

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	2	1	3	3	1	1	1
# contigs (>= 5000 bp)	2	0	1	3	2	1	1	0
# contigs (>= 10000 bp)	2	0	1	2	2	1	1	0
# contigs (>= 25000 bp)	2	0	1	1	0	0	1	0
# contigs (>= 50000 bp)	2	0	1	0	0	0	1	0
Total length (>= 1000 bp)	176172	9616	5396452	64369	24824	15161	64738	3821
Total length (>= 5000 bp)	176172	0	5396452	64369	21828	15161	64738	0
Total length (>= 10000 bp)	176172	0	5396452	58035	21828	15161	64738	0
Total length (>= 25000 bp)	176172	0	5396452	38660	0	0	64738	0
Total length (>= 50000 bp)	176172	0	5396452	0	0	0	64738	0
# contigs	2	2	1	3	3	1	1	1
Largest contig	88086	4808	5396452	38660	10914	15161	64738	3821
Total length	176172	9616	5396452	64369	24824	15161	64738	3821
Reference length	206	206	206	206	206	206	206	206
GC (%)	41.71	42.28	43.29	41.11	40.11	40.68	42.23	41.74
Reference GC (%)	48.06	48.06	48.06	48.06	48.06	48.06	48.06	48.06
N50	88086	4808	5396452	38660	10914	15161	64738	3821
NG50	88086	4808	5396452	38660	10914	15161	64738	3821
N75	88086	4808	5396452	19375	10914	15161	64738	3821
NG75	88086	4808	5396452	38660	10914	15161	64738	3821
L50	1	1	1	1	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	2	1	2	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	0	0	0	0	0	0	0
# unaligned contigs	0 + 2 part	0 + 2 part	0 + 1 part	0 + 3 part	0 + 3 part	0 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	175760	9204	5396246	63751	24206	14955	64532	3615
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	2.000	2.000	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	1456.31	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	206	206	206	206	206	206	206	206
Total aligned length	412	412	206	618	618	206	206	206
NGA50	206	206	206	206	206	206	206	206
NGA75	206	206	206	206	206	206	206	206
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

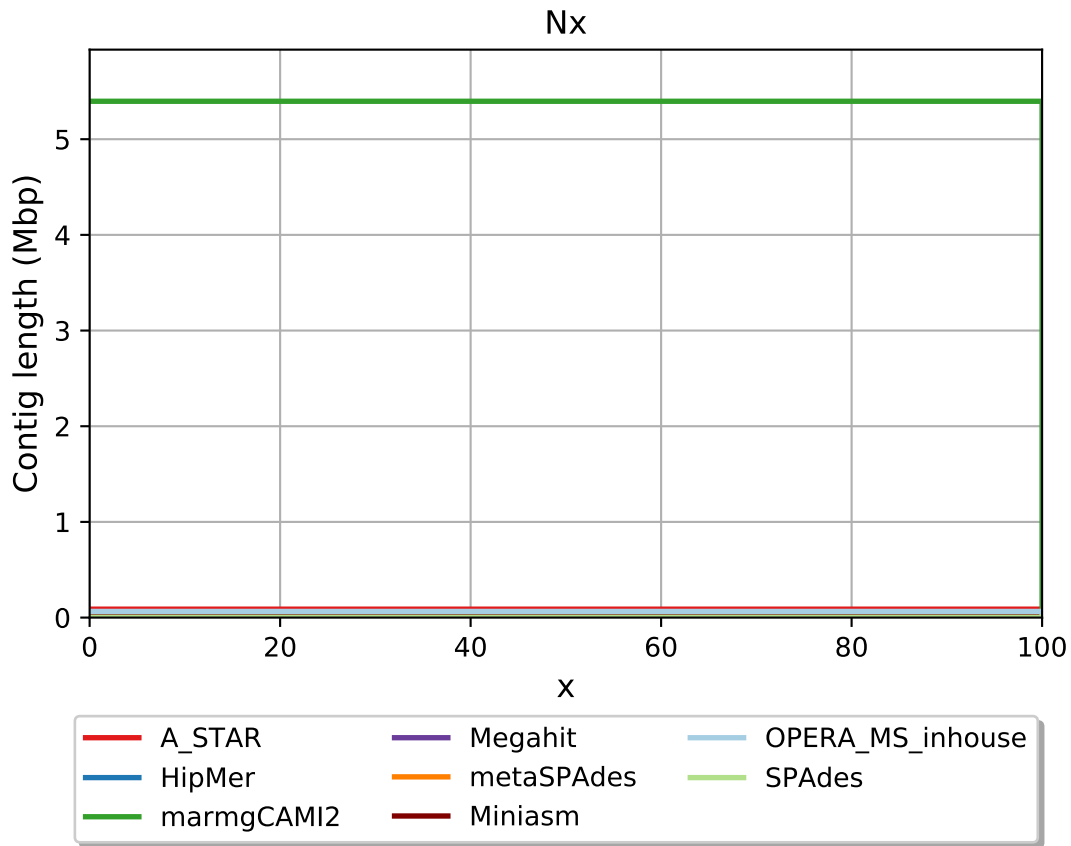
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations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

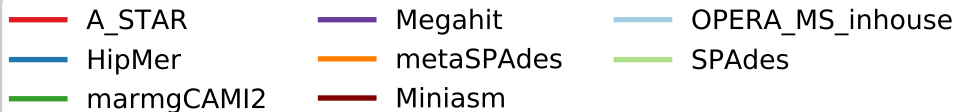
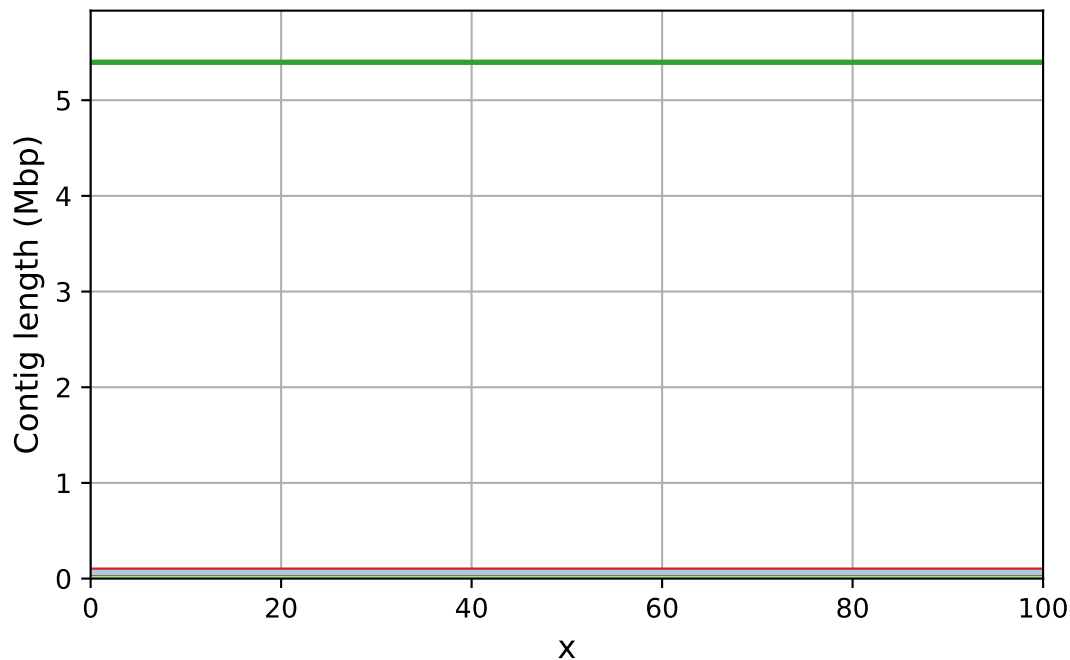
Unaligned report

	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	3	3	1	1	1
Partially unaligned length	175760	9204	5396246	63751	24206	14955	64532	3615
# N's	0	0	0	0	0	0	0	0

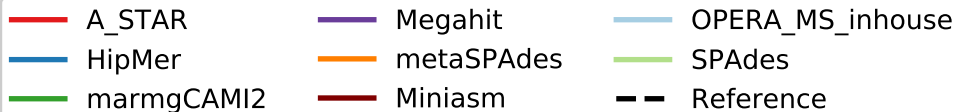
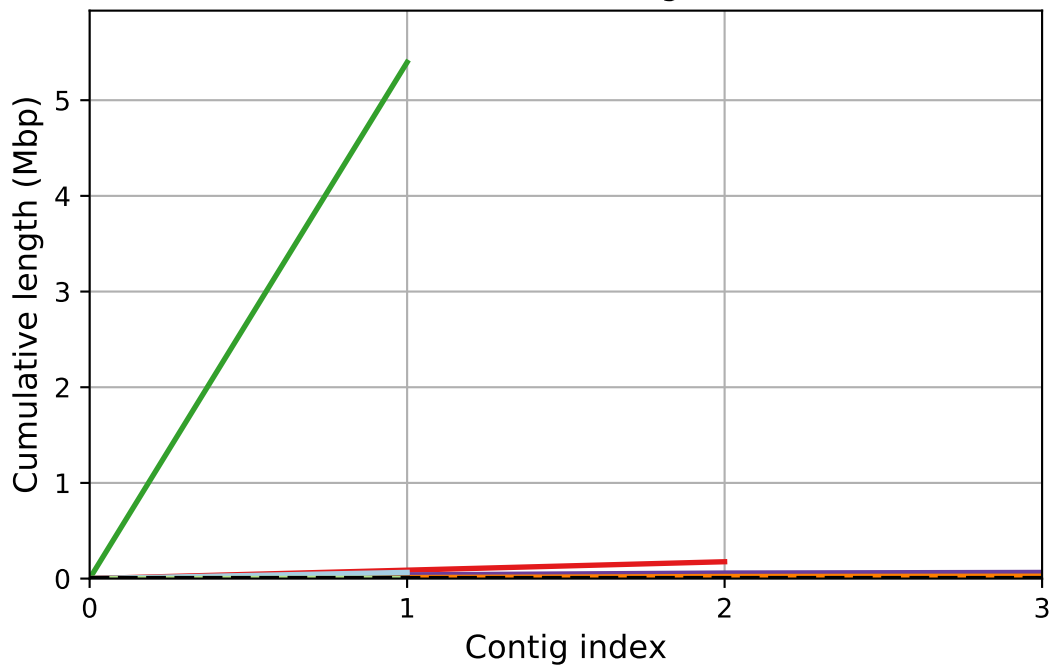
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



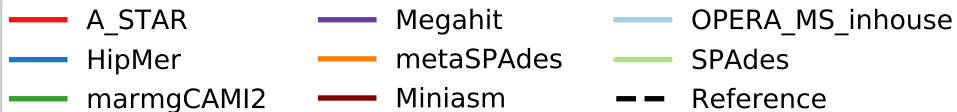
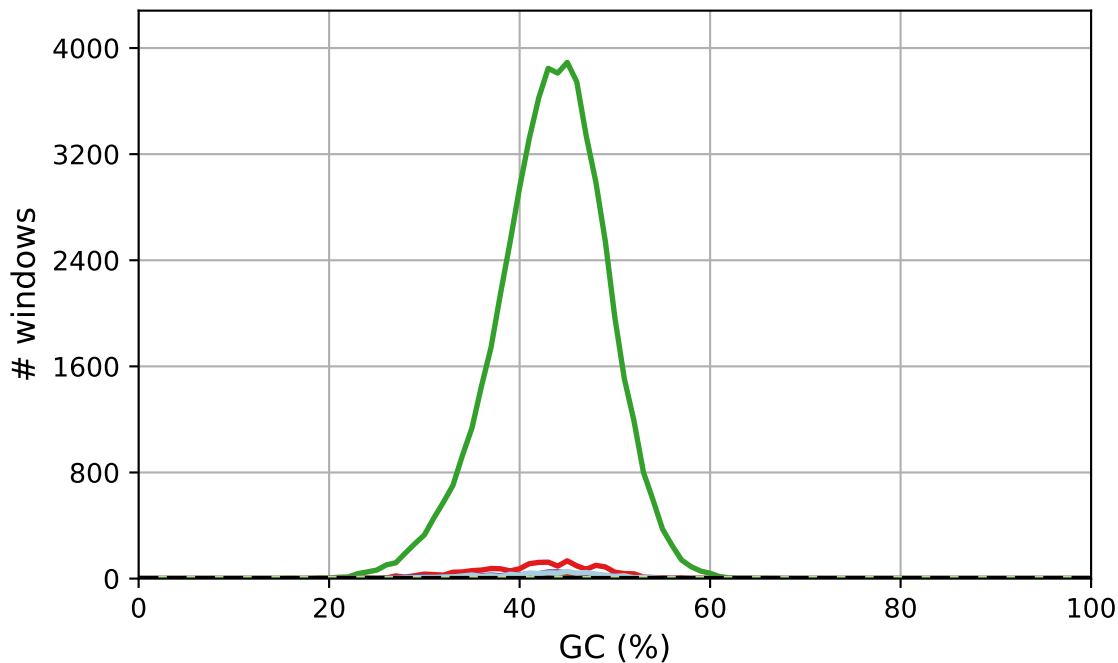
NGx



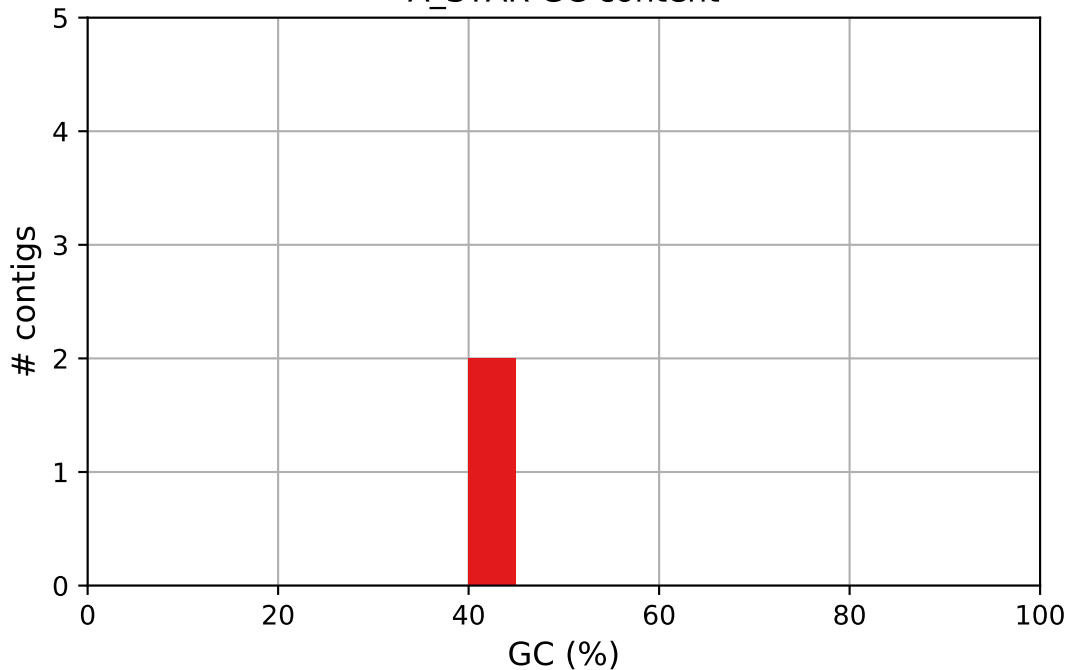
Cumulative length



GC content

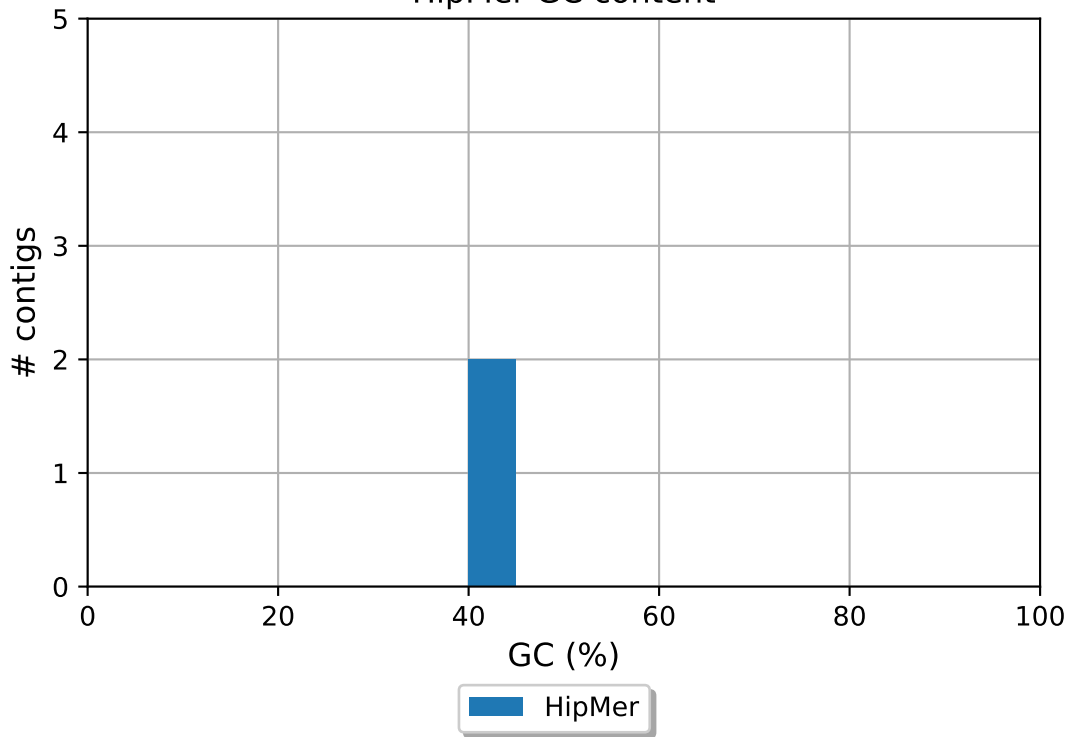


A_STAR GC content

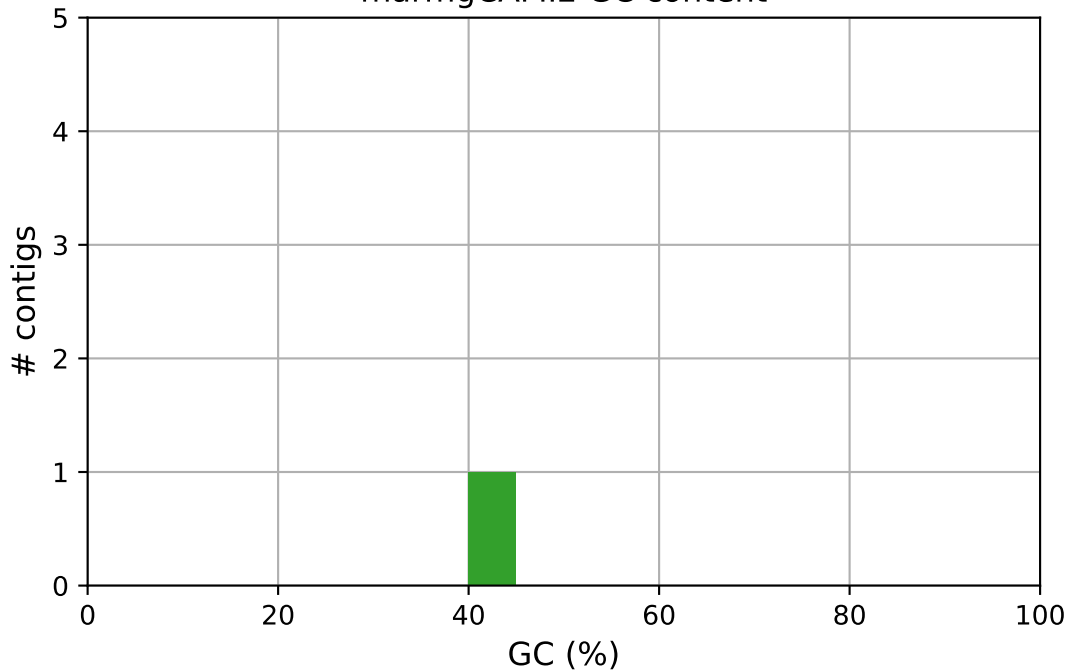


A_STAR

HipMer GC content

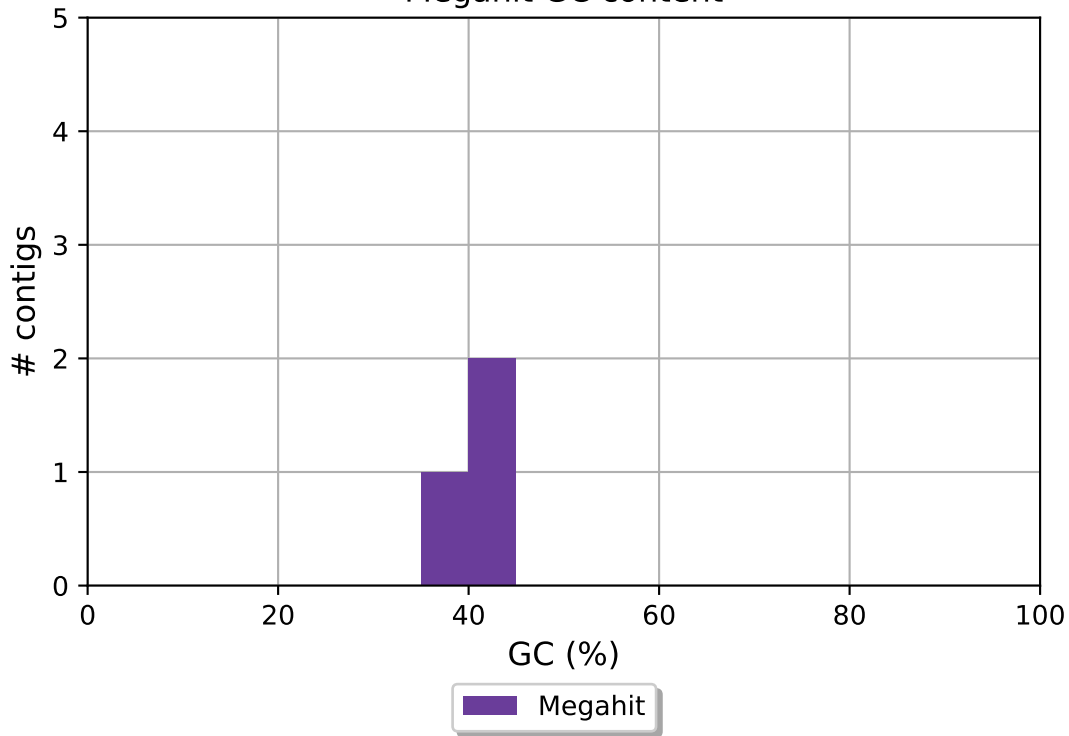


marmgCAMI2 GC content

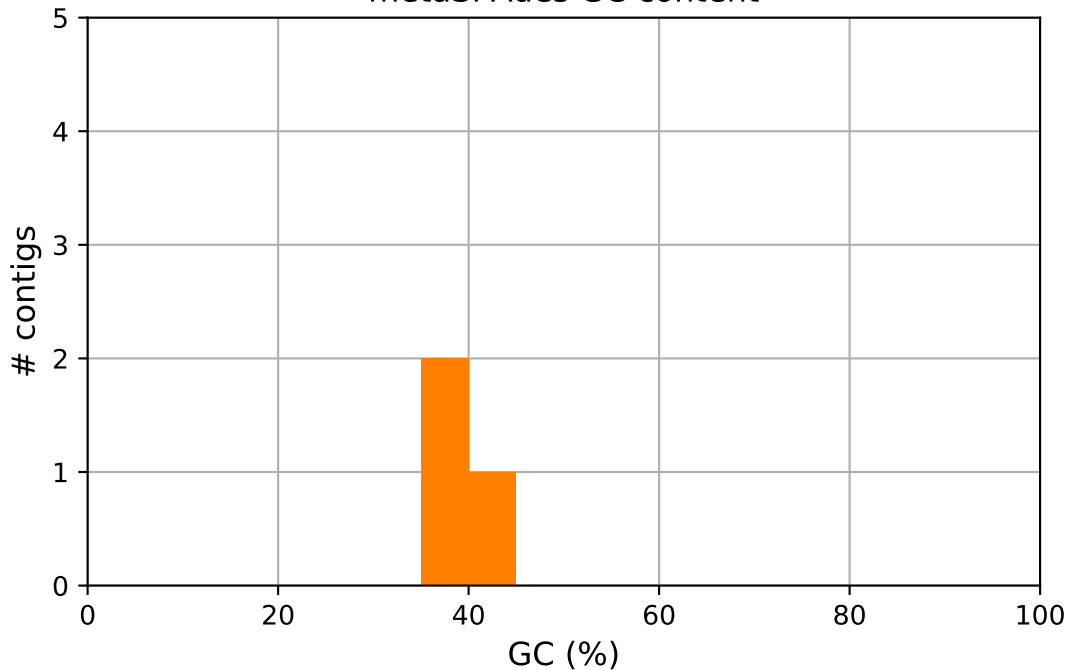


marmgCAMI2

Megahit GC content

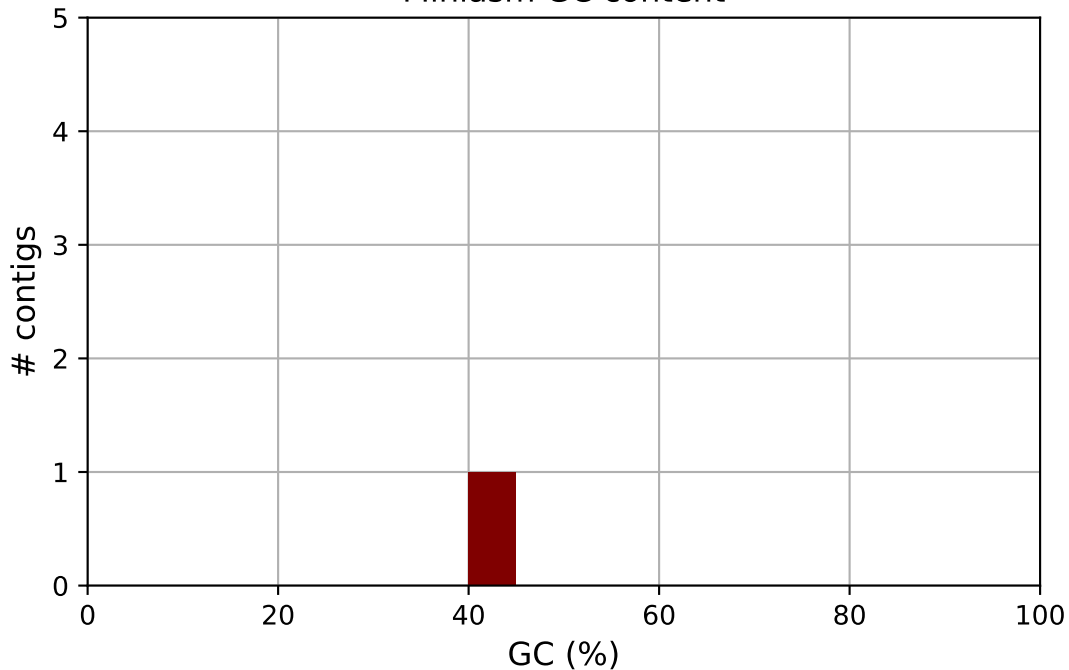


metaSPAdes GC content



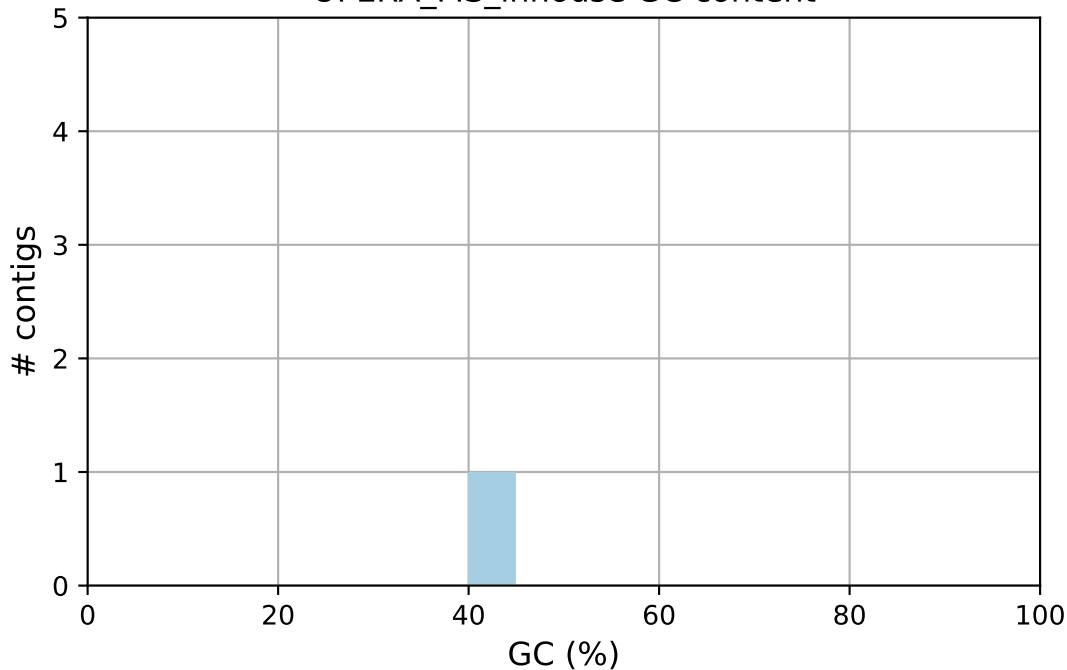
metaSPAdes

Miniasm GC content



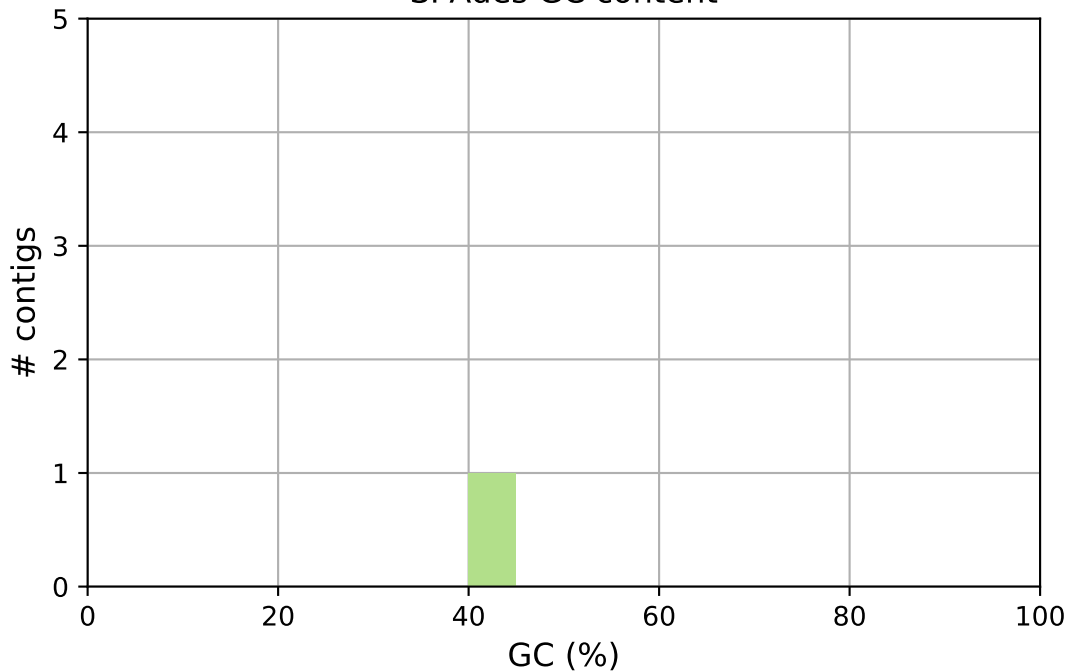
Miniasm

OPERA_MS_inhouse GC content



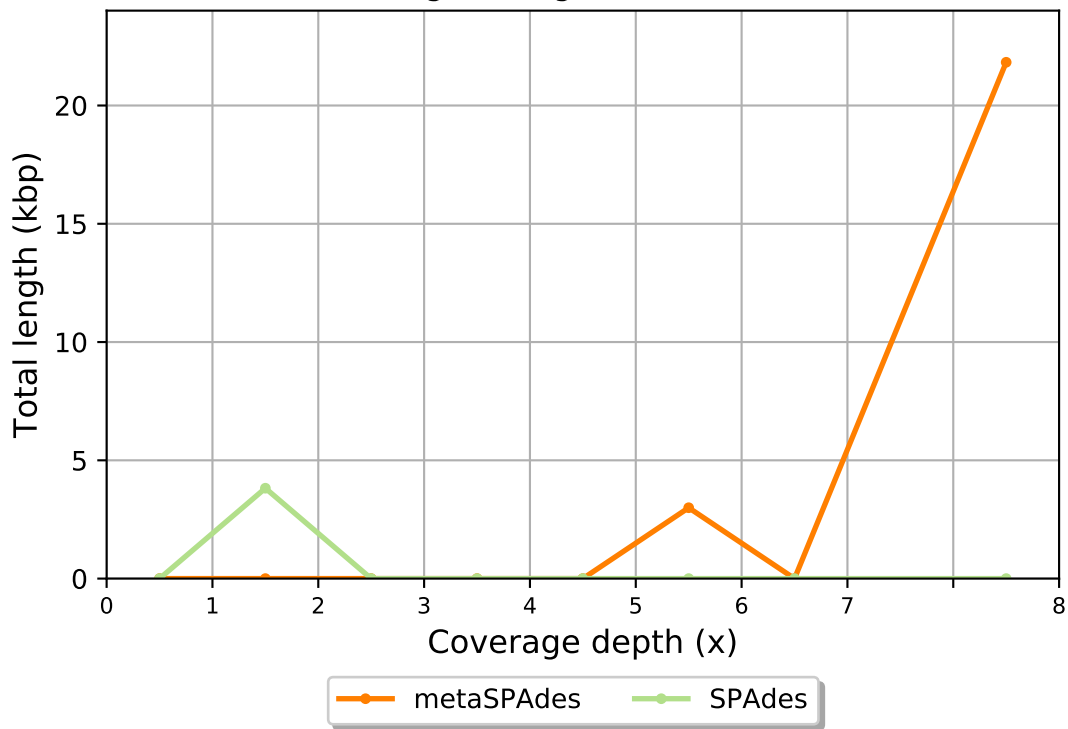
OPERA_MS_inhouse

SPAdes GC content

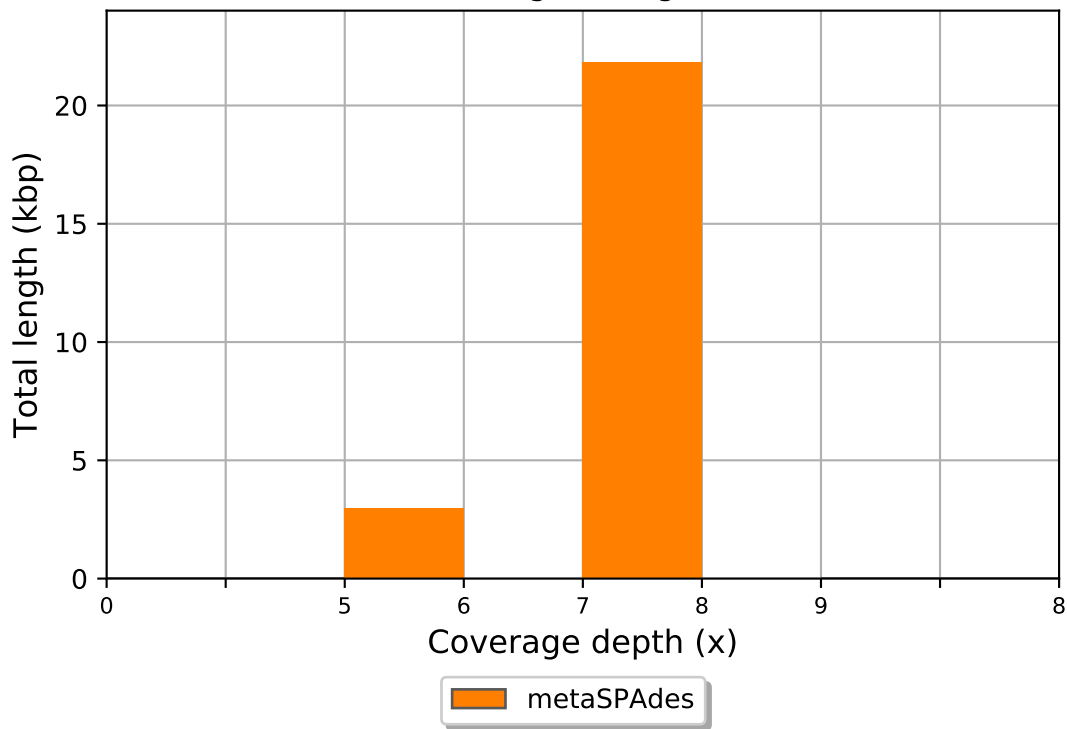


SPAdes

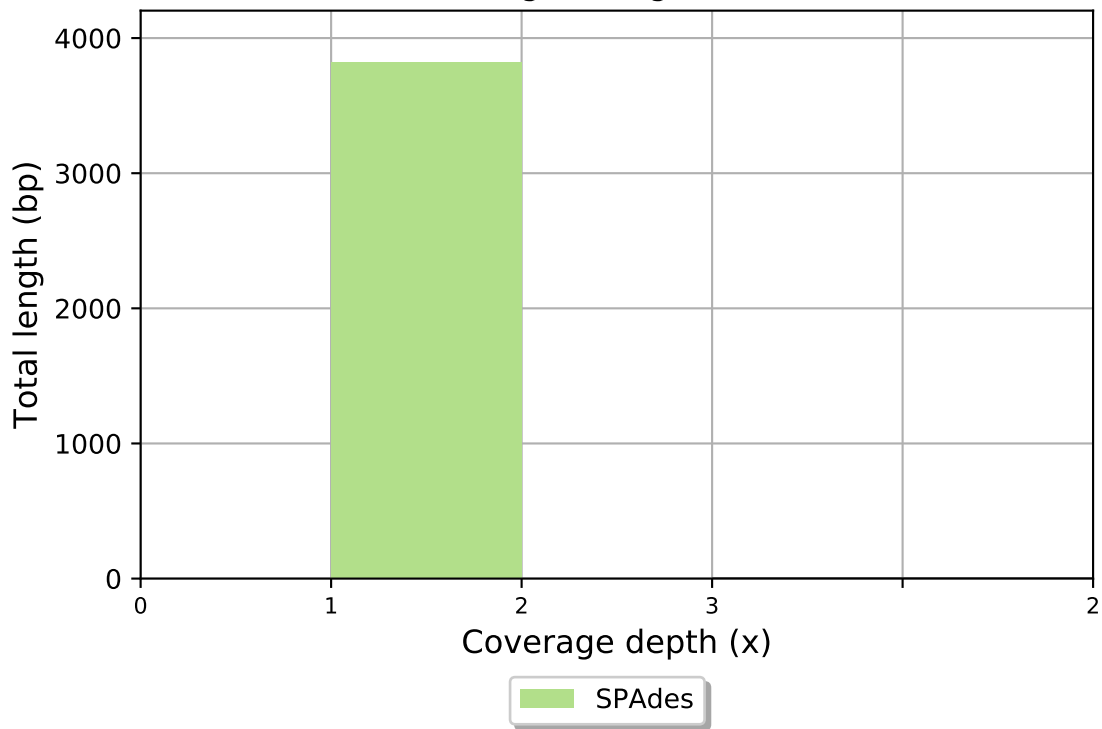
Coverage histogram (bin size: 1x)



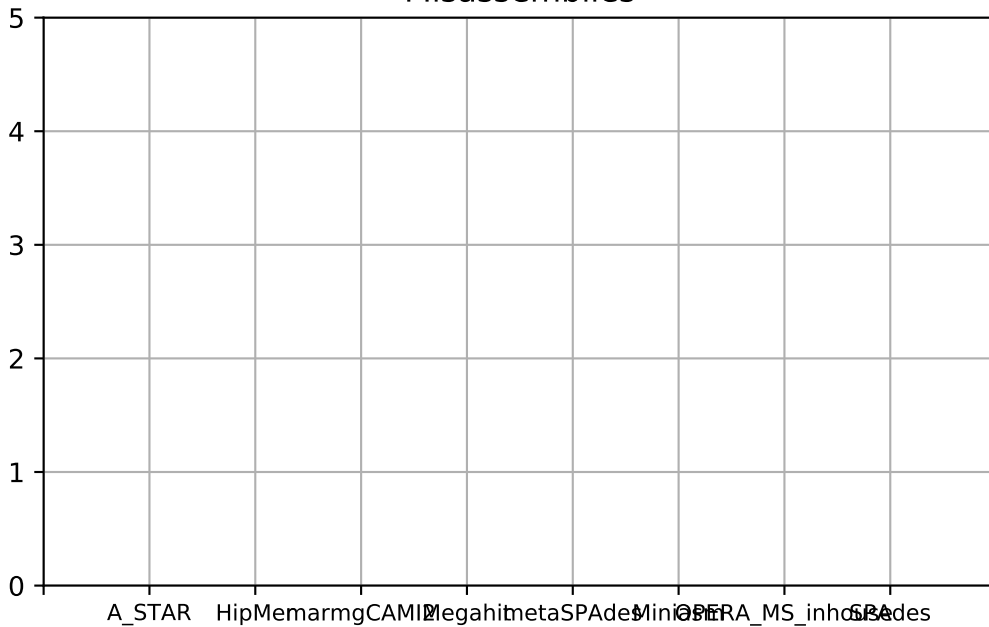
metaSPAdes coverage histogram (bin size: 1x)



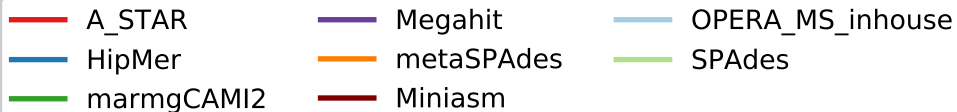
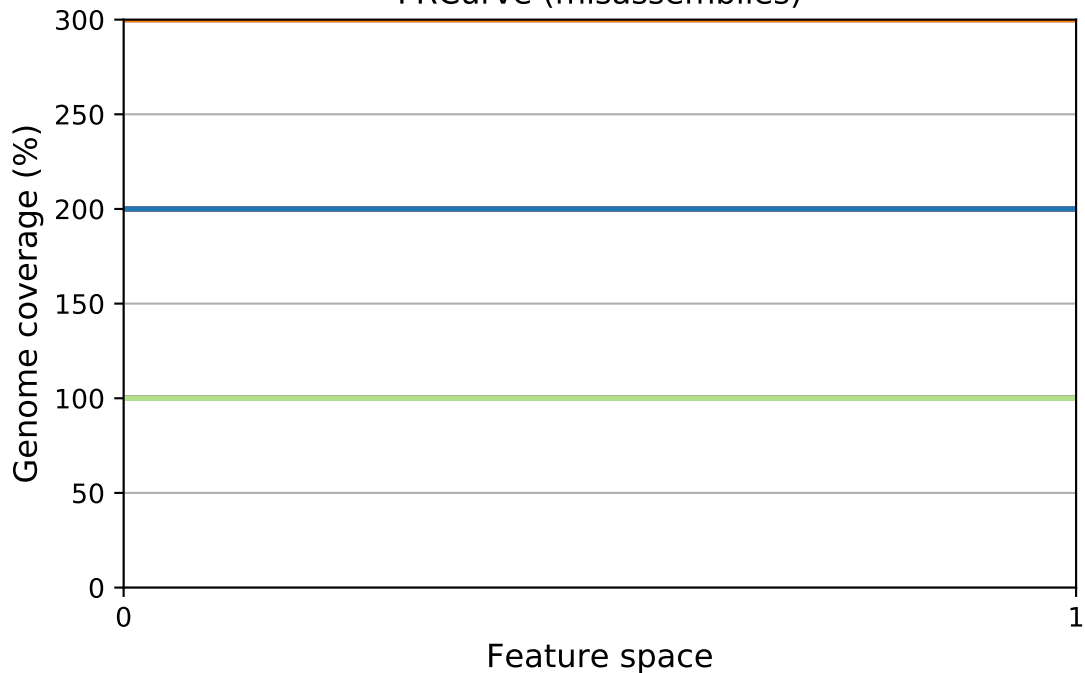
SPAdes coverage histogram (bin size: 1x)



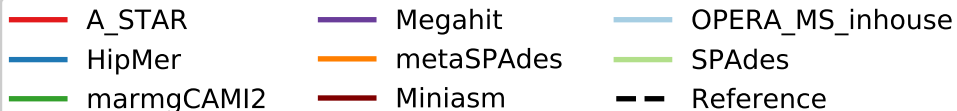
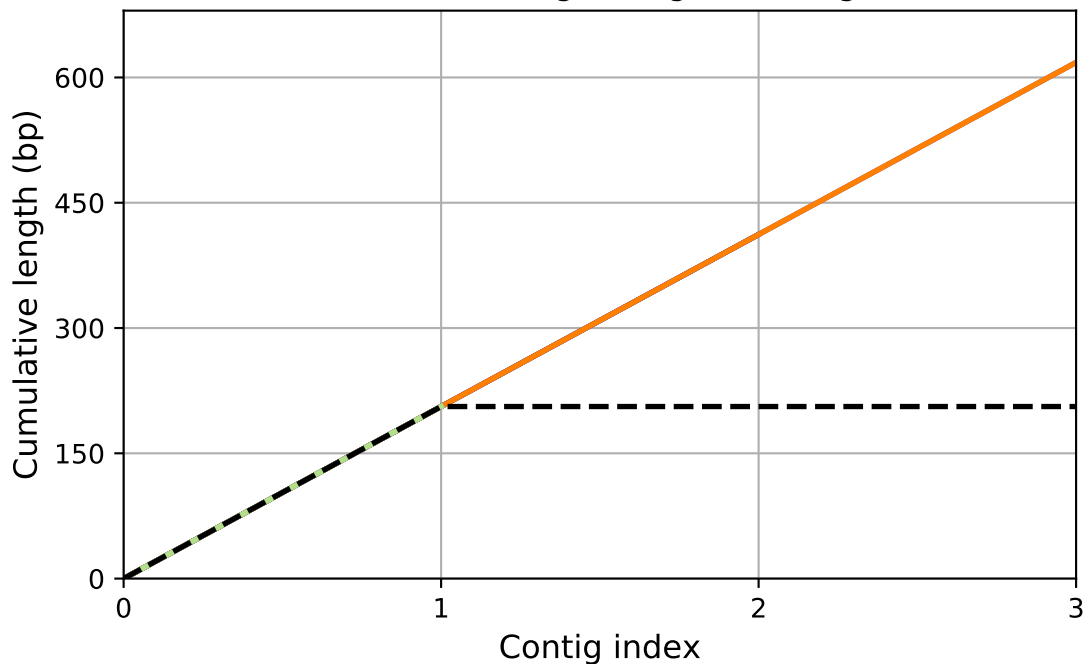
Misassemblies



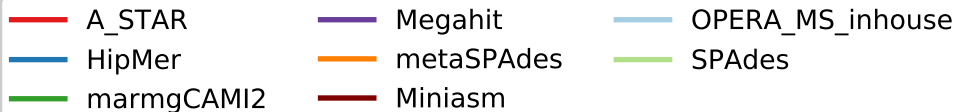
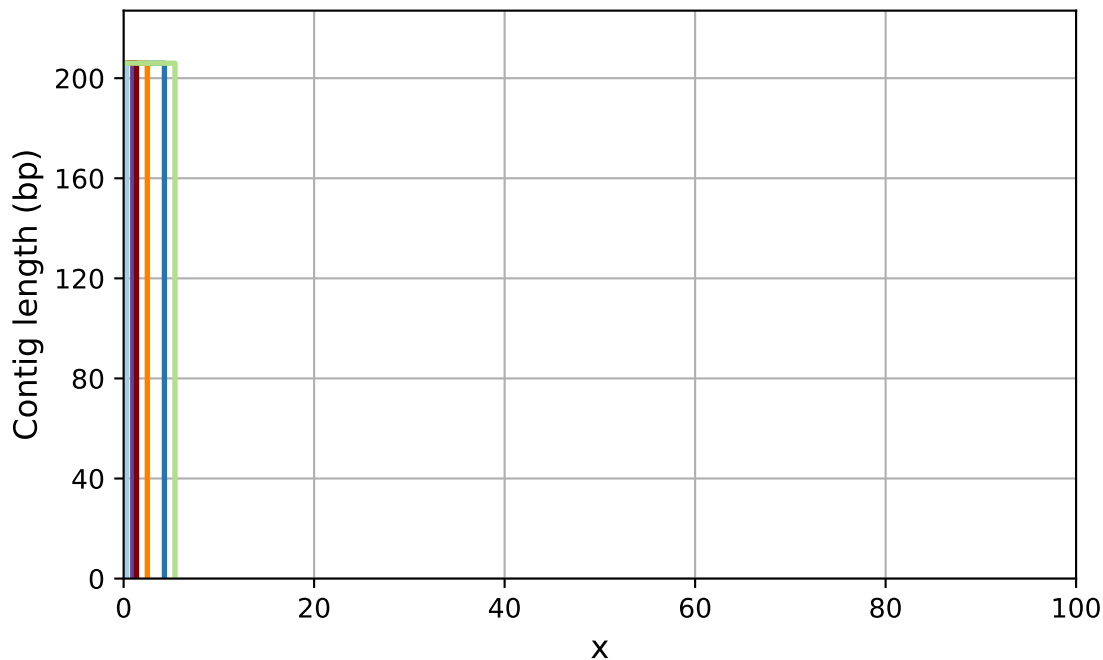
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAX



NGAx

