

Report

	merge_bcalm	merge_bifrost	merge_superreads	merge_tadpole	merge_mr_bcalm	merge_mr_bifrost	merge_mr_superreads	merge_mr_tadpole	merge_anchors	spades	mr_spades	megahit	mr_megahit	repetitive
# contigs (>= 0 bp)	17	16	27	17	17	20	22	18	16	7	4	15	6	41
# contigs (>= 1000 bp)	17	16	27	17	17	20	22	18	16	7	4	15	6	0
# contigs (>= 5000 bp)	14	13	22	14	14	17	19	15	13	6	3	12	3	0
# contigs (>= 10000 bp)	10	10	17	10	10	13	15	11	10	6	3	10	3	0
# contigs (>= 25000 bp)	9	9	13	9	9	11	9	10	9	6	3	10	3	0
# contigs (>= 50000 bp)	3	3	2	3	3	3	3	3	3	3	3	3	2	0
Total length (>= 0 bp)	562331	562444	565623	562558	562001	562146	560942	562076	562572	572804	577948	564643	581605	6905
Total length (>= 1000 bp)	562331	562444	565623	562558	562001	562146	560942	562076	562572	572804	577948	564643	581605	0
Total length (>= 5000 bp)	556513	556636	554209	556698	556281	556469	555318	556350	556779	569544	575930	558438	577948	0
Total length (>= 10000 bp)	529216	537536	517864	529277	529104	529234	528172	529126	537688	569544	575930	546321	577948	0
Total length (>= 25000 bp)	514137	522450	450358	514196	514040	489796	418328	514058	522595	569544	575930	546321	577948	0
Total length (>= 50000 bp)	314555	314510	105279	314516	314531	200427	200315	265673	314582	456664	575930	274827	539574	0
# contigs	17	16	27	17	17	20	22	18	16	7	4	15	6	41
Largest contig	179639	179631	55020	179630	179650	79822	79687	130816	179697	236302	395878	139169	319091	365
Total length	562331	562444	565623	562558	562001	562146	560942	562076	562572	572804	577948	564643	581605	6905
Reference length	580076	580076	580076	580076	580076	580076	580076	580076	580076	580076	580076	580076	580076	580076
GC (%)	31.42	31.42	31.41	31.43	31.42	31.41	31.42	31.42	31.43	31.58	31.66	31.47	31.71	39.23
Reference GC (%)	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69	31.69
N50	55025	55022	30331	55021	55055	41117	39461	48835	55019	163847	395878	42296	319091	184
NG50	55025	55022	30331	55021	55055	41117	37652	48835	55019	163847	395878	42296	319091	-
N90	27065	27075	10417	27077	27062	24410	15128	27055	27106	37734	60118	37742	220483	111
NG90	15079	27075	9052	15081	15064	15028	13770	15068	27106	37734	60118	34738	220483	-
auN	86889.8	87762.7	32032.5	86856.7	86921.9	45428.7	43161.2	64191.7	87797.3	157372.3	302314.1	69999.8	261189.0	195.6
auNG	84231.8	85095.1	31234.4	84233.7	84213.5	44024.5	41737.6	62199.8	85147.9	155399.5	301205.0	68137.4	261877.5	2.3
L50	3	3	8	3	3	5	5	4	3	2	1	4	1	15
LG50	3	3	8	3	3	5	6	4	3	2	1	4	1	-
L90	9	9	17	9	9	12	14	10	9	5	3	9	2	35
LG90	10	9	18	10	10	13	15	11	9	5	3	10	2	-
# misassemblies	0	0	0	0	0	0	0	0	0	1	1	0	1	0
# misassembled contigs	0	0	0	0	0	0	0	0	0	1	1	0	1	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0	163847	119934	0	220483	0
# local misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 1 part	1 + 0 part	0 + 0 part	1 + 0 part	0 + 0 part
Unaligned length	0	0	0	0	0	0	0	0	0	680	2018	0	1267	0
Genome fraction (%)	96.841	96.826	96.823	96.861	96.766	96.747	96.618	96.801	96.871	98.675	99.256	97.233	99.640	1.078
Duplication ratio	1.000	1.000	1.006	1.000	1.000	1.001	1.000	1.000	1.000	0.999	1.000	1.000	1.004	1.104
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	72.81	69.61	70.79	74.39	67.88	67.49	67.08	72.83	73.14	215.13	248.88	98.77	291.59	0.00
# indels per 100 kbp	18.51	17.09	16.99	18.86	17.10	16.38	16.41	18.16	18.86	63.31	75.38	28.37	87.20	0.00
Largest alignment	179639	179620	55020	179621	179650	79712	79687	130816	179680	236176	395873	139169	319091	365
Total aligned length	561758	561670	565042	561925	561324	561529	560516	561553	561932	571745	575771	563953	580273	6905
NA50	54988	55022	30291	54987	55010	41117	39405	48814	55016	83749	395873	42296	319091	184
NGA50	54988	55022	30291	54987	55010	41117	37637	48814	55016	83749	395873	42296	319091	-
NA90	27065	27073	10417	27036	27062	24410	15119	27055	27070	37687	60004	37731	38374	111
NGA90	15079	15086	9052	15081	15062	15015	13770	15065	27070	37687	60004	34731	38374	-
auNA	86855.7	87678.1	32002.9	86812.4	86859.1	45368.9	43143.1	64165.0	87745.9	133802.6	291959.1	69957.0	237480.8	195.6
auNGA	84198.8	85013.0	31205.6	84190.7	84152.6	43966.5	41720.0	62173.9	85098.1	132125.2	290888.0	68095.8	238106.8	2.3
LA50	3	3	8	3	3	5	5	4	3	2	1	4	1	15
LGA50	3	3	8	3	3	5	6	4	3	2	1	4	1	-
LA90	9	9	17	9	9	12	14	10	9	6	3	9	3	35
LGA90	10	10	18	10	10	13	15	11	9	6	3	10	3	-

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

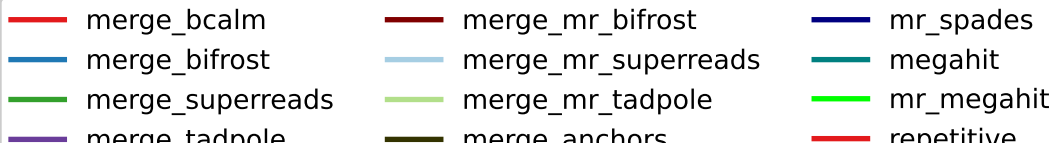
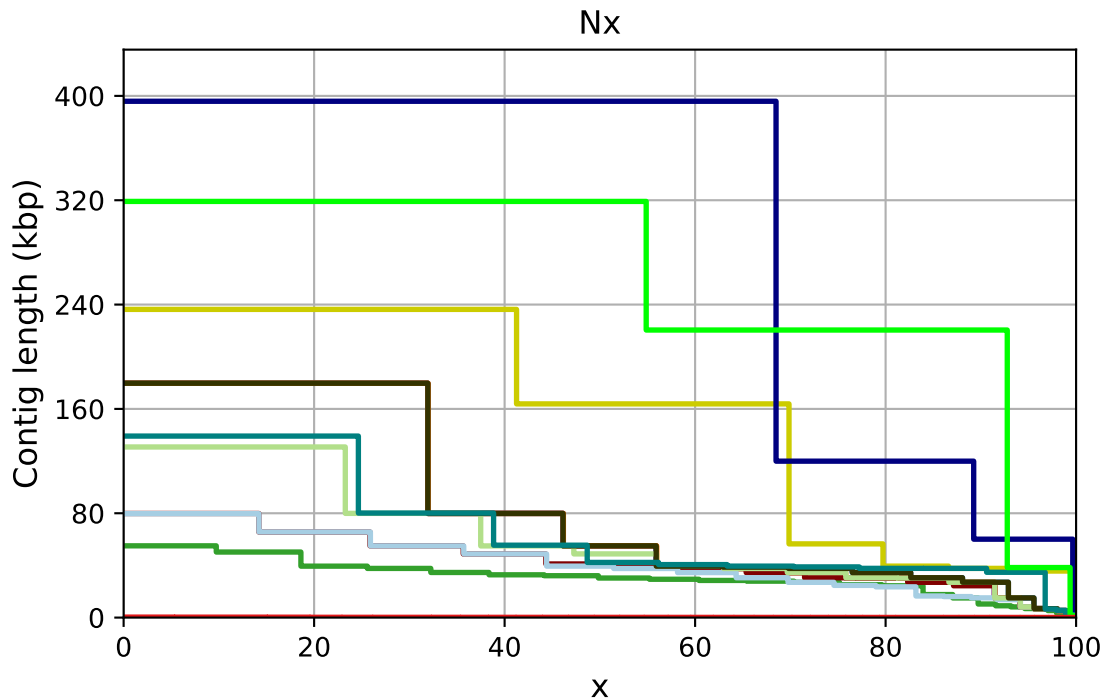
	merge_bcalm	merge_bifrost	merge_superreads	merge_tadpole	merge_mr_bcalm	merge_mr_bifrost	merge_mr_superreads	merge_mr_tadpole	merge_anchors	spades	mr_spades	megahit	mr_megahit	repetitive
# misassemblies	0	0	0	0	0	0	0	0	0	1	1	0	1	0
# contig misassemblies	0	0	0	0	0	0	0	0	0	1	1	0	1	0
# c. relocations	0	0	0	0	0	0	0	0	0	1	1	0	1	0
# c. translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0	1	1	0	1	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0	163847	119934	0	220483	0
# local misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# mismatches	409	391	400	418	381	379	376	409	411	1230	1433	557	1692	0
# indels	104	96	96	106	96	92	92	102	106	362	434	160	506	0
# indels (<= 5 bp)	97	89	88	99	89	85	85	95	99	335	408	148	466	0
# indels (> 5 bp)	7	7	8	7	7	7	7	7	7	27	26	12	40	0
Indels length	259	249	260	265	249	239	239	255	265	1496	1069	605	1659	0

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

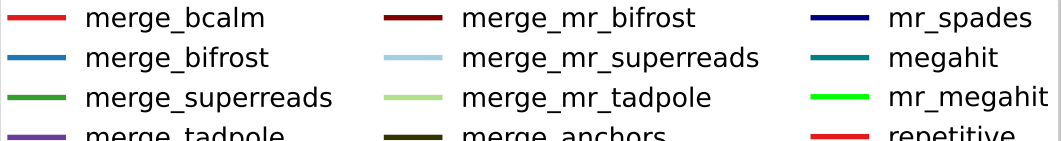
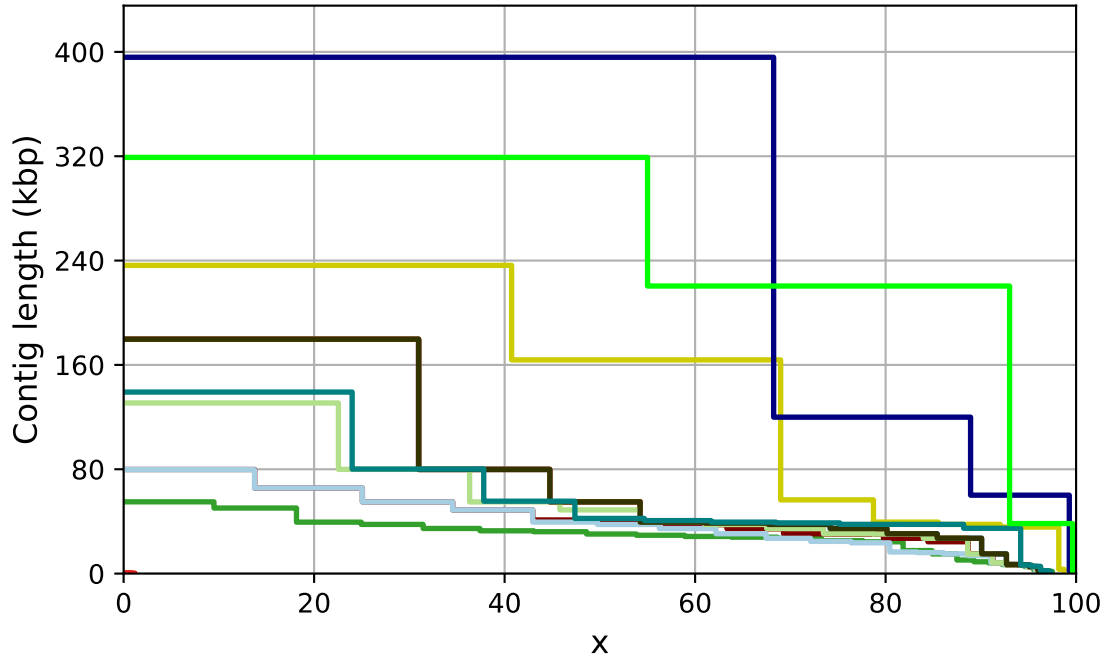
Unaligned report

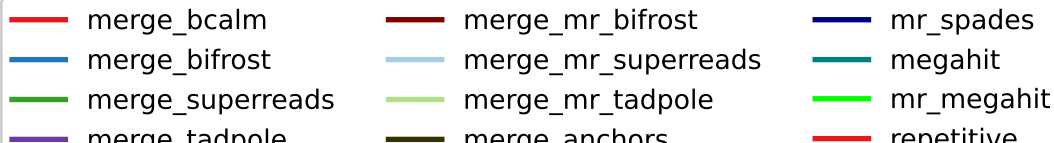
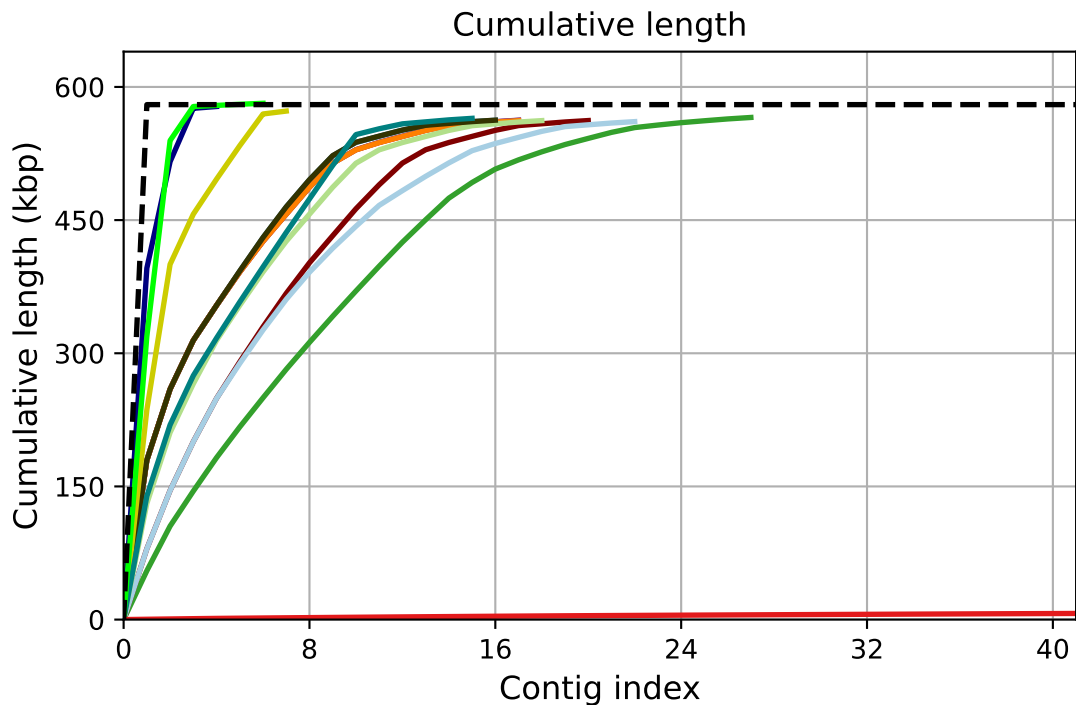
	merge_bcalm	merge_bifrost	merge_superreads	merge_tadpole	merge_mr_bcalm	merge_mr_bifrost	merge_mr_superreads	merge_mr_tadpole	merge_anchors	spades	mr_spades	megahit	mr_megahit	repetitive
# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	1	0	1	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	2018	0	1267	0
# partially unaligned contigs	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0	0	680	0	0	0	0
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0

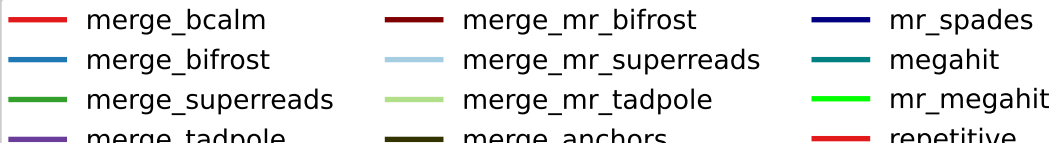
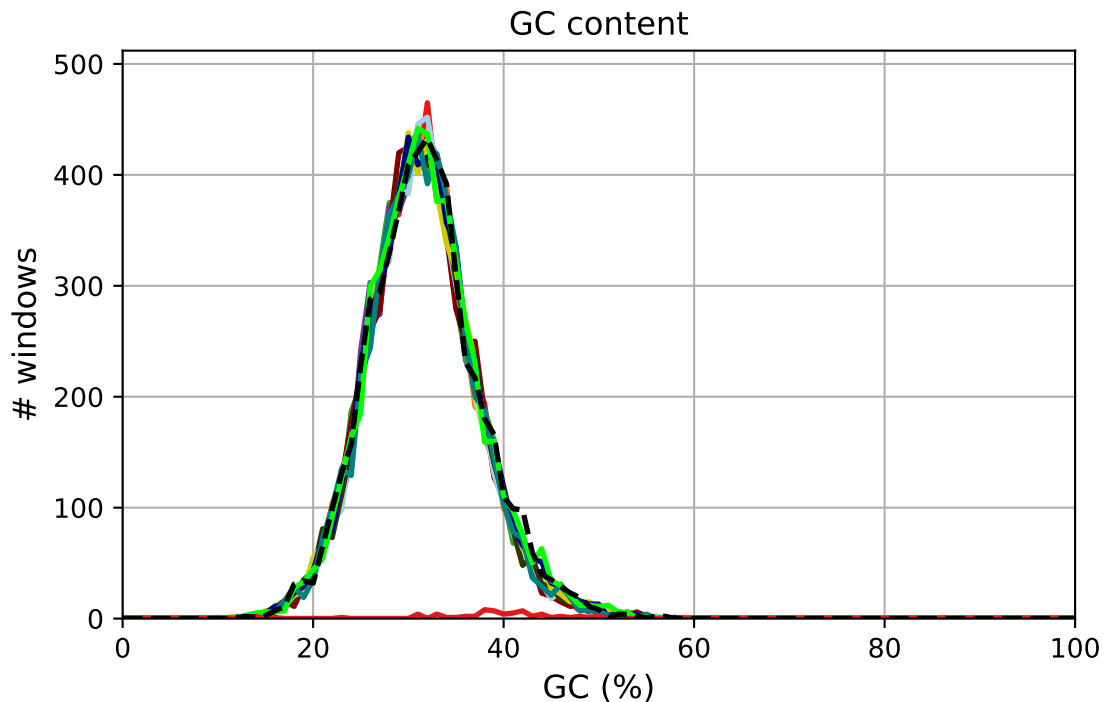
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



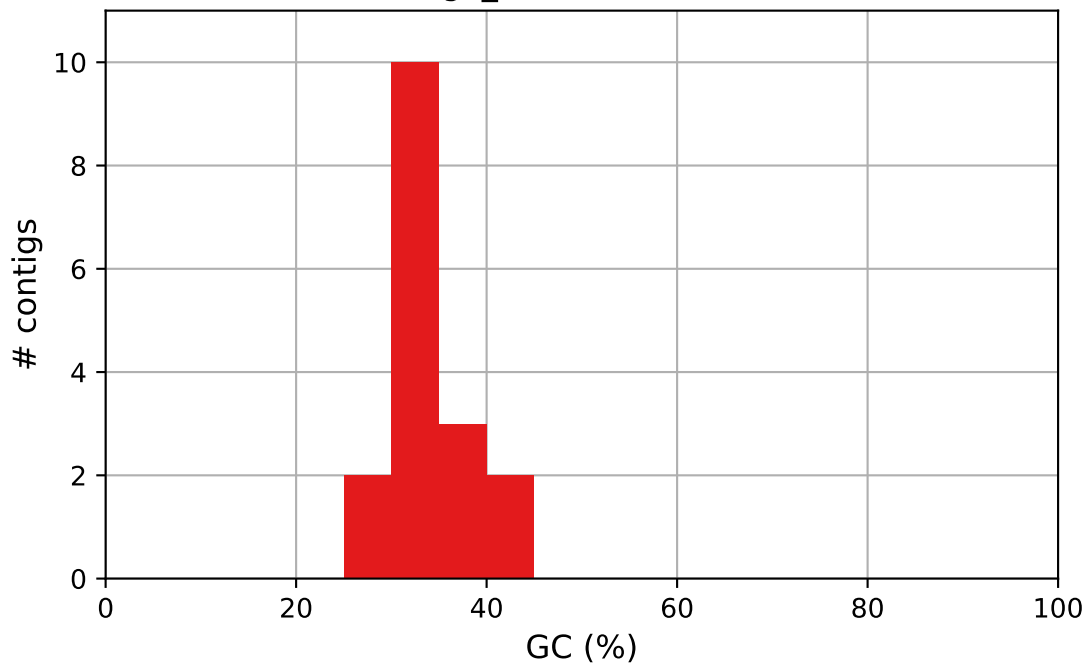
NGx





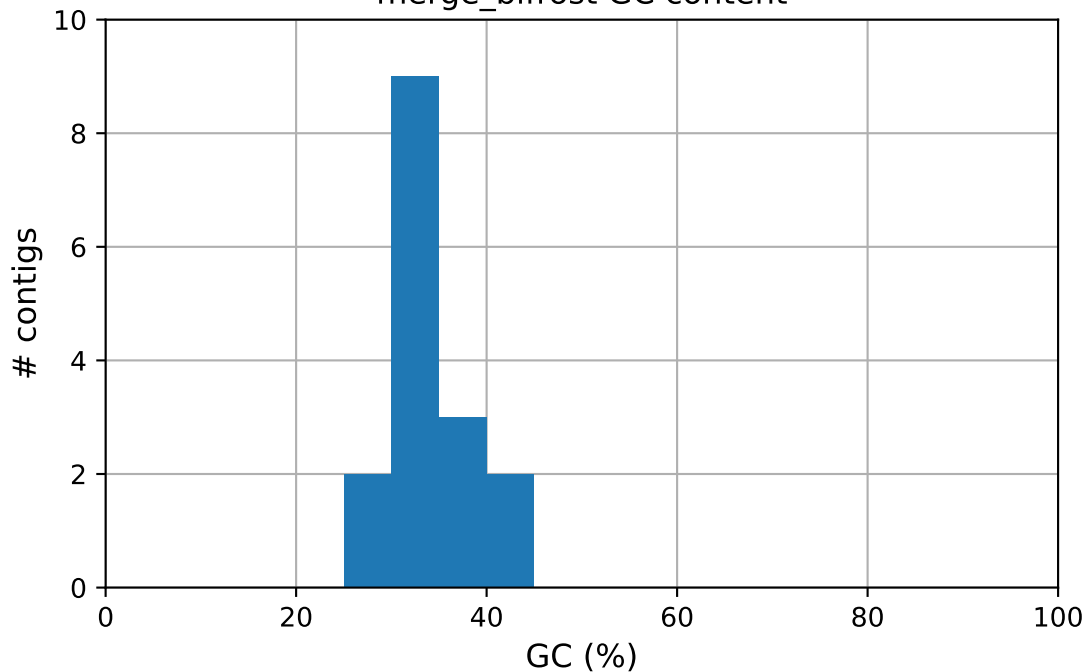


merge_bcalm GC content



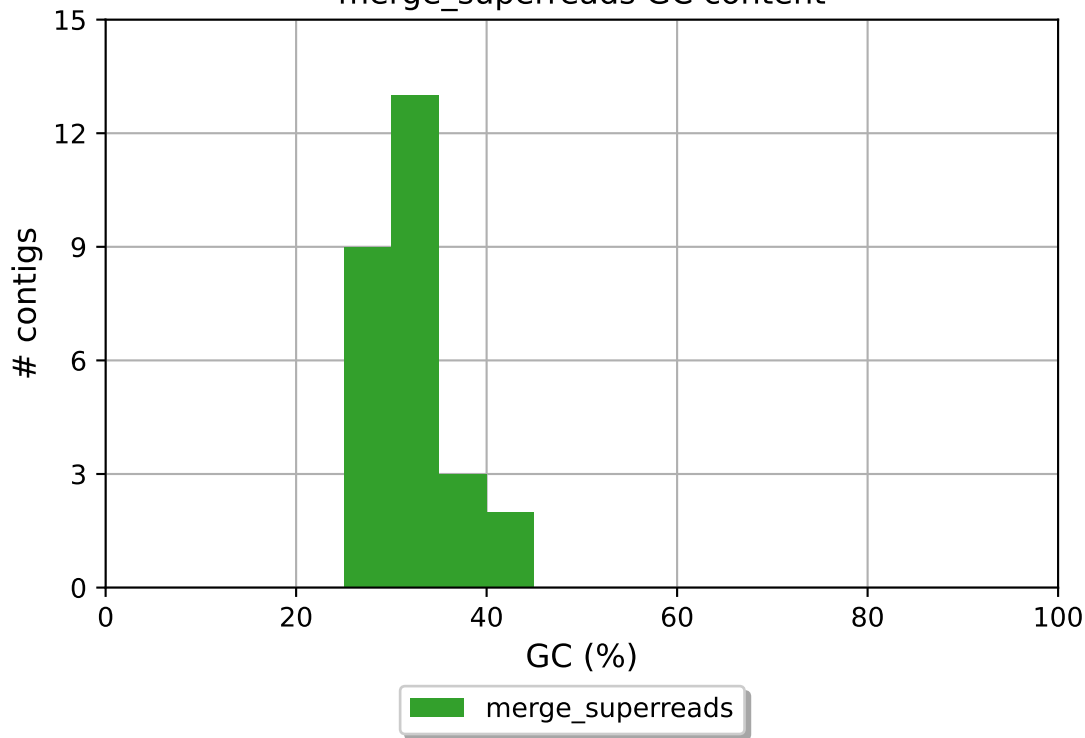
merge_bcalm

merge_bifrost GC content

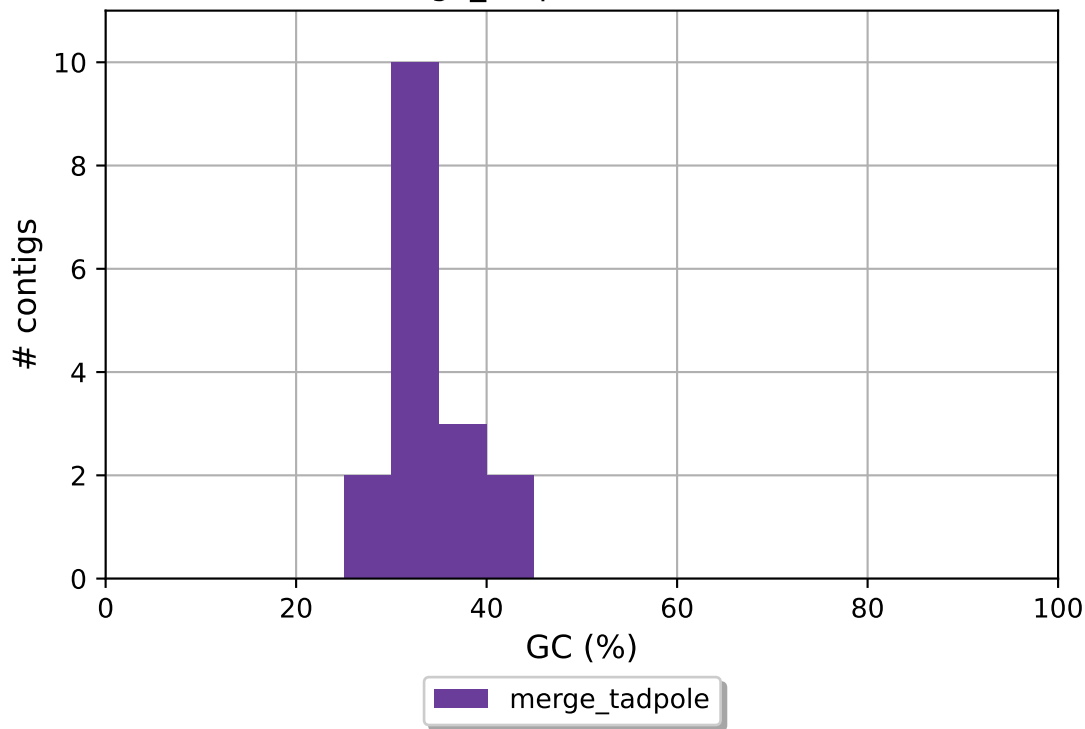


merge_bifrost

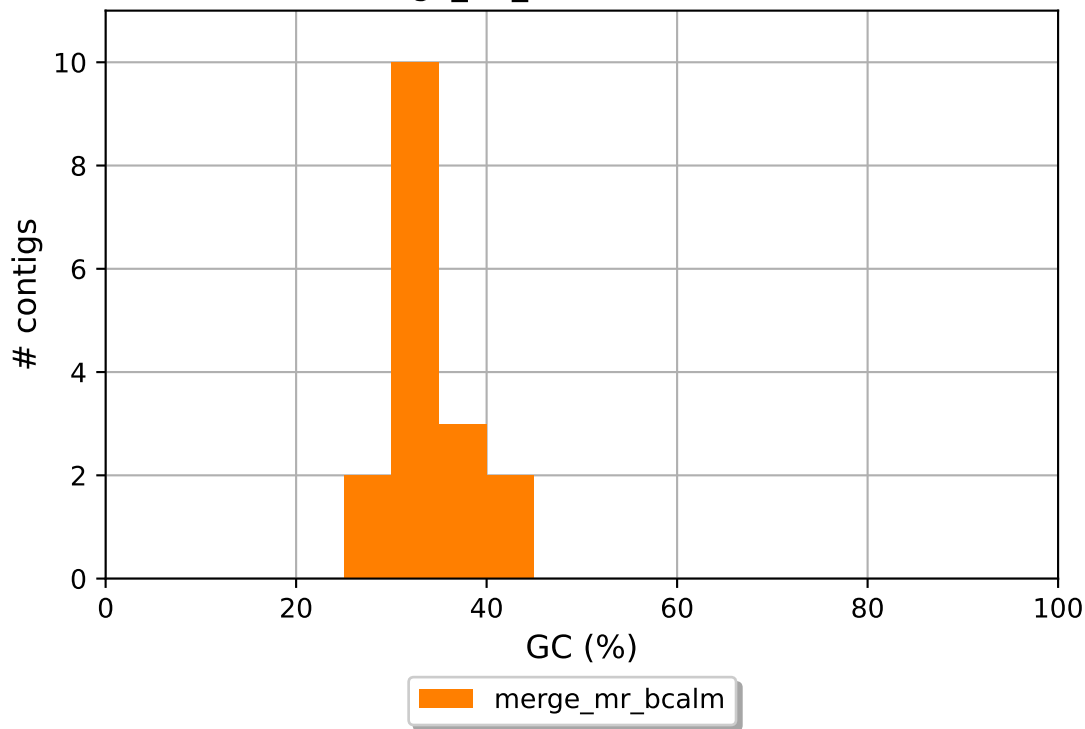
merge_superreads GC content



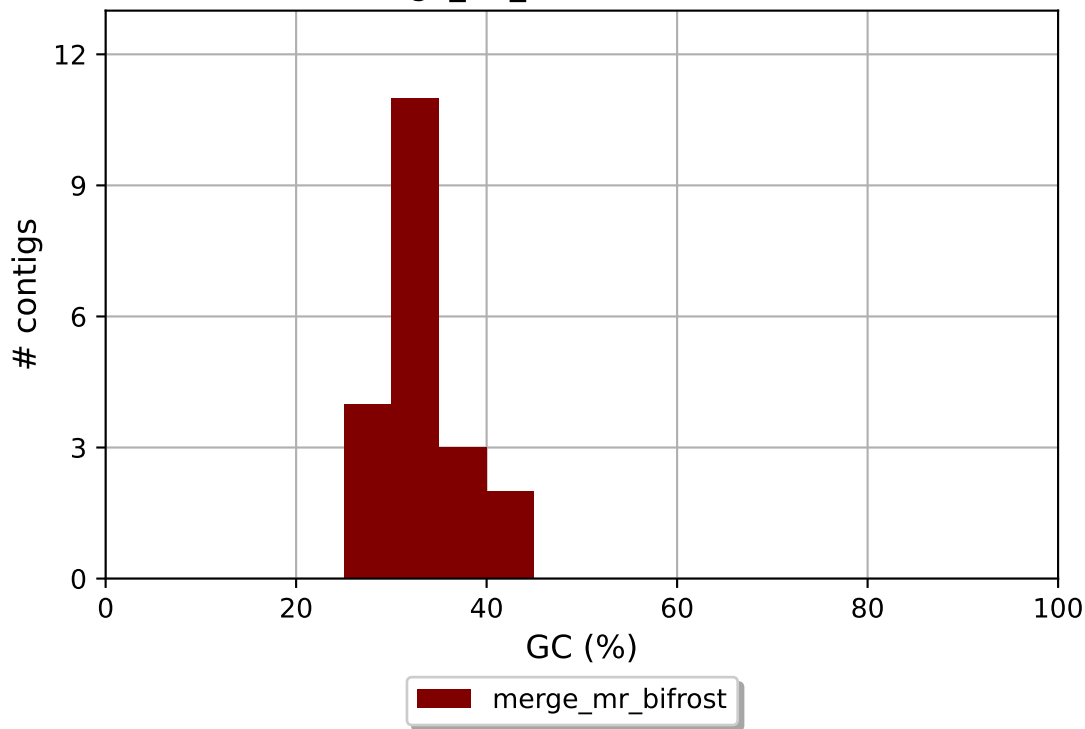
merge_tadpole GC content



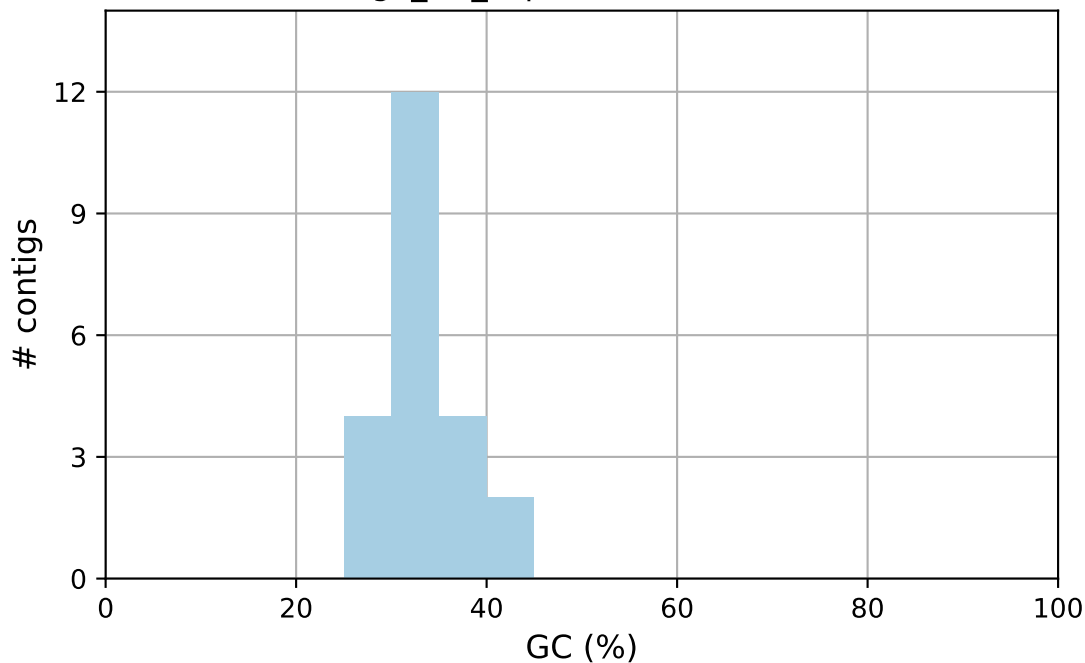
merge_mr_bcalm GC content



merge_mr_bifrost GC content

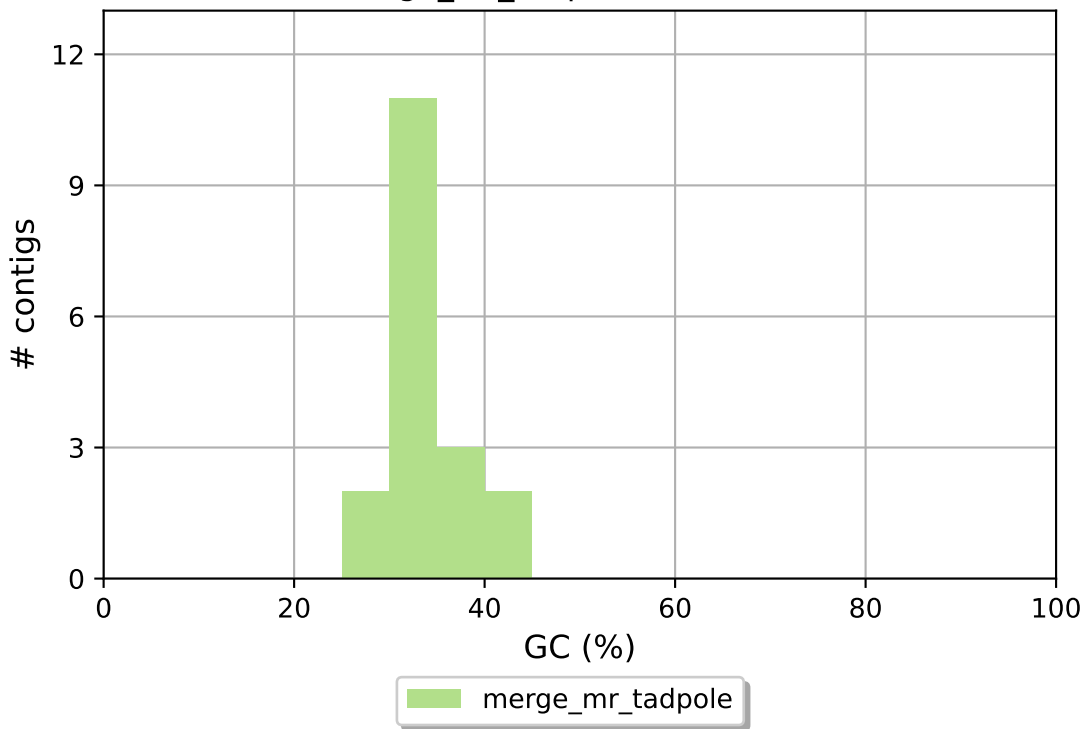


merge_mr_superreads GC content

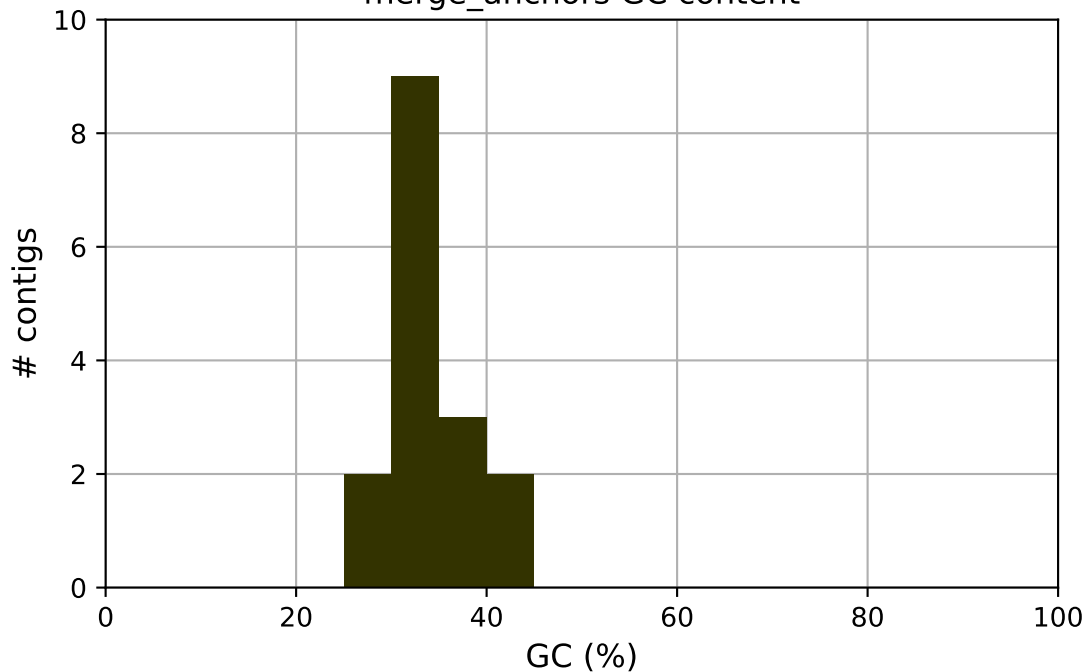


merge_mr_superreads

merge_mr_tadpole GC content

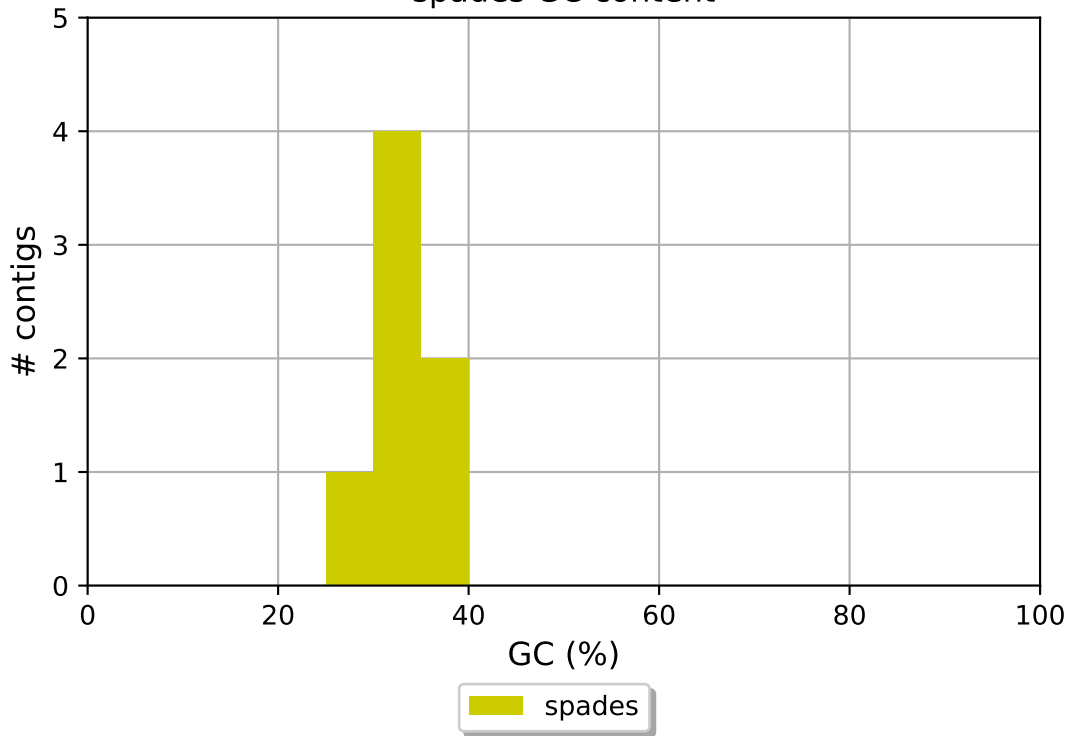


merge_anchors GC content

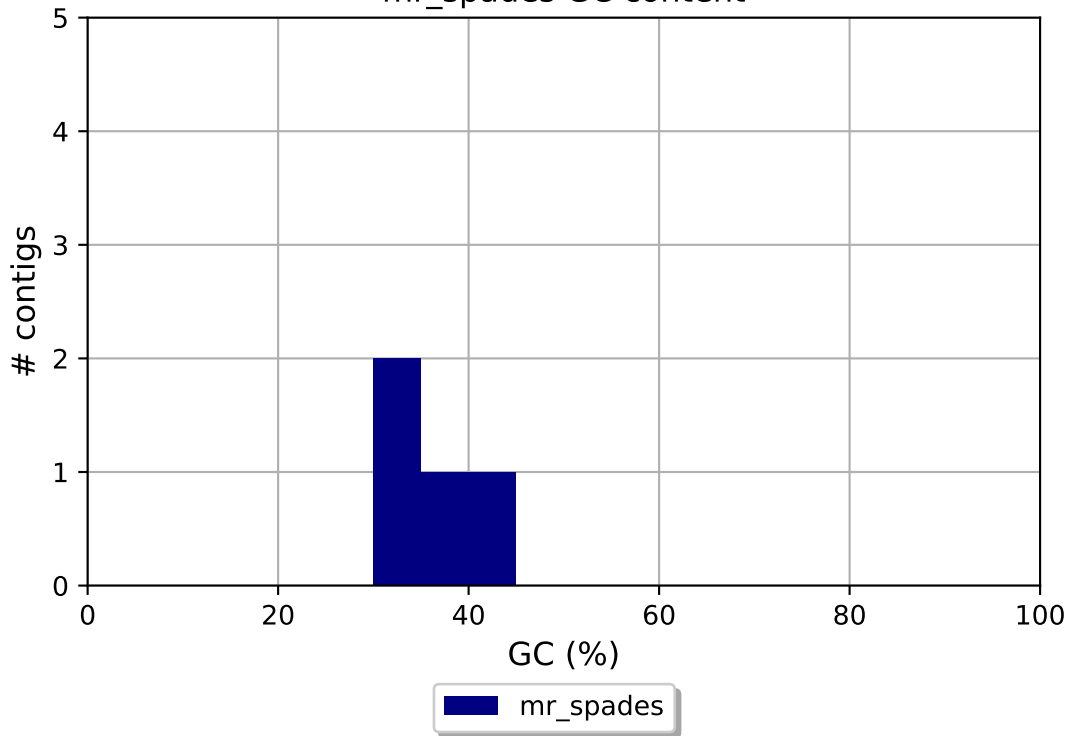


merge_anchors

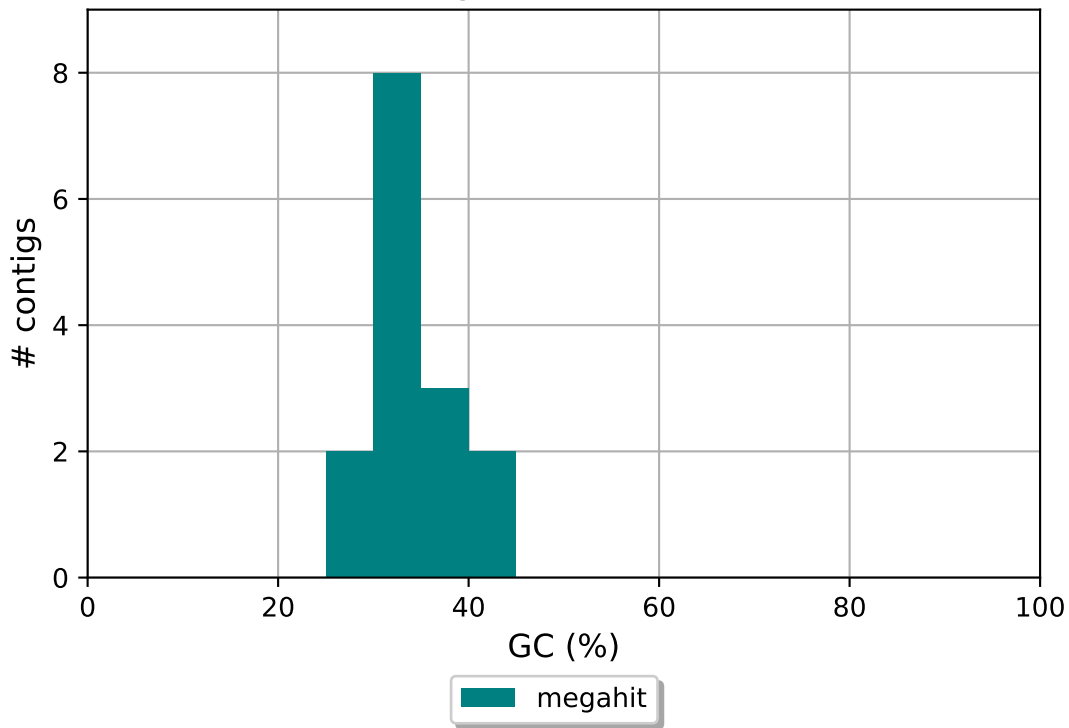
spades GC content



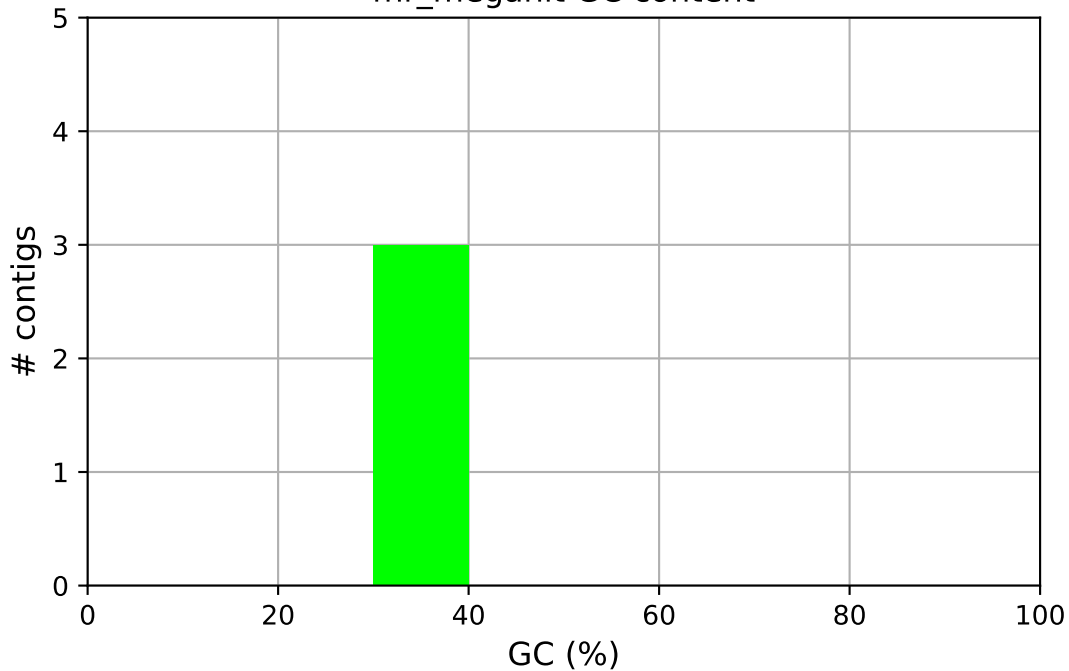
mr_spades GC content



megahit GC content

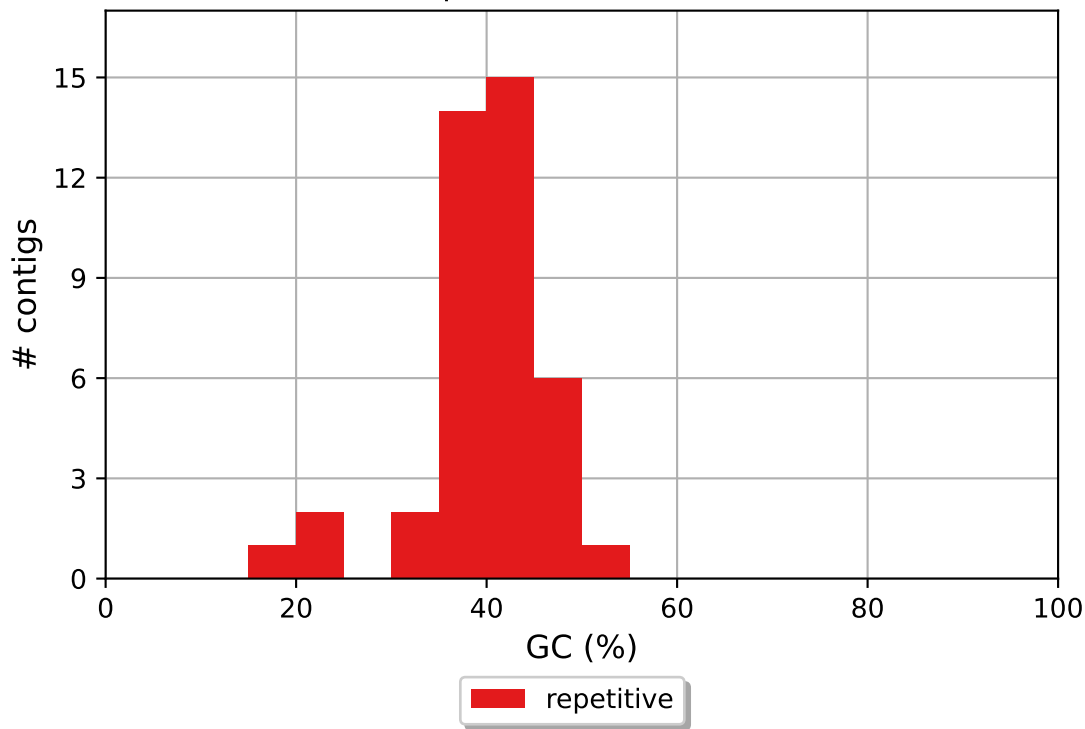


mr_megahit GC content

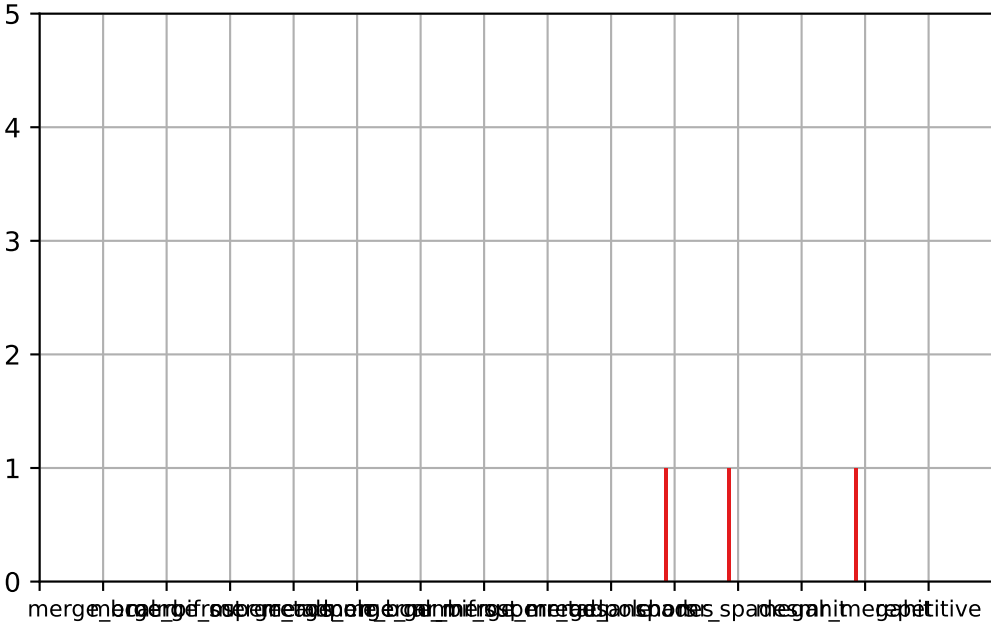


mr_megahit

repetitive GC content

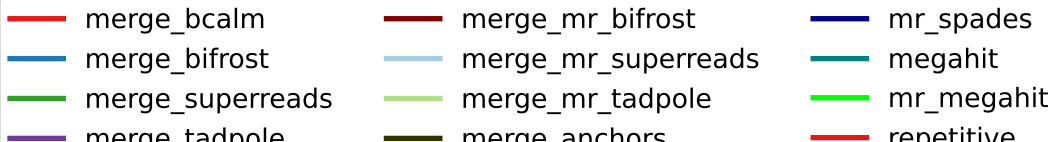
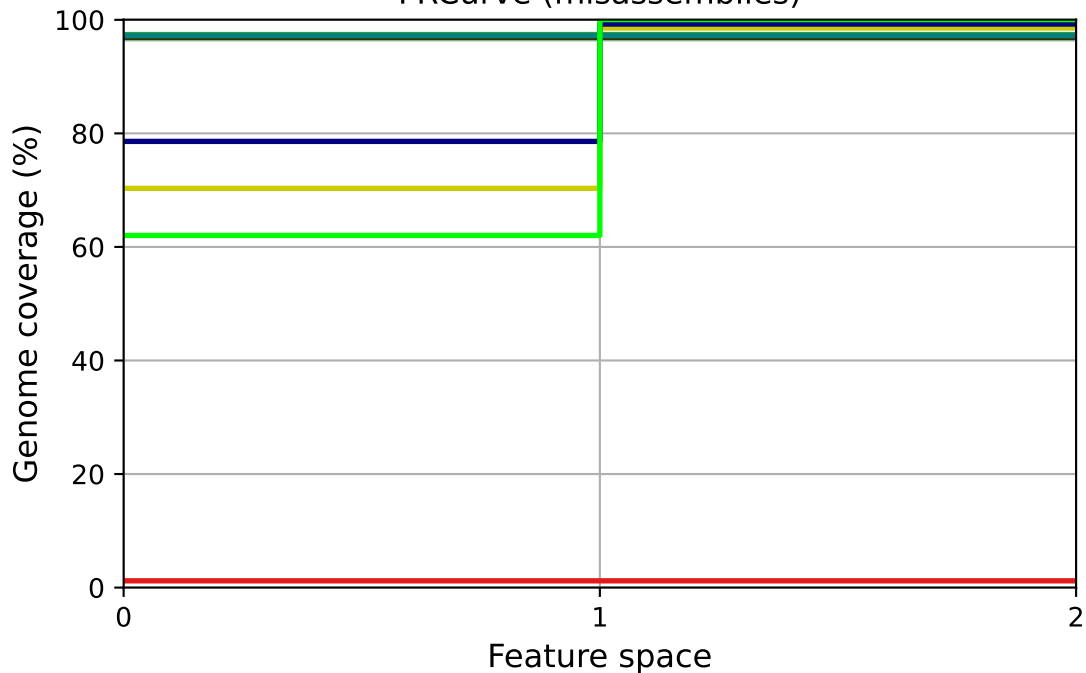


Misassemblies

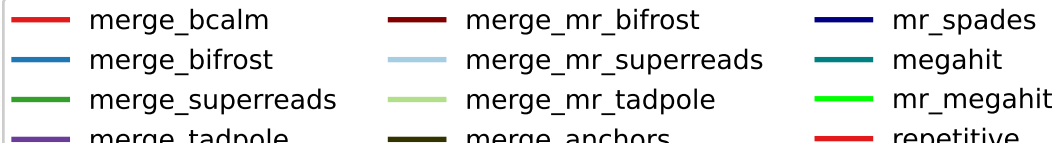
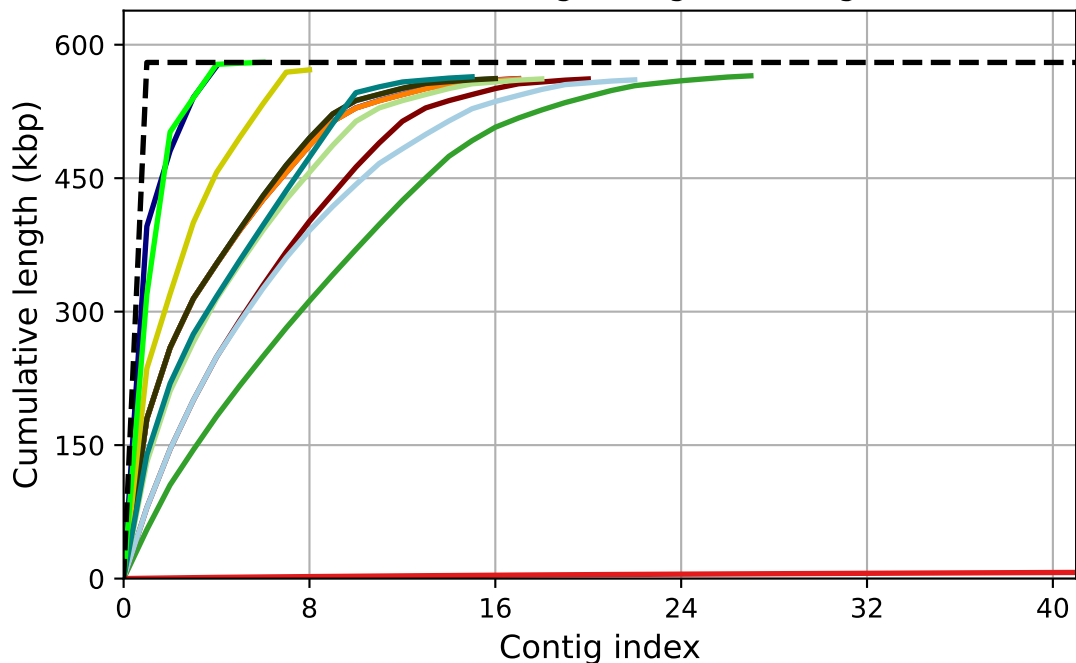


relocations

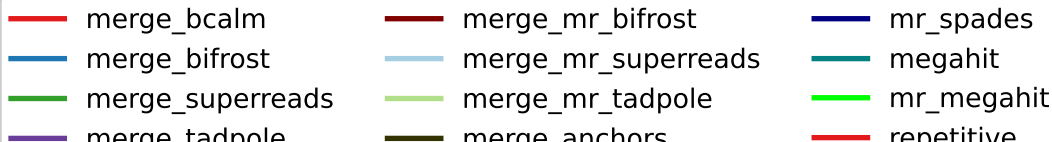
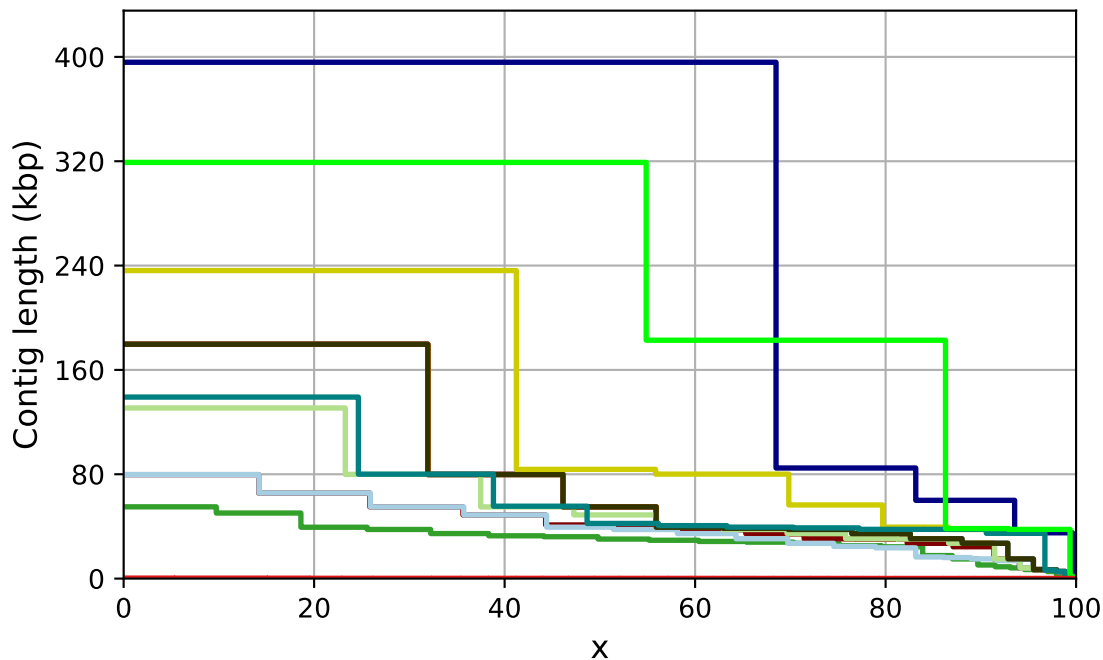
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

