

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	4	2	1	6	6	2	2	3
# contigs (>= 5000 bp)	4	0	1	1	1	0	2	1
# contigs (>= 10000 bp)	4	0	1	1	1	0	2	0
# contigs (>= 25000 bp)	0	0	1	0	0	0	1	0
# contigs (>= 50000 bp)	0	0	1	0	0	0	0	0
Total length (>= 1000 bp)	51284	3405	1584791	23831	21560	5682	46714	10244
Total length (>= 5000 bp)	51284	0	1584791	12930	10215	0	46714	5567
Total length (>= 10000 bp)	51284	0	1584791	12930	10215	0	46714	0
Total length (>= 25000 bp)	0	0	1584791	0	0	0	28333	0
Total length (>= 50000 bp)	0	0	1584791	0	0	0	0	0
# contigs	4	6	1	9	6	2	2	3
Largest contig	15231	1855	1584791	12930	10215	3403	28333	5567
Total length	51284	6366	1584791	26102	21560	5682	46714	10244
Reference length	2397	2397	2397	2397	2397	2397	2397	2397
GC (%)	40.41	36.91	39.92	33.73	40.45	36.98	37.68	38.47
Reference GC (%)	37.00	37.00	37.00	37.00	37.00	37.00	37.00	37.00
N50	15231	1550	1584791	4184	3791	3403	28333	5567
NG50	15231	1855	1584791	12930	10215	3403	28333	5567
N75	10411	895	1584791	1534	3791	2279	18381	3043
NG75	15231	1855	1584791	12930	10215	3403	28333	5567
L50	2	2	1	2	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	3	4	1	4	3	2	2	2
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	2	0	1	0	0	0	0	0
# unaligned contigs	0 + 4 part	0 + 2 part	0 + 1 part	0 + 4 part	0 + 3 part	0 + 2 part	0 + 2 part	0 + 2 part
Unaligned length	47178	2244	1582394	17470	14044	3299	44317	7208
Genome fraction (%)	83.813	77.680	100.000	100.000	100.000	99.416	100.000	100.000
Duplication ratio	2.044	2.214	1.000	3.601	3.136	1.000	1.000	1.267
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	1095.07	0.00	0.00	2044.22	125.16	0.00	41.72	166.88
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	865	733	1251	1251	1251	1251	1251	1146
Total aligned length	4106	3498	2397	7502	7191	2383	2397	2548
NA50	-	428	-	-	-	-	-	-
NGA50	865	611	1251	1251	1251	1251	1251	928
NGA75	739	583	1146	1251	1251	1132	1146	928
LA50	-	6	-	-	-	-	-	-
LGA50	2	2	1	1	1	1	1	2
LGA75	3	3	2	2	2	2	2	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

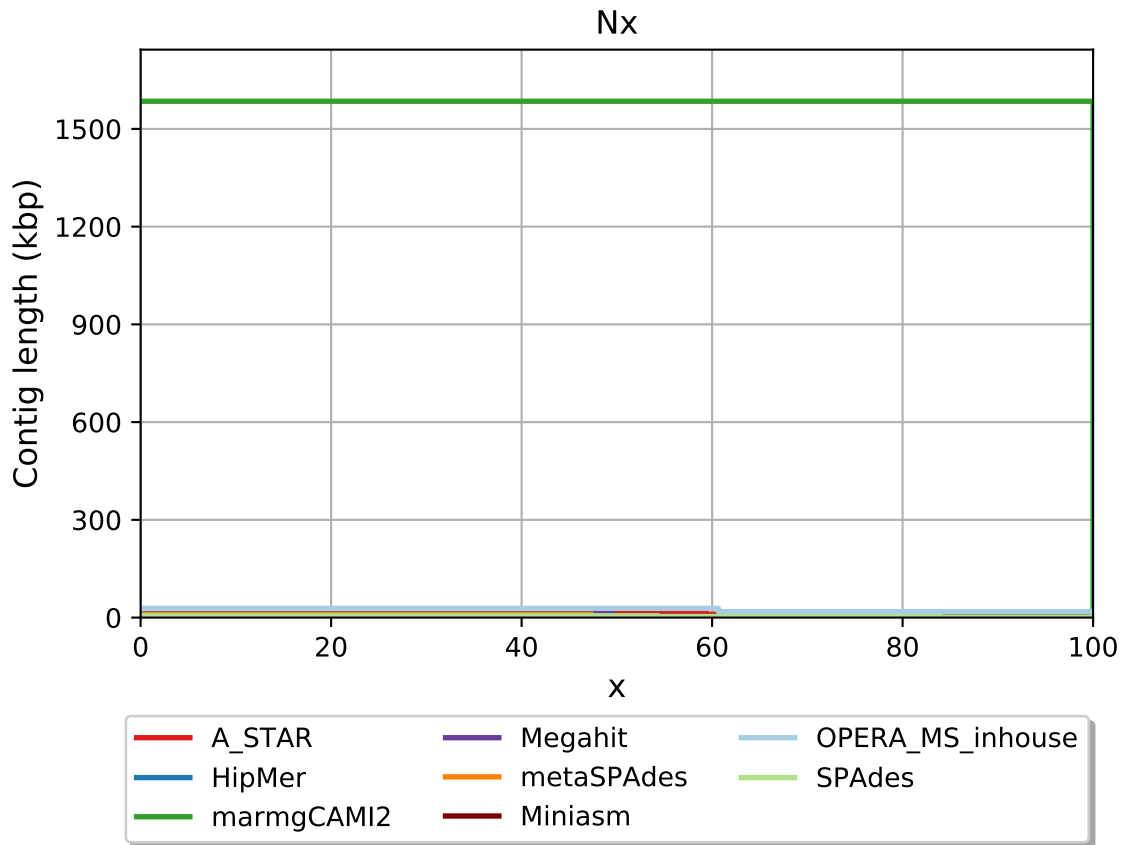
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	2	2	0	4	3	2	2	2
# possible misassemblies	2	2	0	5	4	2	4	2
# 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	2	0	1	0	0	0	0	0
# mismatches	22	0	0	49	3	0	1	4
# 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).

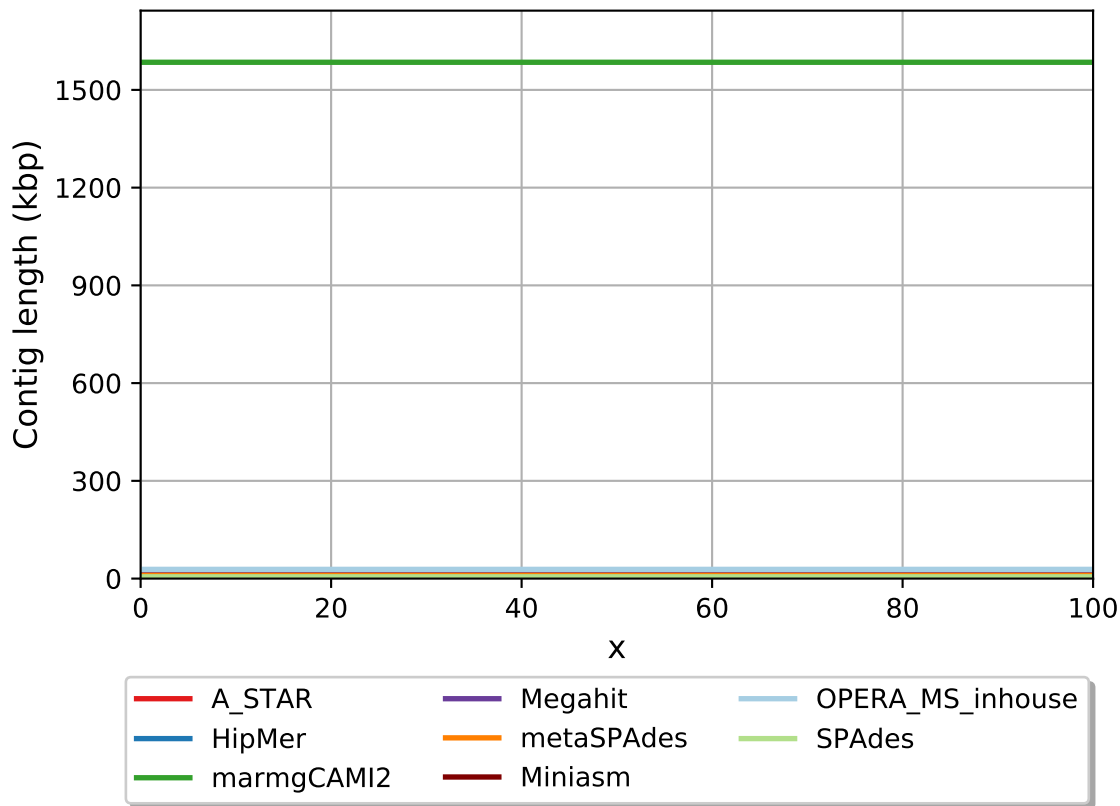
Unaligned report

	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	4	2	1	4	3	2	2	2
Partially unaligned length	47178	2244	1582394	17470	14044	3299	44317	7208
# N's	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).



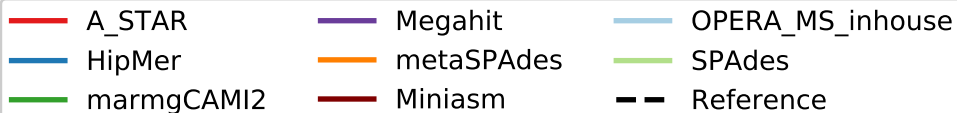
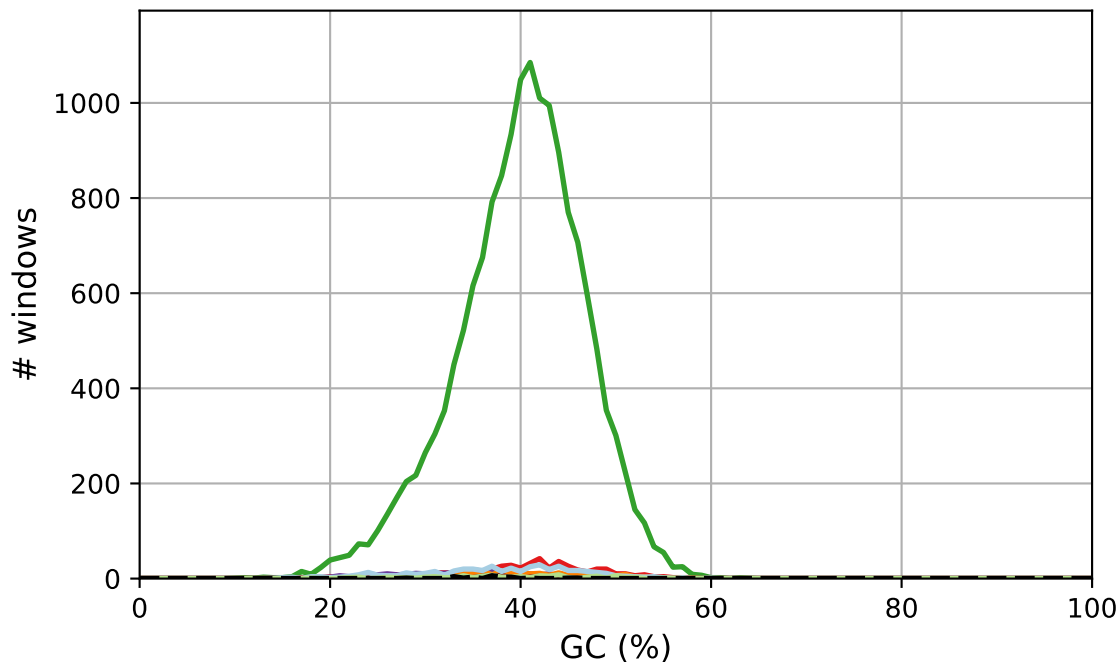
NGx



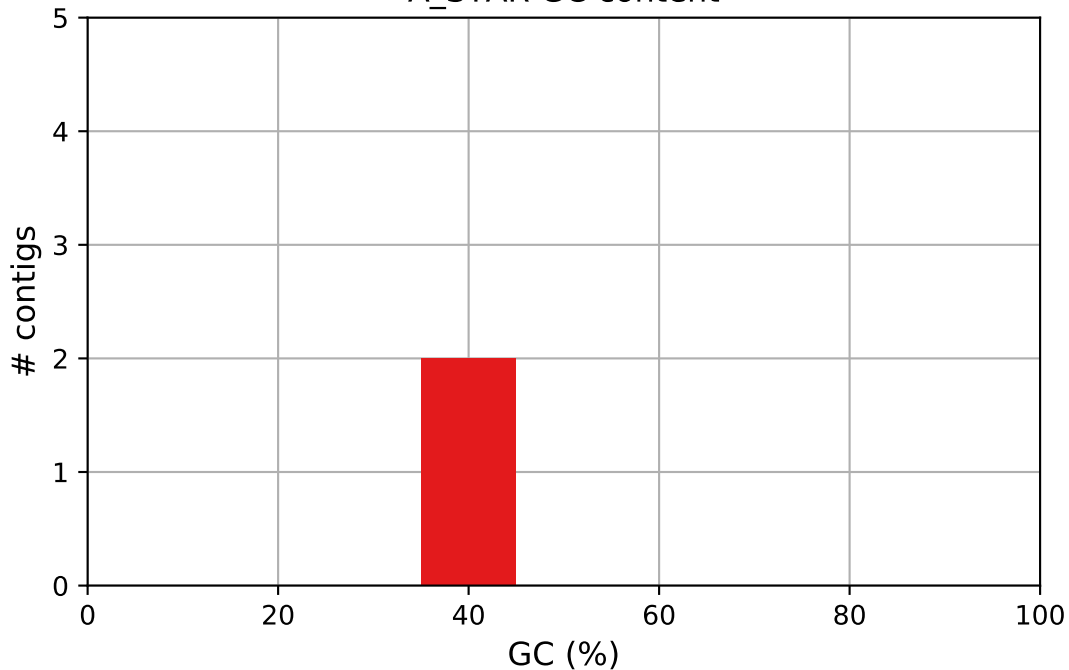
Contig index	Contig 0 (green)	Contig 1 (blue)	Contig 2 (red)	Contig 3 (orange)	Contig 4 (purple)	Contig 5 (dashed black)
0	0	0	0	0	0	0
1	100	2	0	0	0	0
2	0	10	1	0	0	0
3	0	5	2	0	0	0
4	0	2	5	0	0	0
5	0	1	2	1	0	0
6	0	0	1	2	0	0
7	0	0	0	1	0	0
8	0	0	0	0	1	0.5



GC content

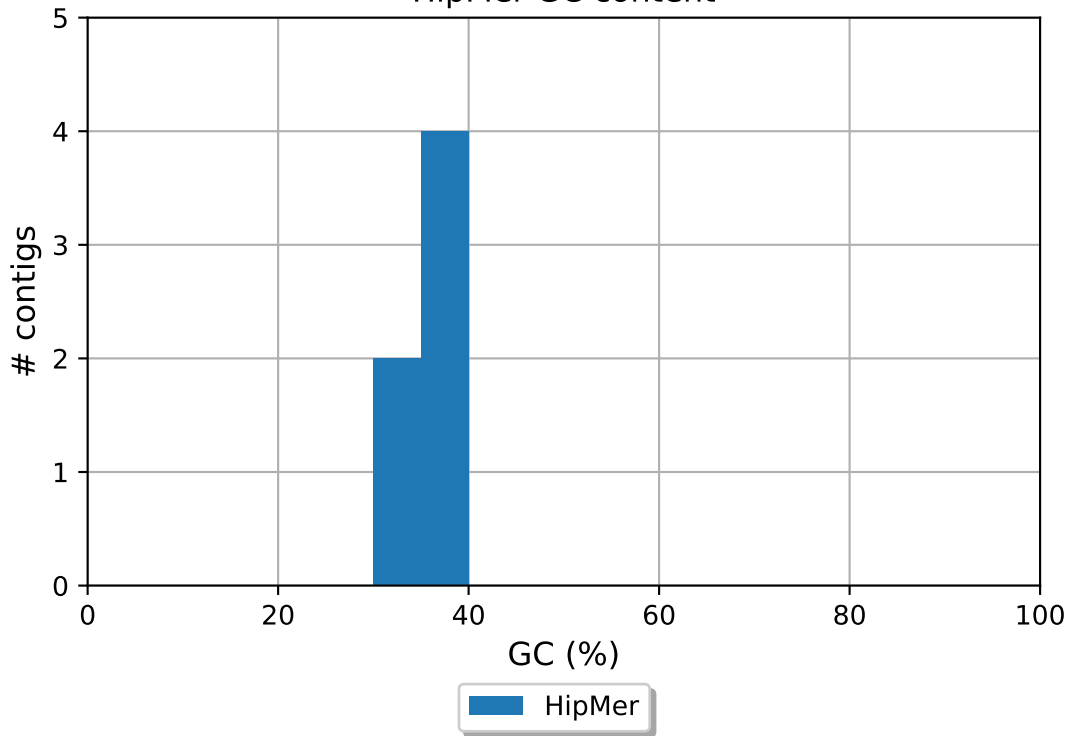


A_STAR GC content

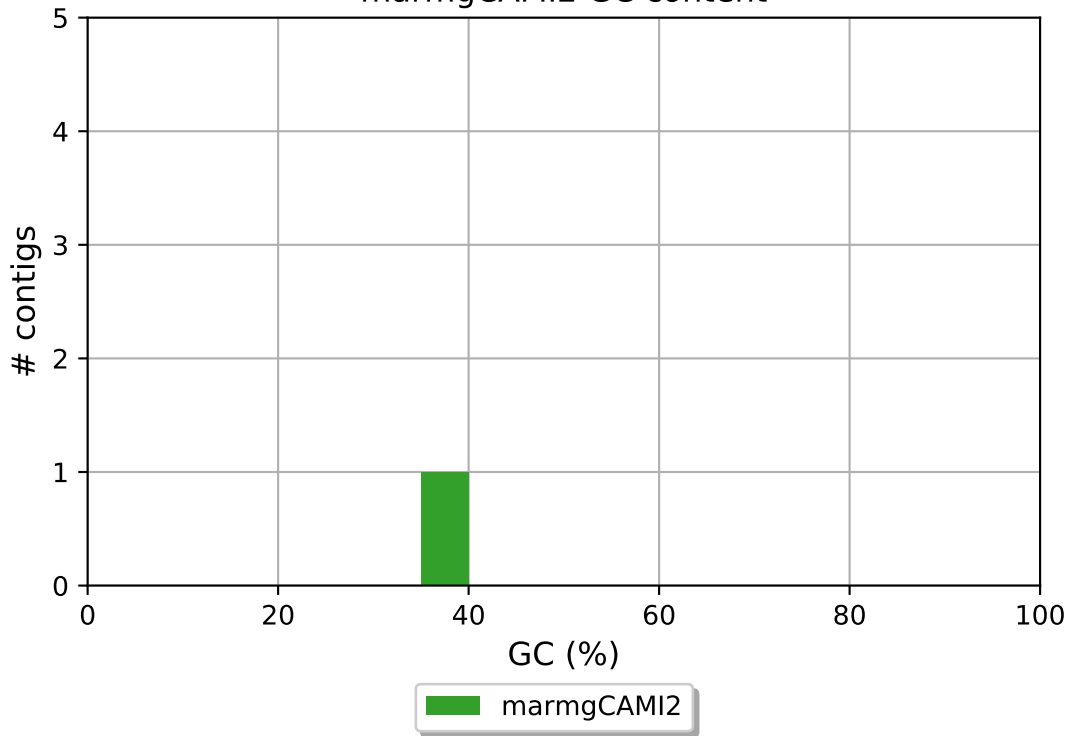


A_STAR

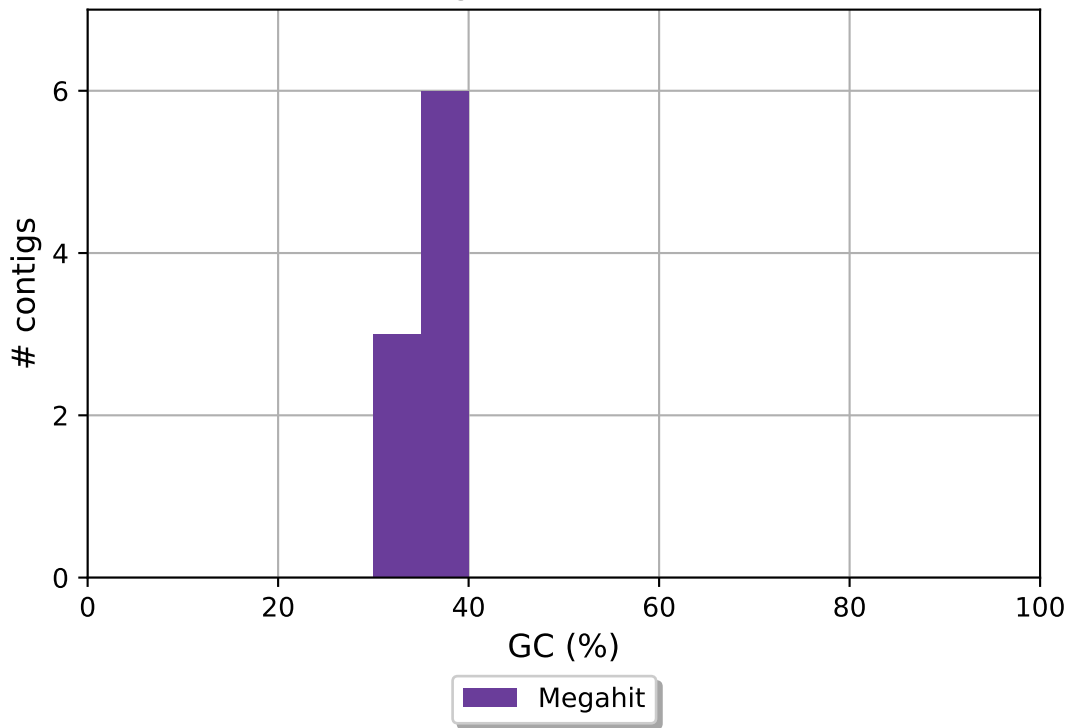
HipMer GC content



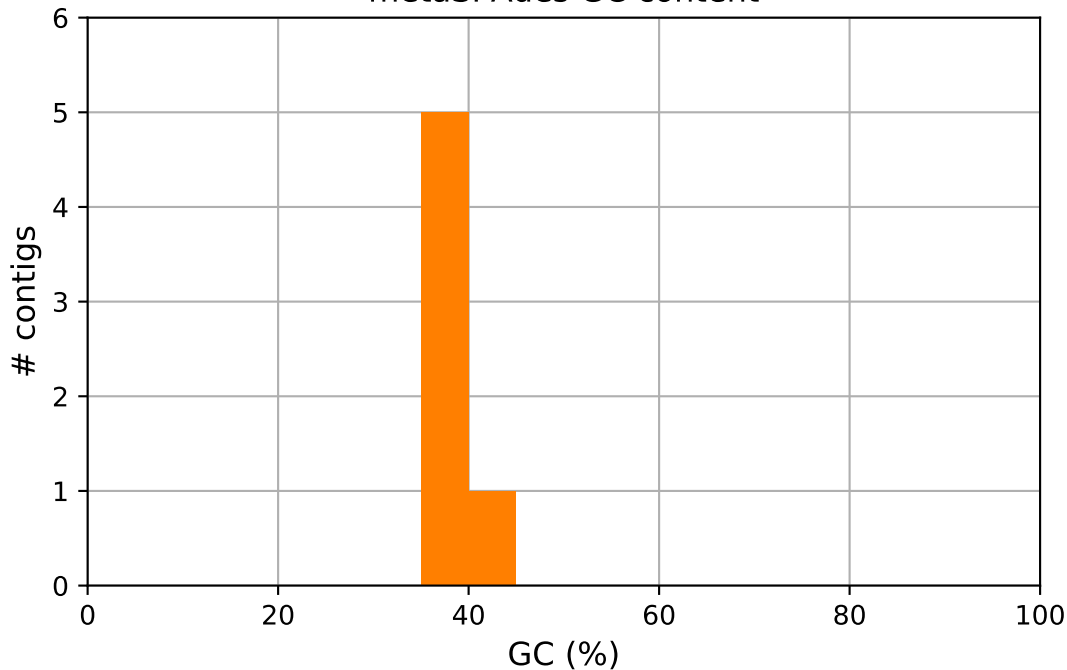
marmgCAMI2 GC content



Megahit GC content

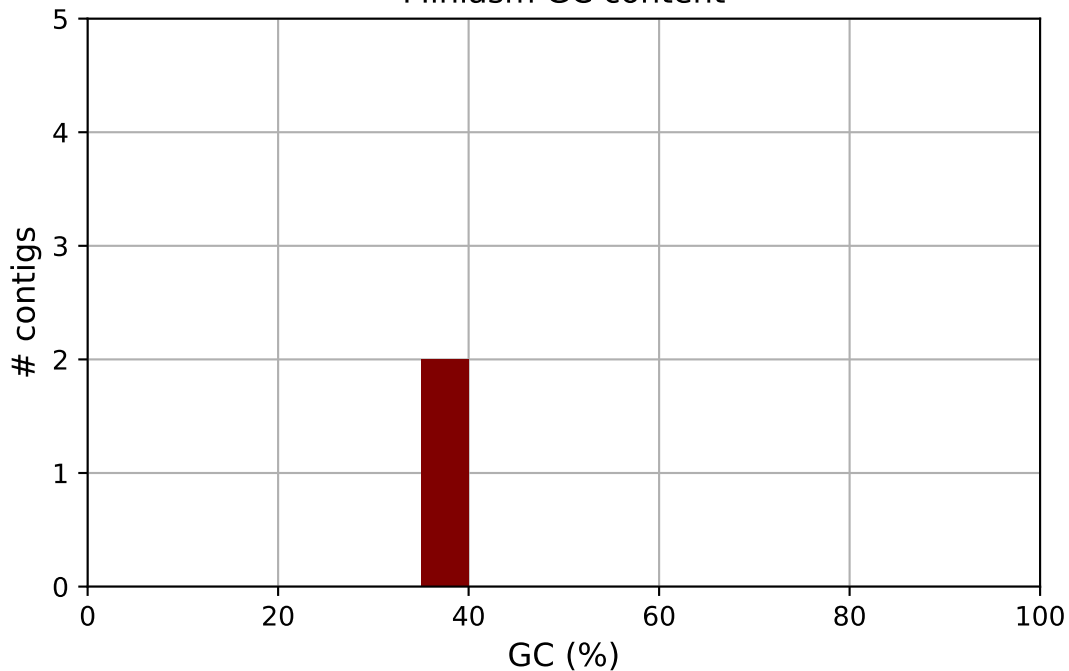


metaSPAdes GC content



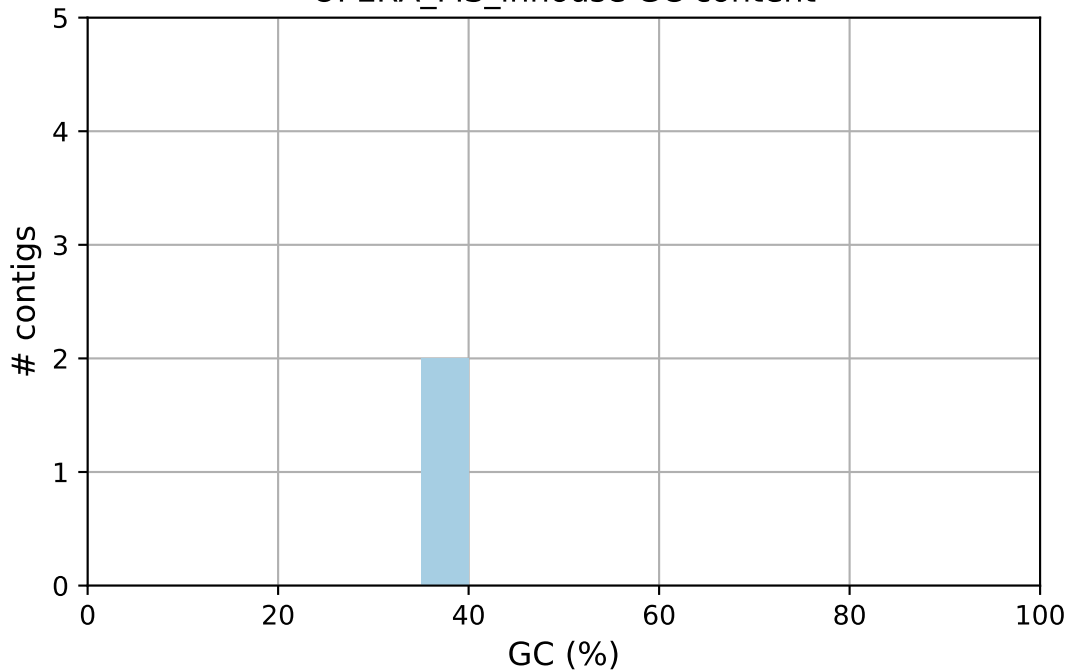
metaSPAdes

Miniasm GC content



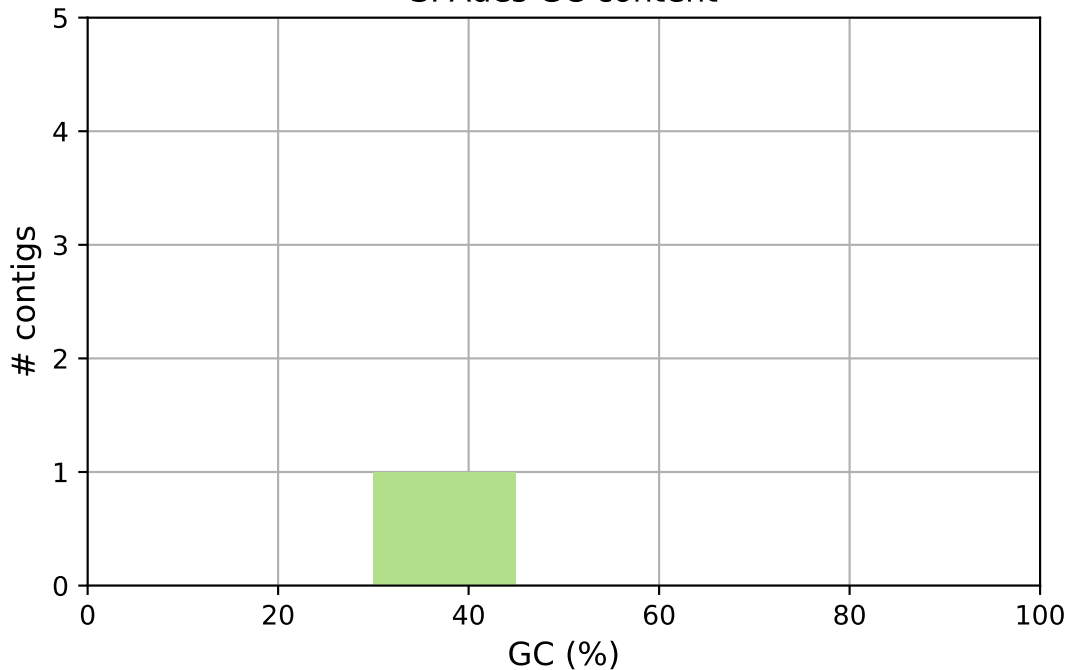
Miniasm

OPERA_MS_inhouse GC content



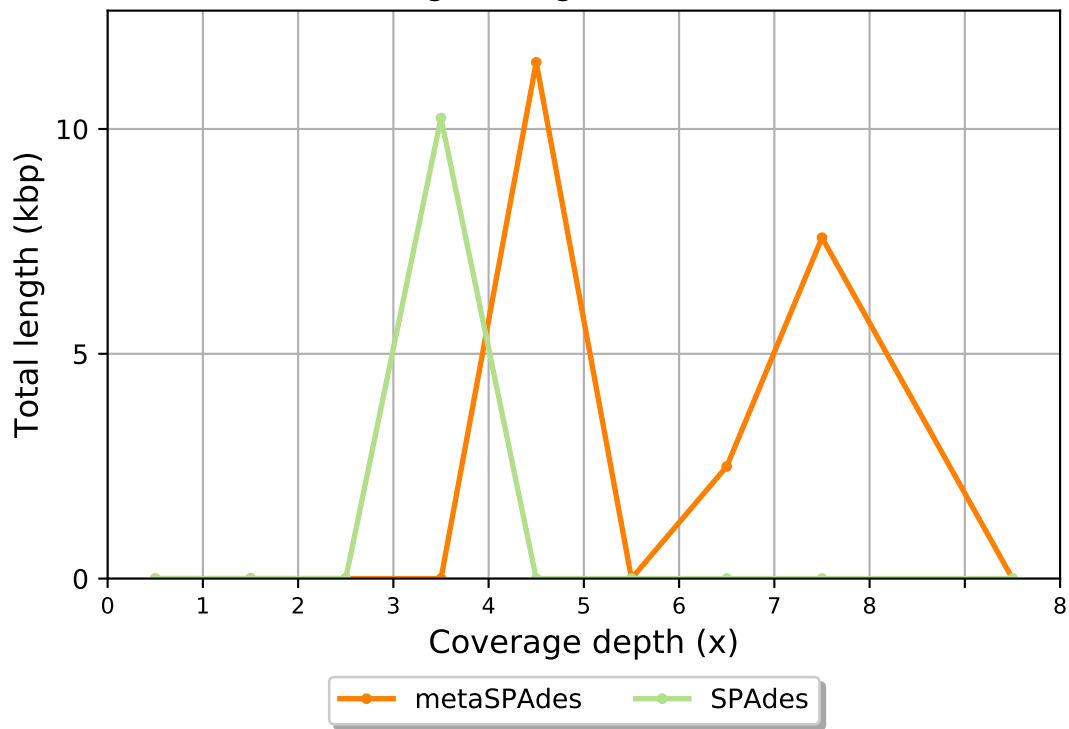
OPERA_MS_inhouse

SPAdes GC content

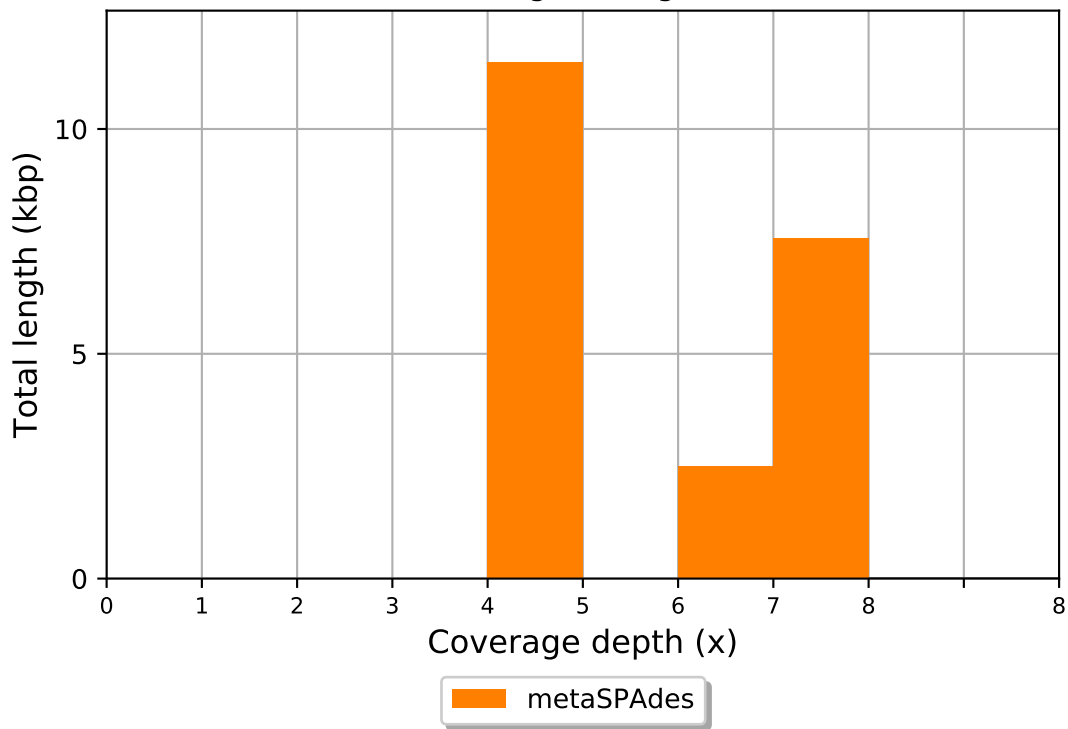


SPAdes

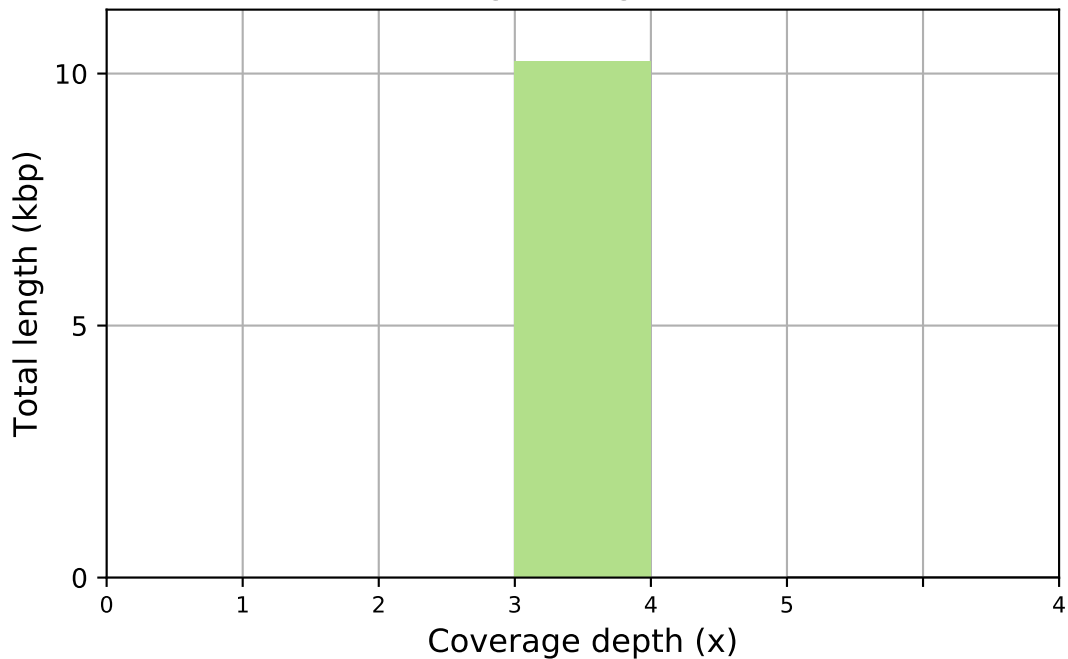
Coverage histogram (bin size: 1x)



metaSPAdes coverage histogram (bin size: 1x)

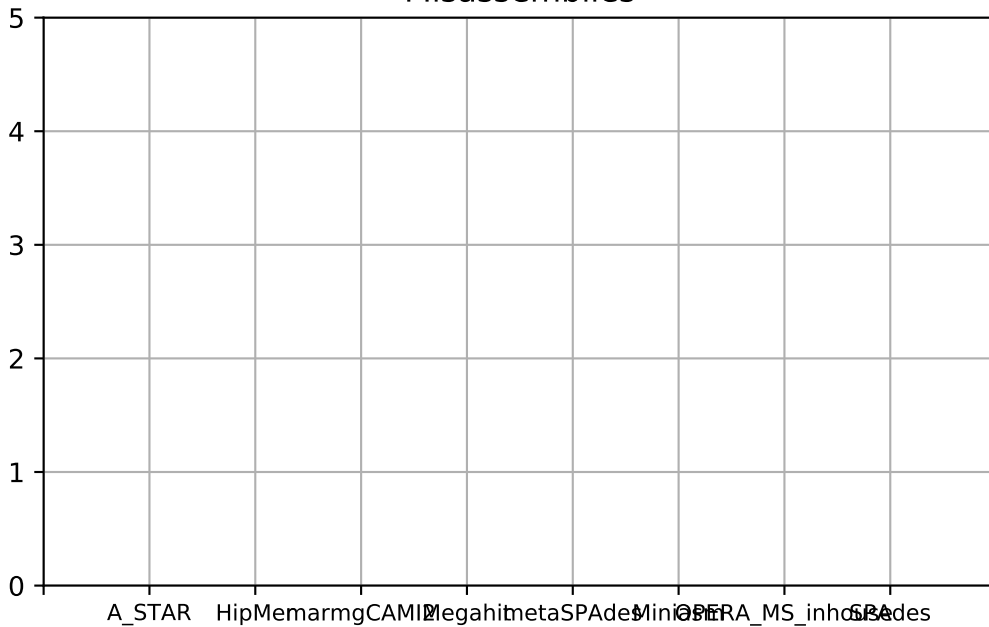


SPAdes coverage histogram (bin size: 1x)

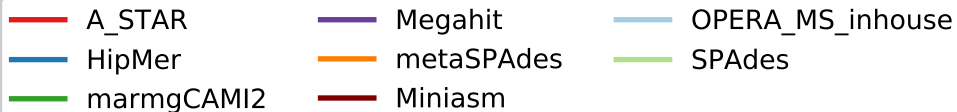
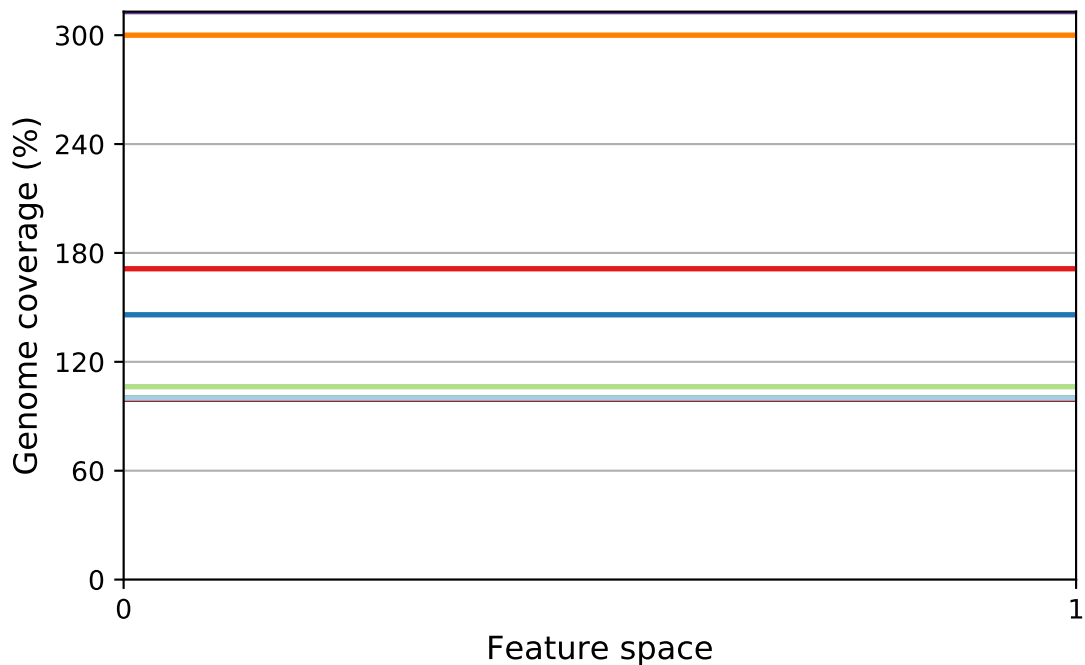


SPAdes

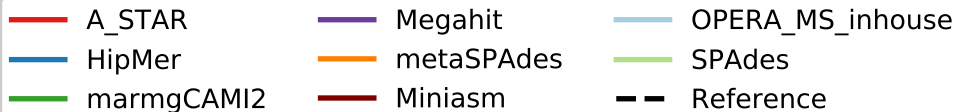
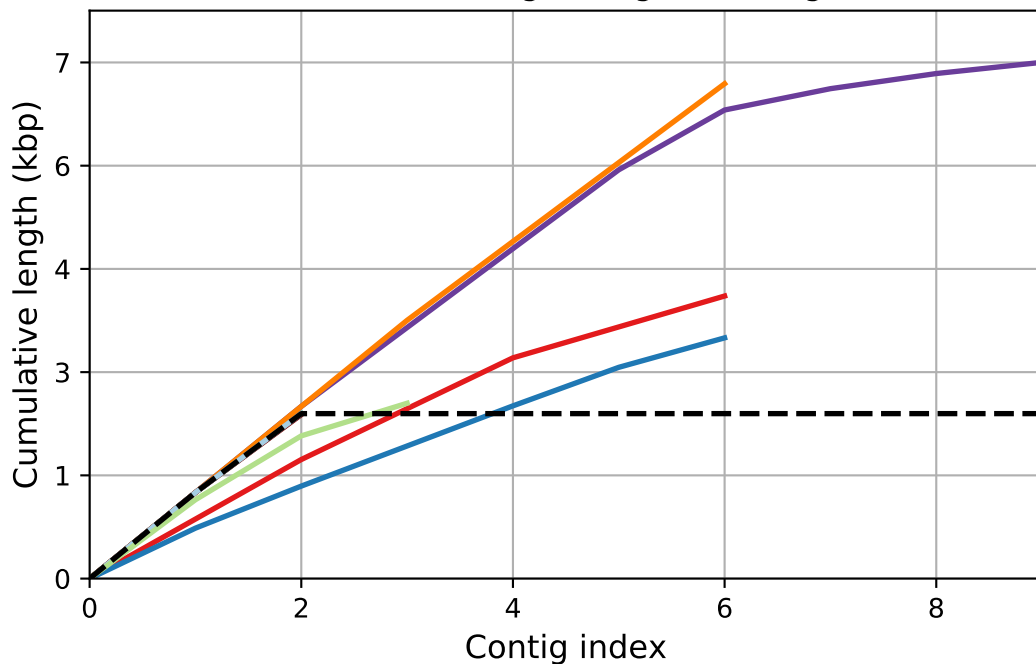
Misassemblies



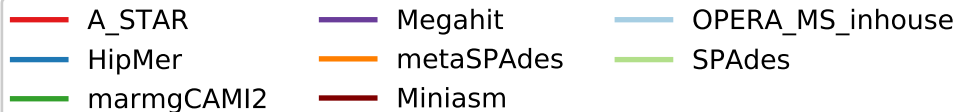
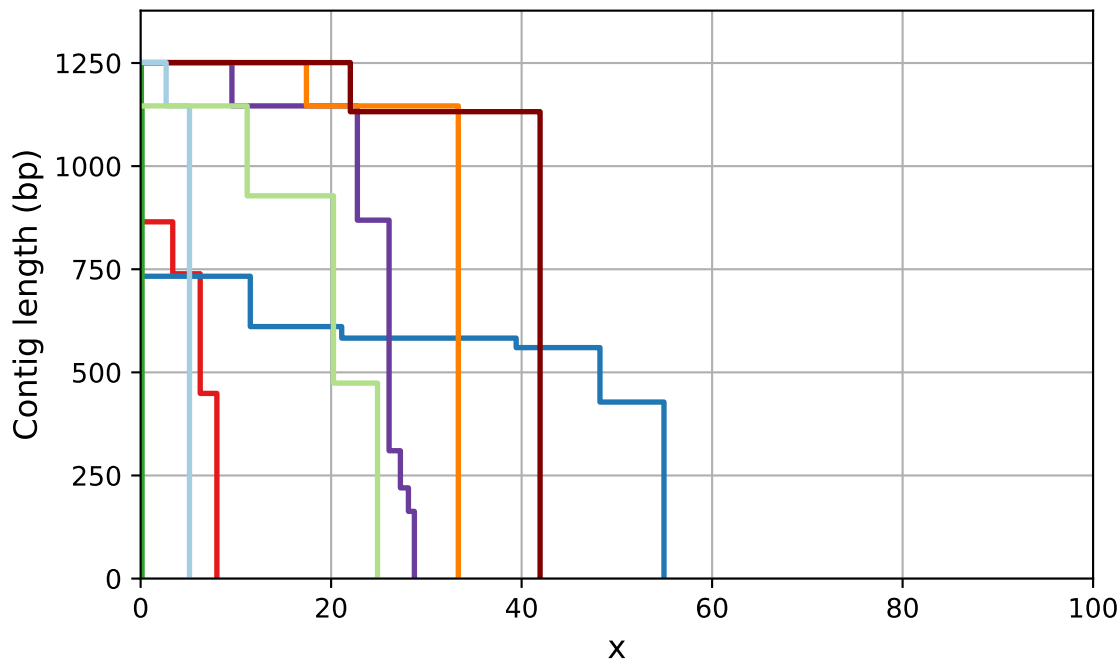
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

