

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	2	1	4	3	2	1	1
# contigs (>= 5000 bp)	1	2	1	2	3	2	1	1
# contigs (>= 10000 bp)	0	2	1	2	3	2	1	0
# contigs (>= 25000 bp)	0	2	1	1	1	2	1	0
# contigs (>= 50000 bp)	0	2	1	1	1	1	1	0
Total length (>= 1000 bp)	9419	847780	3389983	225712	143444	327453	190198	5532
Total length (>= 5000 bp)	7134	847780	3389983	220592	143444	327453	190198	5532
Total length (>= 10000 bp)	0	847780	3389983	220592	143444	327453	190198	0
Total length (>= 25000 bp)	0	847780	3389983	198036	113468	327453	190198	0
Total length (>= 50000 bp)	0	847780	3389983	198036	113468	280460	190198	0
# contigs	2	2	1	4	3	2	1	1
Largest contig	7134	747964	3389983	198036	113468	280460	190198	5532
Total length	9419	847780	3389983	225712	143444	327453	190198	5532
Reference length	510	510	510	510	510	510	510	510
GC (%)	41.71	37.34	37.29	37.73	38.22	37.87	37.74	39.95
Reference GC (%)	58.63	58.63	58.63	58.63	58.63	58.63	58.63	58.63
N50	7134	747964	3389983	198036	113468	280460	190198	5532
NG50	7134	747964	3389983	198036	113468	280460	190198	5532
N75	7134	747964	3389983	198036	113468	280460	190198	5532
NG75	7134	747964	3389983	198036	113468	280460	190198	5532
L50	1	1	1	1	1	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	1	1	1	1	1	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	0	0	0	0	0	0	0
# unaligned contigs	0 + 2 part	0 + 2 part	0 + 1 part	0 + 4 part	0 + 3 part	0 + 2 part	0 + 1 part	0 + 1 part
Unaligned length	6423	846730	3389473	224068	141914	326712	189687	5022
Genome fraction (%)	94.706	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	6.203	2.059	1.000	3.224	3.000	1.453	1.002	1.000
# N's per 100 kbp	21552.18	3.54	0.00	0.00	0.00	0.00	0.53	0.00
# mismatches per 100 kbp	1656.31	0.00	0.00	588.24	0.00	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	483	510	510	510	510	510	510	510
Total aligned length	966	1020	510	1644	1530	741	510	510
NGA50	483	510	510	510	510	510	510	510
NGA75	483	510	510	510	510	510	510	510
LGA50	1	1	1	1	1	1	1	1
LGA75	1	1	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

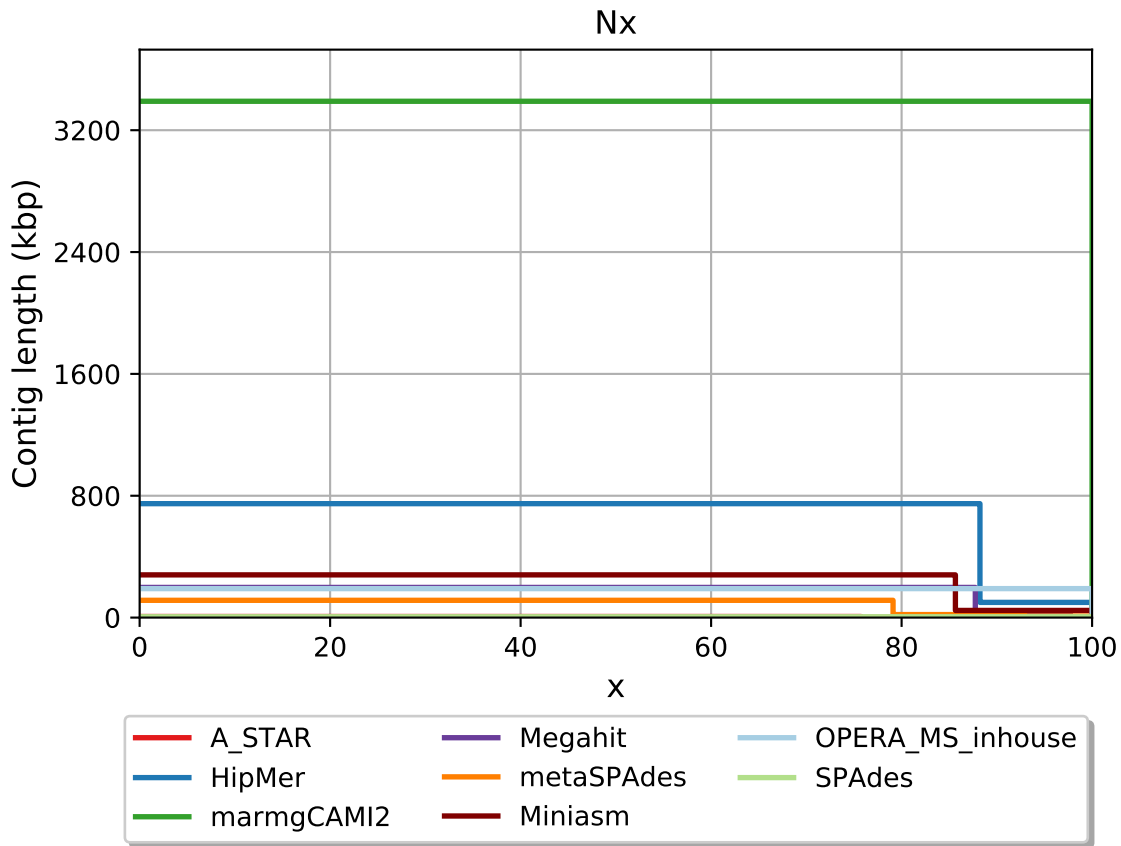
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	1	4	3	2	1	1
# possible misassemblies	4	4	2	6	6	4	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	0	0	0	0	0	0	0	0
# mismatches	8	0	0	3	0	0	0	0
# 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).

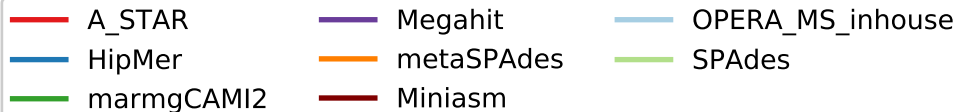
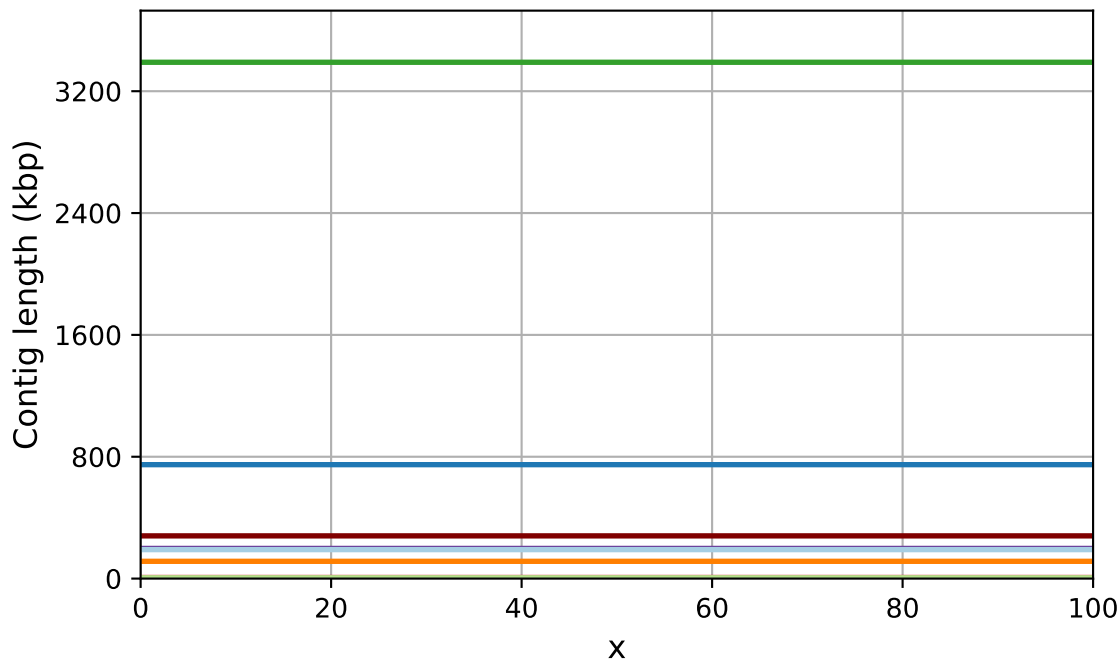
Unaligned report

	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	2	1	4	3	2	1	1
Partially unaligned length	6423	846730	3389473	224068	141914	326712	189687	5022
# N's	2030	30	0	0	0	0	1	0

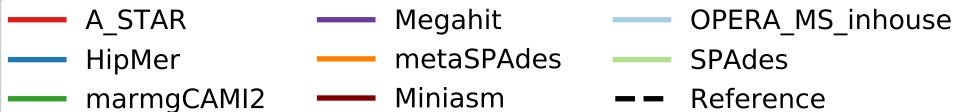
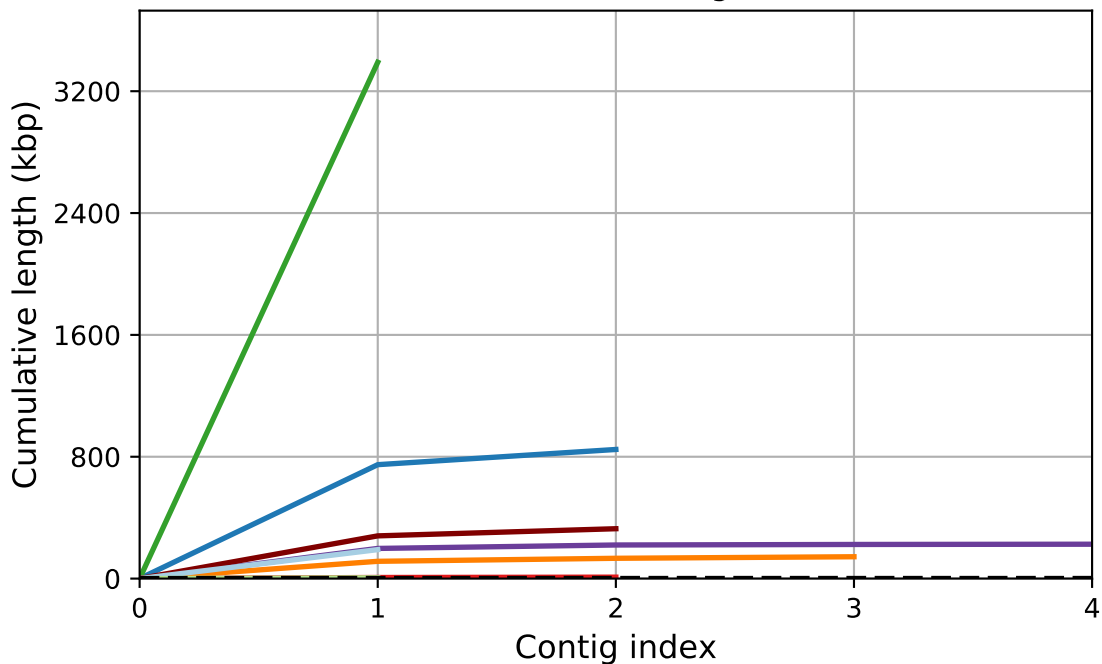
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



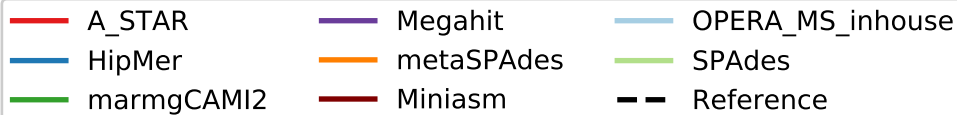
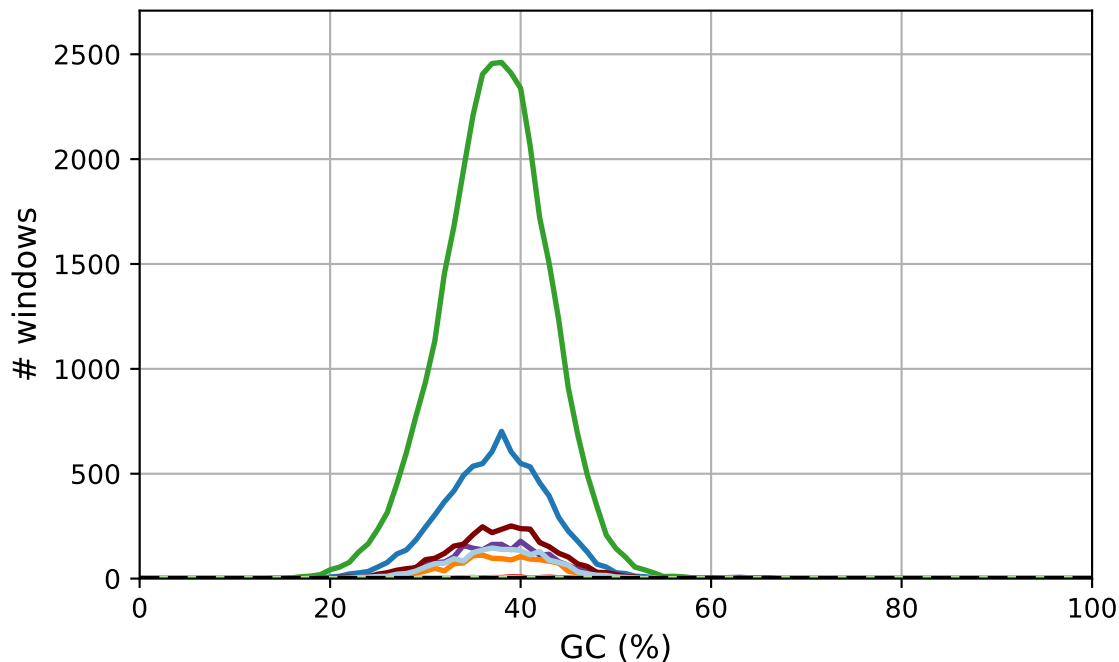
NGx



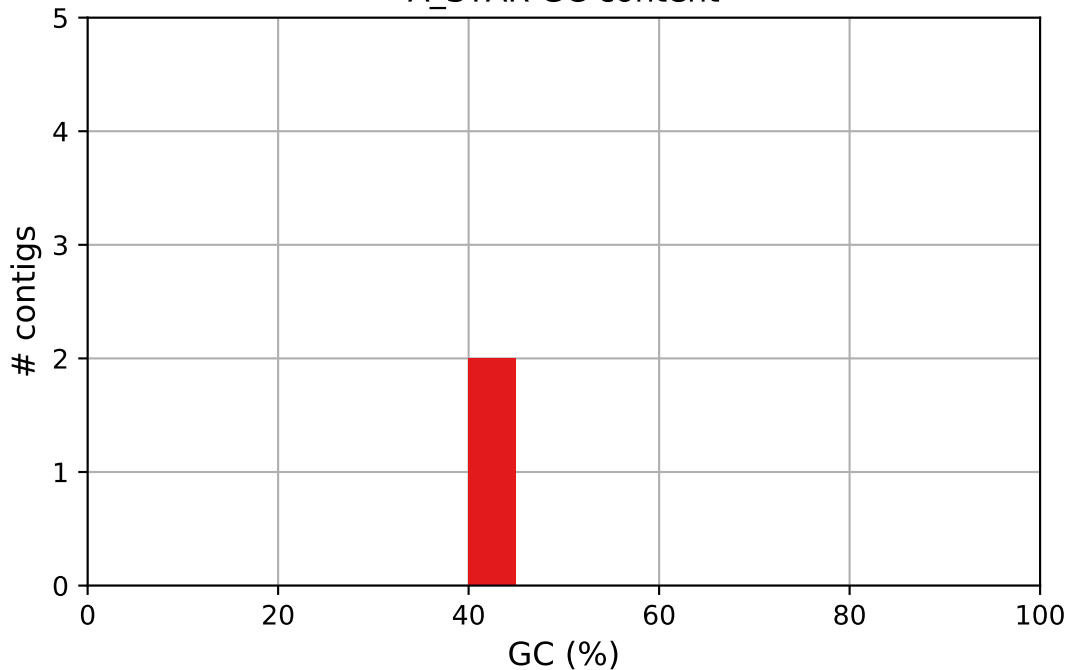
Cumulative length



GC content

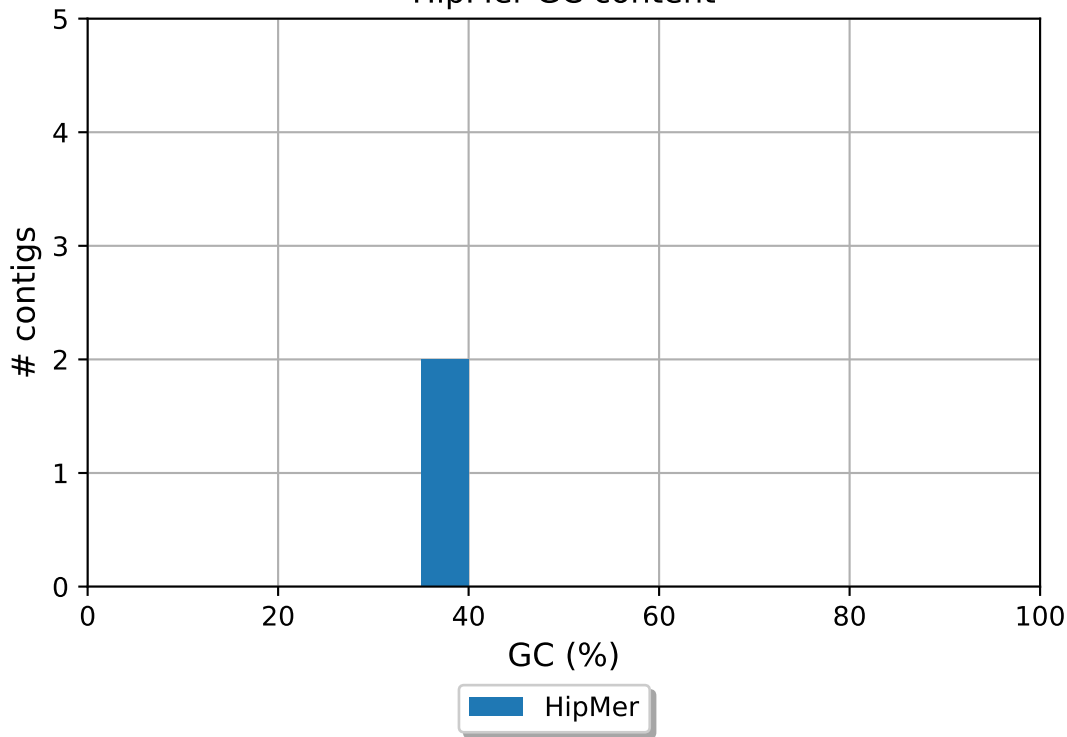


A_STAR GC content

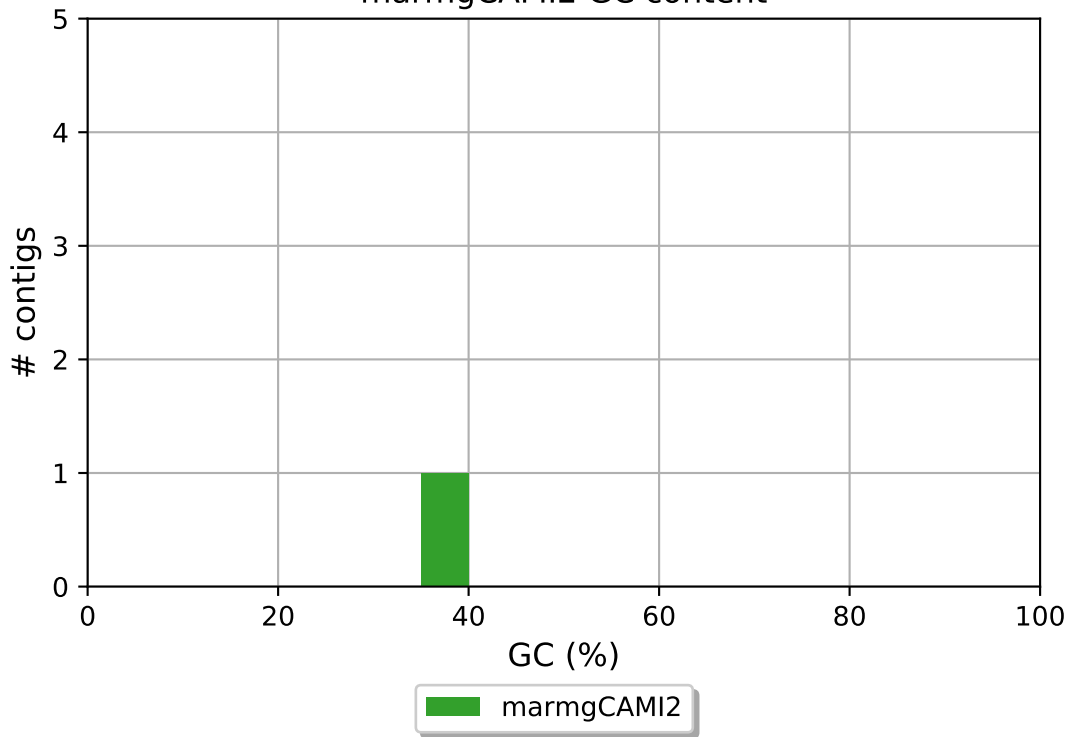


A_STAR

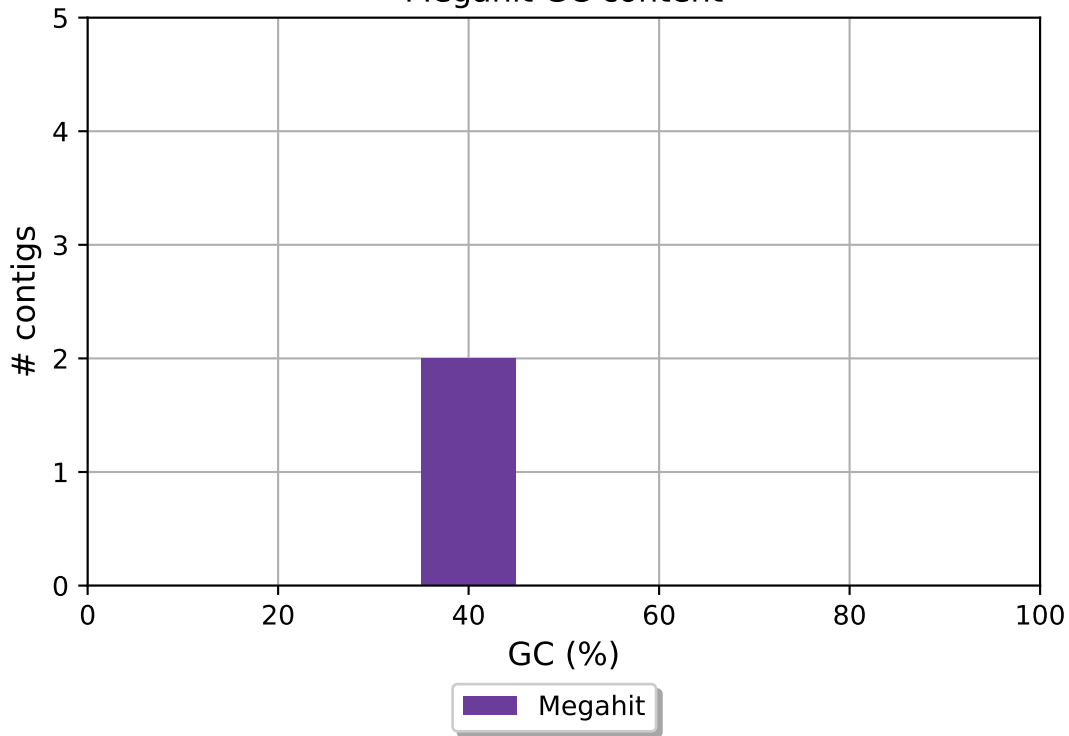
HipMer GC content



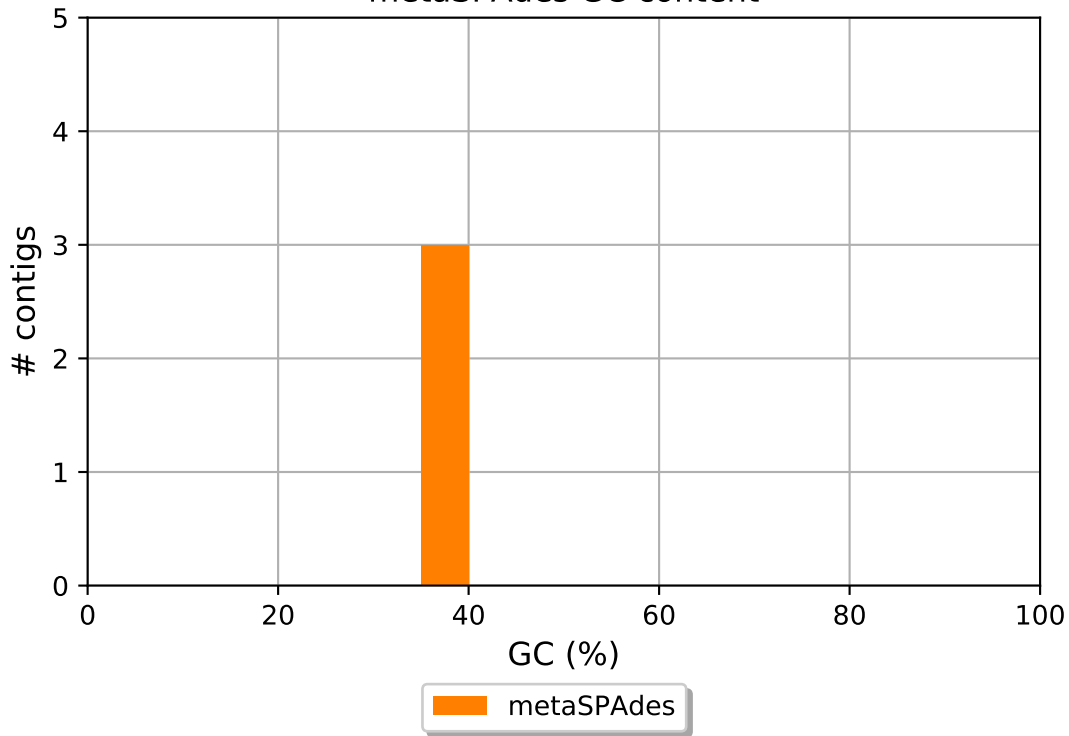
marmgCAMI2 GC content



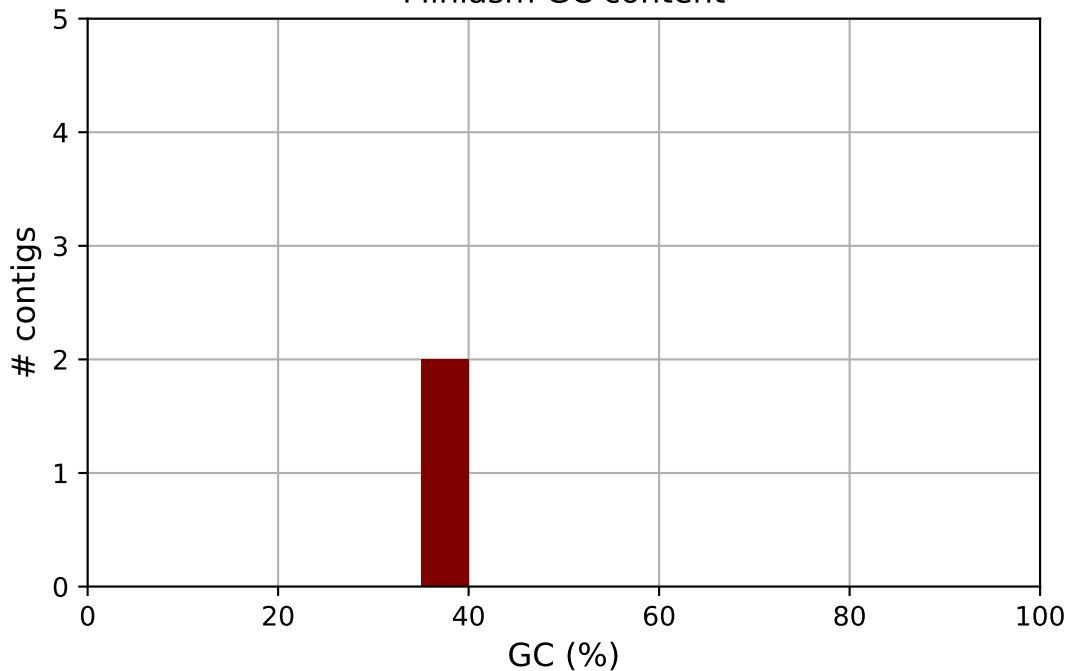
Megahit GC content



metaSPAdes GC content

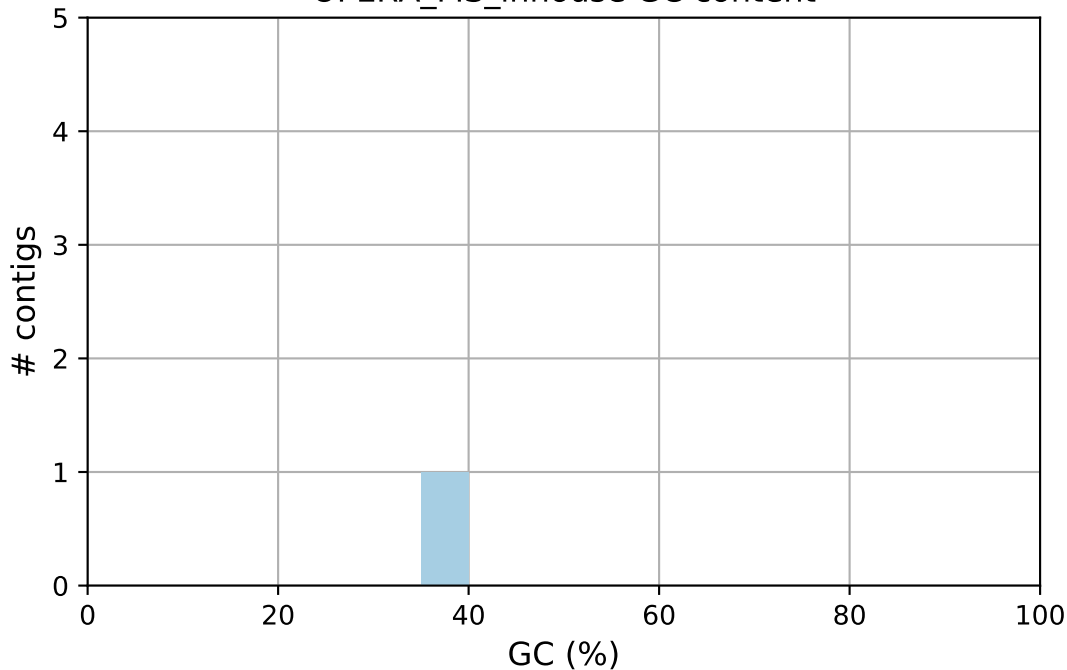


Miniasm GC content



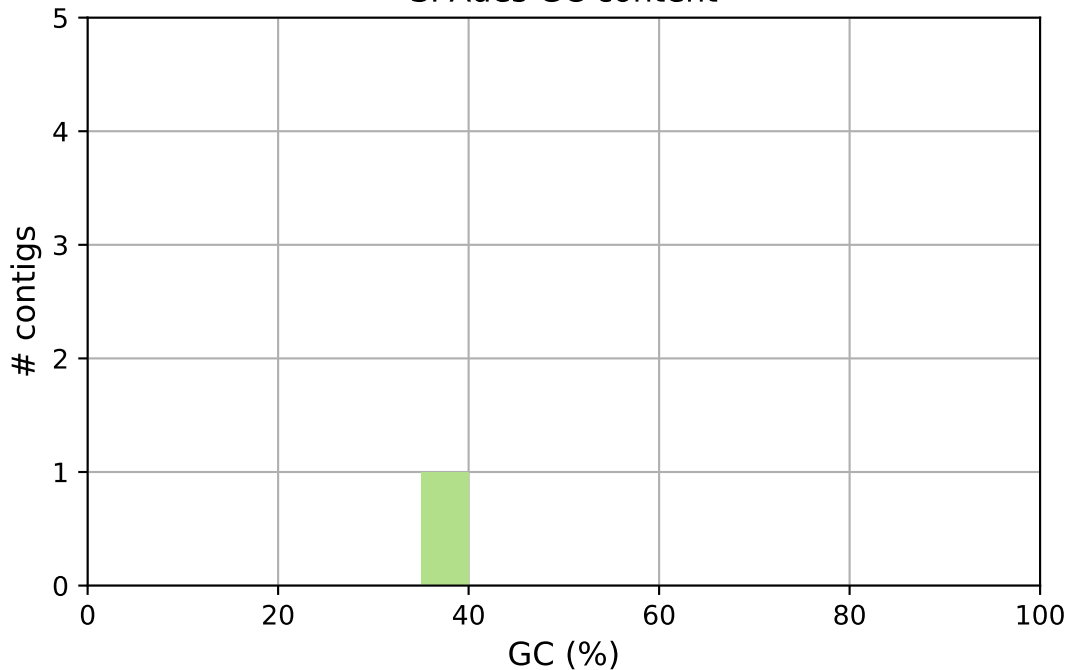
Miniasm

OPERA_MS_inhouse GC content



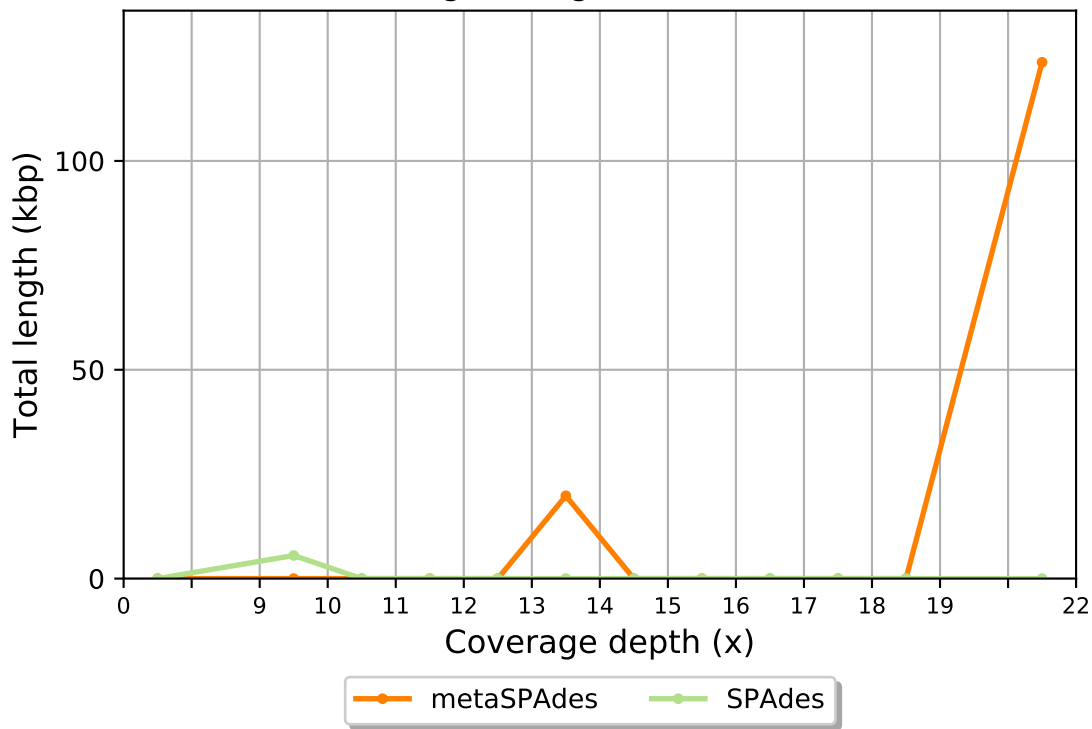
OPERA_MS_inhouse

SPAdes GC content

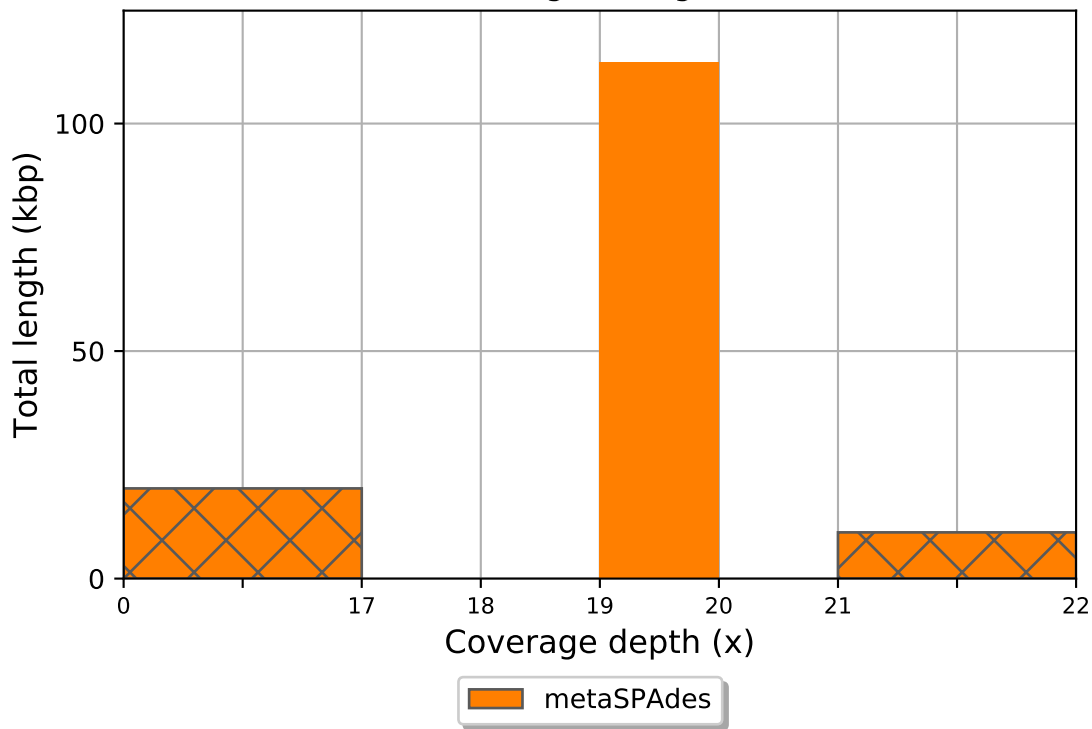


SPAdes

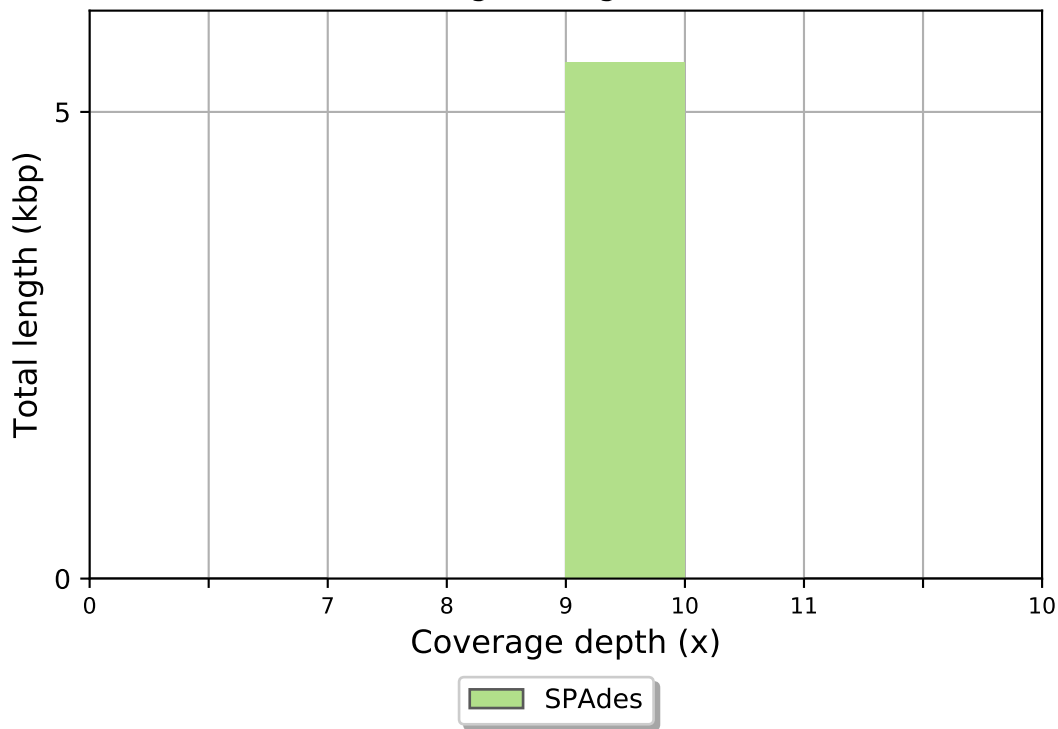
Coverage histogram (bin size: 1x)



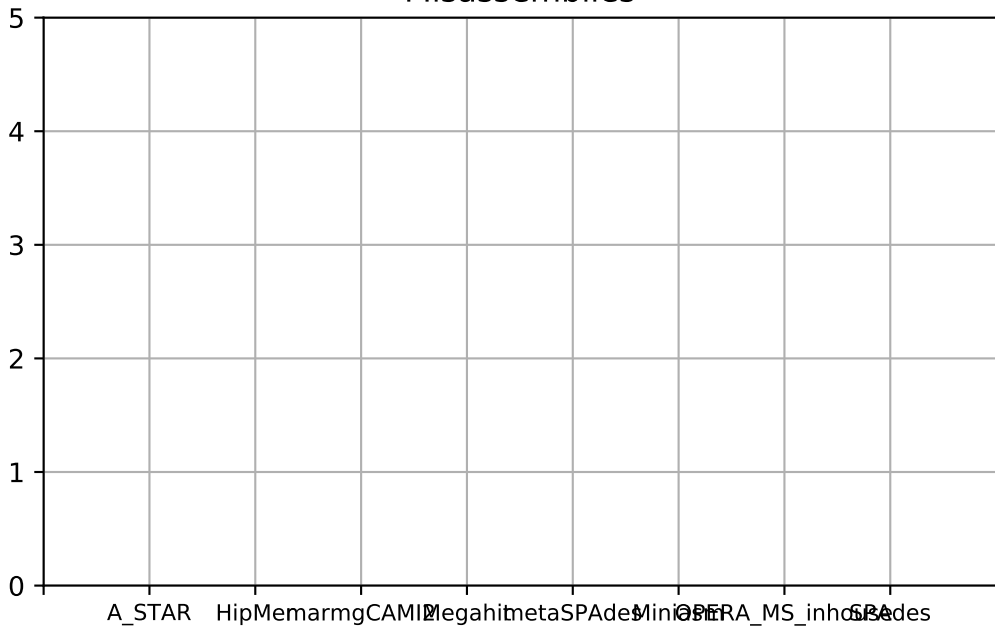
metaSPAdes coverage histogram (bin size: 1x)



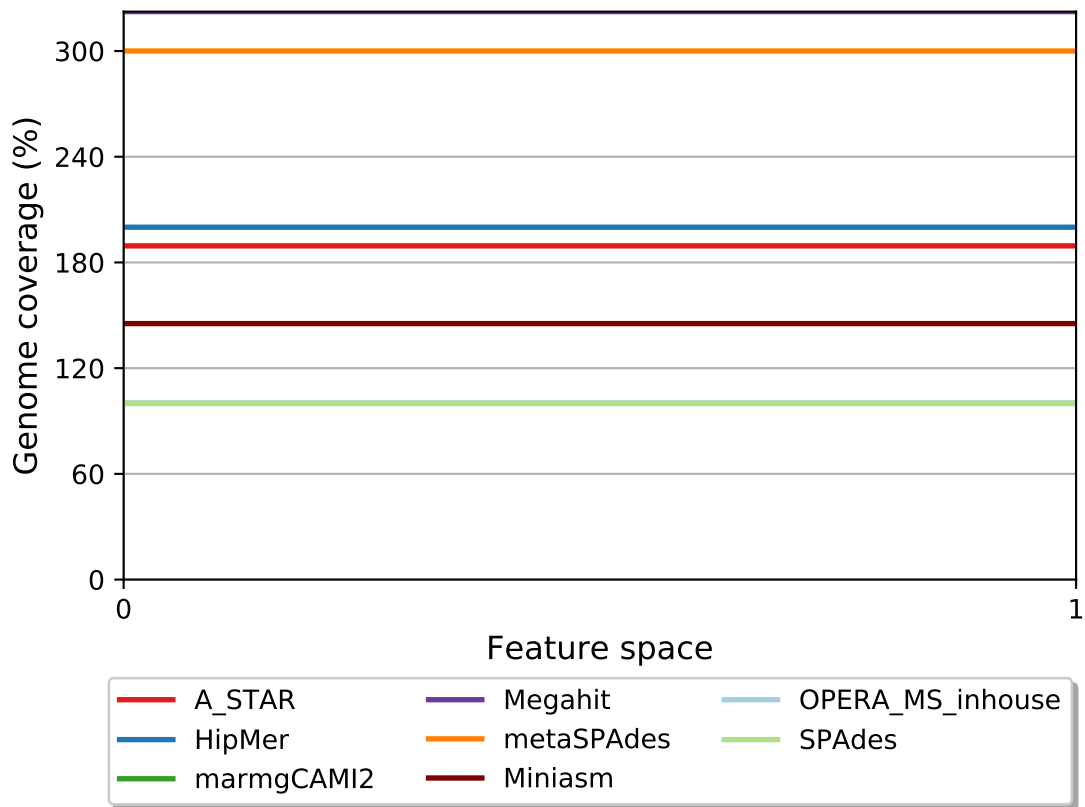
SPAdes coverage histogram (bin size: 1x)



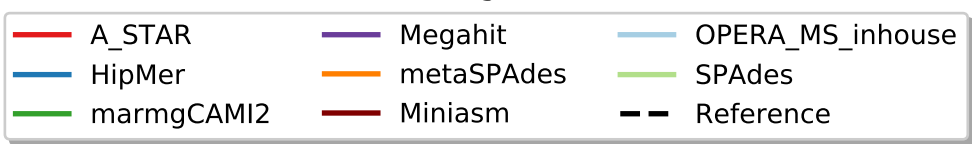
Misassemblies



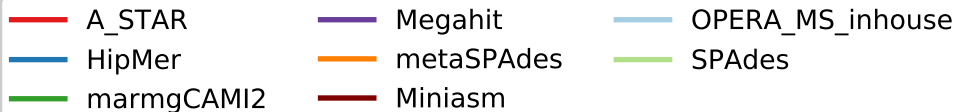
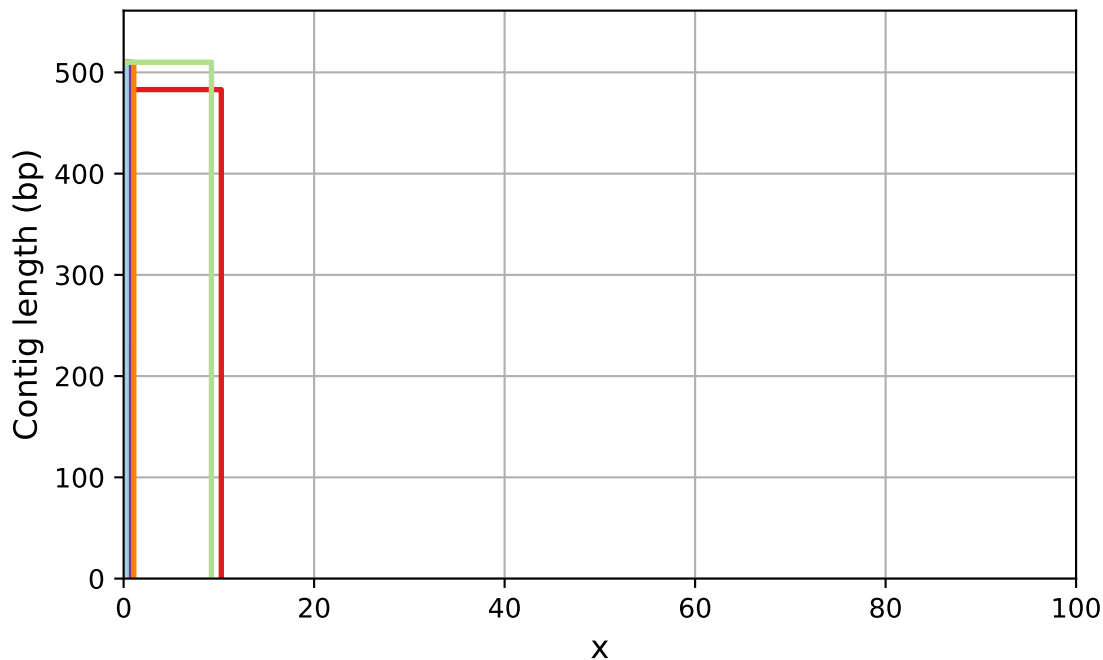
FRCurve (misassemblies)



Contig index	n=1 (dashed black)	n=2 (solid red)	n=3 (solid orange)	n=4 (solid purple)
0	0.00	0.00	0.00	0.00
1	0.50	0.50	0.50	0.50
2	0.50	0.75	0.75	0.75
3	0.50	0.75	1.00	1.00
4	0.50	0.75	1.00	1.125



NAx



NGAx

