

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	4	4	1	8	3	1	1	1
# contigs (>= 5000 bp)	2	4	1	5	3	1	1	1
# contigs (>= 10000 bp)	2	4	1	5	3	1	1	1
# contigs (>= 25000 bp)	2	2	1	2	3	1	1	0
# contigs (>= 50000 bp)	2	0	1	1	2	1	0	0
Total length (>= 1000 bp)	154710	87393	3665852	194470	208419	50405	44893	13545
Total length (>= 5000 bp)	152562	87393	3665852	189335	208419	50405	44893	13545
Total length (>= 10000 bp)	152562	87393	3665852	189335	208419	50405	44893	13545
Total length (>= 25000 bp)	152562	50418	3665852	134542	208419	50405	44893	0
Total length (>= 50000 bp)	152562	0	3665852	90815	182892	50405	0	0
# contigs	8	4	1	9	3	1	1	1
Largest contig	76281	25209	3665852	90815	91446	50405	44893	13545
Total length	157464	87393	3665852	195027	208419	50405	44893	13545
Reference length	6799	6799	6799	6799	6799	6799	6799	6799
GC (%)	53.15	52.29	55.11	53.32	53.58	52.84	52.28	56.94
Reference GC (%)	58.27	58.27	58.27	58.27	58.27	58.27	58.27	58.27
N50	76281	25209	3665852	43727	91446	50405	44893	13545
NG50	76281	25209	3665852	90815	91446	50405	44893	13545
N75	76281	18927	3665852	24001	91446	50405	44893	13545
NG75	76281	25209	3665852	90815	91446	50405	44893	13545
L50	2	2	1	2	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	3	1	3	2	1	1	1
LG75	1	1	1	1	1	1	1	1
# misassemblies	2	0	0	0	0	0	0	0
# misassembled contigs	2	0	0	0	0	0	0	0
Misassembled contigs length	2148	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	0	0	0	0	0	0
# unaligned contigs	0 + 2 part	0 + 4 part	0 + 1 part	0 + 5 part	0 + 3 part	0 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	148890	74185	3659053	179273	188022	43606	38159	6746
Genome fraction (%)	58.994	99.824	100.000	100.000	100.000	100.000	99.941	100.000
Duplication ratio	2.138	1.946	1.000	2.317	3.000	1.000	0.991	1.000
# 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	648.22	0.00	0.00	970.73	0.00	0.00	117.73	0.00
# indels per 100 kbp	0.00	0.00	0.00	58.83	0.00	0.00	14.72	0.00
Largest alignment	981	4157	6799	6738	6799	6799	6734	6799
Total aligned length	8482	13208	6799	15313	20397	6799	6734	6799
NA50	-	-	-	-	-	-	-	6799
NGA50	943	4157	6799	6738	6799	6799	6734	6799
NGA75	855	3791	6799	6738	6799	6799	6734	6799
LA50	-	-	-	-	-	-	-	1
LGA50	4	1	1	1	1	1	1	1
LGA75	6	2	1	1	1	1	1	1

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

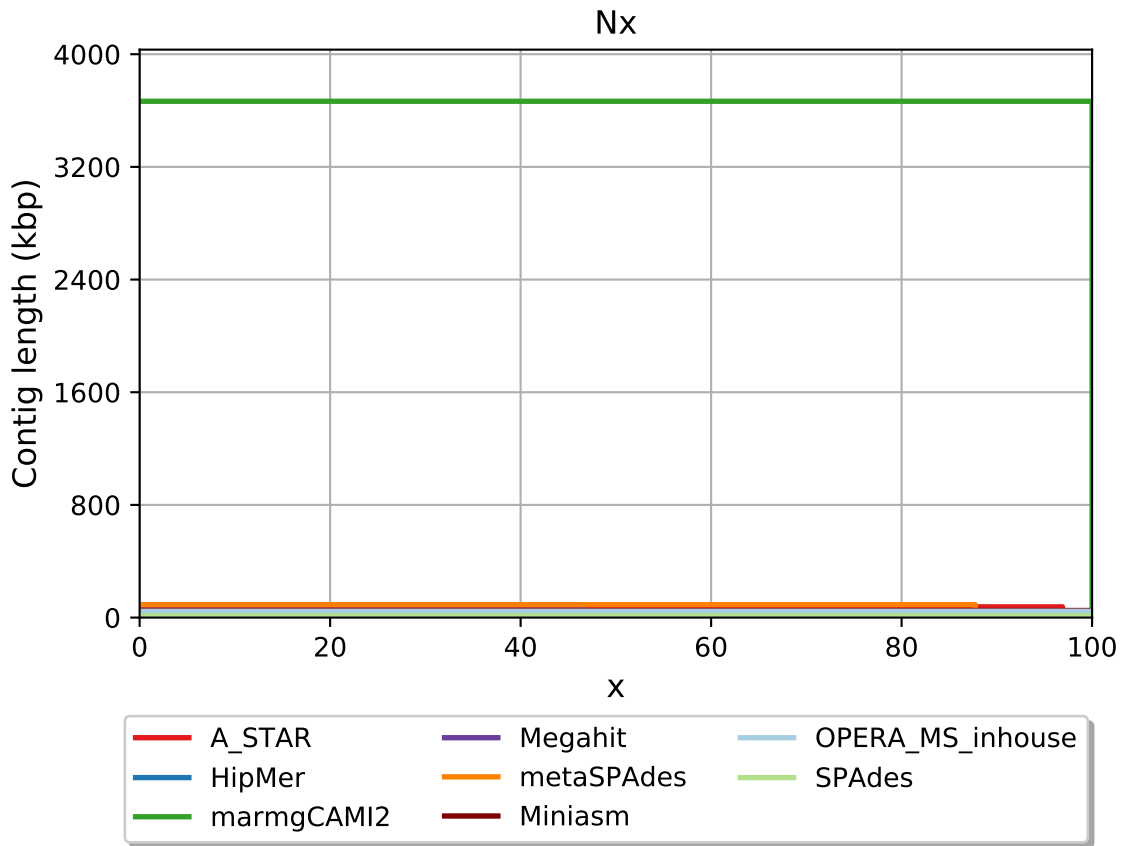
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	2	0	0	0	0	0	0	0
# contig misassemblies	2	0	0	0	0	0	0	0
# c. relocations	2	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	2	0	0	0	0	0	0	0
Misassembled contigs length	2148	0	0	0	0	0	0	0
# possibly misassembled contigs	0	4	1	5	3	1	1	1
# possible misassemblies	0	4	2	6	6	2	2	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	0	0	0	0	0	0
# mismatches	26	0	0	66	0	0	8	0
# indels	0	0	0	4	0	0	1	0
# indels (<= 5 bp)	0	0	0	1	0	0	0	0
# indels (> 5 bp)	0	0	0	3	0	0	1	0
Indels length	0	0	0	81	0	0	61	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).

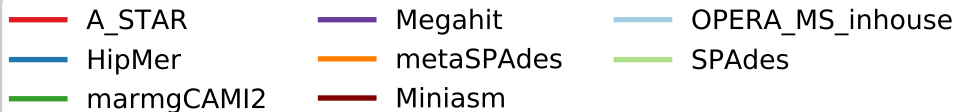
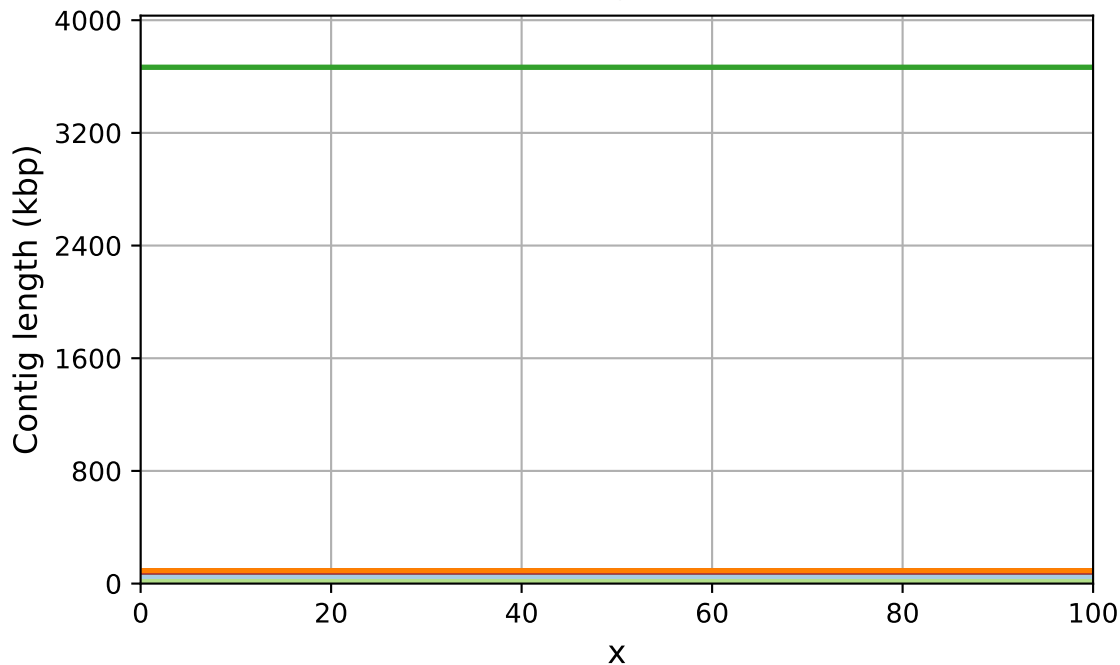
Unaligned report

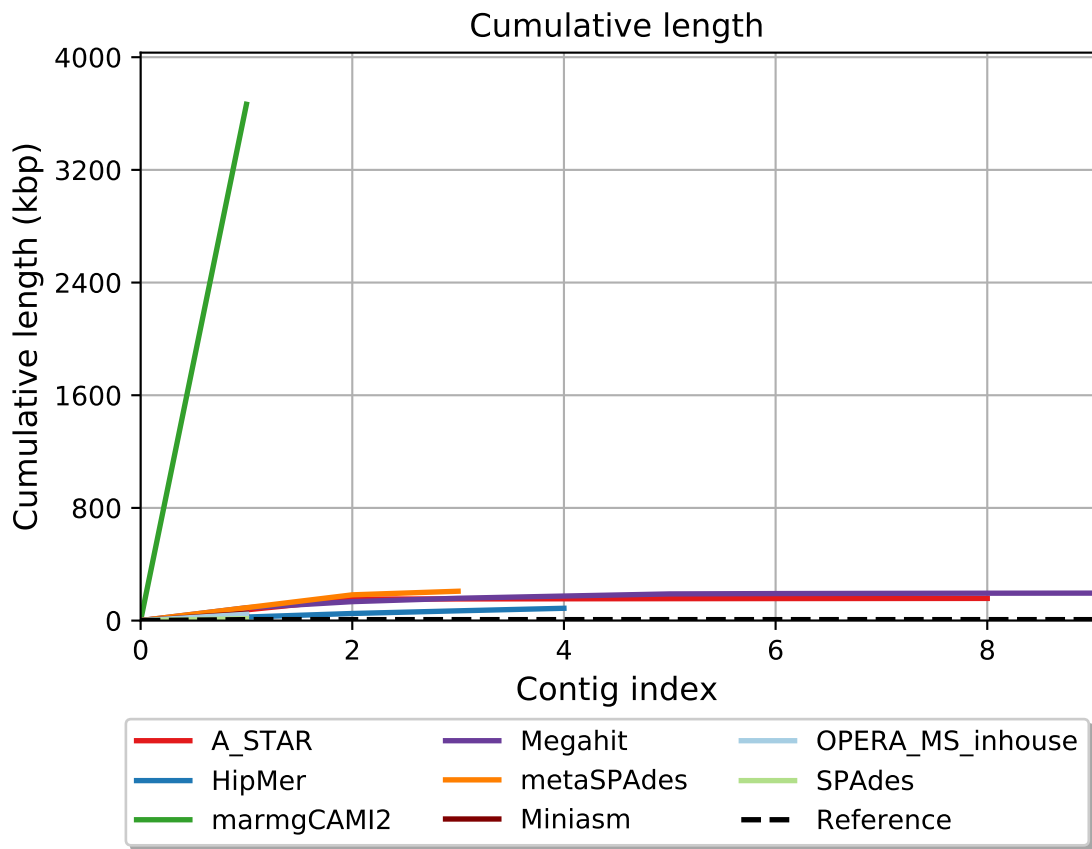
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	2	4	1	5	3	1	1	1
Partially unaligned length	148890	74185	3659053	179273	188022	43606	38159	6746
# N's	0	0	0	0	0	0	0	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).

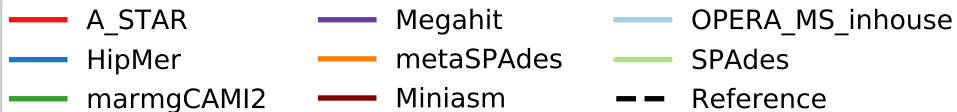
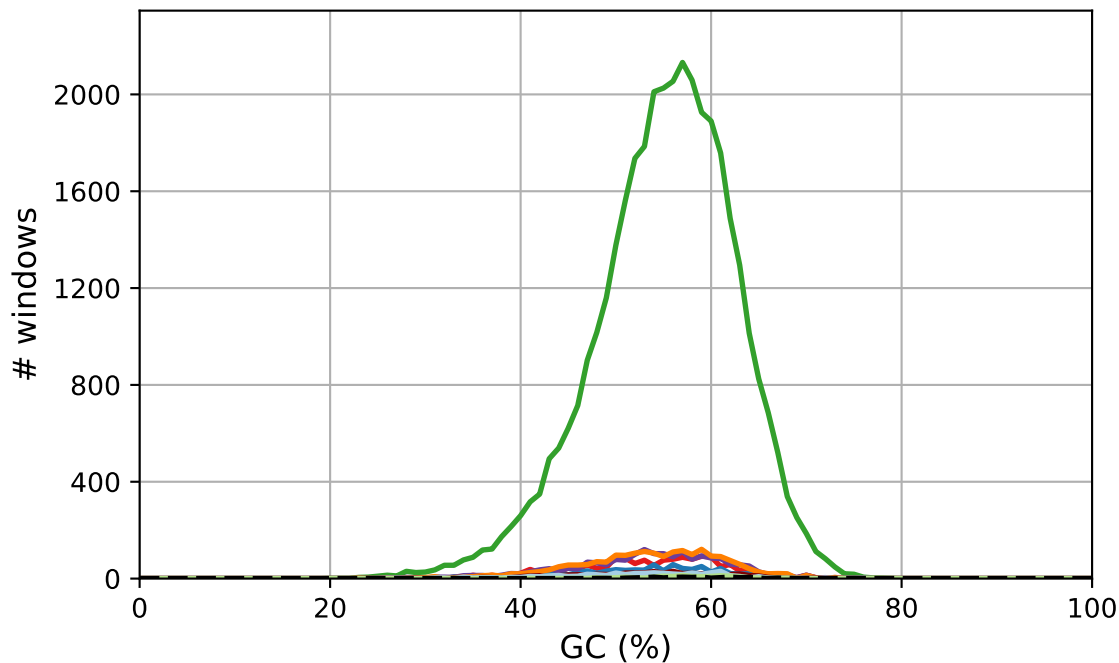


NGx

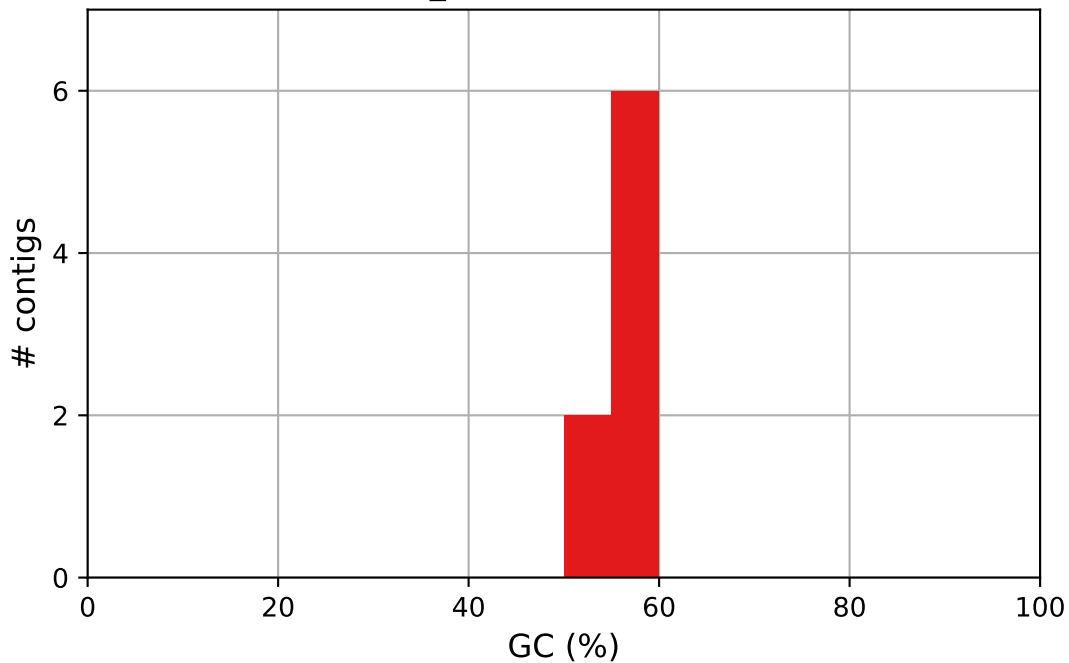




GC content

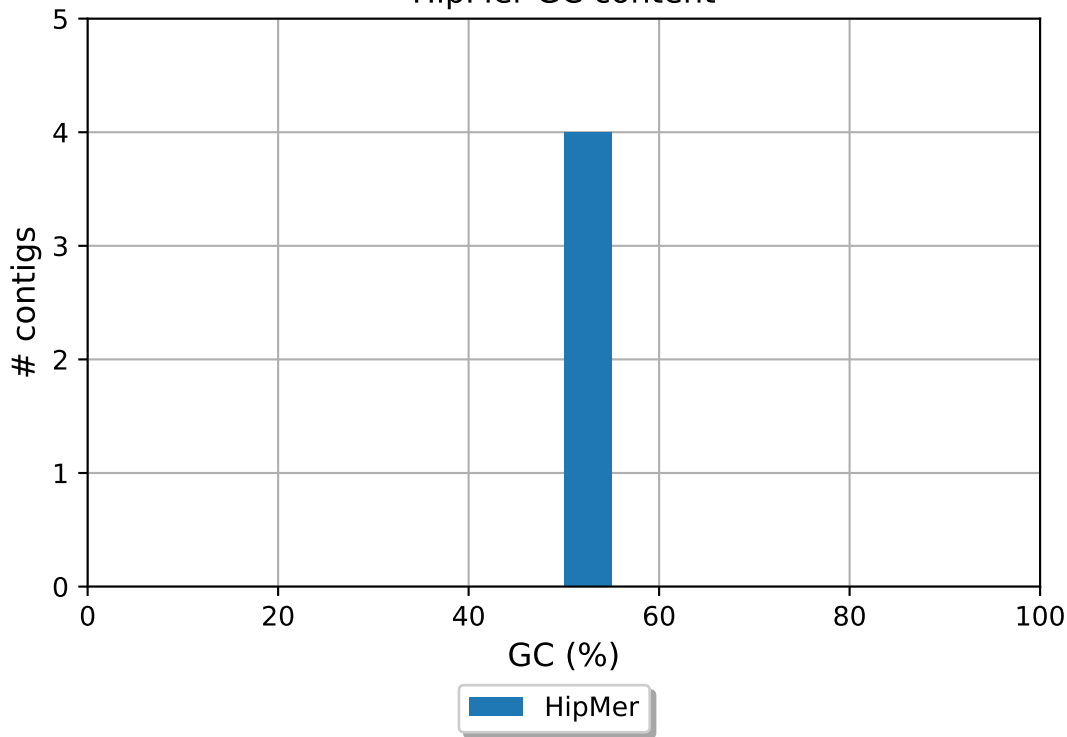


A_STAR GC content

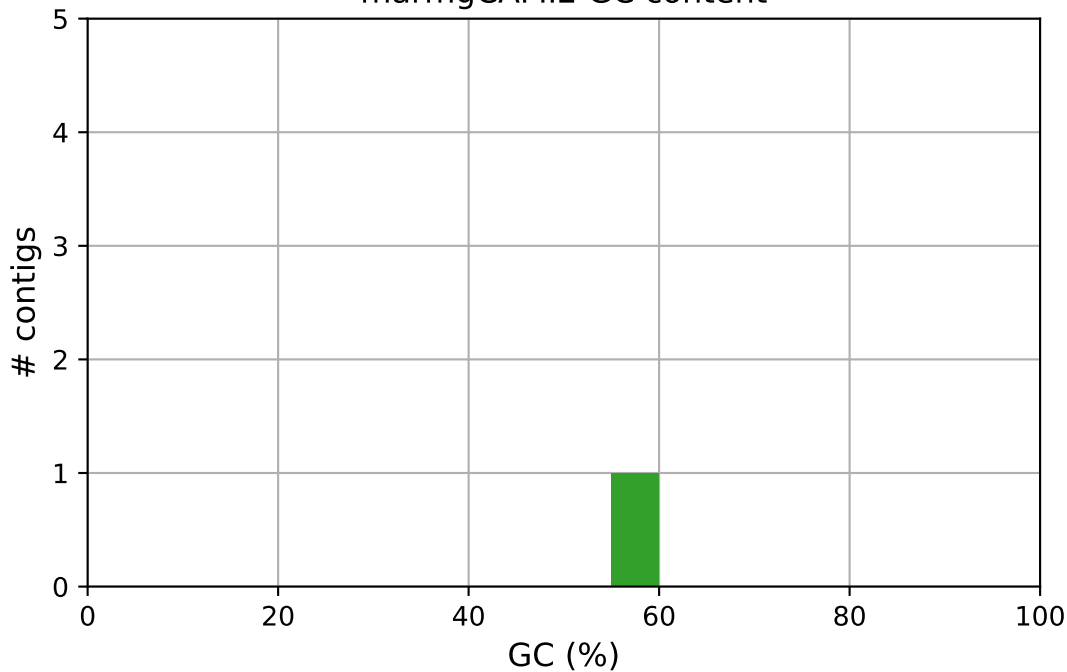


A_STAR

HipMer GC content

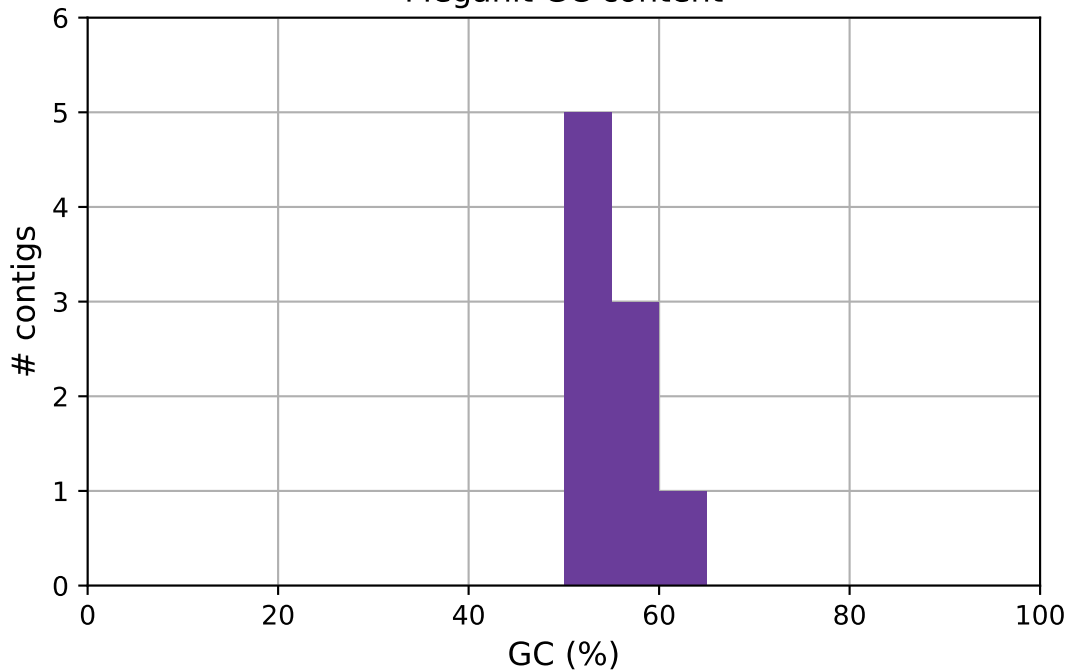


marmgCAMI2 GC content



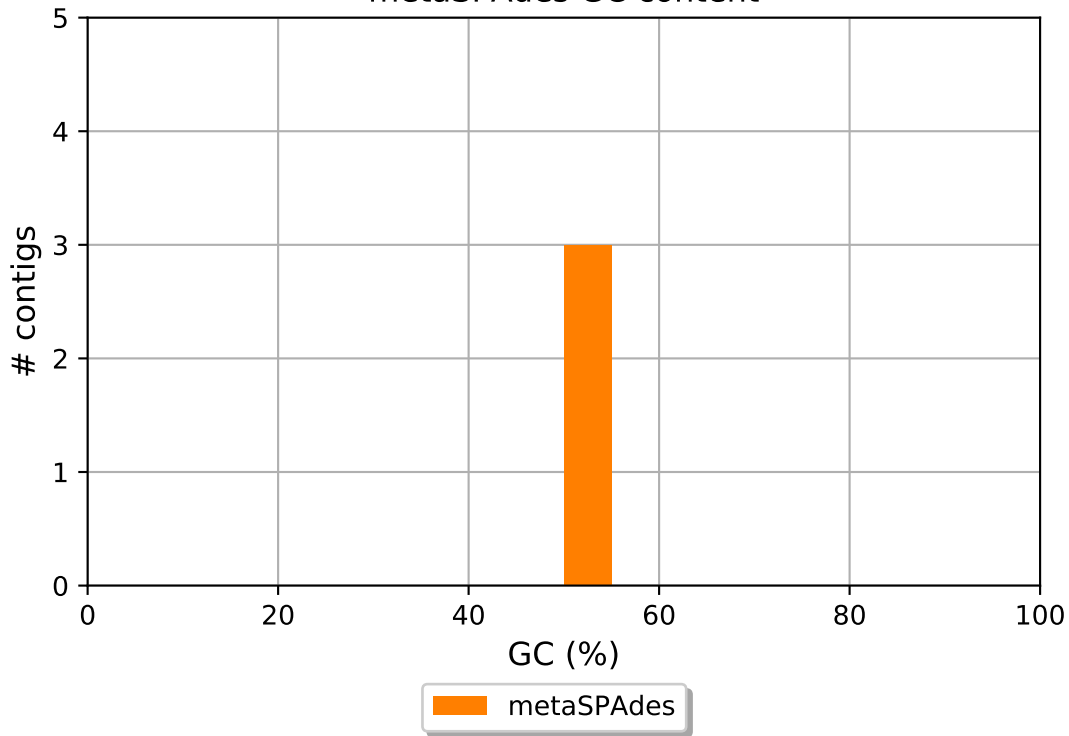
marmgCAMI2

Megahit GC content

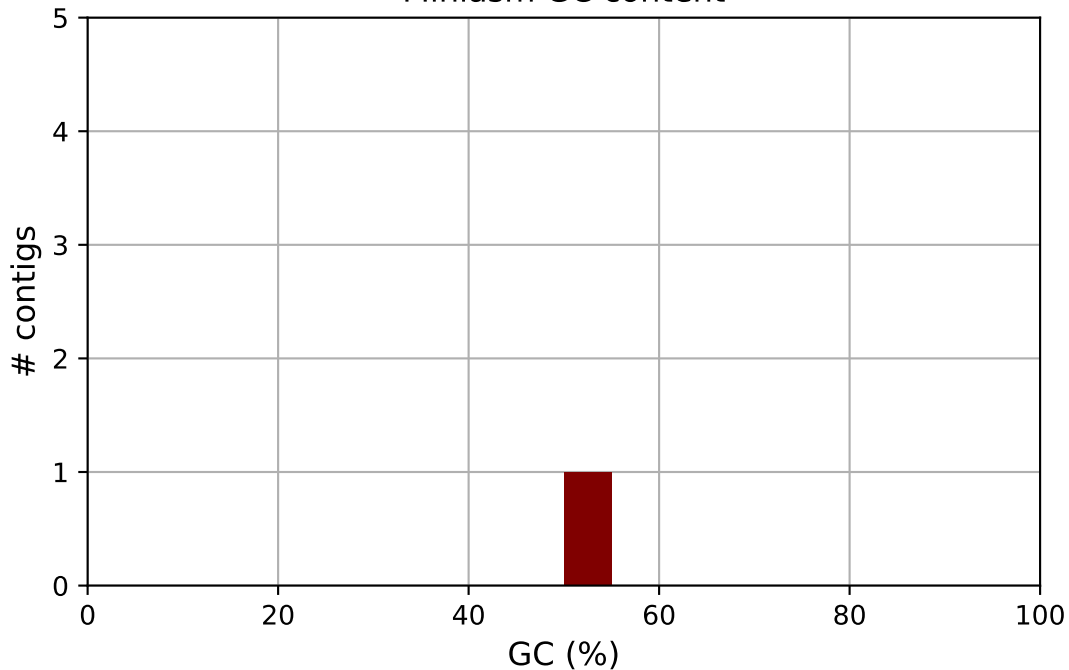


Megahit

metaSPAdes GC content

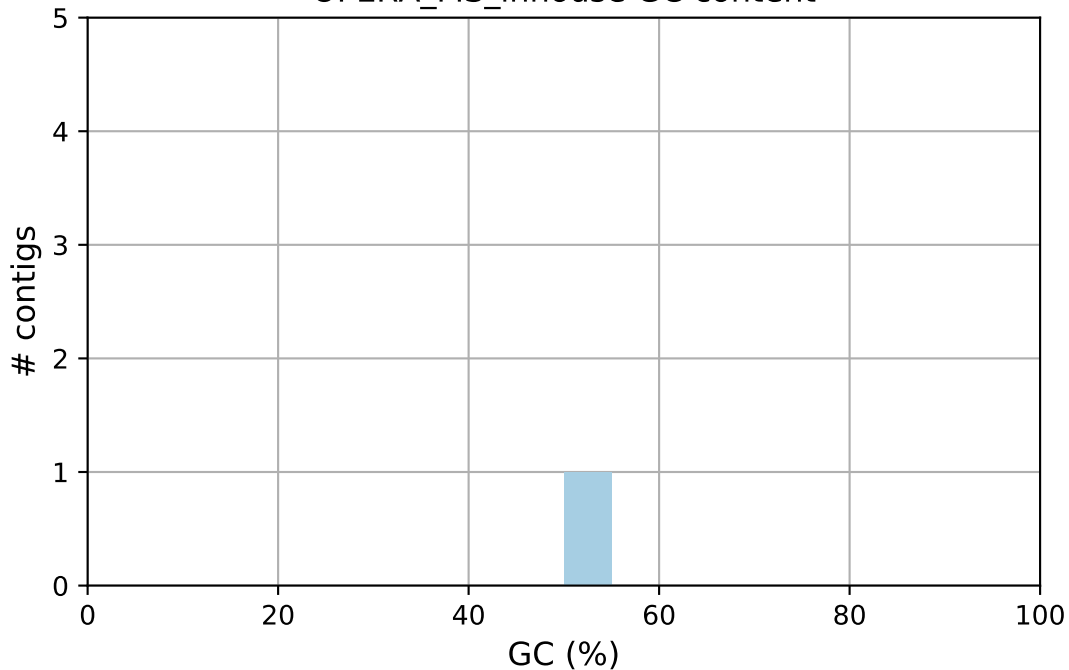


Miniasm GC content



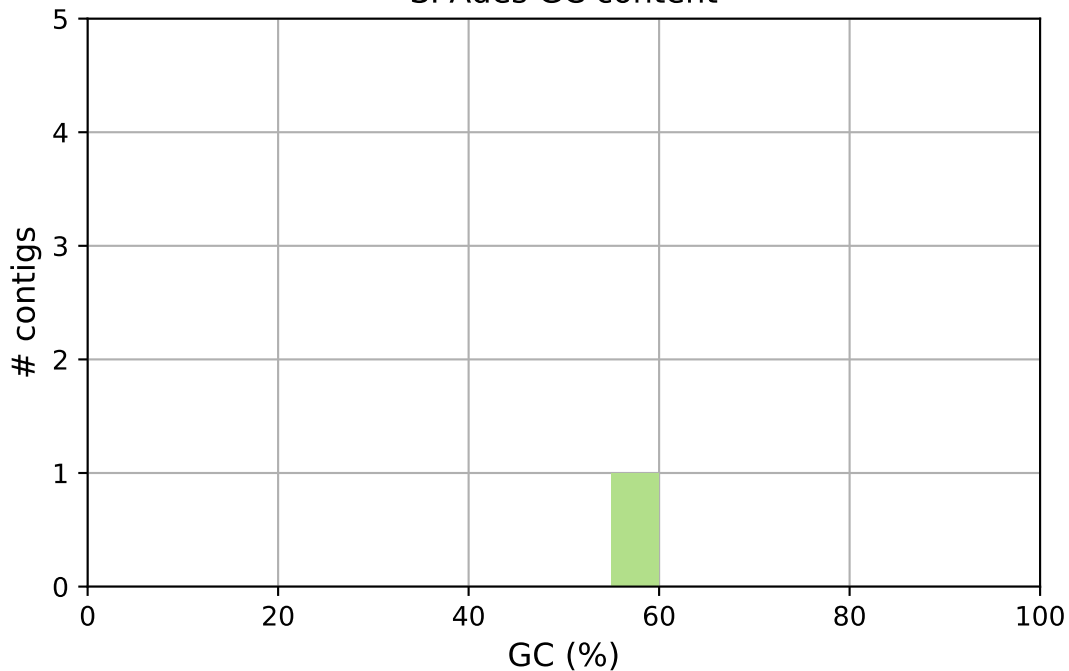
Miniasm

OPERA_MS_inhouse GC content



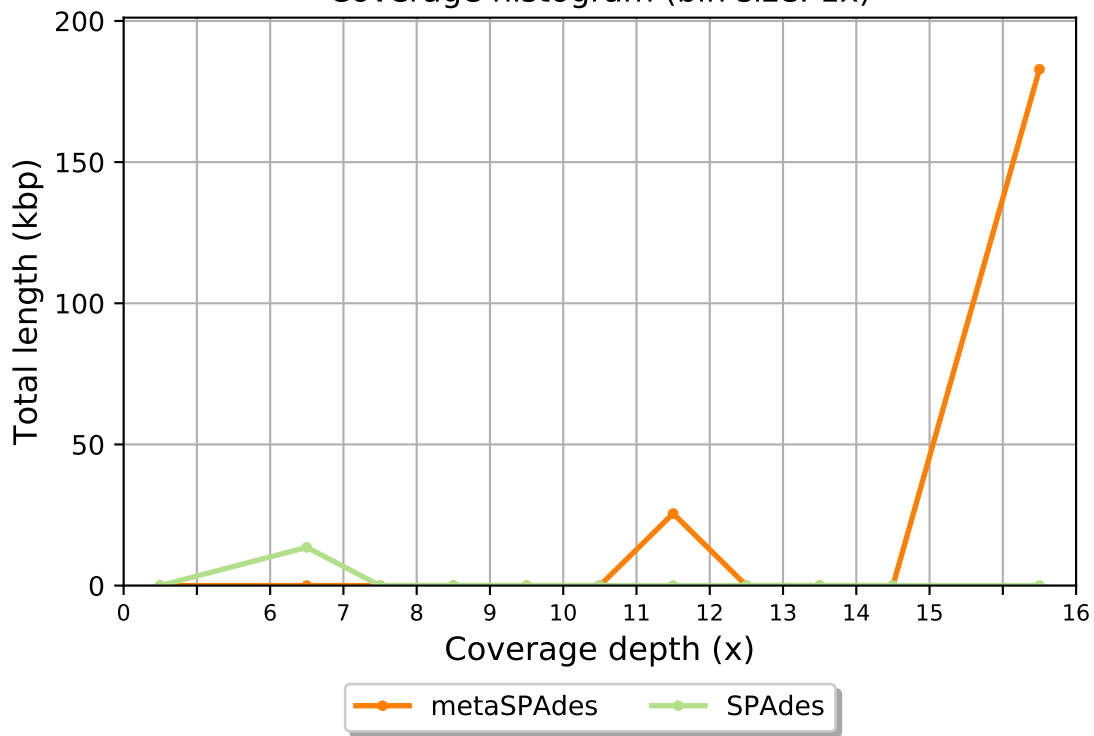
OPERA_MS_inhouse

SPAdes GC content

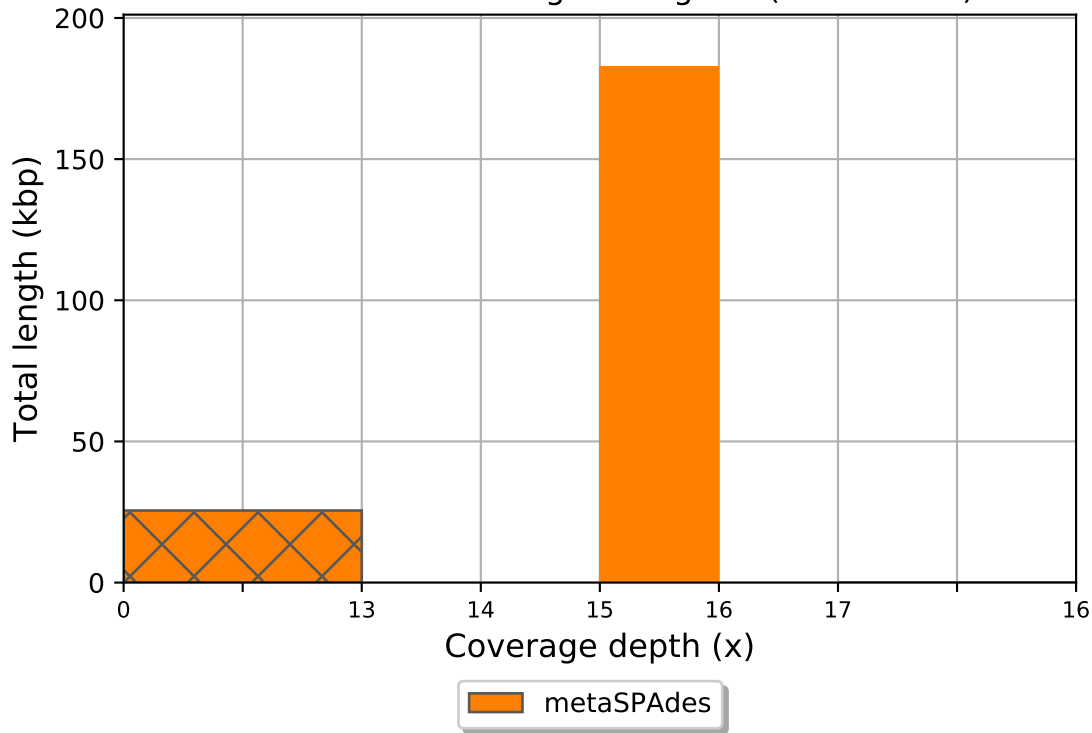


SPAdes

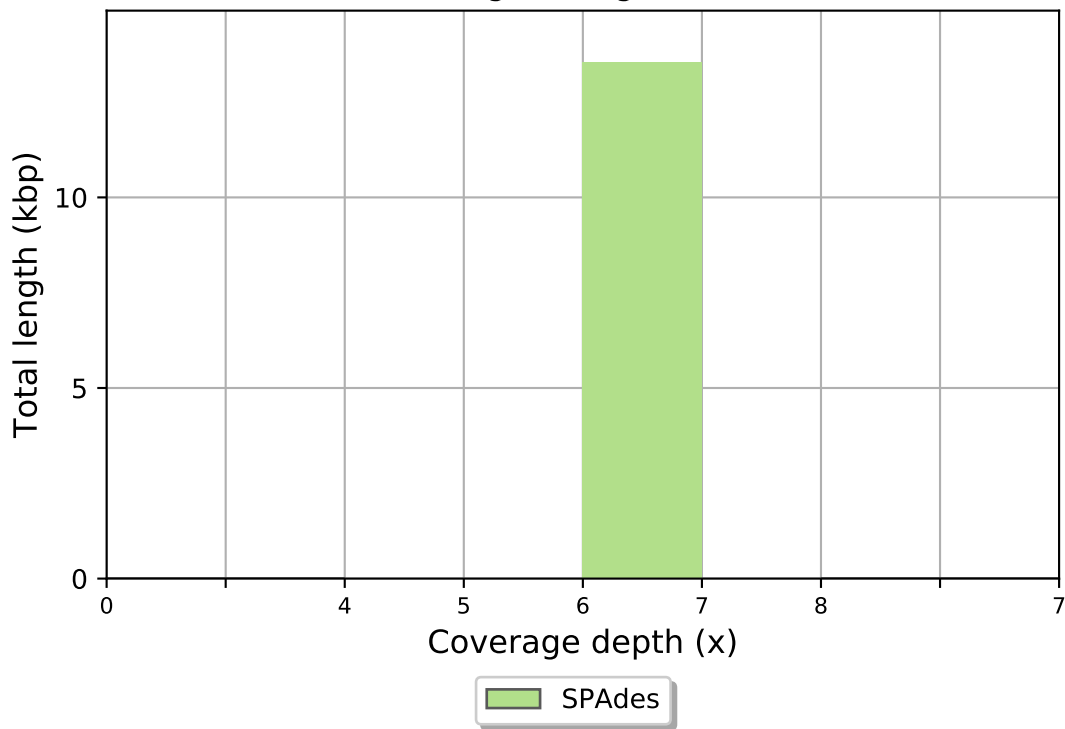
Coverage histogram (bin size: 1x)



metaSPAdes coverage histogram (bin size: 1x)



SPAdes coverage histogram (bin size: 1x)

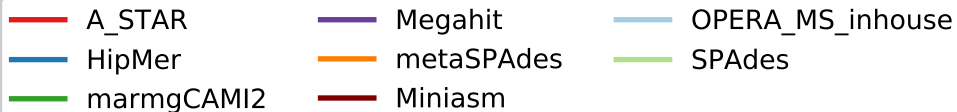
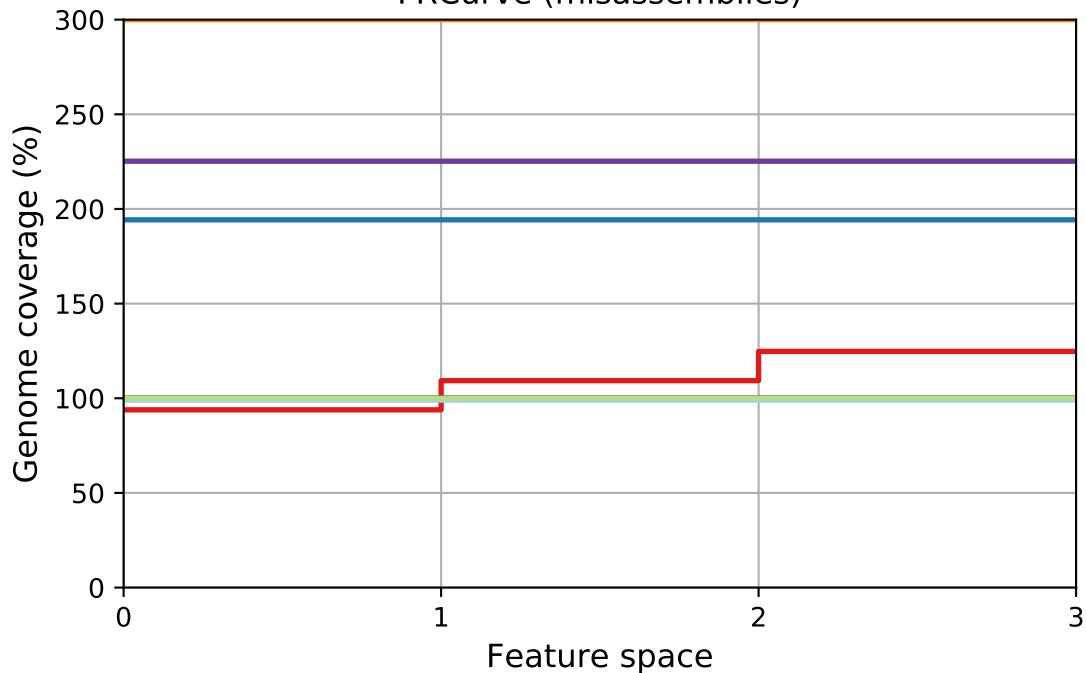


Misassemblies

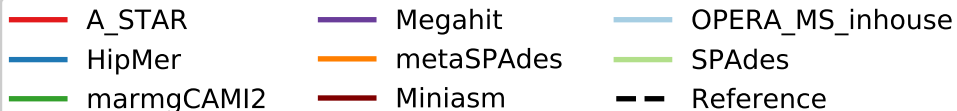
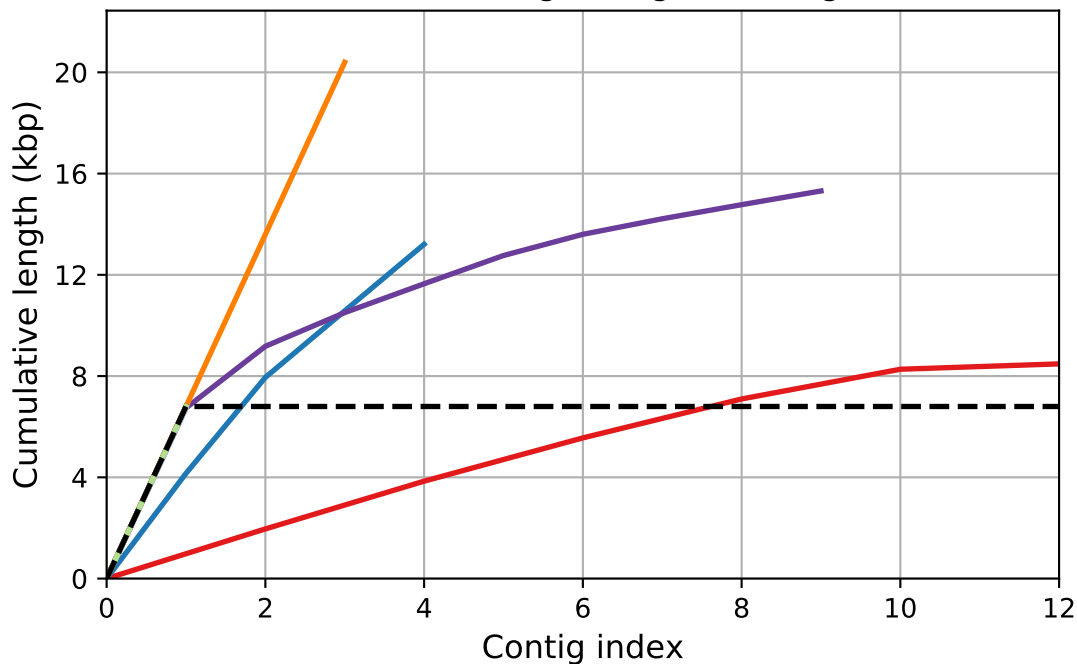


 # relocations

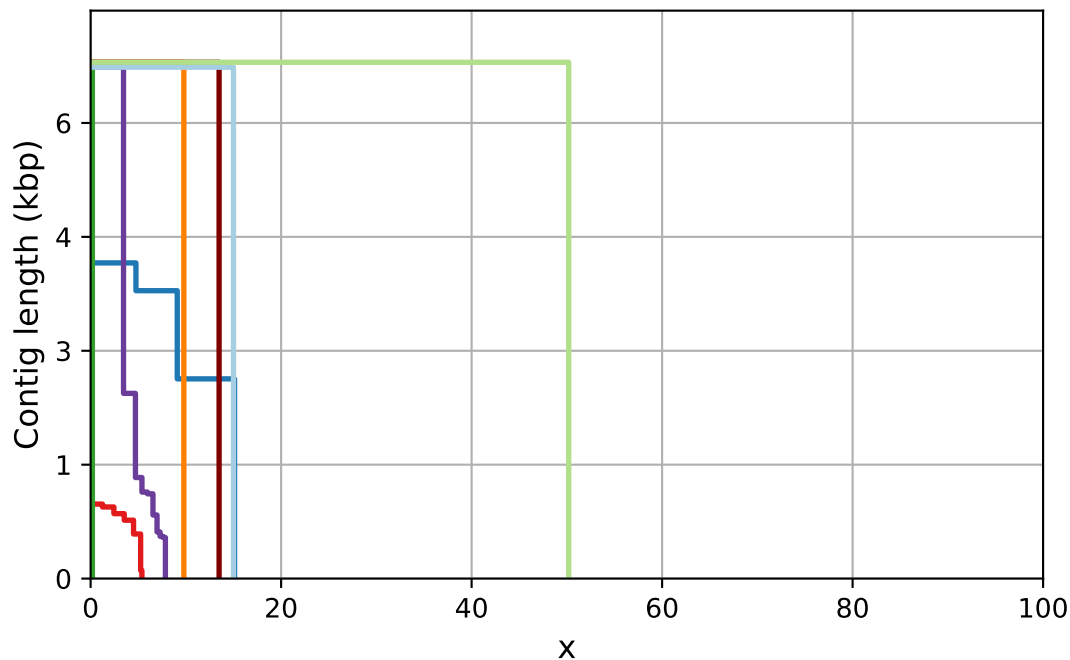
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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

NGAx

