

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	4	1	3	3	1	1	1
# contigs (>= 5000 bp)	0	4	1	3	3	1	1	1
# contigs (>= 10000 bp)	0	3	1	3	3	1	1	0
# contigs (>= 25000 bp)	0	3	1	2	3	1	1	0
# contigs (>= 50000 bp)	0	2	1	1	3	1	1	0
Total length (>= 1000 bp)	3720	191032	5132065	133016	235844	76823	65484	9063
Total length (>= 5000 bp)	0	191032	5132065	133016	235844	76823	65484	9063
Total length (>= 10000 bp)	0	185761	5132065	133016	235844	76823	65484	0
Total length (>= 25000 bp)	0	185761	5132065	109864	235844	76823	65484	0
Total length (>= 50000 bp)	0	137138	5132065	66378	235844	76823	65484	0
# contigs	2	4	1	3	3	1	1	1
Largest contig	1860	81572	5132065	66378	82233	76823	65484	9063
Total length	3720	191032	5132065	133016	235844	76823	65484	9063
Reference length	298	298	298	298	298	298	298	298
GC (%)	43.98	41.83	41.31	41.40	41.43	41.96	41.42	41.70
Reference GC (%)	33.56	33.56	33.56	33.56	33.56	33.56	33.56	33.56
N50	1860	55566	5132065	43486	82233	76823	65484	9063
NG50	1860	81572	5132065	66378	82233	76823	65484	9063
N75	1860	48623	5132065	43486	71378	76823	65484	9063
NG75	1860	81572	5132065	66378	82233	76823	65484	9063
L50	1	2	1	2	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	3	1	2	3	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 + 4 part	0 + 1 part	0 + 3 part	0 + 3 part	0 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	3124	190334	5131767	132122	234950	76525	65186	8765
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	2.000	2.342	1.000	3.000	3.000	1.000	1.000	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	0.00	0.00	0.00	0.00	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	298	180	298	298	298	298	298	298
Total aligned length	596	698	298	894	894	298	298	298
NGA50	298	180	298	298	298	298	298	298
NGA75	298	180	298	298	298	298	298	298
LGA50	1	1	1	1	1	1	1	1
LGA75	1	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	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	4	1	3	3	1	1	1
# possible misassemblies	2	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	0	0	0	0	0	0	0	0
# mismatches	0	0	0	0	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

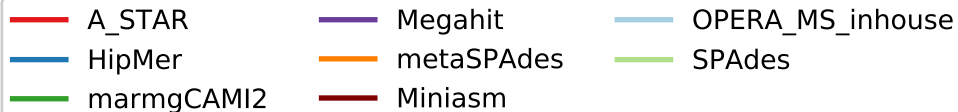
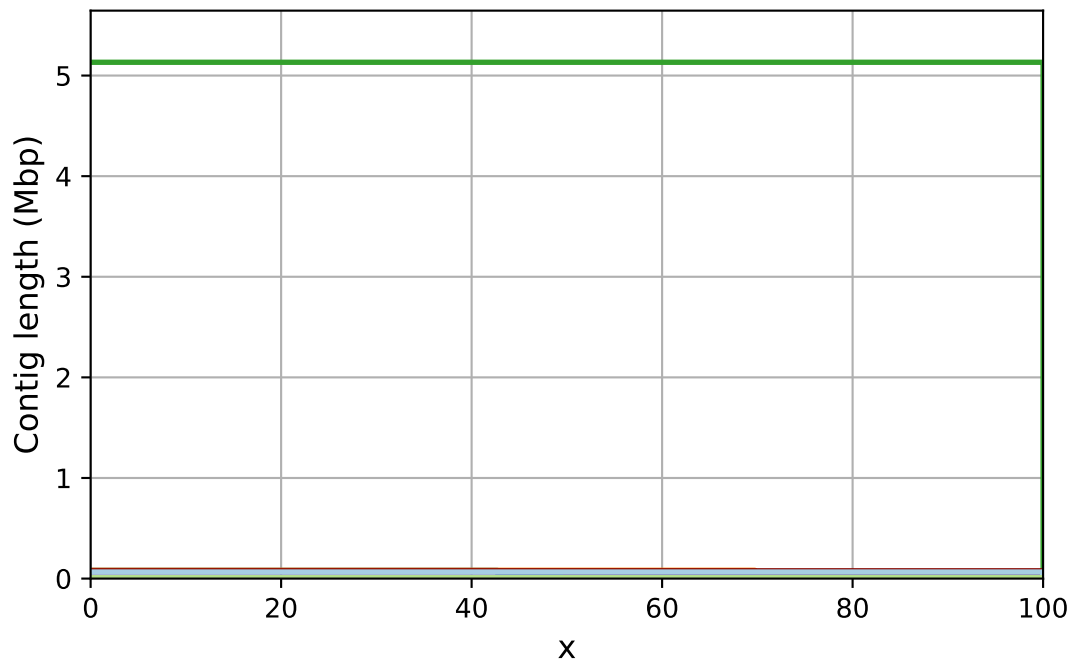
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

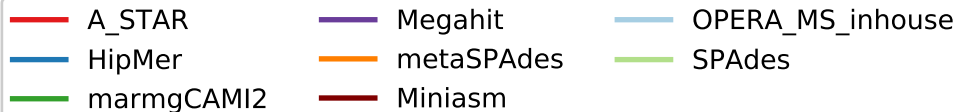
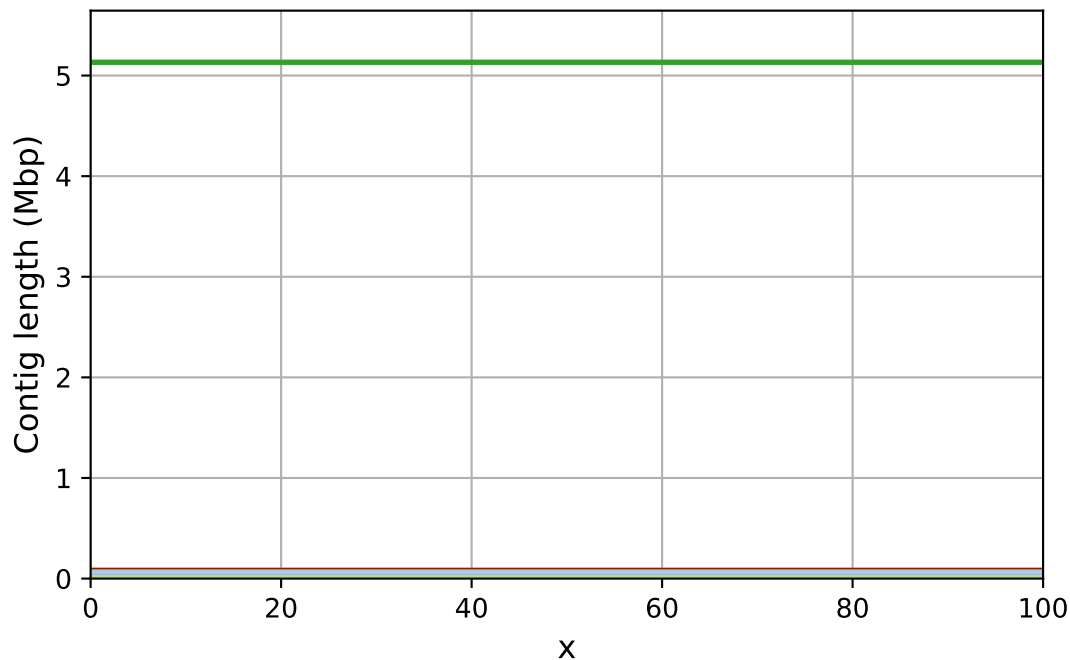
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	2	4	1	3	3	1	1	1
Partially unaligned length	3124	190334	5131767	132122	234950	76525	65186	8765
# N's	0	0	0	0	0	0	0	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).

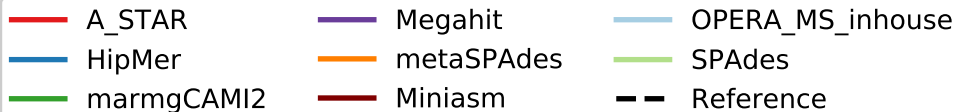
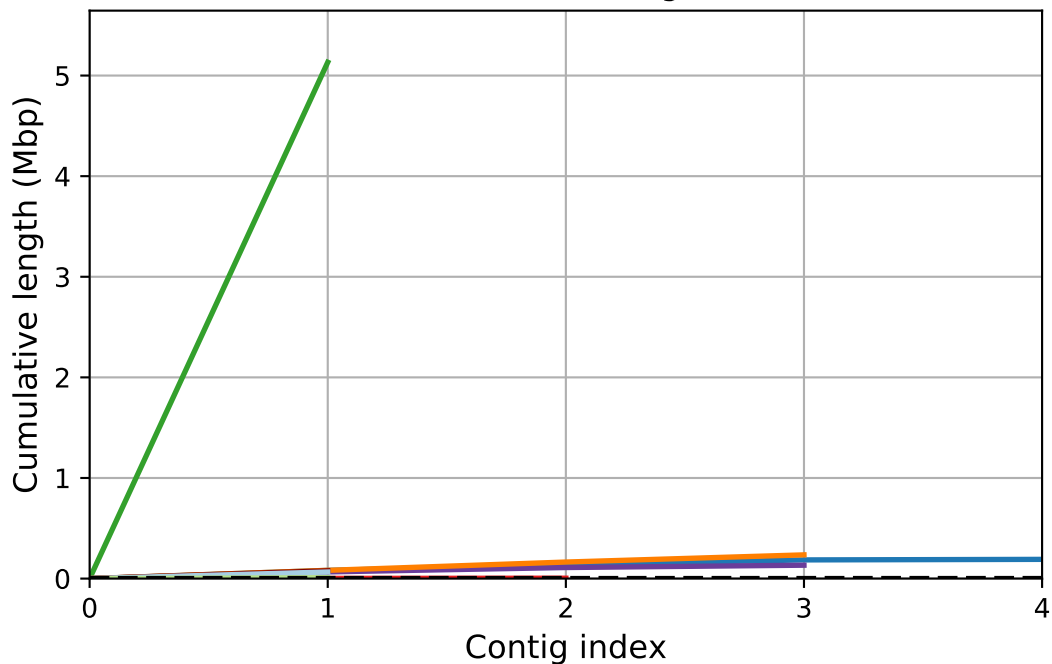
Nx



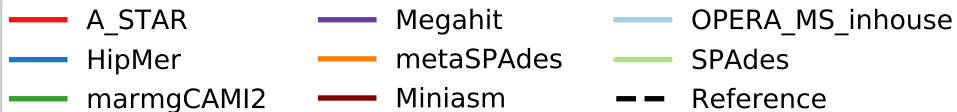
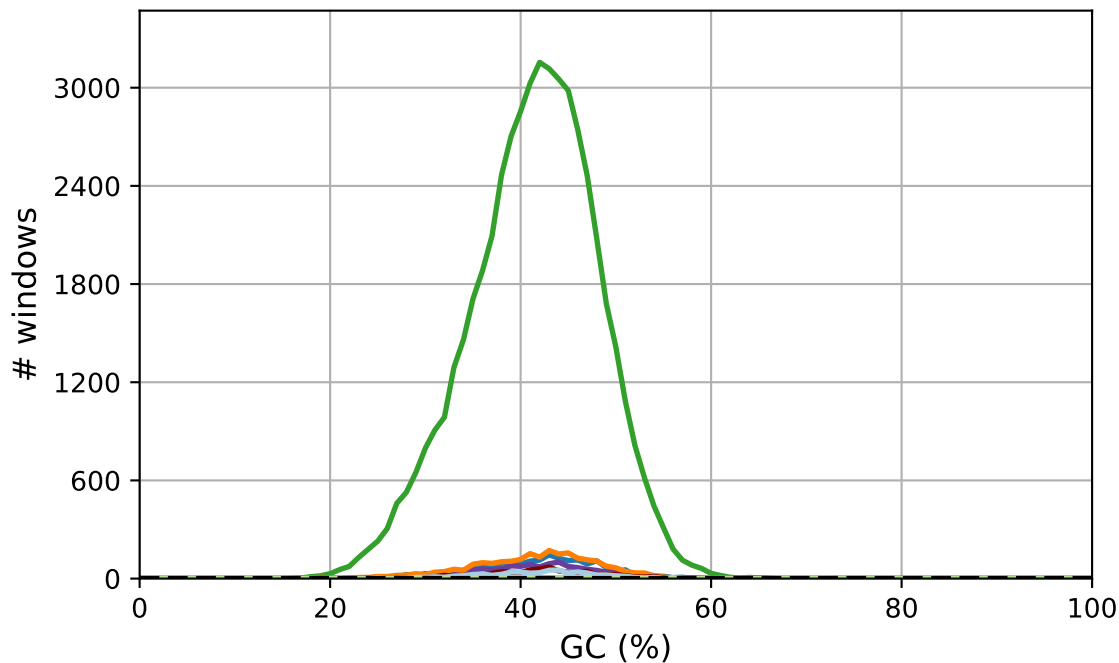
NGx



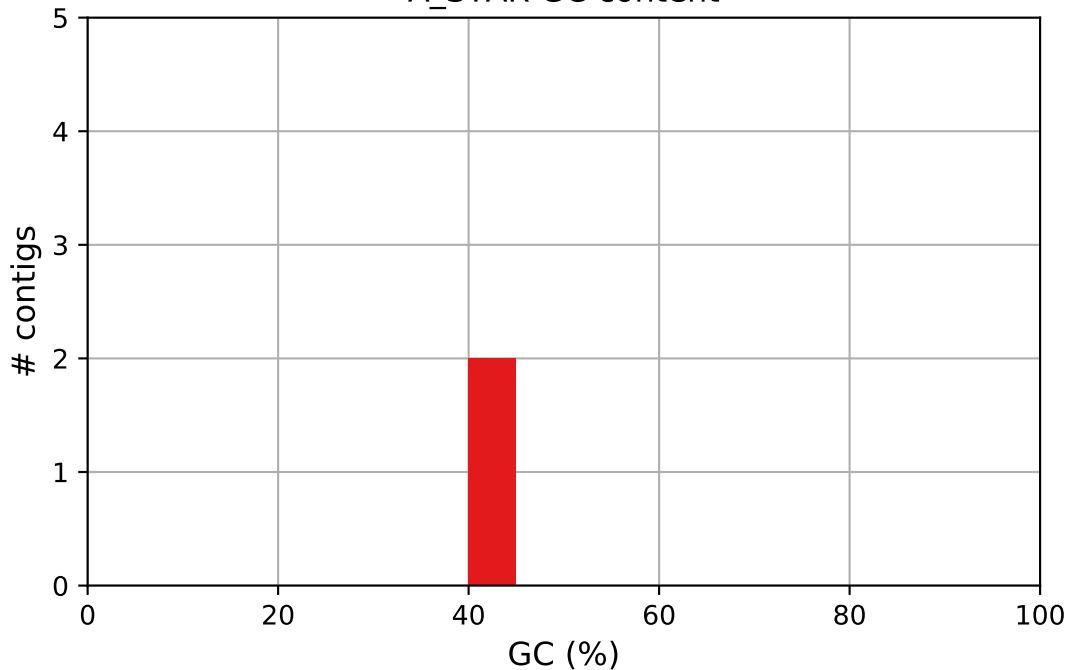
Cumulative length



GC content

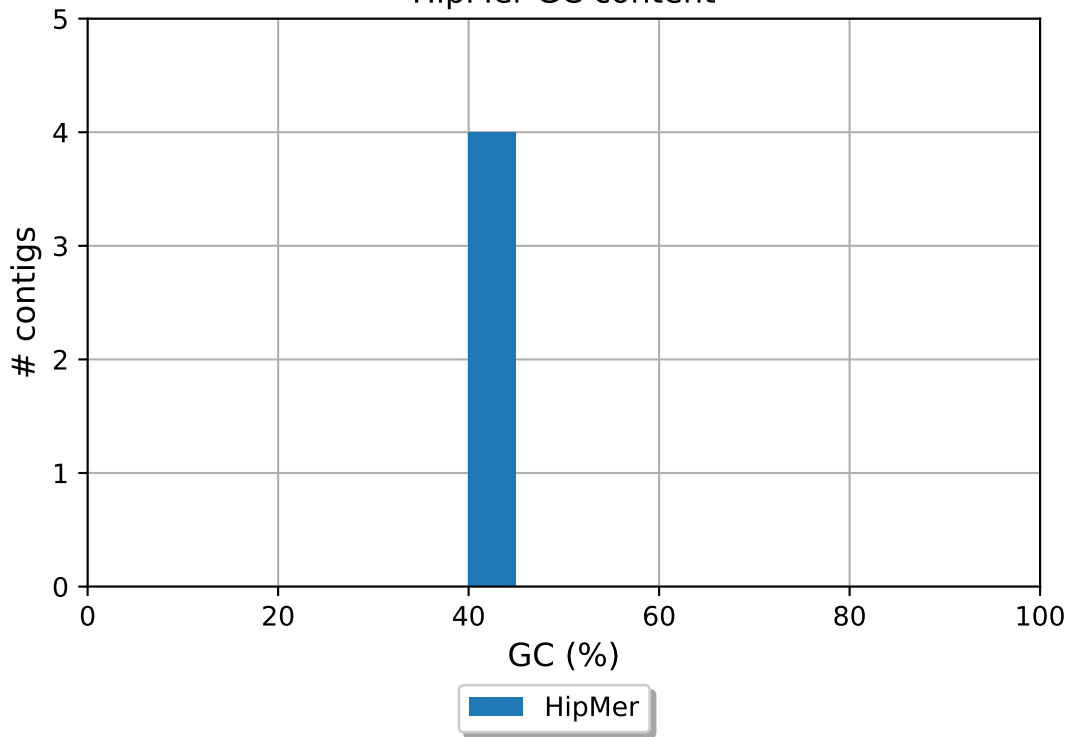


A_STAR GC content

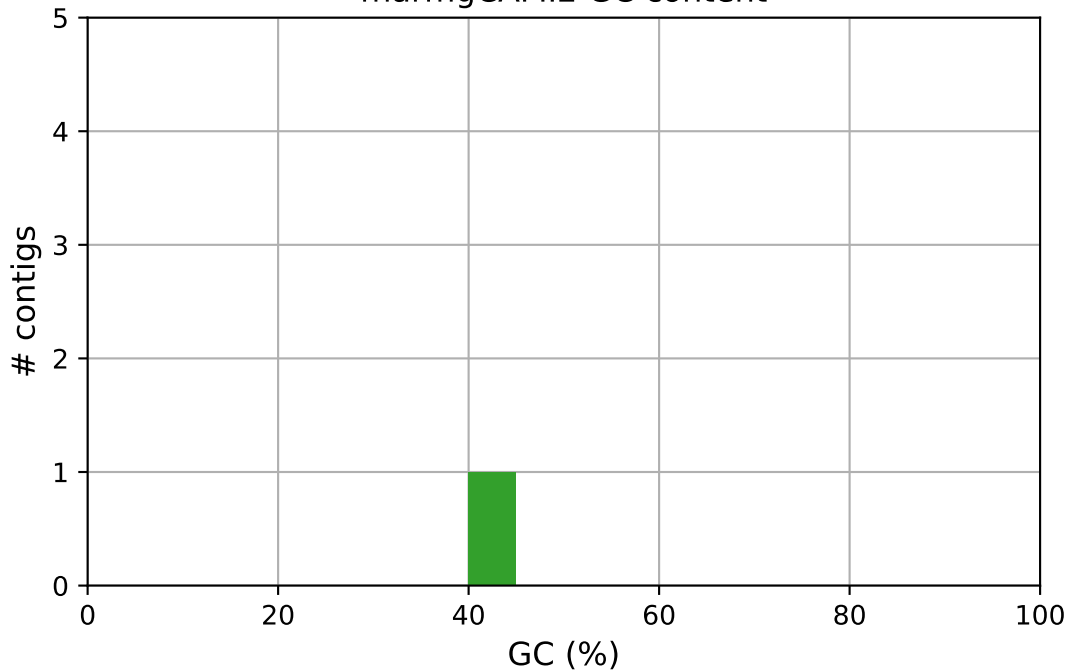


A_STAR

HipMer GC content

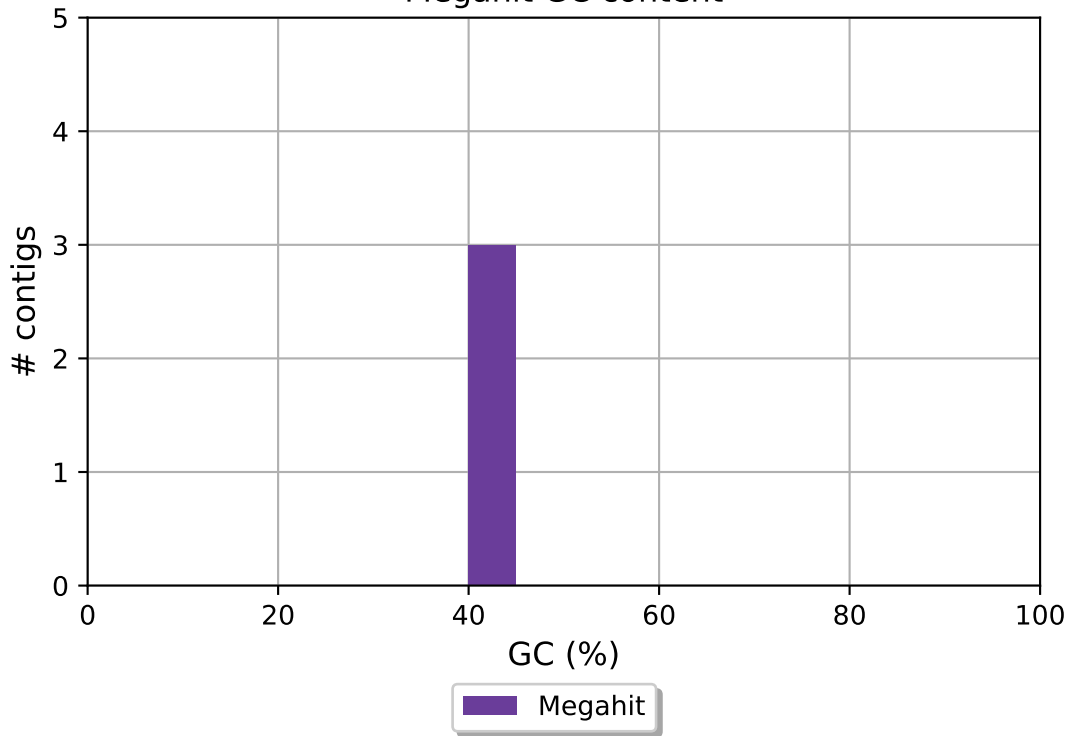


marmgCAMI2 GC content

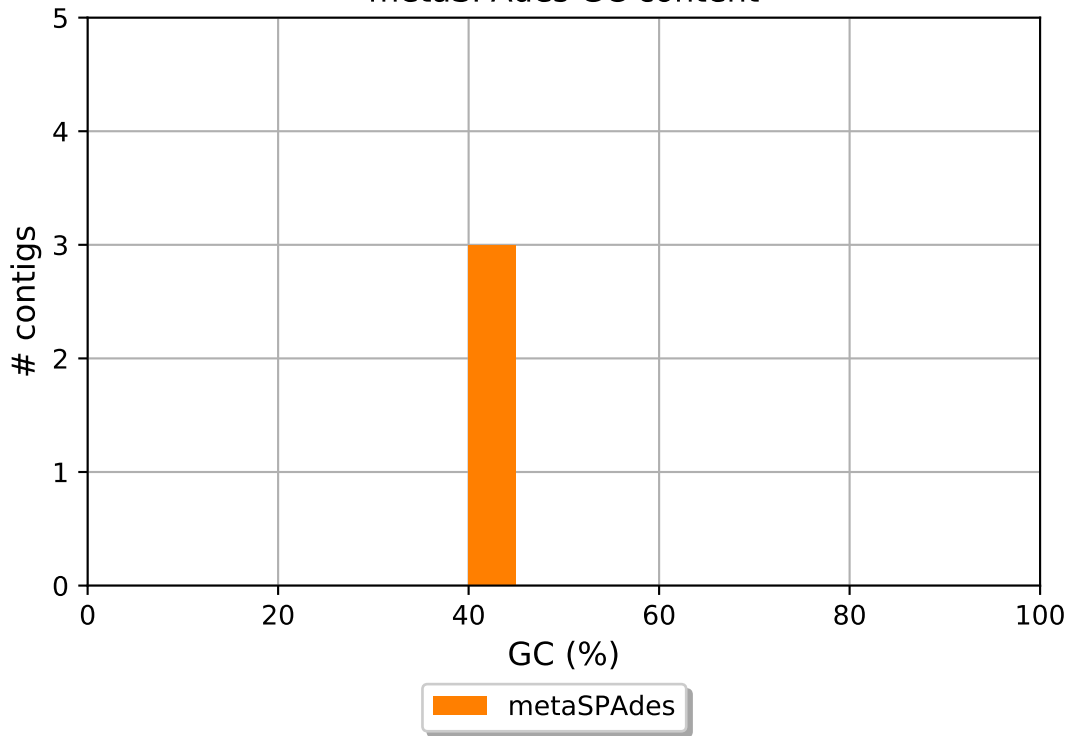


marmgCAMI2

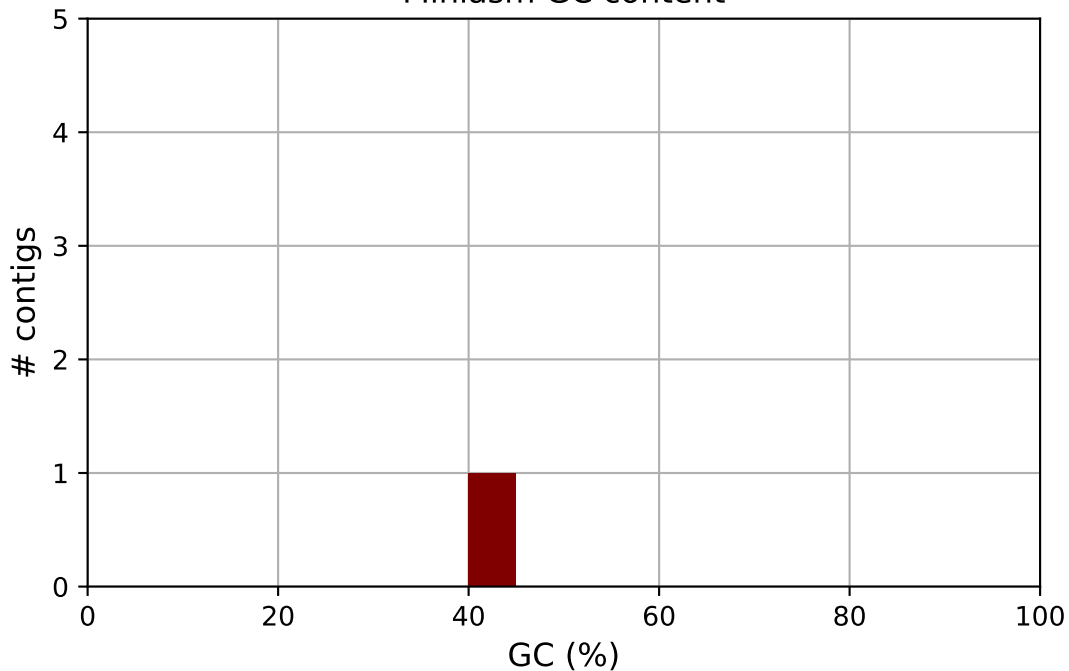
Megahit GC content



metaSPAdes GC content

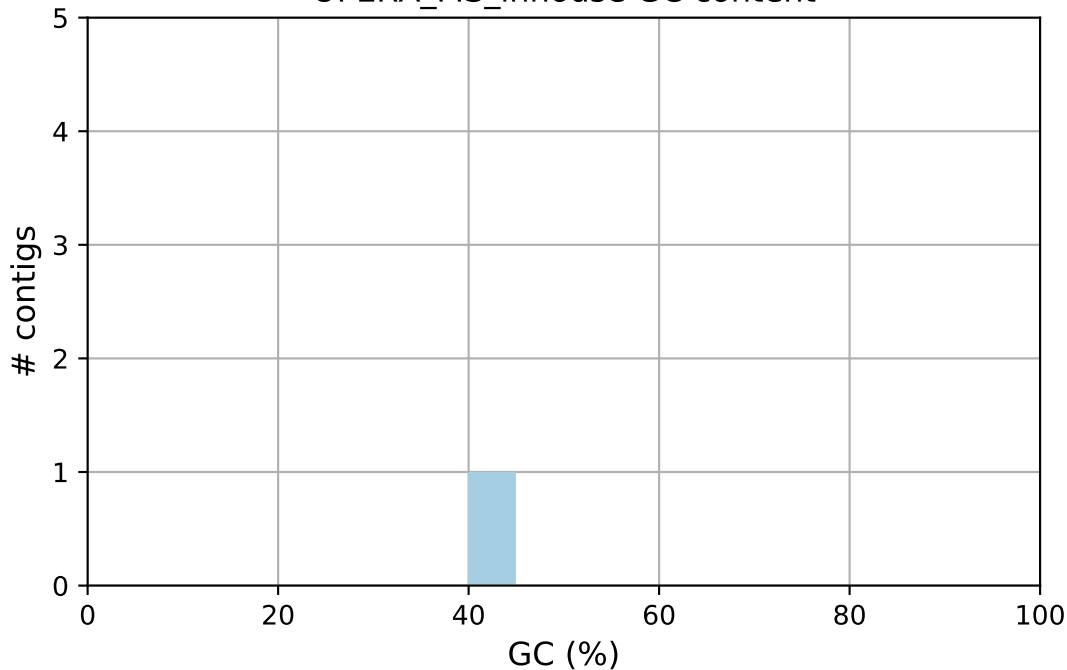


Miniasm GC content



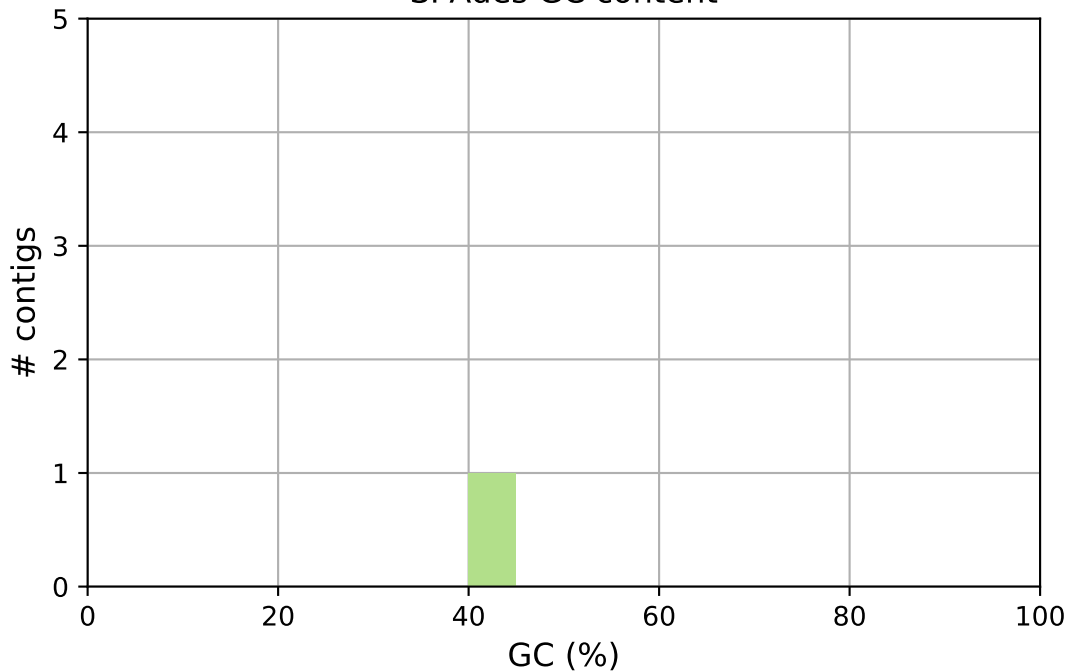
Miniasm

OPERA_MS_inhouse GC content



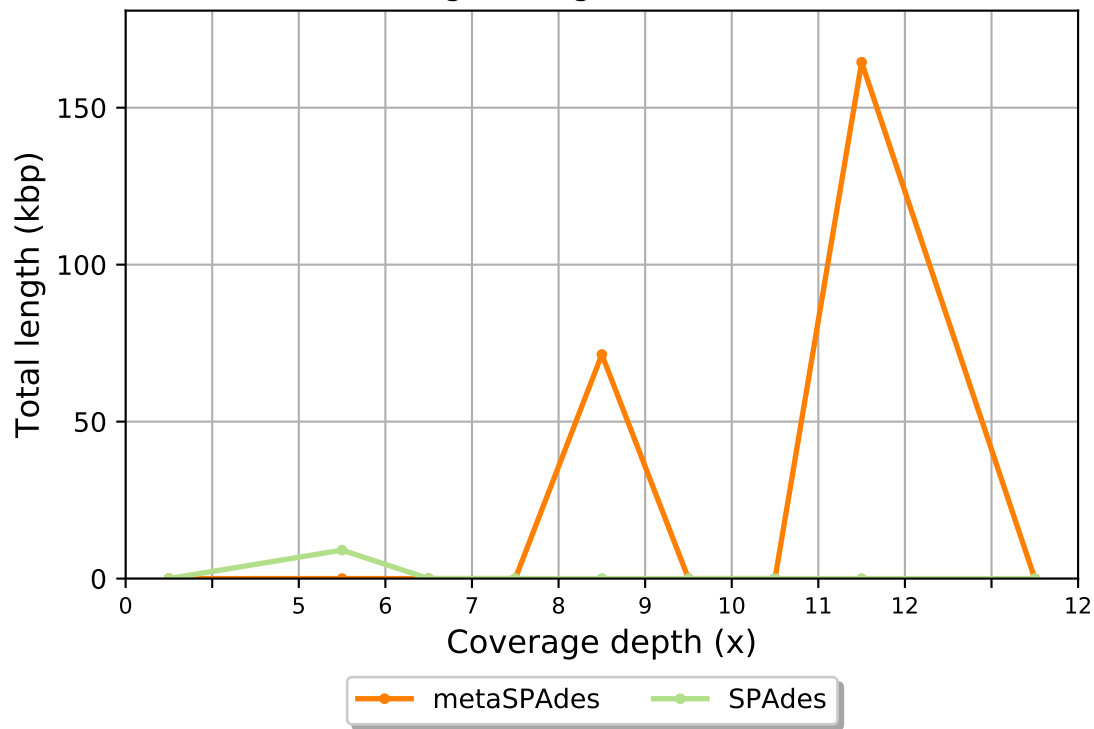
OPERA_MS_inhouse

SPAdes GC content

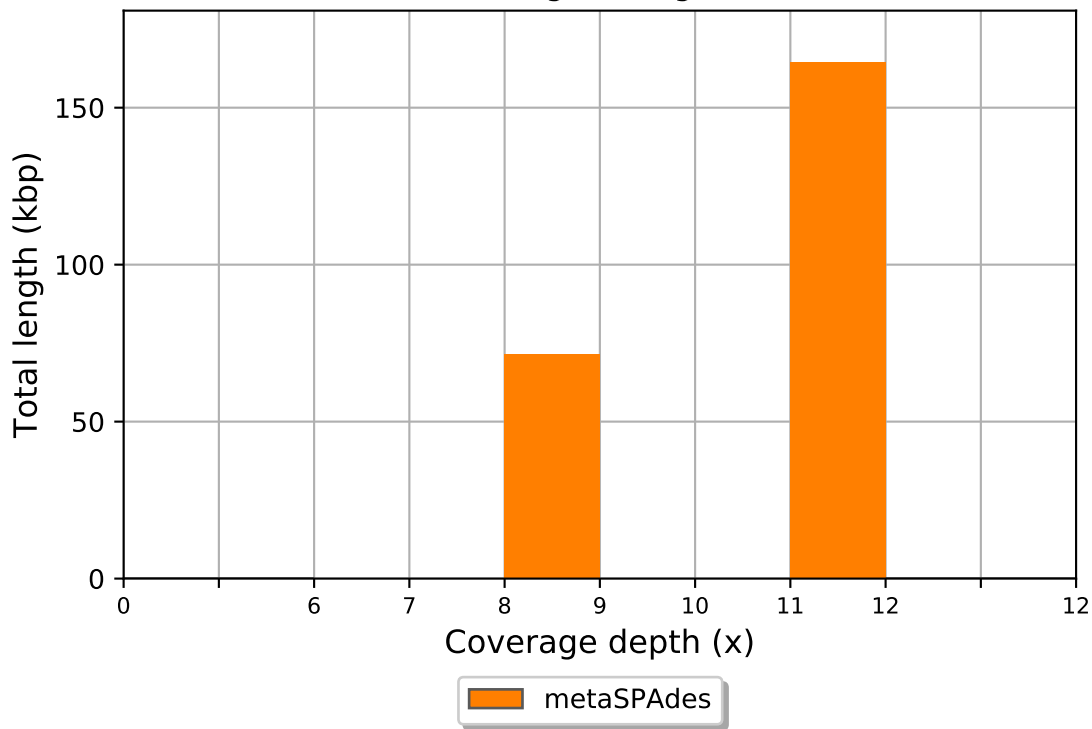


SPAdes

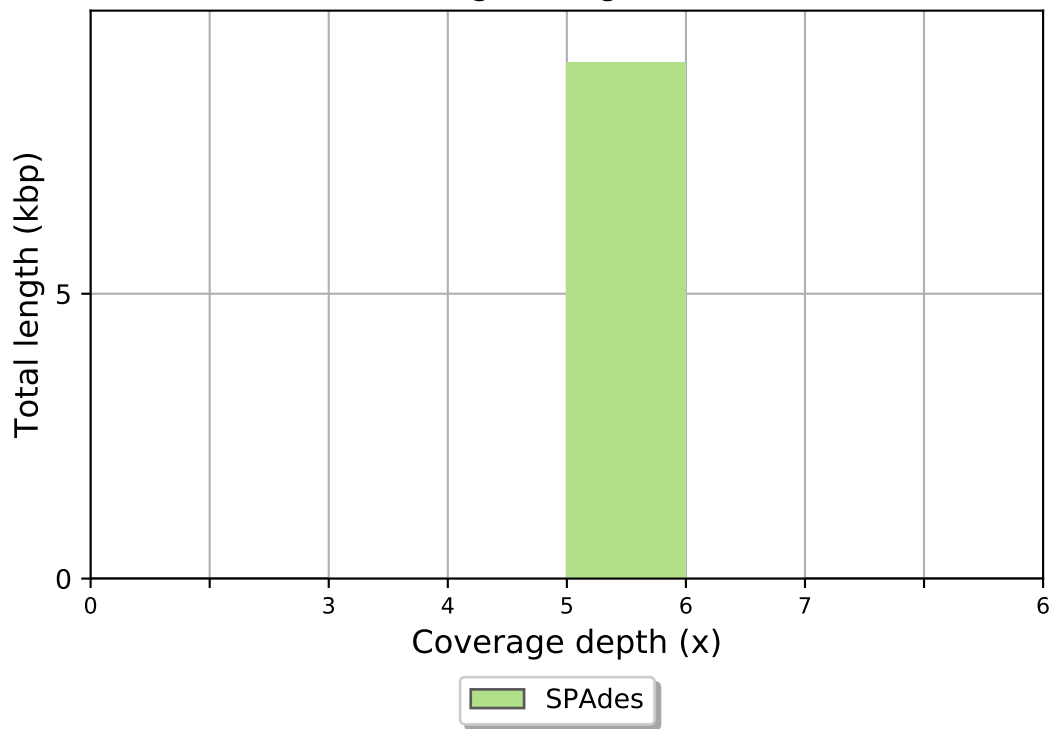
Coverage histogram (bin size: 1x)



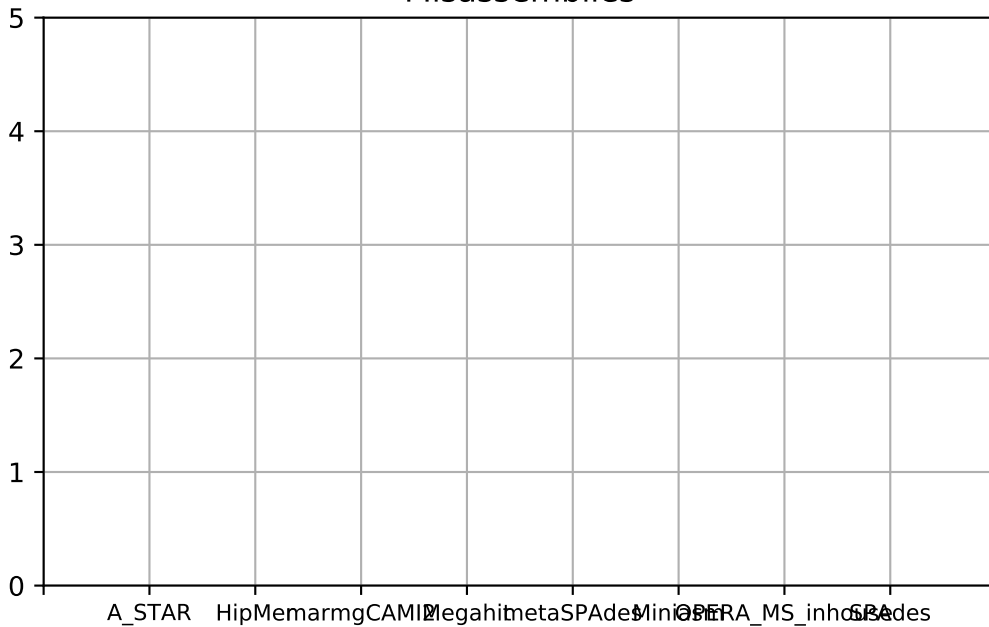
metaSPAdes coverage histogram (bin size: 1x)



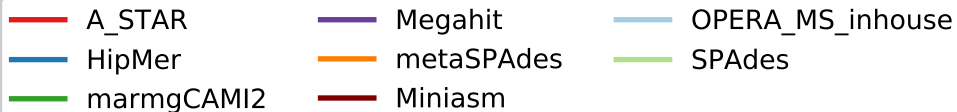
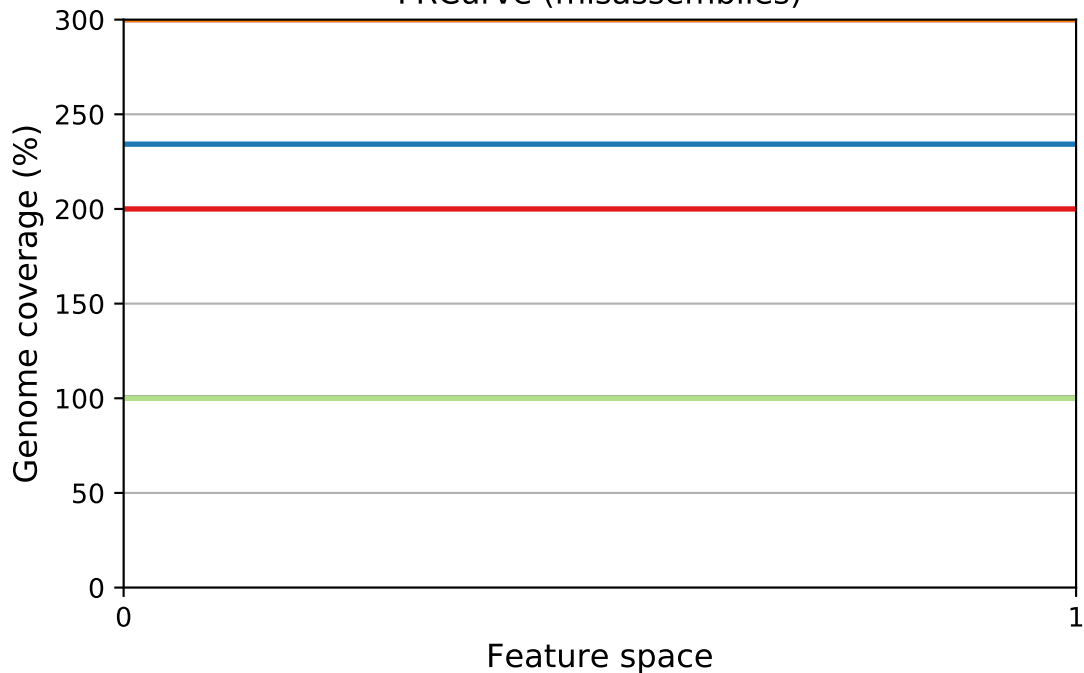
SPAdes coverage histogram (bin size: 1x)



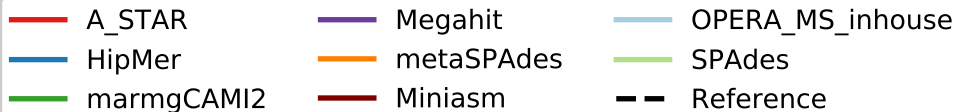
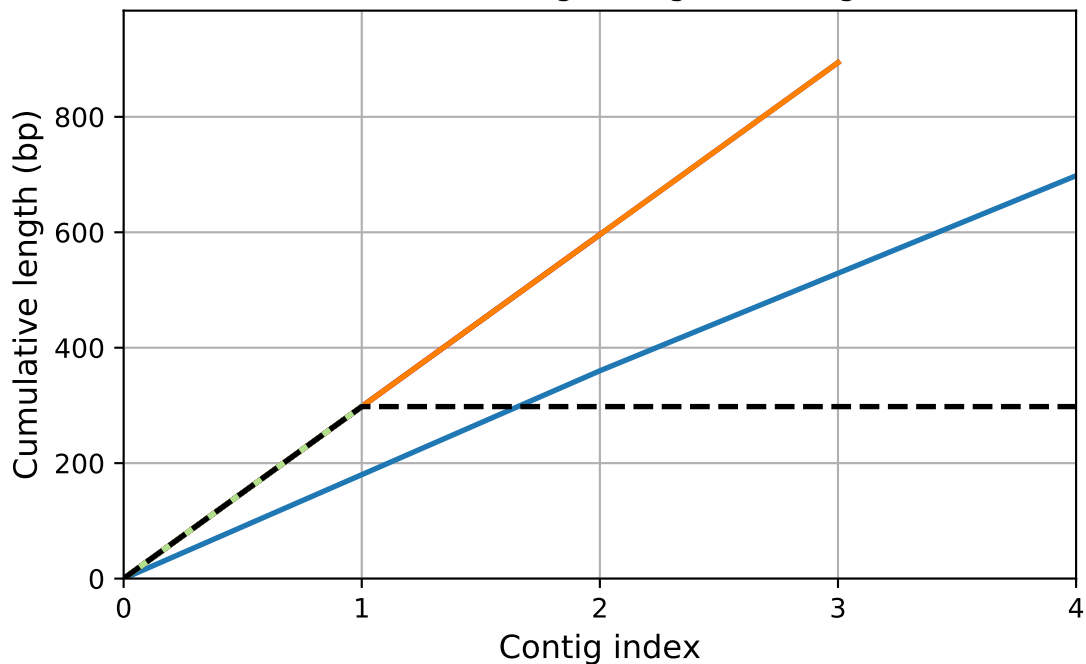
Misassemblies



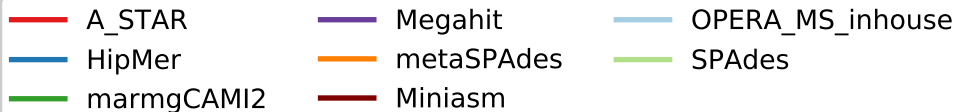
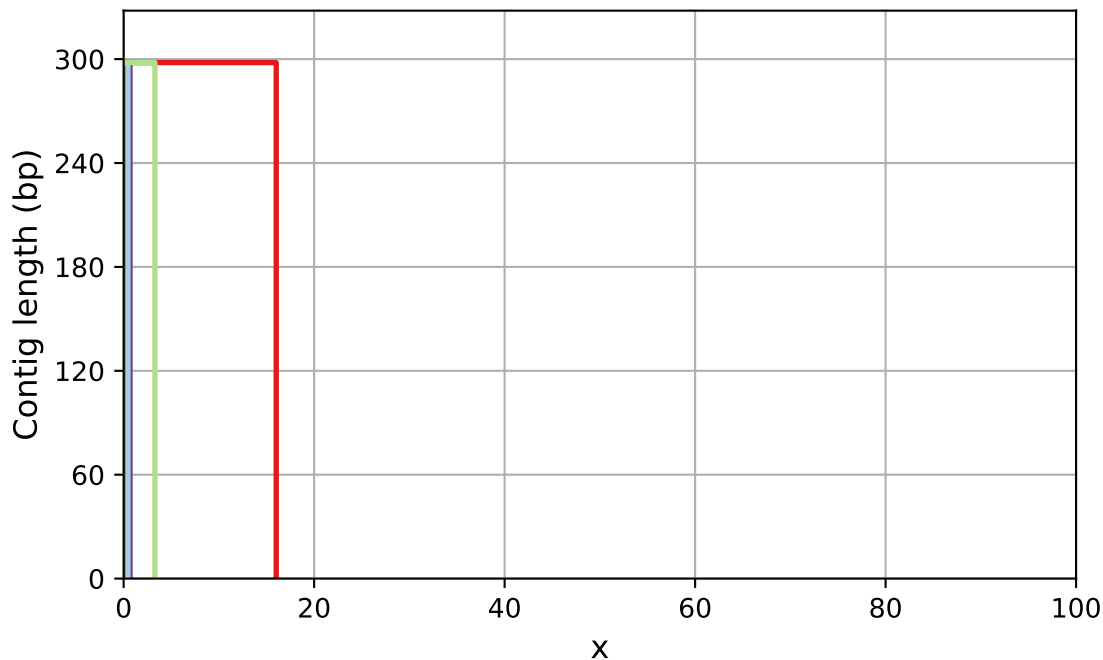
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

