maxbin2	Methanoculleus sp012797575	3.47 Mb	1,045	4,453	59.15%	96.05%	80.26%	archaea
MAXBIN__061	maxbin2	UBA5436 sp012522435	2.99 Mb	1,147	3,734	37.10%	97.18%	28.17%	bacteria
MAXBIN__063	maxbin2	DTU012 sp012837335	2.92 Mb	588	15,803	47.13%	97.18%	19.72%	bacteria
MAXBIN__017	maxbin2	Acetomicrobium sp012518015	3.12 Mb	1,108	3,596	45.01%	95.77%	88.73%	bacteria
MAXBIN__004	maxbin2	DTU010 sp900018335	2.51 Mb	115	57,891	56.62%	95.77%	49.30%	bacteria
MAXBIN__066	maxbin2	Fermentimonas sp012839475	4.18 Mb	1,069	14,323	51.72%	92.96%	53.52%	bacteria
MAXBIN__007	maxbin2	UBA3910 sp002391465	2.72 Mb	316	71,325	51.89%	92.96%	4.23%	bacteria
MAXBIN__014	maxbin2	UBA4179 sp002381125	2.59 Mb	712	5,466	41.80%	92.96%	21.13%	bacteria
MAXBIN__009	maxbin2	DTU013 sp002385815	2.67 Mb	170	43,354	47.28%	91.55%	1.41%	bacteria
MAXBIN__001	maxbin2	UBA3900 sp002391675	2.57 Mb	245	47,247	51.24%	91.55%	0.00%	bacteria
MAXBIN__025	maxbin2	DTU065 sp001512545	2.65 Mb	688	6,473	48.76%	90.14%	21.13%	bacteria
MAXBIN__038	maxbin2	DTU067 sp001512995	1.60 Mb	316	8,447	47.43%	90.14%	5.63%	bacteria
MAXBIN__015	maxbin2	UBA4971 sp900019985	2.35 Mb	605	6,474	49.61%	88.73%	22.54%	bacteria
MAXBIN__016	maxbin2	Lenti-01 sp002304915	2.17 Mb	785	3,733	60.47%	88.73%	7.04%	bacteria
MAXBIN__023	maxbin2	JAAYQA01 sp012519495	2.38 Mb	812	4,123	52.36%	85.92%	47.89%	bacteria
MAXBIN__011	maxbin2	Thermoclostridium sp012518025	2.07 Mb	227	17,710	47.14%	85.92%	0.00%	bacteria
MAXBIN__005	maxbin2	DUQW01 sp012837585	971.55 Kb	329	3,519	31.77%	85.92%	1.41%	bacteria
MAXBIN__006	maxbin2	UBA3906 sp002391555	1.91 Mb	113	27,283	40.98%	84.51%	0.00%	bacteria
MAXBIN__043	maxbin2	DTU012 sp012520795	2.79 Mb	777	7,191	50.27%	83.10%	14.08%	bacteria
MAXBIN__021	maxbin2	JAAZPQ01 sp012797175	2.09 Mb	566	9,294	52.12%	83.10%	39.44%	bacteria
MAXBIN__032	maxbin2	DTU059 sp012523705	3.46 Mb	1,528	2,509	39.96%	81.69%	47.89%	bacteria
MAXBIN__058	maxbin2	Paludibacter sp012519425	3.37 Mb	1,385	2,900	40.84%	81.69%	26.76%	bacteria
MAXBIN__013	maxbin2	UBA4923 sp012841015	3.08 Mb	697	7,460	48.40%	81.69%	38.03%	bacteria
MAXBIN__042	maxbin2	UBA3946 sp002385755	1.34 Mb	438	3,841	48.94%	80.28%	7.04%	bacteria
MAXBIN__028	maxbin2	JAAZLA01 sp012799545	1.84 Mb	771	2,882	38.76%	78.87%	19.72%	bacteria
MAXBIN__049	maxbin2	JAAZJW01 sp012519835	2.82 Mb	1,561	1,769	39.74%	74.65%	59.15%	bacteria
MAXBIN__060	maxbin2	DTU015 sp012837895	1.69 Mb	868	2,077	51.86%	74.65%	28.17%	bacteria
MAXBIN__068	maxbin2	DUPA01 sp012838515	1.47 Mb	835	1,815	41.73%	74.65%	26.76%	bacteria
MAXBIN__040	maxbin2	Herbivorax sp012517995	2.74 Mb	1,741	1,543	35.18%	70.42%	40.85%	bacteria
MAXBIN__027	maxbin2	Geofilum sp002411385	3.11 Mb	1,246	3,007	43.54%	67.61%	14.08%	bacteria
MAXBIN__031	maxbin2	UBA1402 sp002305085	2.92 Mb	926	4,863	47.08%	67.61%	29.58%	bacteria

Bin	Source	Taxonomy	Total Size	Num Contigs	N50	GC Content	Compl.	Red.	SCG Domain:
MAXBIN__034	maxbin2	Clostridium sp003541575	1.69 Mb	1,012	1,608	35.79%	66.20%	74.65%	bacteria
MAXBIN__054	maxbin2	DTU010 sp012837385	1.88 Mb	918	2,178	51.56%	64.79%	33.80%	bacteria
MAXBIN__037	maxbin2	JAAYEV01 sp012728565	1.42 Mb	944	1,488	50.84%	64.79%	16.90%	bacteria
MAXBIN__044	maxbin2	UBA4923 sp012841145	1.29 Mb	231	14,822	50.19%	63.38%	38.03%	bacteria
MAXBIN__048	maxbin2	UBA3941 sp002385665	2.70 Mb	1,707	1,535	46.08%	61.97%	38.03%	bacteria
MAXBIN__035	maxbin2	JAAZPQ01 sp012840855	1.65 Mb	882	1,733	57.96%	61.97%	29.58%	bacteria
MAXBIN__059	maxbin2	UBA9076 sp003537975	1.95 Mb	1,171	1,580	34.23%	59.15%	35.21%	bacteria
MAXBIN__041	maxbin2	DTU012 sp900019385	2.29 Mb	1,040	2,467	54.71%	54.93%	25.35%	bacteria
MAXBIN__012	maxbin2	UBA1179 sp002340405	2.36 Mb	618	6,512	47.78%	53.52%	5.63%	bacteria
MAXBIN__002	maxbin2	DTU010 sp002391385	2.16 Mb	112	29,425	59.45%	52.11%	5.63%	bacteria
MAXBIN__024	maxbin2	JAAYSA01 sp012518455	294.12 Kb	79	5,990	35.26%	52.11%	29.58%	bacteria
MAXBIN__056	maxbin2	DTU010 sp012837385	3.72 Mb	1,423	3,223	54.44%	50.70%	36.62%	bacteria
MAXBIN__050	maxbin2	UBA5420 sp012838305	2.42 Mb	1,488	1,583	48.96%	50.70%	35.21%	bacteria
MAXBIN__033	maxbin2	UBA4923	888.91 Kb	175	8,960	52.19%	47.89%	11.27%	bacteria
MAXBIN__030	maxbin2	UBA1361 sp002306335	976.70 Kb	180	11,842	35.77%	46.48%	4.23%	bacteria
MAXBIN__008	maxbin2	DTU049 sp001512885	845.01 Kb	533	1,587	32.22%	46.48%	0.00%	bacteria
MAXBIN__036	maxbin2	N/A	2.11 Mb	1,241	1,660	55.46%	43.66%	14.08%	bacteria
MAXBIN__026	maxbin2	Sedimentibacter sp012520455	963.08 Kb	544	1,785	40.02%	43.66%	23.94%	bacteria
MAXBIN__055	maxbin2	Bacteria	1.32 Mb	895	1,442	54.35%	40.85%	8.45%	bacteria
MAXBIN__053	maxbin2	DTU059 sp012523685	670.22 Kb	427	1,504	39.80%	40.85%	12.68%	bacteria
MAXBIN__051	maxbin2	UBA5453 sp002427375	659.13 Kb	234	3,930	32.66%	40.85%	15.49%	bacteria
MAXBIN__019	maxbin2	UBA1361 sp002306335	214.38 Kb	64	6,822	37.66%	40.85%	1.41%	bacteria
MAXBIN__065	maxbin2	UBA5453 sp002427375	672.52 Kb	358	1,932	31.05%	38.03%	8.45%	bacteria
MAXBIN__067	maxbin2	Amphibacillus sp012838505	788.56 Kb	477	1,582	41.38%	36.62%	25.35%	bacteria
MAXBIN__018	maxbin2	Clostridia	1.49 Mb	777	1,878	35.50%	33.80%	9.86%	bacteria
MAXBIN__052	maxbin2	JAAYTL01 sp012518035	1.52 Mb	877	1,742	40.01%	32.39%	9.86%	bacteria
MAXBIN__069	maxbin2	UBA5455 sp012518415	319.39 Kb	193	1,680	37.12%	32.39%	0.00%	bacteria
MAXBIN__020	maxbin2	Geofilum sp002411385	2.50 Mb	1,308	1,953	45.28%	30.99%	5.63%	bacteria
MAXBIN__064	maxbin2	UBA5455 sp012518415	660.57 Kb	396	1,610	41.70%	29.58%	16.90%	bacteria
MAXBIN__047	maxbin2	UBA4923	799.30 Kb	290	3,166	54.43%	28.17%	8.45%	bacteria
MAXBIN__045	maxbin2	Bacteria	736.86 Kb	204	6,432	51.42%	22.54%	1.41%	bacteria
MAXBIN__039	maxbin2	Bacteria	2.91 Mb	1,381	2,155	43.99%	0.00%	0.00%	blank
MAXBIN__046	maxbin2	Mobilitalea sp012518975	2.70 Mb	1,674	1,552	38.97%	0.00%	0.00%	blank
MAXBIN__022	maxbin2	Methanoculleus bourgensis	1.94 Mb	1,066	1,867	63.37%	0.00%	0.00%	blank
MAXBIN__057	maxbin2	DUPI01 sp012838395	1.10 Mb	678	1,540	31.10%	0.00%	0.00%	blank
MAXBIN__003	maxbin2	N/A	1.08 Mb	480	2,532	42.62%	0.00%	0.00%	blank
MAXBIN__029	maxbin2	UBA3950 sp002385475	1.07 Mb	651	1,620	42.04%	0.00%	0.00%	blank

Bin	Source	Taxonomy	Total Size	Num Contigs	N50	GC Content	Compl.	Red.	SCG Domain
MAXBIN__062	maxbin2	DTU029 sp001512435	1.06 Mb	730	1,414	44.43%	0.00%	0.00%	blank

Across Samples (3)

std coverage	mean coverage	mean coverage Q2Q3	detection	abundance	variability
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TAB-delimited matrix file for std_coverage: bins_across_samples/std_coverage.txt (bins_across_samples/std_coverage.txt)

Bin	BGR_1 ...	BGR_1 ...	BGR_1 ...
MAXBIN__061	1.31	5.63	1.61
MAXBIN__063	1.28	3.54	1.93
MAXBIN__010	3.61	3.10	2.64
MAXBIN__017	2.78	2.45	2.55
MAXBIN__004	9.19	7.19	9.00
MAXBIN__066	0.92	0.93	4.94
MAXBIN__007	6.19	9.70	6.03
MAXBIN__014	3.25	7.00	3.31
MAXBIN__009	3.96	3.49	6.04
MAXBIN__001	10.50	7.46	16.49
MAXBIN__025	2.43	2.18	2.67
MAXBIN__038	2.07	0.92	3.71
MAXBIN__015	2.81	1.15	2.36
MAXBIN__016	2.63	0.15	2.16
MAXBIN__023	2.35	1.27	1.66
MAXBIN__011	3.46	2.12	2.98
MAXBIN__005	10.12	3.39	4.24
MAXBIN__006	5.99	8.18	5.14
MAXBIN__043	1.93	0.51	2.83
MAXBIN__021	2.54	1.98	2.17
MAXBIN__032	2.32	1.86	2.41
MAXBIN__058	1.43	1.68	3.25
MAXBIN__013	3.01	3.08	2.79
MAXBIN__042	1.94	1.43	2.55
MAXBIN__028	2.48	2.08	2.94
MAXBIN__049	1.77	1.94	1.74
MAXBIN__060	1.14	0.98	1.81
MAXBIN__068	0.27	2.03	1.79
MAXBIN__040	2.08	2.46	2.49
MAXBIN__027	2.34	1.20	1.99
MAXBIN__031	2.20	0.52	3.48
MAXBIN__034	2.14	2.15	2.28
MAXBIN__054	1.36	2.01	1.88
MAXBIN__037	1.79	0.38	1.48
MAXBIN__044	2.06	5.09	5.04
MAXBIN__048	1.51	0.89	1.61
MAXBIN__035	1.86	1.07	1.37
MAXBIN__059	1.35	3.17	2.77
MAXBIN__041	1.98	0.66	2.25
MAXBIN__012	3.60	1.77	4.33

Bin	BGR_1 ...	BGR_1 ...	BGR_1 ...
MAXBIN__002	10.94	11.30	7.79
MAXBIN__024	3.03	4.34	7.88
MAXBIN__056	1.32	2.01	1.95
MAXBIN__050	2.01	1.96	2.56
MAXBIN__033	2.36	5.86	4.39
MAXBIN__030	2.80	4.38	6.95
MAXBIN__008	5.98	0.70	3.72
MAXBIN__036	1.94	1.34	1.83
MAXBIN__026	2.59	2.41	2.62
MAXBIN__055	1.28	0.50	1.41
MAXBIN__053	1.43	2.16	2.24
MAXBIN__051	2.03	3.94	4.83
MAXBIN__019	2.79	3.83	6.39
MAXBIN__065	1.17	4.14	2.16
MAXBIN__067	0.67	2.49	2.36
MAXBIN__018	3.00	2.74	2.81
MAXBIN__052	1.62	1.53	2.05
MAXBIN__069	0.10	2.62	1.20
MAXBIN__020	2.90	3.62	4.18
MAXBIN__064	1.05	2.90	2.86
MAXBIN__047	1.66	4.81	4.20
MAXBIN__045	1.77	4.66	4.61
MAXBIN__039	1.88	2.21	2.75
MAXBIN__046	1.81	2.31	2.63
MAXBIN__022	2.42	2.07	1.99
MAXBIN__057	1.58	2.92	2.77
MAXBIN__003	13.96	12.26	18.04
MAXBIN__029	2.20	0.28	1.67
MAXBIN__062	1.11	1.56	1.21

Percent Recruitment											
<p>This panel shows how much of the mapped data is recruited by each bin (and how much of the mapped data was not binned under 'splits_not_binned' column). The way these percents calculated is quite simple: summarize the mean coverage of each split in each bin, and normalize every bin with respect to each other. It is critical to remember that these values do not take the unasssembled data into account. This is how you should read this table: "<i>X percent of all mapped reads in Sample Y mapped to splits that were binned into bin Z</i>".</p> <p>TAB-delimited matrix file for percent recruitment: bins_across_samples/bins_percent_recruitment.txt (bins_across_samples/bins_percent_recruitment.txt)</p>											
Sample	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI ...	MAXBI
BGR_130305_bam_sorted	4.86	1.81	6.26	1.82	2.36	0.87	2.69	2.40	0.74	3.18	...
BGR_130527_bam_sorted	3.48	1.74	5.42	1.12	0.77	1.33	3.66	0.23	0.56	2.26	...
BGR_130708_bam_sorted	6.20	0.98	6.82	1.56	0.75	0.52	2.61	0.98	1.04	1.50	...

Gene calls (their functions, coverage and detection across samples, etc)			
<p>An overview of genes and functions based on the information found in the contigs database. If you haven't assigned any functions, these tables will only contain coverages of ORFs across samples.</p>			
Bin	Total Size	Num Genes Identified	Tabular data

Bin	Total Size	Num Genes Identified	Tabular data
MAXBIN__061	2.99 Mb	3,384	genes (bin_by_bin/MAXBIN__061/MAXBIN__061-gene_calls.txt) gene_coverages detection
MAXBIN__063	2.92 Mb	3,113	genes (bin_by_bin/MAXBIN__063/MAXBIN__063-gene_calls.txt) gene_coverages detection
MAXBIN__010	3.47 Mb	4,231	genes (bin_by_bin/MAXBIN__010/MAXBIN__010-gene_calls.txt) gene_coverages detection
MAXBIN__017	3.12 Mb	3,899	genes (bin_by_bin/MAXBIN__017/MAXBIN__017-gene_calls.txt) gene_coverages detection
MAXBIN__004	2.51 Mb	2,546	genes (bin_by_bin/MAXBIN__004/MAXBIN__004-gene_calls.txt) gene_coverages detection
MAXBIN__066	4.18 Mb	3,900	genes (bin_by_bin/MAXBIN__066/MAXBIN__066-gene_calls.txt) gene_coverages detection
MAXBIN__007	2.72 Mb	2,866	genes (bin_by_bin/MAXBIN__007/MAXBIN__007-gene_calls.txt) gene_coverages detection
MAXBIN__014	2.59 Mb	2,692	genes (bin_by_bin/MAXBIN__014/MAXBIN__014-gene_calls.txt) gene_coverages detection
MAXBIN__009	2.67 Mb	2,437	genes (bin_by_bin/MAXBIN__009/MAXBIN__009-gene_calls.txt) gene_coverages detection
MAXBIN__001	2.57 Mb	2,206	genes (bin_by_bin/MAXBIN__001/MAXBIN__001-gene_calls.txt) gene_coverages detection
MAXBIN__025	2.65 Mb	2,954	genes (bin_by_bin/MAXBIN__025/MAXBIN__025-gene_calls.txt) gene_coverages detection
MAXBIN__038	1.60 Mb	1,686	genes (bin_by_bin/MAXBIN__038/MAXBIN__038-gene_calls.txt) gene_coverages detection
MAXBIN__015	2.35 Mb	2,515	genes (bin_by_bin/MAXBIN__015/MAXBIN__015-gene_calls.txt) gene_coverages detection
MAXBIN__016	2.17 Mb	2,410	genes (bin_by_bin/MAXBIN__016/MAXBIN__016-gene_calls.txt) gene_coverages detection
MAXBIN__023	2.38 Mb	2,901	genes (bin_by_bin/MAXBIN__023/MAXBIN__023-gene_calls.txt) gene_coverages detection
MAXBIN__011	2.07 Mb	1,959	genes (bin_by_bin/MAXBIN__011/MAXBIN__011-gene_calls.txt) gene_coverages detection
MAXBIN__005	971.55 Kb	1,032	genes (bin_by_bin/MAXBIN__005/MAXBIN__005-gene_calls.txt) gene_coverages detection
MAXBIN__006	1.91 Mb	1,786	genes (bin_by_bin/MAXBIN__006/MAXBIN__006-gene_calls.txt) gene_coverages detection
MAXBIN__043	2.79 Mb	3,148	genes (bin_by_bin/MAXBIN__043/MAXBIN__043-gene_calls.txt) gene_coverages detection
MAXBIN__021	2.09 Mb	2,406	genes (bin_by_bin/MAXBIN__021/MAXBIN__021-gene_calls.txt) gene_coverages detection
MAXBIN__032	3.46 Mb	3,941	genes (bin_by_bin/MAXBIN__032/MAXBIN__032-gene_calls.txt) gene_coverages detection
MAXBIN__058	3.37 Mb	3,585	genes (bin_by_bin/MAXBIN__058/MAXBIN__058-gene_calls.txt) gene_coverages detection
MAXBIN__013	3.08 Mb	3,147	genes (bin_by_bin/MAXBIN__013/MAXBIN__013-gene_calls.txt) gene_coverages detection
MAXBIN__042	1.34 Mb	1,434	genes (bin_by_bin/MAXBIN__042/MAXBIN__042-gene_calls.txt) gene_coverages detection
MAXBIN__028	1.84 Mb	2,193	genes (bin_by_bin/MAXBIN__028/MAXBIN__028-gene_calls.txt) gene_coverages detection
MAXBIN__049	2.82 Mb	3,722	genes (bin_by_bin/MAXBIN__049/MAXBIN__049-gene_calls.txt) gene_coverages detection
MAXBIN__060	1.69 Mb	2,229	genes (bin_by_bin/MAXBIN__060/MAXBIN__060-gene_calls.txt) gene_coverages detection
MAXBIN__068	1.47 Mb	2,010	genes (bin_by_bin/MAXBIN__068/MAXBIN__068-gene_calls.txt) gene_coverages detection
MAXBIN__040	2.74 Mb	3,856	genes (bin_by_bin/MAXBIN__040/MAXBIN__040-gene_calls.txt) gene_coverages detection
MAXBIN__027	3.11 Mb	3,218	genes (bin_by_bin/MAXBIN__027/MAXBIN__027-gene_calls.txt) gene_coverages detection
MAXBIN__031	2.92 Mb	3,005	genes (bin_by_bin/MAXBIN__031/MAXBIN__031-gene_calls.txt) gene_coverages detection
MAXBIN__034	1.69 Mb	2,258	genes (bin_by_bin/MAXBIN__034/MAXBIN__034-gene_calls.txt) gene_coverages detection
MAXBIN__054	1.88 Mb	2,560	genes (bin_by_bin/MAXBIN__054/MAXBIN__054-gene_calls.txt) gene_coverages detection
MAXBIN__037	1.42 Mb	2,116	genes (bin_by_bin/MAXBIN__037/MAXBIN__037-gene_calls.txt) gene_coverages detection
MAXBIN__044	1.29 Mb	1,275	genes (bin_by_bin/MAXBIN__044/MAXBIN__044-gene_calls.txt) gene_coverages detection
MAXBIN__048	2.70 Mb	3,786	genes (bin_by_bin/MAXBIN__048/MAXBIN__048-gene_calls.txt) gene_coverages detection
MAXBIN__035	1.65 Mb	2,190	genes (bin_by_bin/MAXBIN__035/MAXBIN__035-gene_calls.txt) gene_coverages detection

Bin	Total Size	Num Genes Identified	Tabular data
MAXBIN__059	1.95 Mb	2,412	genes (bin_by_bin/MAXBIN__059/MAXBIN__059-gene_calls.txt) gene_coverages detection
MAXBIN__041	2.29 Mb	2,747	genes (bin_by_bin/MAXBIN__041/MAXBIN__041-gene_calls.txt) gene_coverages detection
MAXBIN__012	2.36 Mb	2,364	genes (bin_by_bin/MAXBIN__012/MAXBIN__012-gene_calls.txt) gene_coverages detection
MAXBIN__002	2.16 Mb	2,139	genes (bin_by_bin/MAXBIN__002/MAXBIN__002-gene_calls.txt) gene_coverages detection
MAXBIN__024	294.12 Kb	312	genes (bin_by_bin/MAXBIN__024/MAXBIN__024-gene_calls.txt) gene_coverages detection
MAXBIN__056	3.72 Mb	4,629	genes (bin_by_bin/MAXBIN__056/MAXBIN__056-gene_calls.txt) gene_coverages detection
MAXBIN__050	2.42 Mb	3,331	genes (bin_by_bin/MAXBIN__050/MAXBIN__050-gene_calls.txt) gene_coverages detection
MAXBIN__033	888.91 Kb	862	genes (bin_by_bin/MAXBIN__033/MAXBIN__033-gene_calls.txt) gene_coverages detection
MAXBIN__030	976.70 Kb	993	genes (bin_by_bin/MAXBIN__030/MAXBIN__030-gene_calls.txt) gene_coverages detection
MAXBIN__008	845.01 Kb	898	genes (bin_by_bin/MAXBIN__008/MAXBIN__008-gene_calls.txt) gene_coverages detection
MAXBIN__036	2.11 Mb	2,853	genes (bin_by_bin/MAXBIN__036/MAXBIN__036-gene_calls.txt) gene_coverages detection
MAXBIN__026	963.08 Kb	1,345	genes (bin_by_bin/MAXBIN__026/MAXBIN__026-gene_calls.txt) gene_coverages detection
MAXBIN__055	1.32 Mb	1,838	genes (bin_by_bin/MAXBIN__055/MAXBIN__055-gene_calls.txt) gene_coverages detection
MAXBIN__053	670.22 Kb	979	genes (bin_by_bin/MAXBIN__053/MAXBIN__053-gene_calls.txt) gene_coverages detection
MAXBIN__051	659.13 Kb	764	genes (bin_by_bin/MAXBIN__051/MAXBIN__051-gene_calls.txt) gene_coverages detection
MAXBIN__019	214.38 Kb	275	genes (bin_by_bin/MAXBIN__019/MAXBIN__019-gene_calls.txt) gene_coverages detection
MAXBIN__065	672.52 Kb	905	genes (bin_by_bin/MAXBIN__065/MAXBIN__065-gene_calls.txt) gene_coverages detection
MAXBIN__067	788.56 Kb	1,152	genes (bin_by_bin/MAXBIN__067/MAXBIN__067-gene_calls.txt) gene_coverages detection
MAXBIN__018	1.49 Mb	1,896	genes (bin_by_bin/MAXBIN__018/MAXBIN__018-gene_calls.txt) gene_coverages detection
MAXBIN__052	1.52 Mb	1,745	genes (bin_by_bin/MAXBIN__052/MAXBIN__052-gene_calls.txt) gene_coverages detection
MAXBIN__069	319.39 Kb	433	genes (bin_by_bin/MAXBIN__069/MAXBIN__069-gene_calls.txt) gene_coverages detection
MAXBIN__020	2.50 Mb	3,405	genes (bin_by_bin/MAXBIN__020/MAXBIN__020-gene_calls.txt) gene_coverages detection
MAXBIN__064	660.57 Kb	1,017	genes (bin_by_bin/MAXBIN__064/MAXBIN__064-gene_calls.txt) gene_coverages detection
MAXBIN__047	799.30 Kb	897	genes (bin_by_bin/MAXBIN__047/MAXBIN__047-gene_calls.txt) gene_coverages detection
MAXBIN__045	736.86 Kb	822	genes (bin_by_bin/MAXBIN__045/MAXBIN__045-gene_calls.txt) gene_coverages detection
MAXBIN__039	2.91 Mb	3,689	genes (bin_by_bin/MAXBIN__039/MAXBIN__039-gene_calls.txt) gene_coverages detection
MAXBIN__046	2.70 Mb	3,249	genes (bin_by_bin/MAXBIN__046/MAXBIN__046-gene_calls.txt) gene_coverages detection
MAXBIN__022	1.94 Mb	2,705	genes (bin_by_bin/MAXBIN__022/MAXBIN__022-gene_calls.txt) gene_coverages detection
MAXBIN__057	1.10 Mb	1,634	genes (bin_by_bin/MAXBIN__057/MAXBIN__057-gene_calls.txt) gene_coverages detection
MAXBIN__003	1.08 Mb	1,503	genes (bin_by_bin/MAXBIN__003/MAXBIN__003-gene_calls.txt) gene_coverages detection
MAXBIN__029	1.07 Mb	1,343	genes (bin_by_bin/MAXBIN__029/MAXBIN__029-gene_calls.txt) gene_coverages detection
MAXBIN__062	1.06 Mb	1,418	genes (bin_by_bin/MAXBIN__062/MAXBIN__062-gene_calls.txt) gene_coverages detection

Hits for non-single-copy gene HMM profiles

This panel shows you the result of non-single copy gene hits in your bins and contigs for each HMM profile. Here is a table that shows the total number of HMM hits in each bin for each HMM search type (from bins_across_samples/hmm_hit_totals.txt (bins_across_samples/hmm_hit_totals.txt)):

[illegible]

26.01.24, 13:47

26.01.24, 13:47

Bin	Ribosomal_RNA_28S	Ribosomal_RNA_18S	Ribosomal_RNA_12S	Ribosomal_RNA_16S	Ribosomal_RNA_23S	Ribosomal_RNA_5S
MAXBIN__022	None (bin_by_bin/MAXBIN__022 /MAXBIN__022- Ribosomal_RNA_28S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__022 /MAXBIN__022- Ribosomal_RNA_18S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__022 /MAXBIN__022- Ribosomal_RNA_12S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__022 /MAXBIN__022- Ribosomal_RNA_16S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__022 /MAXBIN__022- Ribosomal_RNA_23S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__022 /MAXBIN__022- Ribosomal_RNA_5S-hmm- sequences.txt)
MAXBIN__057	None (bin_by_bin/MAXBIN__057 /MAXBIN__057- Ribosomal_RNA_28S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__057 /MAXBIN__057- Ribosomal_RNA_18S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__057 /MAXBIN__057- Ribosomal_RNA_12S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__057 /MAXBIN__057- Ribosomal_RNA_16S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__057 /MAXBIN__057- Ribosomal_RNA_23S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__057 /MAXBIN__057- Ribosomal_RNA_5S-hmm- sequences.txt)
MAXBIN__003	None (bin_by_bin/MAXBIN__003 /MAXBIN__003- Ribosomal_RNA_28S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__003 /MAXBIN__003- Ribosomal_RNA_18S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__003 /MAXBIN__003- Ribosomal_RNA_12S- hmm-sequences.txt)	4 (bin_by_bin/MAXBIN__003 /MAXBIN__003- Ribosomal_RNA_16S- hmm-sequences.txt)	3 (bin_by_bin/MAXBIN__003 /MAXBIN__003- Ribosomal_RNA_23S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__003 /MAXBIN__003- Ribosomal_RNA_5S-hmm- sequences.txt)
MAXBIN__029	None (bin_by_bin/MAXBIN__029 /MAXBIN__029- Ribosomal_RNA_28S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__029 /MAXBIN__029- Ribosomal_RNA_18S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__029 /MAXBIN__029- Ribosomal_RNA_12S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__029 /MAXBIN__029- Ribosomal_RNA_16S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__029 /MAXBIN__029- Ribosomal_RNA_23S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__029 /MAXBIN__029- Ribosomal_RNA_5S-hmm- sequences.txt)
MAXBIN__062	None (bin_by_bin/MAXBIN__062 /MAXBIN__062- Ribosomal_RNA_28S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__062 /MAXBIN__062- Ribosomal_RNA_18S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__062 /MAXBIN__062- Ribosomal_RNA_12S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__062 /MAXBIN__062- Ribosomal_RNA_16S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__062 /MAXBIN__062- Ribosomal_RNA_23S- hmm-sequences.txt)	None (bin_by_bin/MAXBIN__062 /MAXBIN__062- Ribosomal_RNA_5S-hmm- sequences.txt)

The distribution of each HMM item found in your HMM collections is shown below. Different search types will be presented in their cognate tabs.

Ribosomal RNA 28S	Ribosomal RNA 18S	Ribosomal RNA 12S	Ribosomal RNA 16S	Ribosomal RNA 23S	Ribosomal RNA 5S
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HMM hits in bins for Ribosomal_RNA_28S (from bins_across_samples/hmms_Ribosomal_RNA_28S.txt (bins_across_samples/hmms_Ribosomal_RNA_28S.txt)):

Bin	28S_r ...
MAXBIN__061	None
MAXBIN__063	None
MAXBIN__010	None
MAXBIN__017	None
MAXBIN__004	None
MAXBIN__066	None
MAXBIN__007	None
MAXBIN__014	None
MAXBIN__009	None
MAXBIN__001	None
MAXBIN__025	None
MAXBIN__038	None
MAXBIN__015	None
MAXBIN__016	None
MAXBIN__023	None
MAXBIN__011	None
MAXBIN__005	None
MAXBIN__006	None
MAXBIN__043	None
MAXBIN__021	None
MAXBIN__032	None
MAXBIN__058	None
MAXBIN__013	None
MAXBIN__042	None
MAXBIN__028	None
MAXBIN__049	None
MAXBIN__060	None

Bin	28S_r ...
MAXBIN__068	None
MAXBIN__040	None
MAXBIN__027	None
MAXBIN__031	None
MAXBIN__034	None
MAXBIN__054	None
MAXBIN__037	None
MAXBIN__044	None
MAXBIN__048	None
MAXBIN__035	None
MAXBIN__059	None
MAXBIN__041	None
MAXBIN__012	None
MAXBIN__002	None
MAXBIN__024	None
MAXBIN__056	None
MAXBIN__050	None
MAXBIN__033	None
MAXBIN__030	None
MAXBIN__008	None
MAXBIN__036	None
MAXBIN__026	None
MAXBIN__055	None
MAXBIN__053	None
MAXBIN__051	None
MAXBIN__019	None
MAXBIN__065	None
MAXBIN__067	None
MAXBIN__018	None
MAXBIN__052	None
MAXBIN__069	None
MAXBIN__020	None
MAXBIN__064	None
MAXBIN__047	None
MAXBIN__045	None
MAXBIN__039	None
MAXBIN__046	None
MAXBIN__022	None
MAXBIN__057	None
MAXBIN__003	None
MAXBIN__029	None
MAXBIN__062	None

Misc Data

For layers

The directory misc data layers (misc_data_layers/) contains TAB-delimited files for additional data stored under the following data group names for each **sample/layer** found in the merged database: default.

The **default** data group, which often is added by anvi'o automatically and contains important information, contained these keys: **total_reads_mapped**, **num_SNVs_reported**, **num_INDELs_reported**, **total_reads_kept**.

For items

None found :(