

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	4	1	5	3	1	2	1
# contigs (>= 5000 bp)	2	3	1	4	3	1	2	1
# contigs (>= 10000 bp)	2	3	1	4	3	1	2	0
# contigs (>= 25000 bp)	2	3	1	3	3	1	2	0
# contigs (>= 50000 bp)	2	3	1	3	2	1	2	0
Total length (>= 1000 bp)	120434	759934	5373173	653700	149883	56491	662585	8580
Total length (>= 5000 bp)	120434	758238	5373173	652218	149883	56491	662585	8580
Total length (>= 10000 bp)	120434	758238	5373173	652218	149883	56491	662585	0
Total length (>= 25000 bp)	120434	758238	5373173	629390	149883	56491	662585	0
Total length (>= 50000 bp)	120434	758238	5373173	629390	114654	56491	662585	0
# contigs	4	4	1	5	3	1	2	1
Largest contig	60217	522768	5373173	517479	57327	56491	555914	8580
Total length	121454	759934	5373173	653700	149883	56491	662585	8580
Reference length	913	913	913	913	913	913	913	913
GC (%)	37.97	38.03	38.01	37.97	38.02	38.00	37.98	37.83
Reference GC (%)	41.62	41.62	41.62	41.62	41.62	41.62	41.62	41.62
N50	60217	522768	5373173	517479	57327	56491	555914	8580
NG50	60217	522768	5373173	517479	57327	56491	555914	8580
N75	60217	180083	5373173	517479	57327	56491	555914	8580
NG75	60217	522768	5373173	517479	57327	56491	555914	8580
L50	2	1	1	1	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	2	1	1	2	1	1	1
LG75	1	1	1	1	1	1	1	1
# misassemblies	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	1	0	0	0	0	0	1
# unaligned contigs	0 + 2 part	0 + 4 part	0 + 1 part	0 + 5 part	0 + 3 part	0 + 1 part	0 + 2 part	0 + 1 part
Unaligned length	119746	758652	5372260	652519	147162	56226	662032	7438
Genome fraction (%)	77.218	76.999	100.000	71.961	100.000	29.025	60.570	100.000
Duplication ratio	2.423	1.824	1.000	1.798	2.980	1.000	1.000	1.251
# N's per 100 kbp	0.00	0.79	0.00	0.00	0.00	0.00	0.00	2331.00
# mismatches per 100 kbp	0.00	568.99	0.00	3044.14	657.17	0.00	1084.99	547.65
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	361	400	913	345	913	265	307	679
Total aligned length	1410	1276	913	1181	2721	265	553	942
NGA50	361	303	913	312	913	-	246	679
NGA75	361	303	913	254	913	-	-	263
LGA50	2	2	1	2	1	-	2	1
LGA75	2	2	1	3	1	-	-	2

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0
# possibly misassembled contigs	0	3	1	5	3	1	2	0
# possible misassemblies	0	3	2	6	4	1	2	0
# local misassemblies	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	1	0	0	0	0	0	1
# mismatches	0	4	0	20	6	0	6	5
# indels	0	0	0	0	0	0	0	0
# indels (<= 5 bp)	0	0	0	0	0	0	0	0
# indels (> 5 bp)	0	0	0	0	0	0	0	0
Indels length	0	0	0	0	0	0	0	0

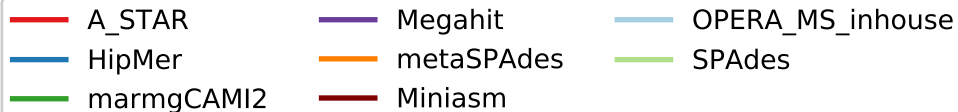
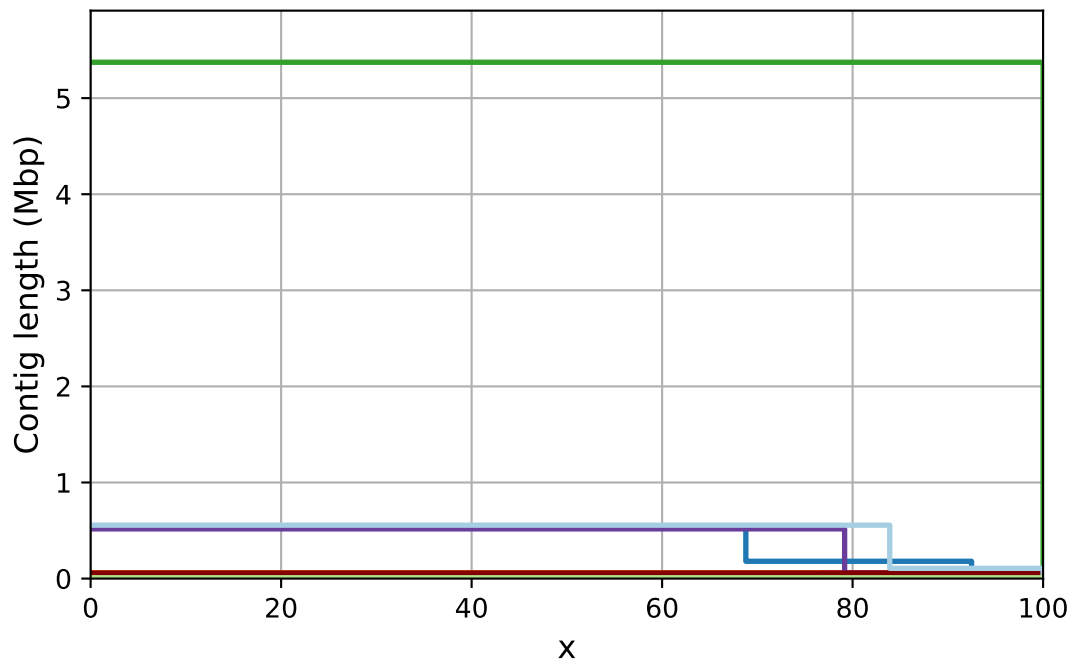
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

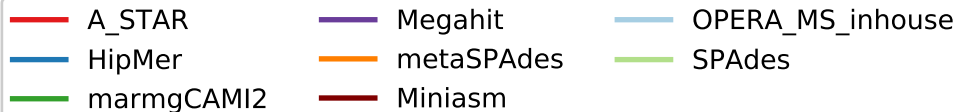
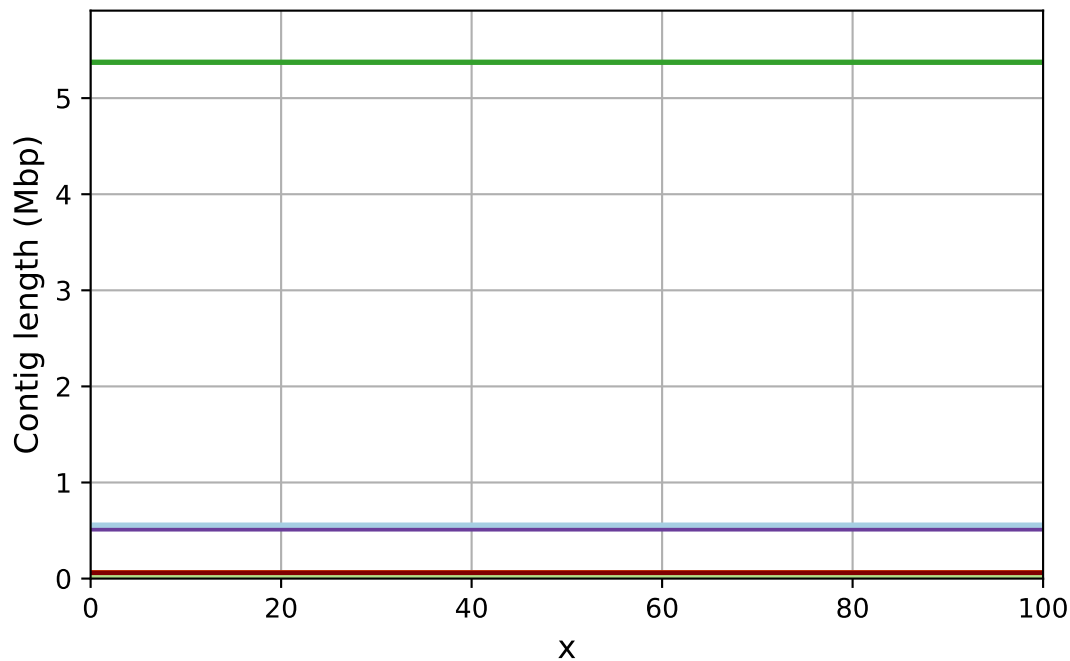
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	2	4	1	5	3	1	2	1
Partially unaligned length	119746	758652	5372260	652519	147162	56226	662032	7438
# N's	0	6	0	0	0	0	0	200

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

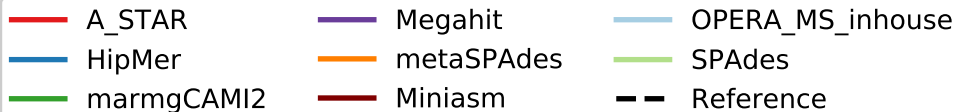
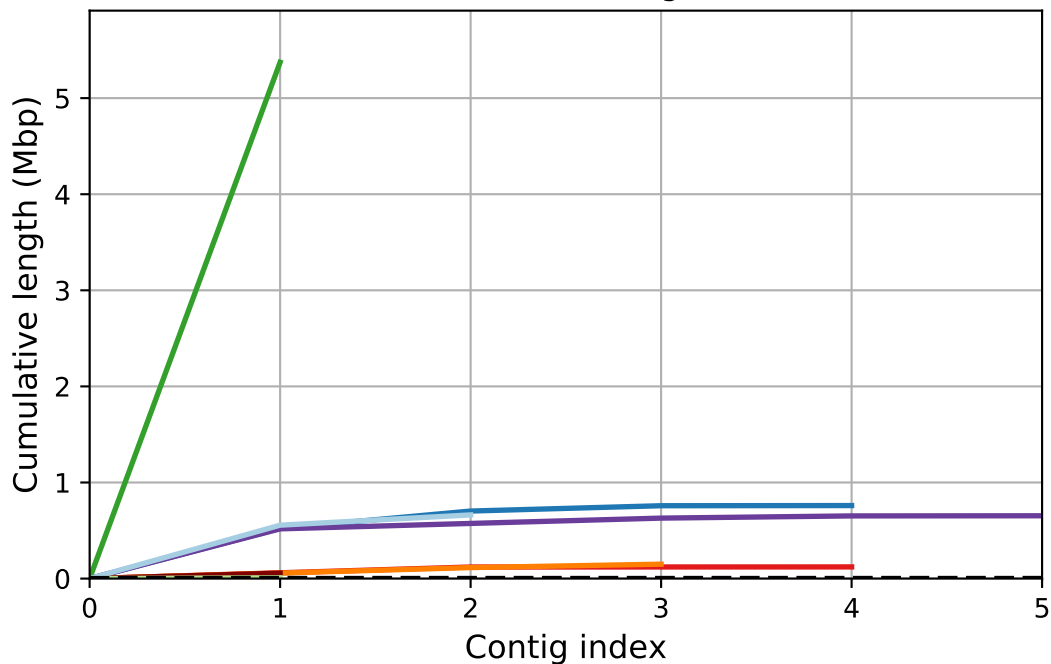
Nx

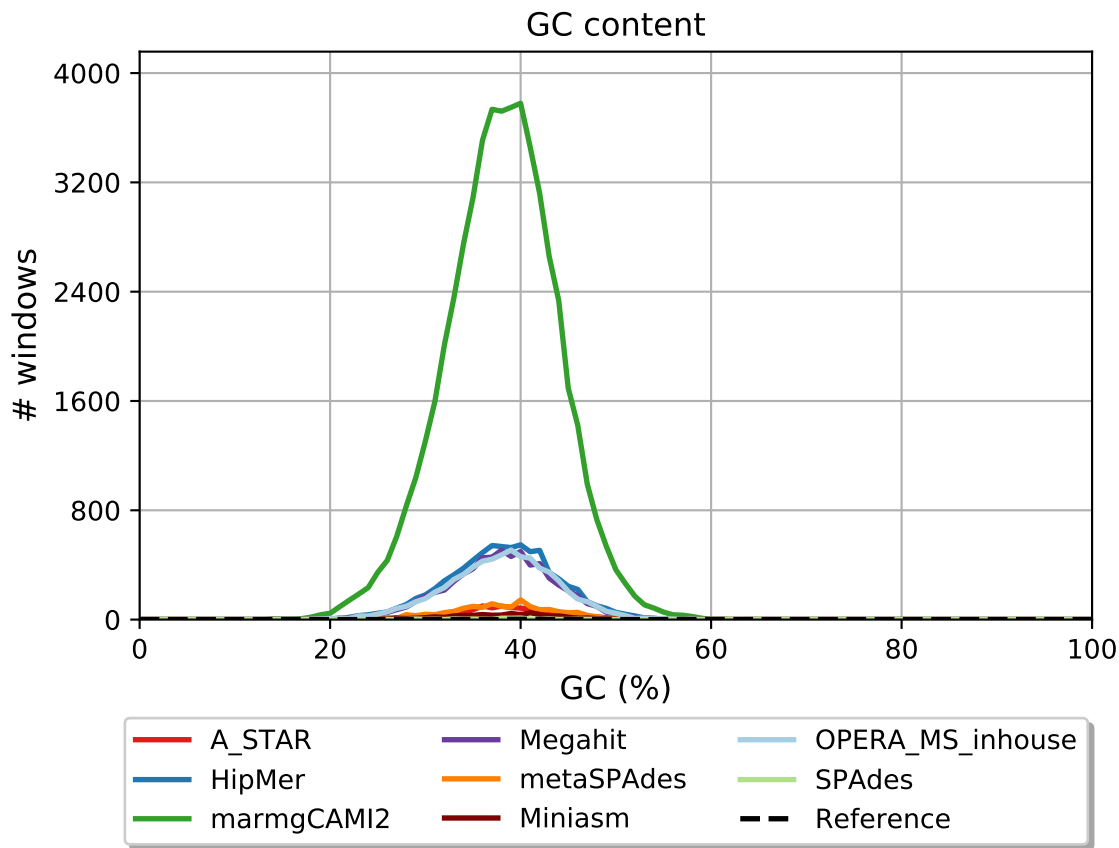


NGx

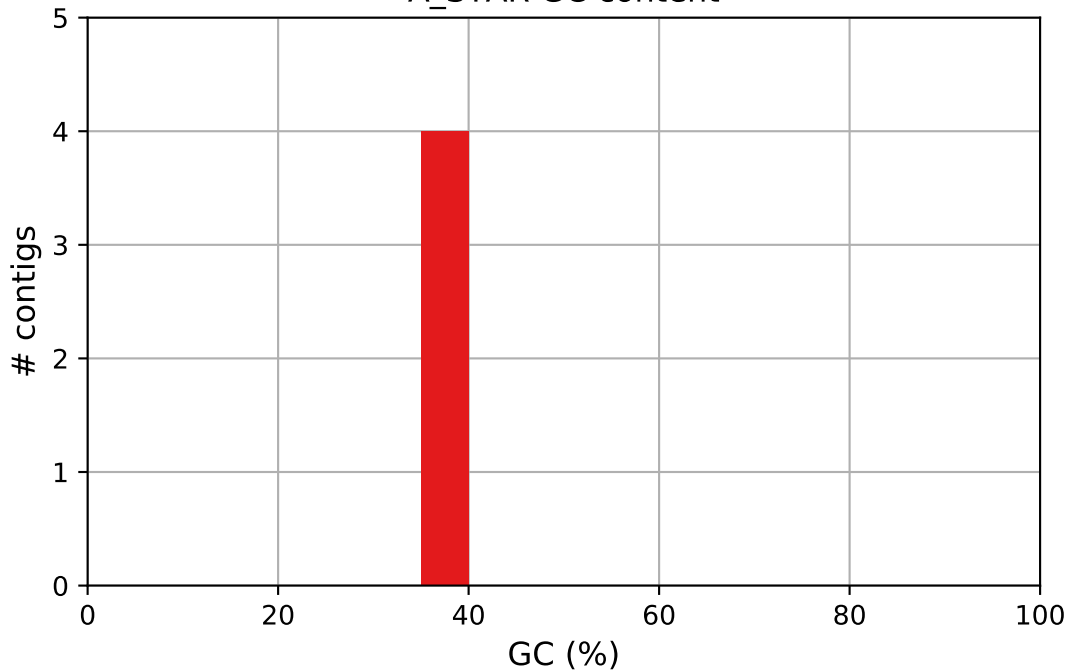


Cumulative length



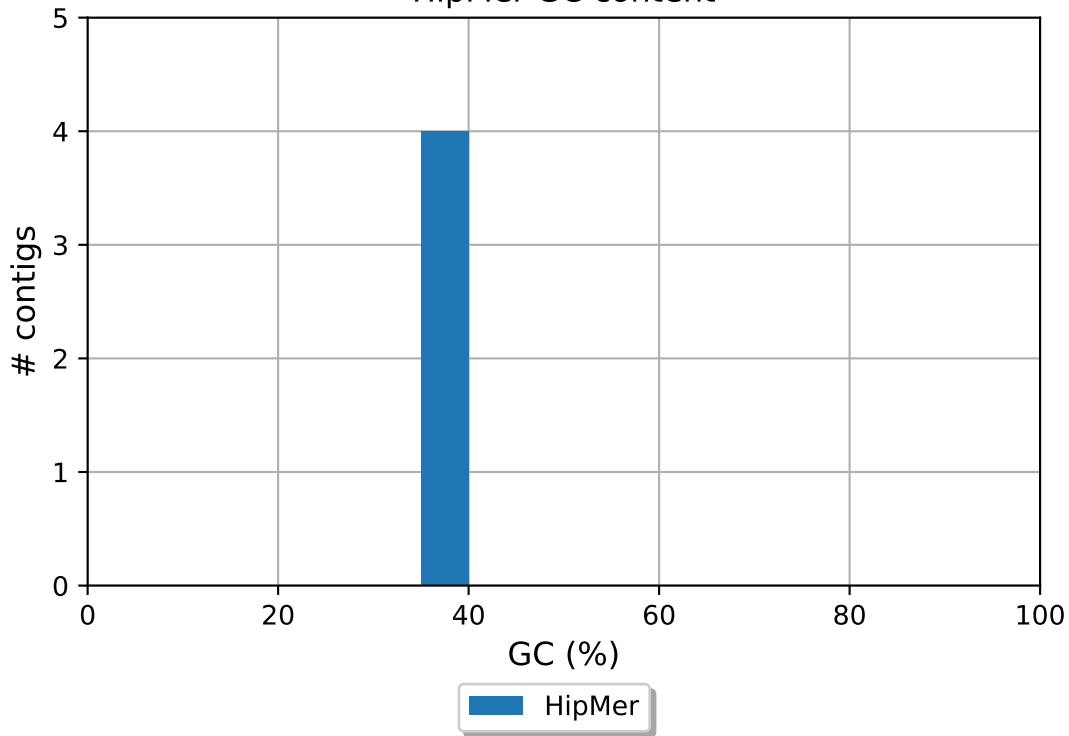


A_STAR GC content

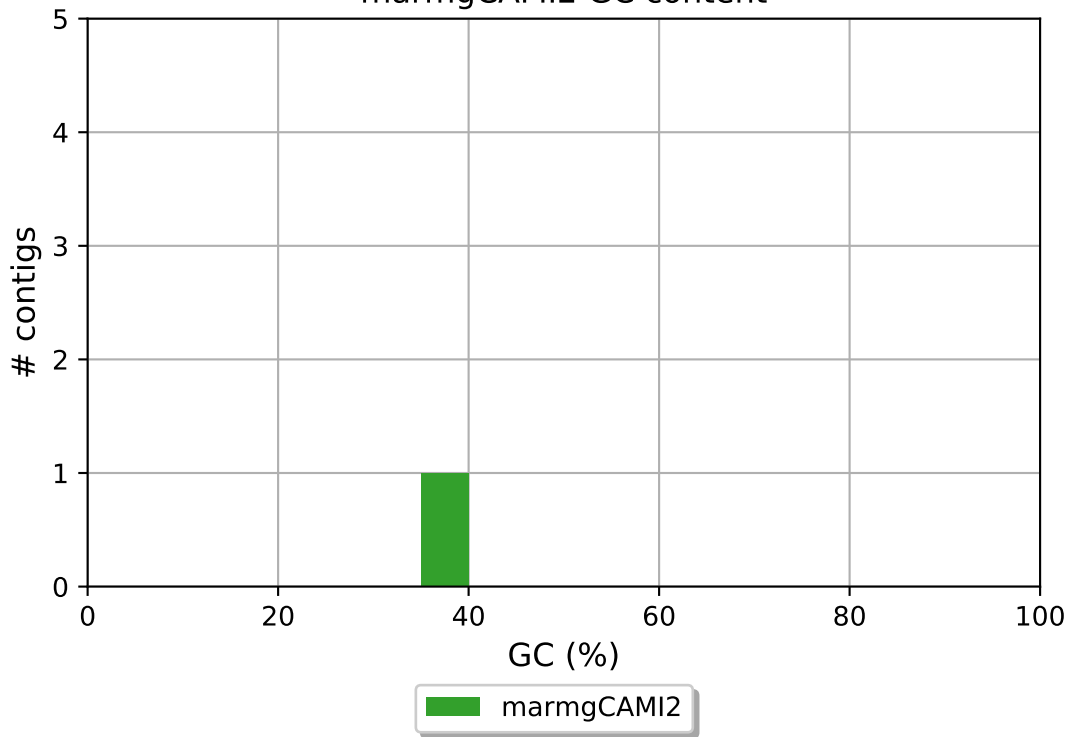


A_STAR

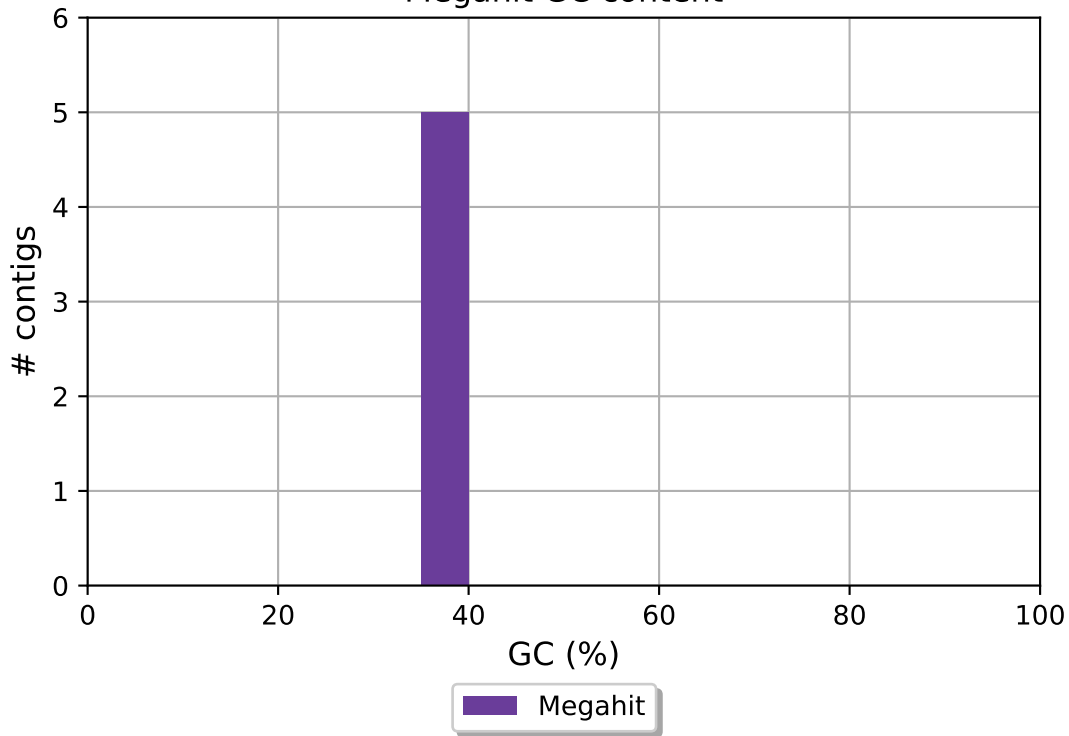
HipMer GC content



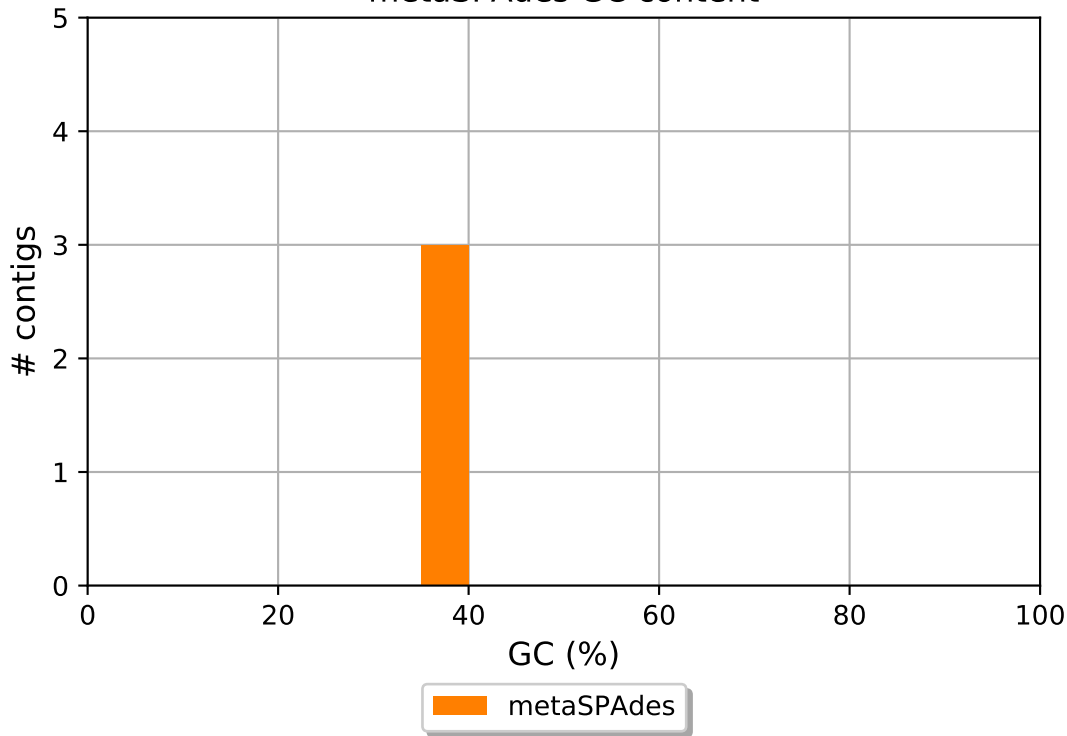
marmgCAMI2 GC content



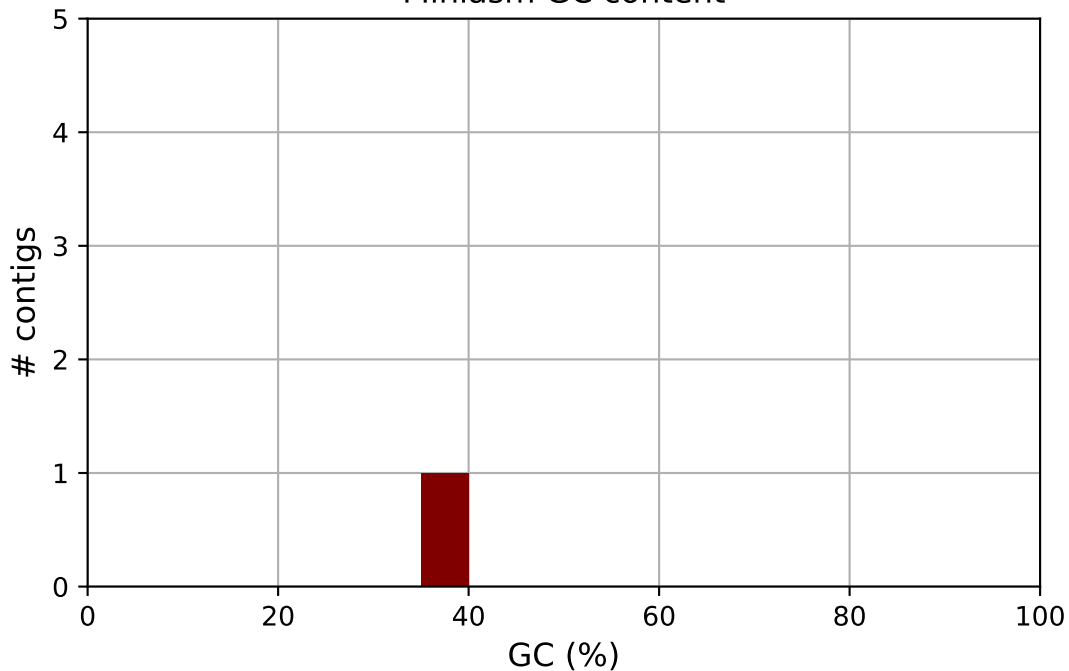
Megahit GC content



metaSPAdes GC content

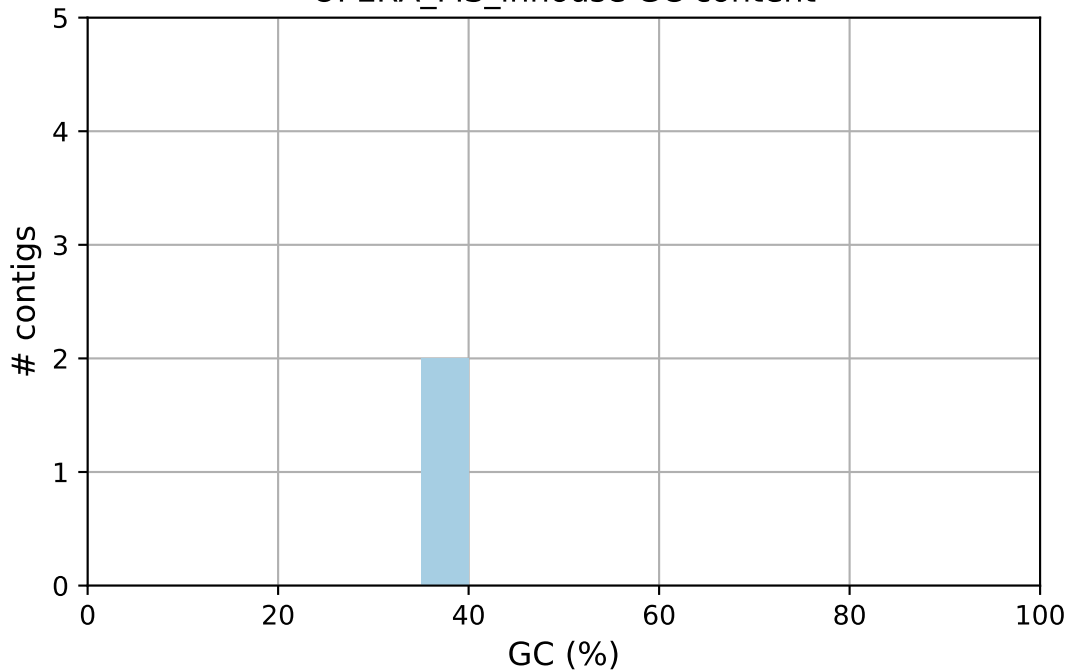


Miniasm GC content



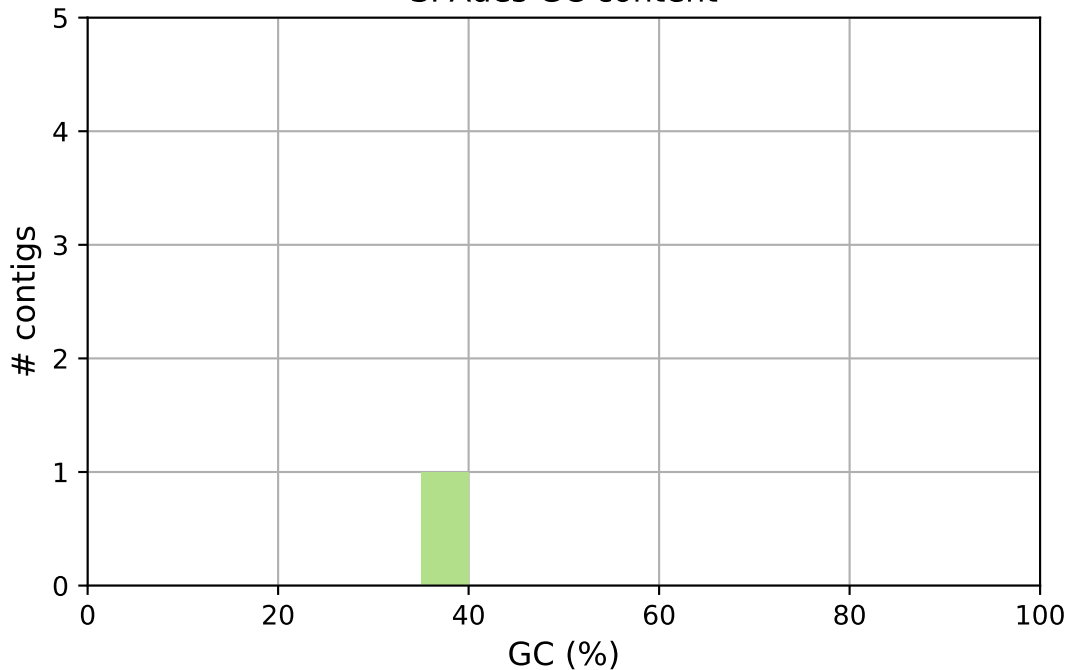
Miniasm

OPERA_MS_inhouse GC content



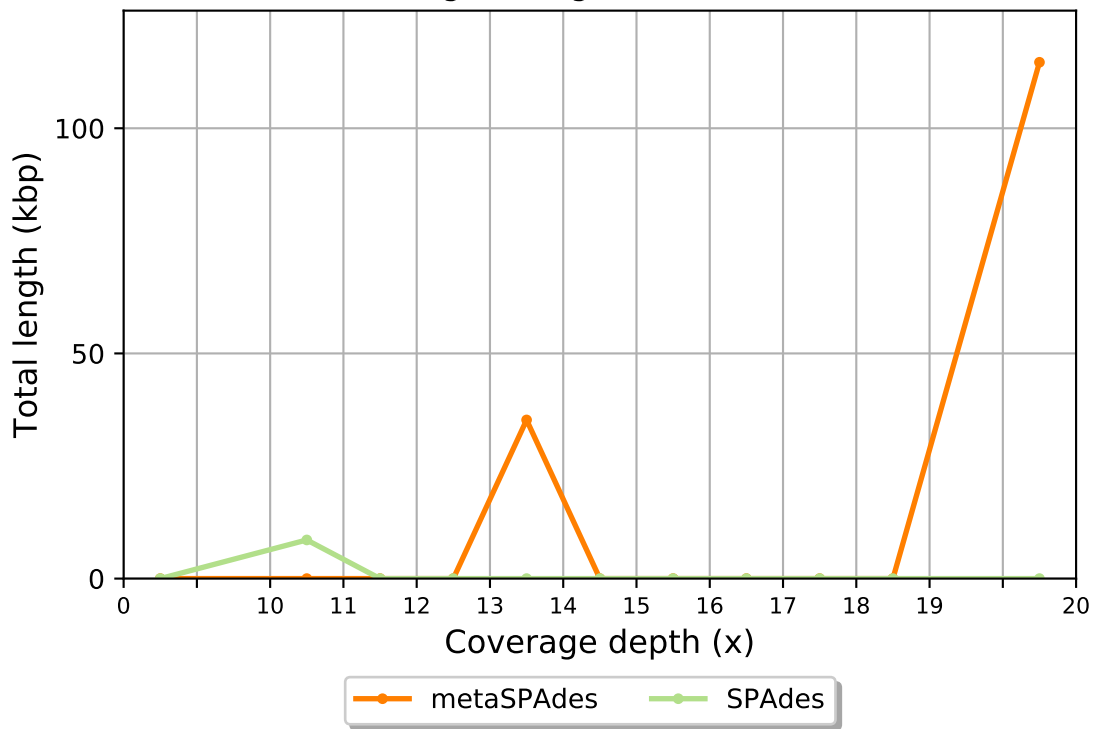
OPERA_MS_inhouse

SPAdes GC content

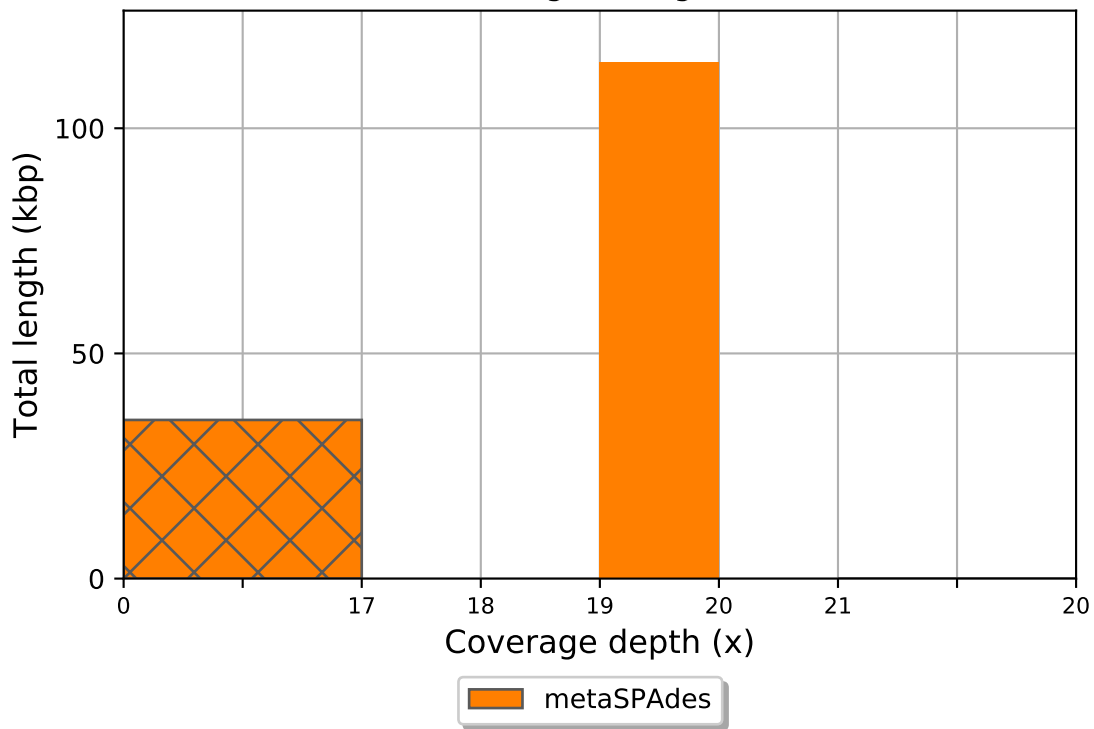


SPAdes

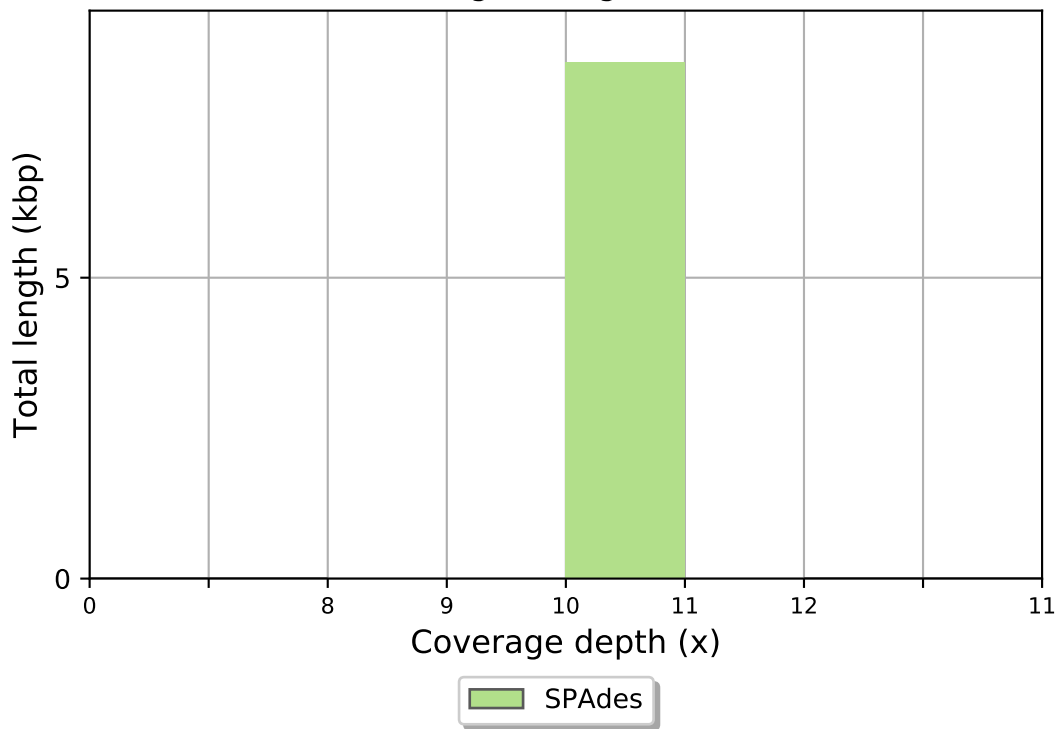
Coverage histogram (bin size: 1x)



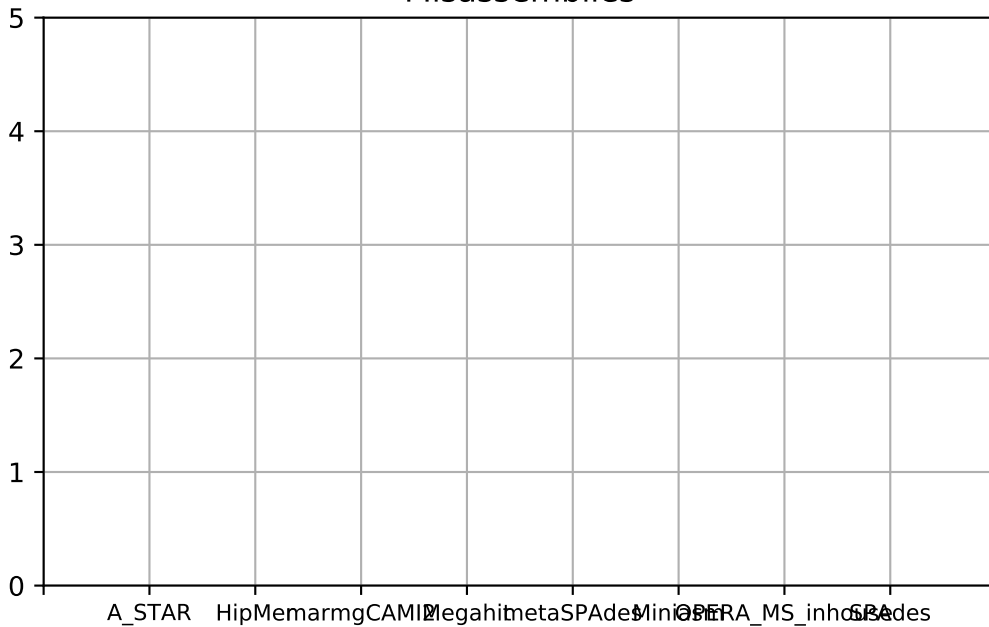
metaSPAdes coverage histogram (bin size: 1x)



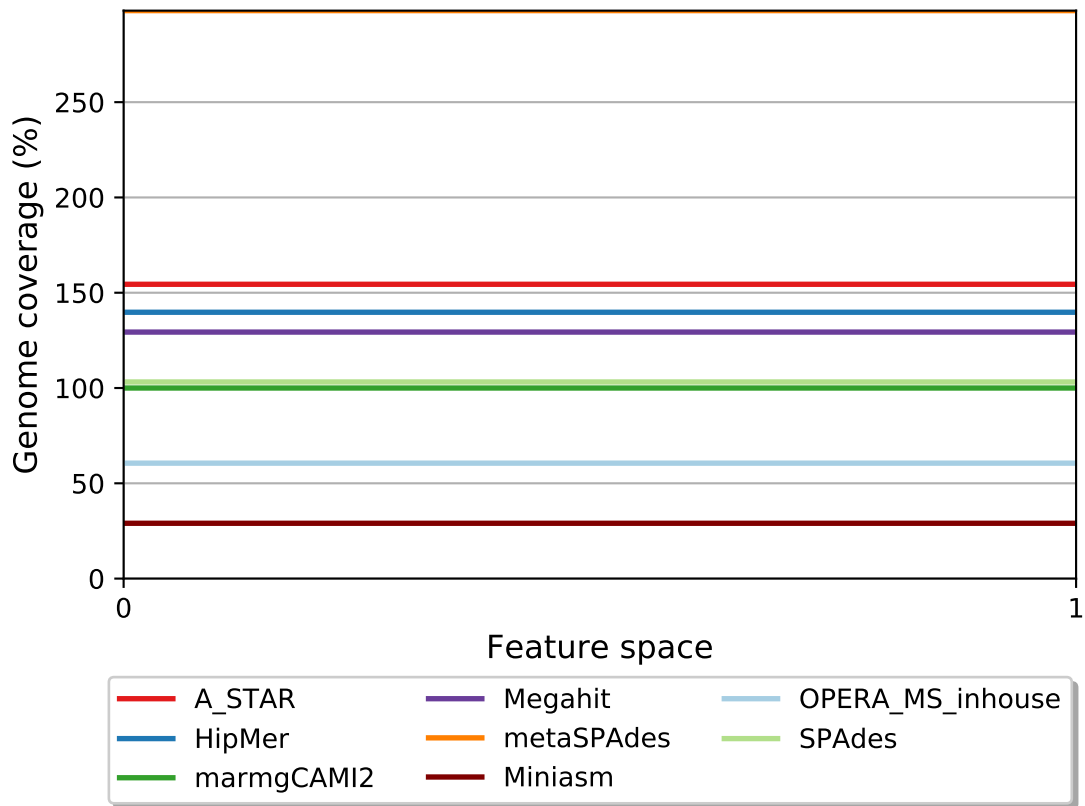
SPAdes coverage histogram (bin size: 1x)



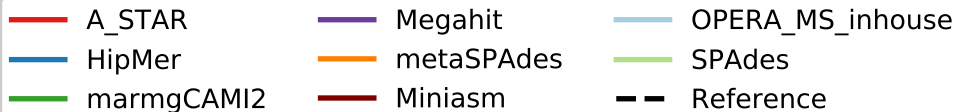
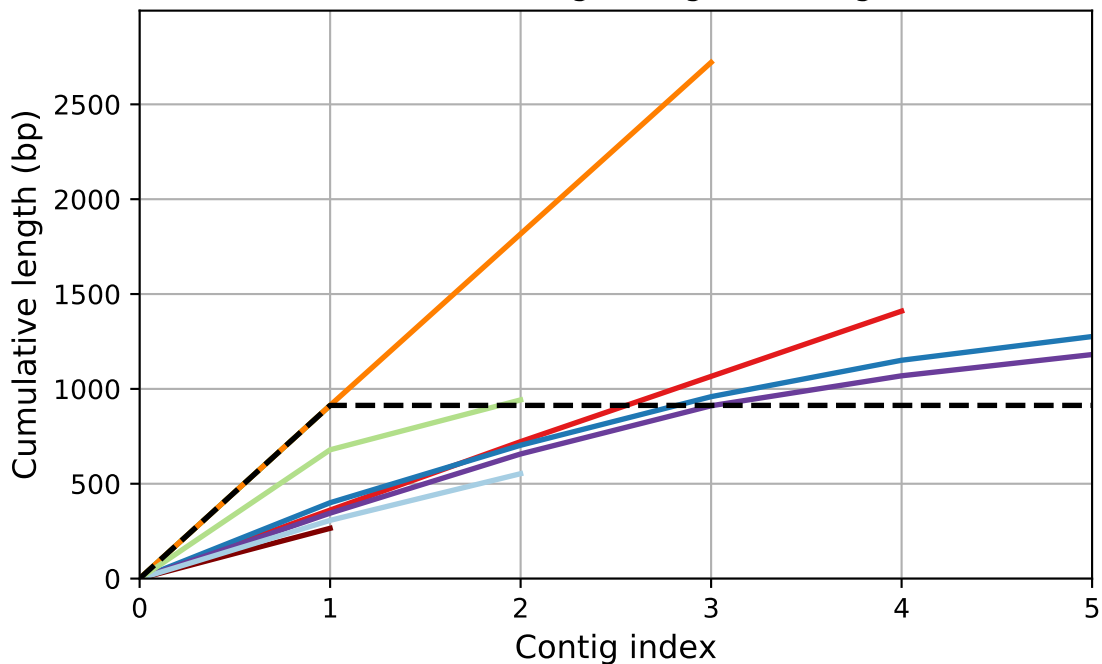
Misassemblies



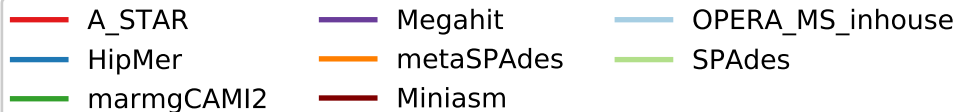
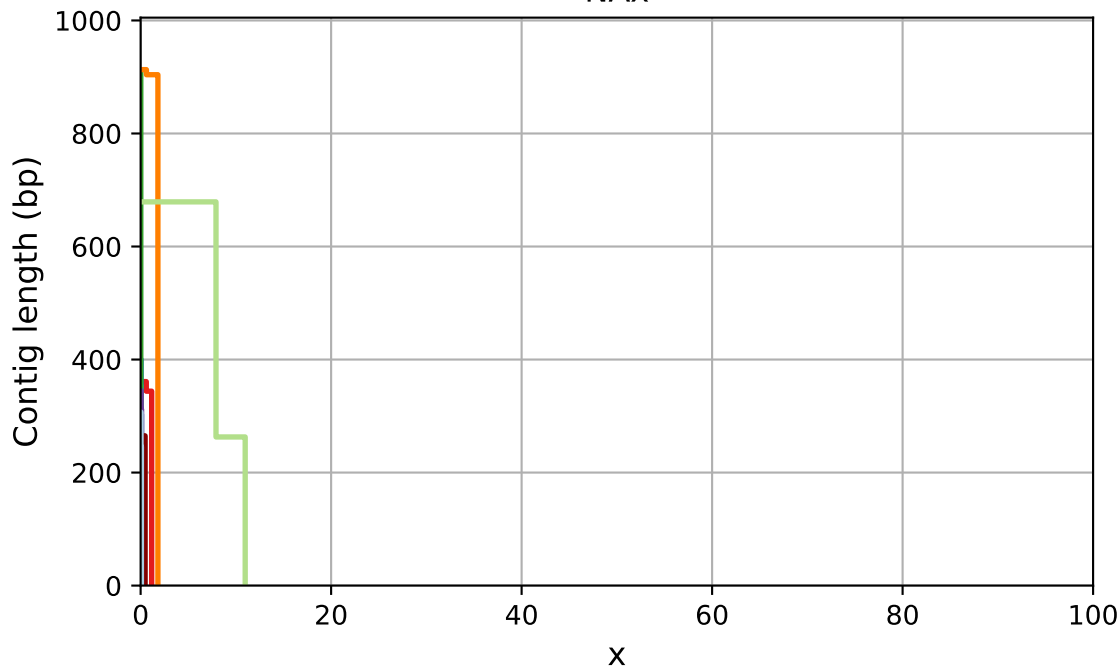
FRCurve (misassemblies)



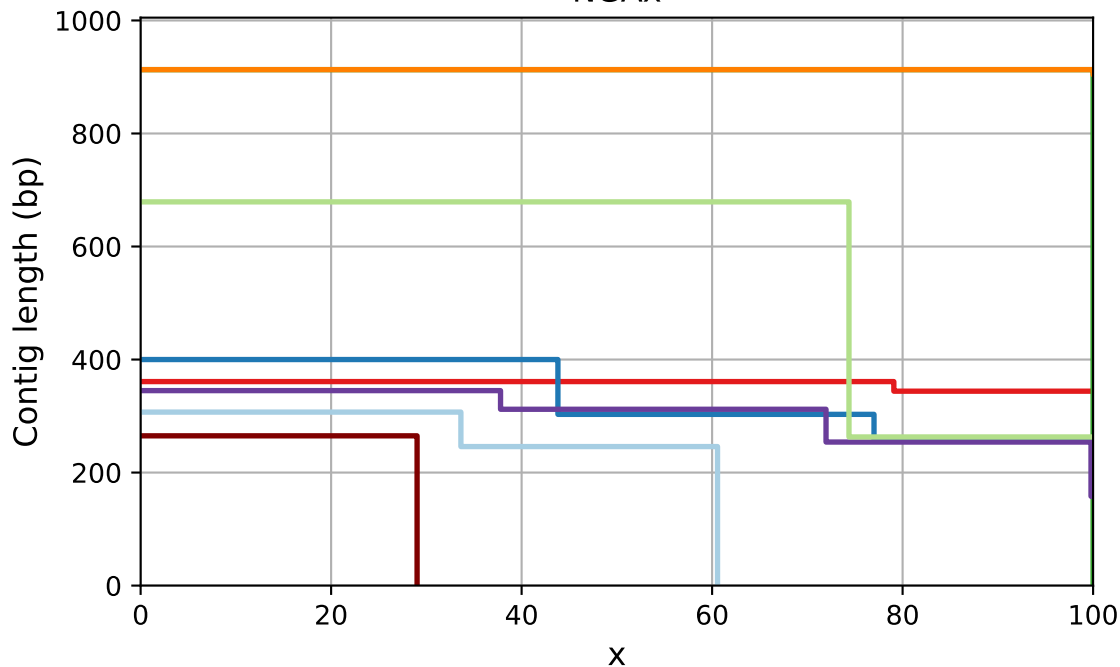
Cumulative length (aligned contigs)



NAx



NGAx



- | | | |
|---|--|---|
| — A_STAR | — Megahit | — OPERA_MS_inhouse |
| — HipMer | — metaSPAdes | — SPAdes |
| — marmgCAMI2 | — Miniasm | |

