

# Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	1	2	1	3	1	1	1
# contigs (>= 5000 bp)	1	1	1	1	0	0	0
# contigs (>= 10000 bp)	1	0	1	0	0	0	0
# contigs (>= 25000 bp)	0	0	1	0	0	0	0
# contigs (>= 50000 bp)	0	0	1	0	0	0	0
Total length (>= 1000 bp)	23644	8432	4480493	11817	3802	1304	2305
Total length (>= 5000 bp)	23644	6521	4480493	6394	0	0	0
Total length (>= 10000 bp)	23644	0	4480493	0	0	0	0
Total length (>= 25000 bp)	0	0	4480493	0	0	0	0
Total length (>= 50000 bp)	0	0	4480493	0	0	0	0
# contigs	2	2	1	5	3	1	1
Largest contig	23644	6521	4480493	6394	3802	1304	2305
Total length	24578	8432	4480493	13263	5607	1304	2305
Reference length	652	652	652	652	652	652	652
GC (%)	44.97	46.99	44.61	45.43	45.91	47.55	45.38
Reference GC (%)	59.05	59.05	59.05	59.05	59.05	59.05	59.05
N50	23644	6521	4480493	4395	3802	1304	2305
NG50	23644	6521	4480493	6394	3802	1304	2305
N75	23644	6521	4480493	4395	903	1304	2305
NG75	23644	6521	4480493	6394	3802	1304	2305
L50	1	1	1	2	1	1	1
LG50	1	1	1	1	1	1	1
L75	1	1	1	2	2	1	1
LG75	1	1	1	1	1	1	1
# misassemblies	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0
# unaligned mis. contigs	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 + 1 part	0 + 1 part
Unaligned length	20253	7162	4479841	11835	5092	1119	2060
Genome fraction (%)	28.528	96.319	100.000	97.546	56.288	28.374	37.577
Duplication ratio	23.253	2.022	1.000	2.245	1.403	1.000	1.000
# N's per 100 kbp	16091.63	71.16	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	7526.88	636.94	0.00	3773.58	1634.88	3783.78	816.33
# indels per 100 kbp	0.00	159.24	0.00	0.00	0.00	0.00	0.00
Largest alignment	186	639	652	253	219	185	245
Total aligned length	371	1267	652	1065	515	185	245
NGA50	185	639	652	238	148	-	-
NGA75	-	639	652	238	148	-	-
LGA50	2	1	1	2	2	-	-
LGA75	-	1	1	2	3	-	-

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

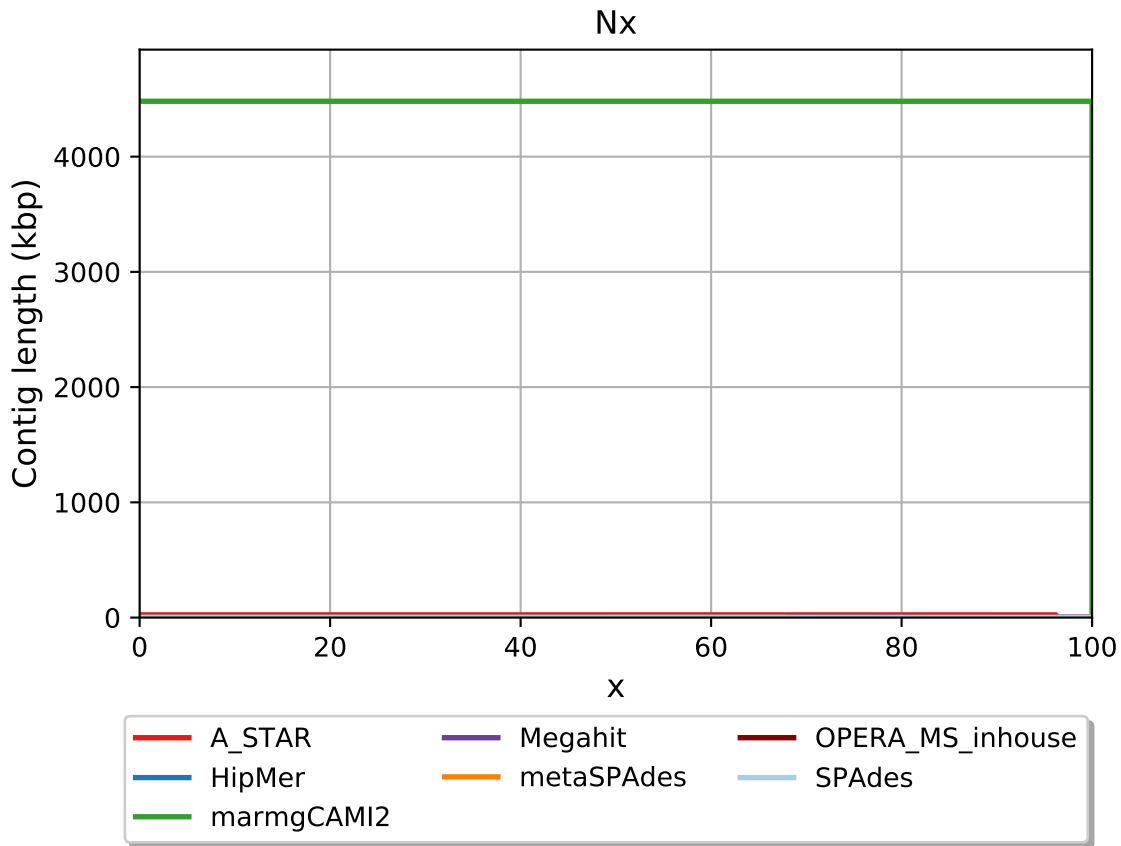
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0
# possibly misassembled contigs	2	1	1	4	3	1	1
# possible misassemblies	3	2	2	4	3	1	1
# local misassemblies	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0
# mismatches	14	4	0	24	6	7	2
# indels	0	1	0	0	0	0	0
# indels (<= 5 bp)	0	0	0	0	0	0	0
# indels (> 5 bp)	0	1	0	0	0	0	0
Indels length	0	11	0	0	0	0	0

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

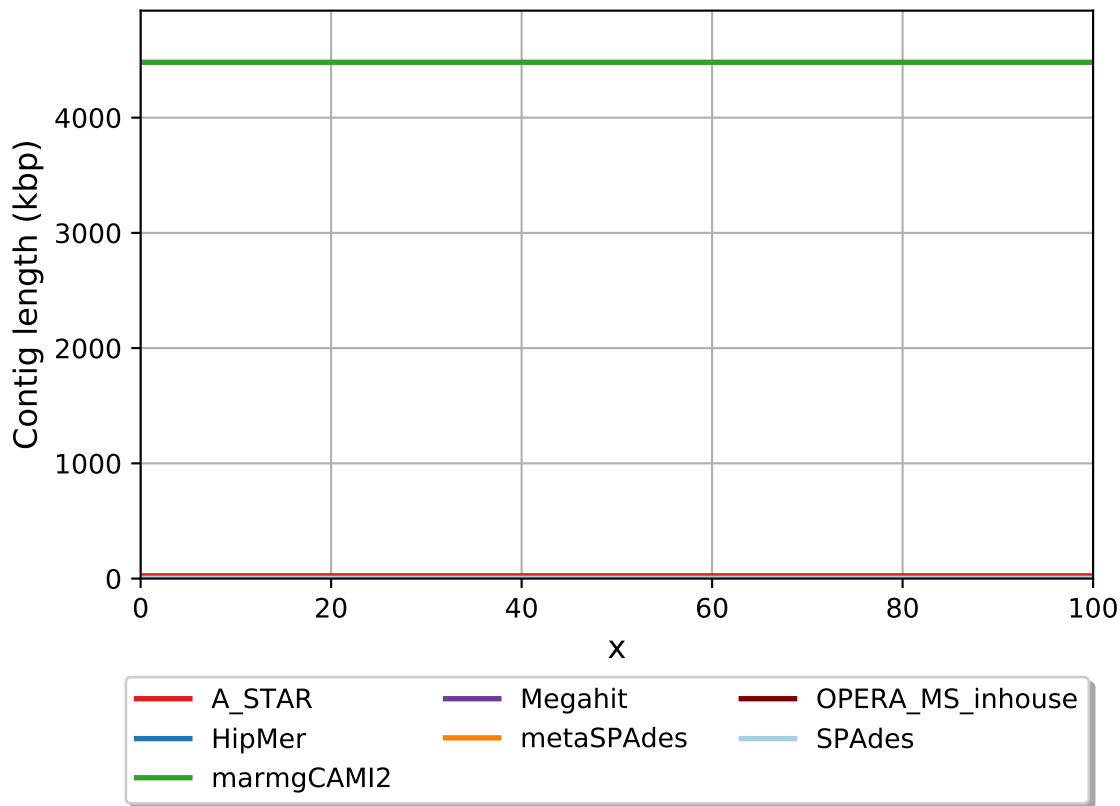
## Unaligned report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0
# partially unaligned contigs	2	2	1	4	3	1	1
Partially unaligned length	20253	7162	4479841	11835	5092	1119	2060
# N's	3955	6	0	0	0	0	0

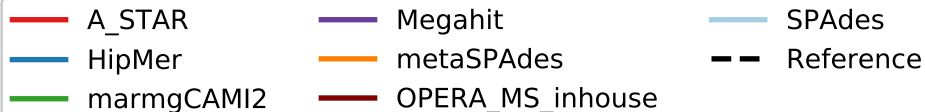
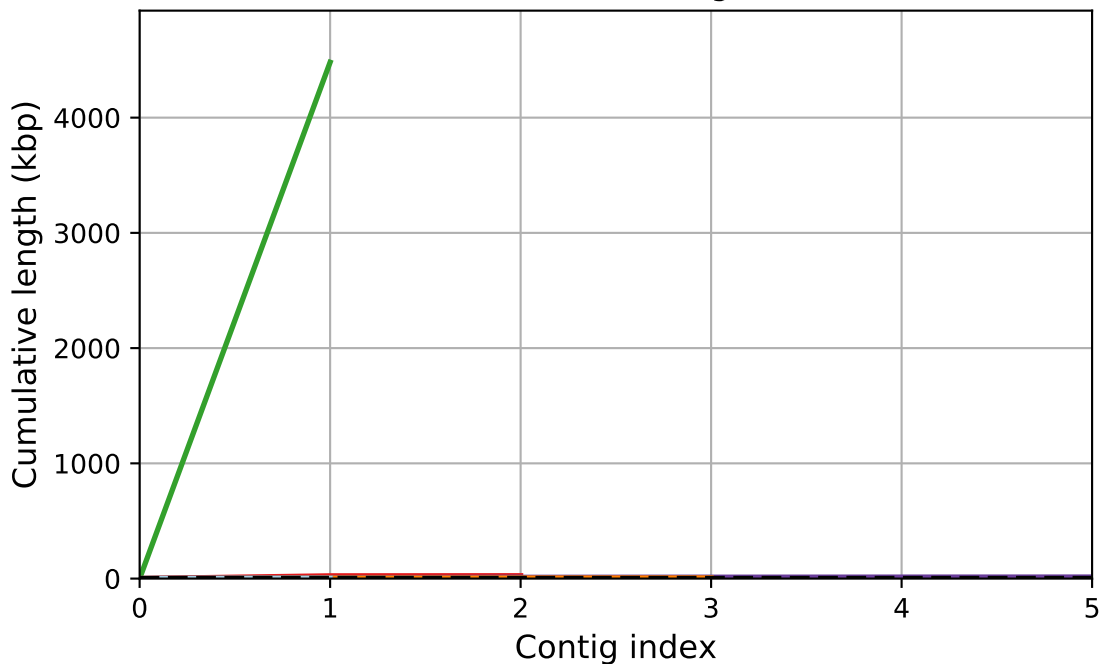
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



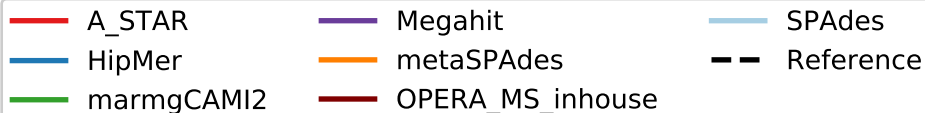
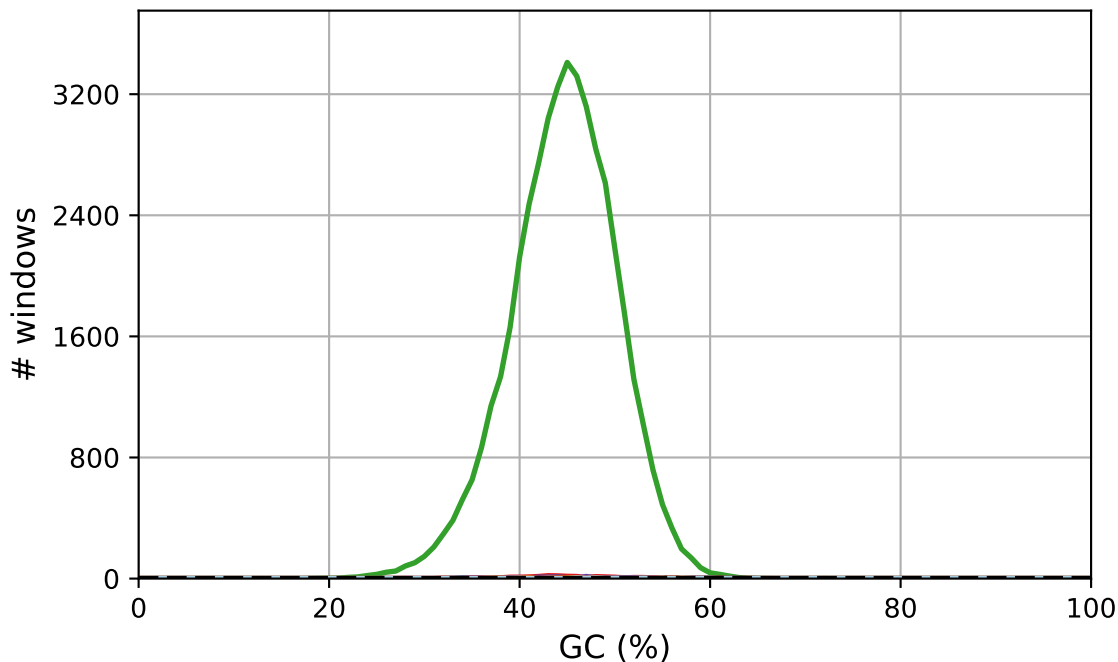
# NGx



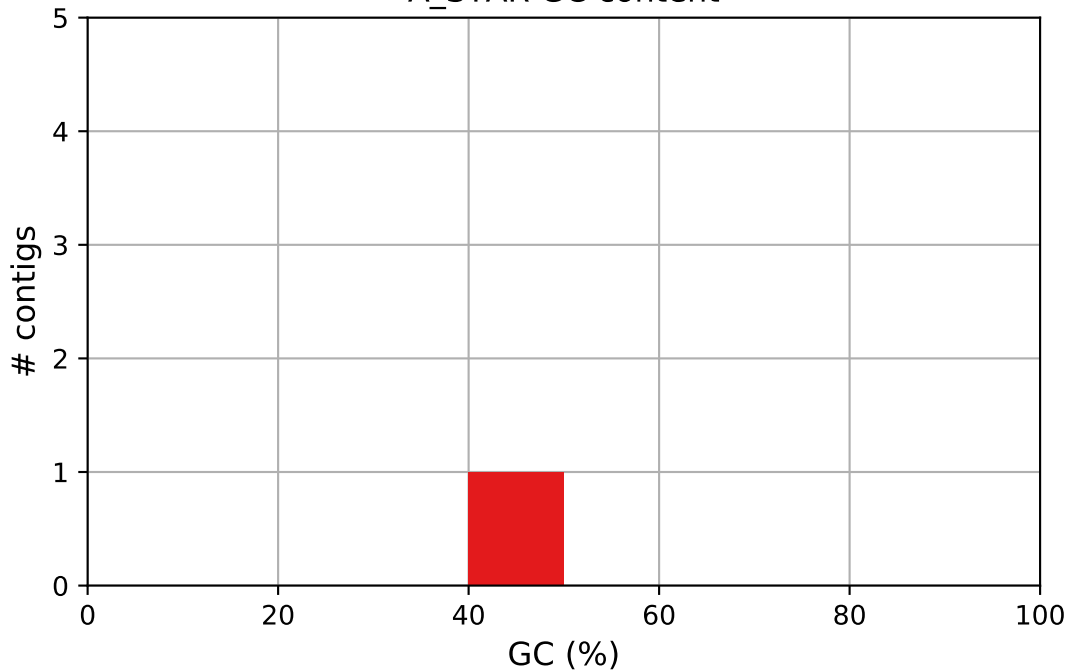
Cumulative length



## GC content



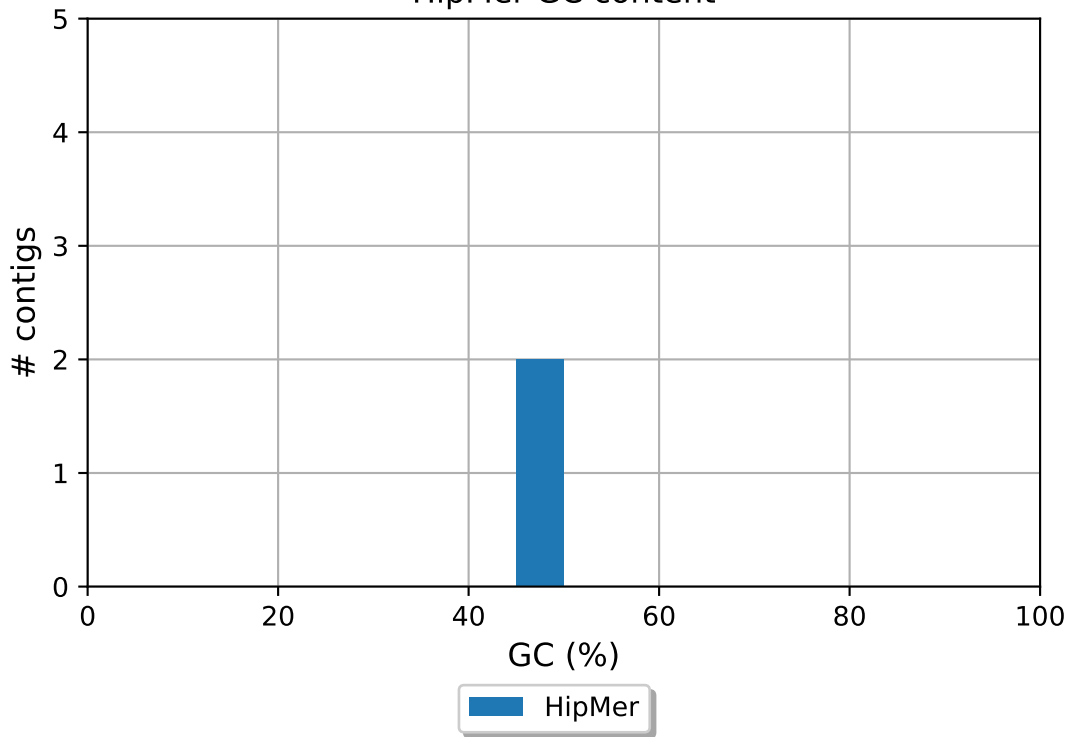
# A\_STAR GC content



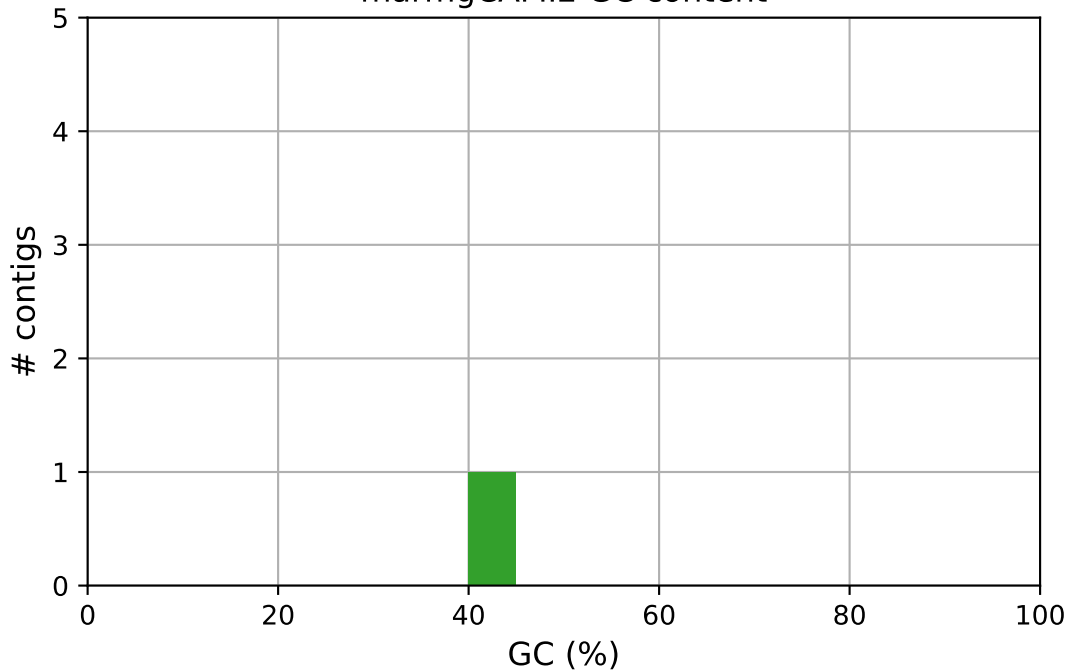
A\_STAR



# HipMer GC content

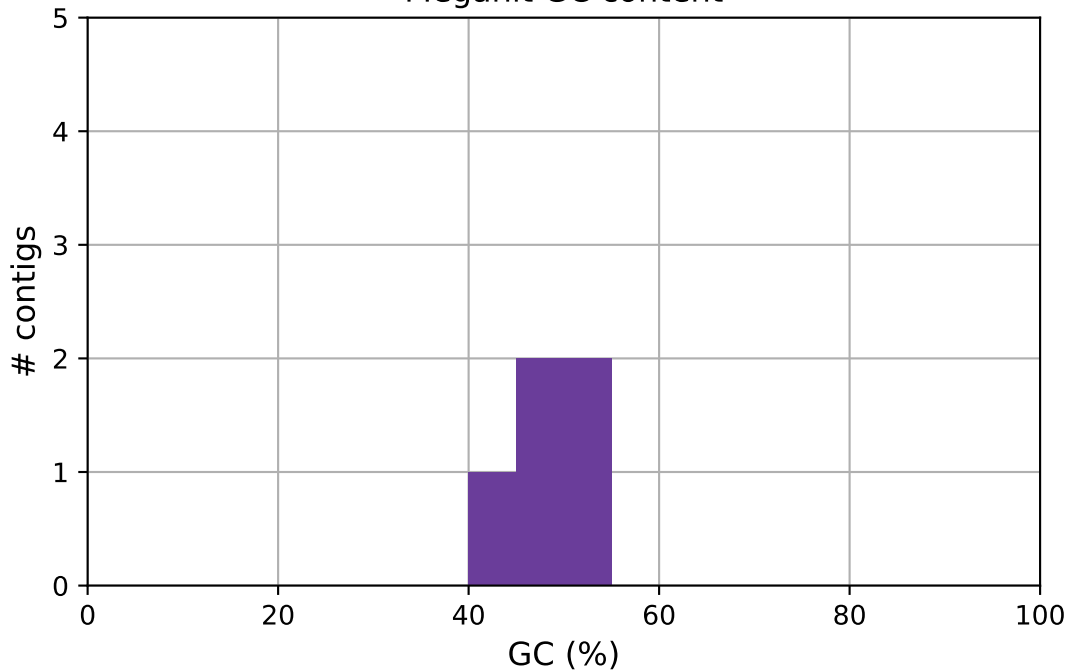


marmgCAMI2 GC content



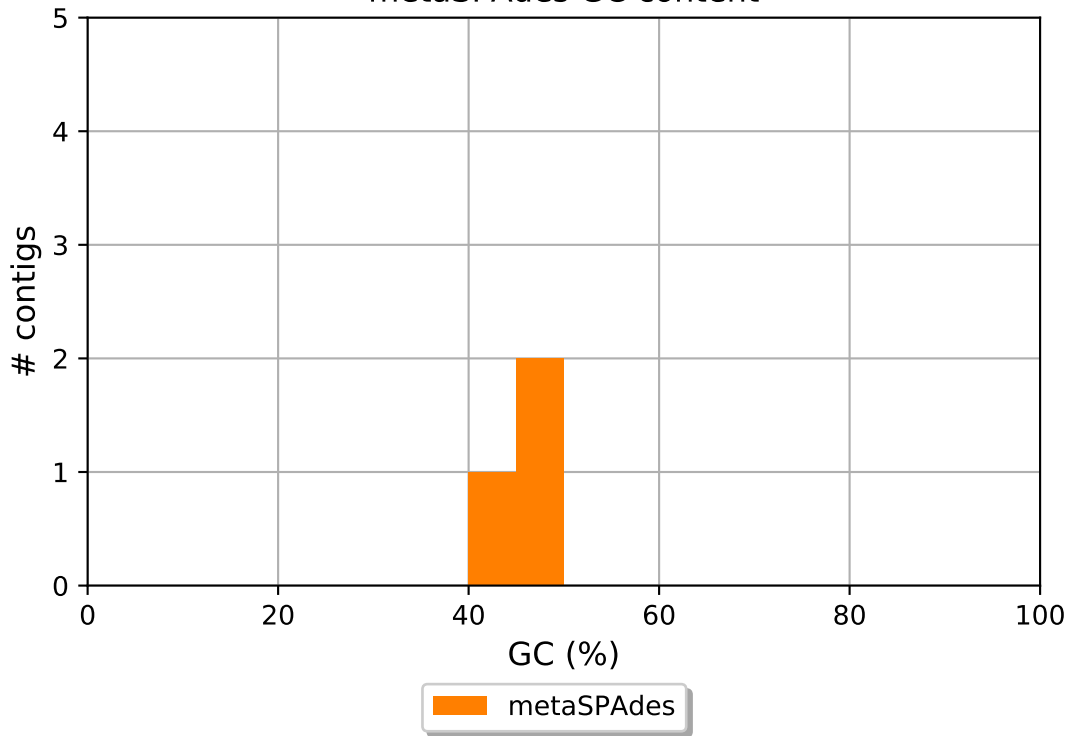
marmgCAMI2

Megahit GC content

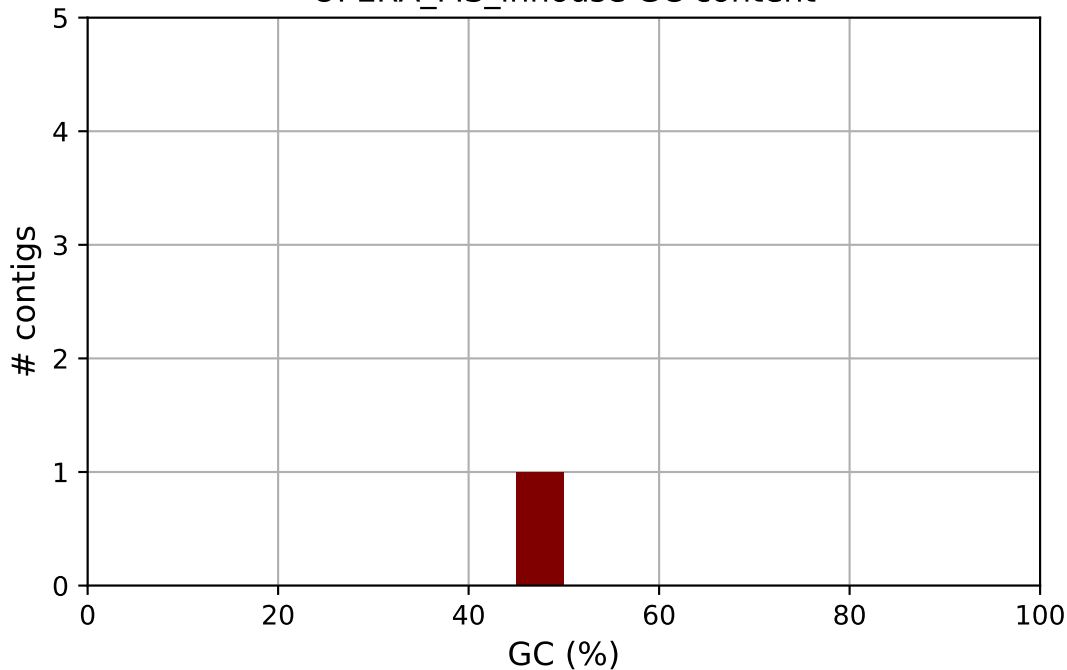


Megahit

metaSPAdes GC content

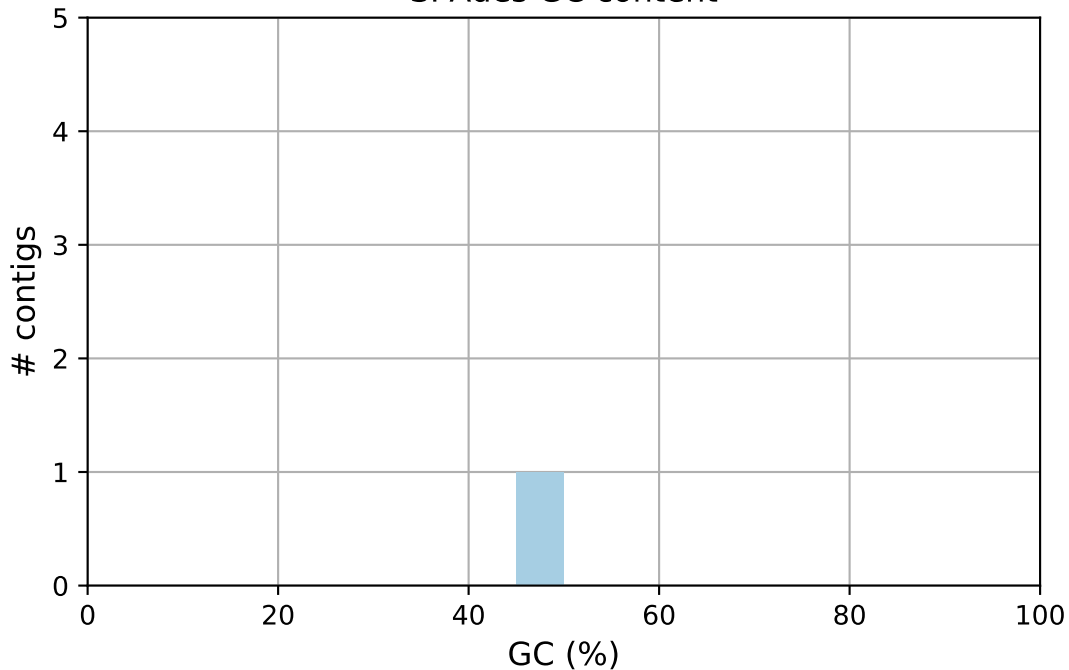


OPERA\_MS\_inhouse GC content



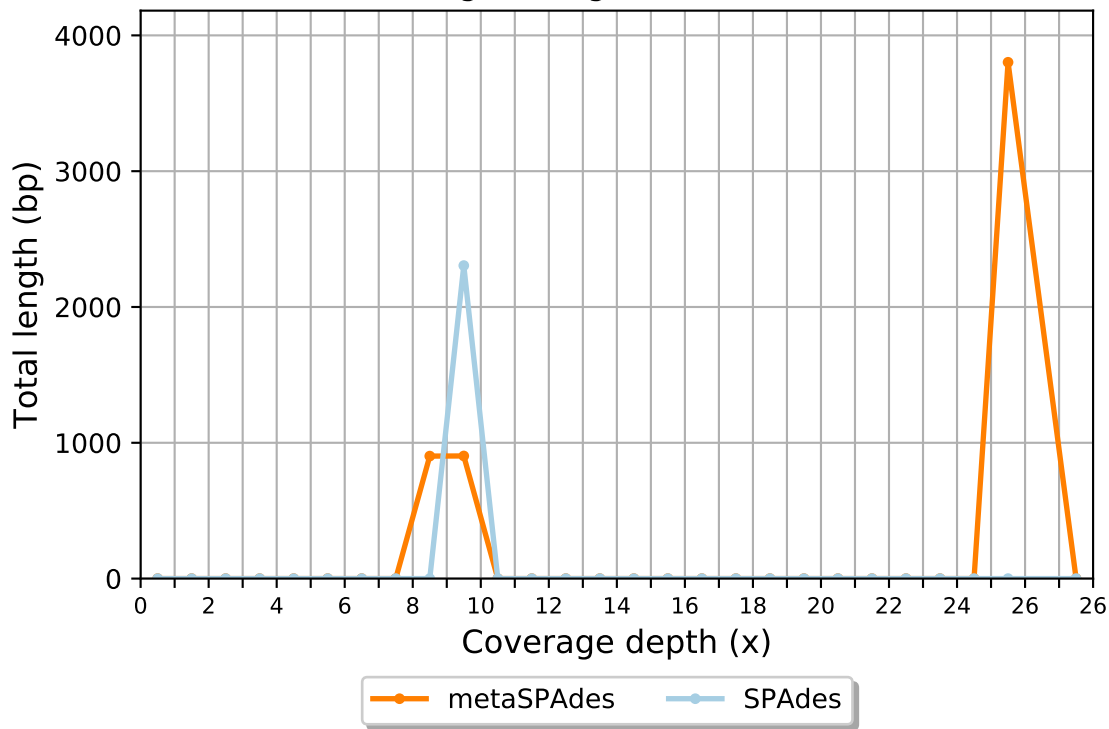
OPERA\_MS\_inhouse

# SPAdes GC content

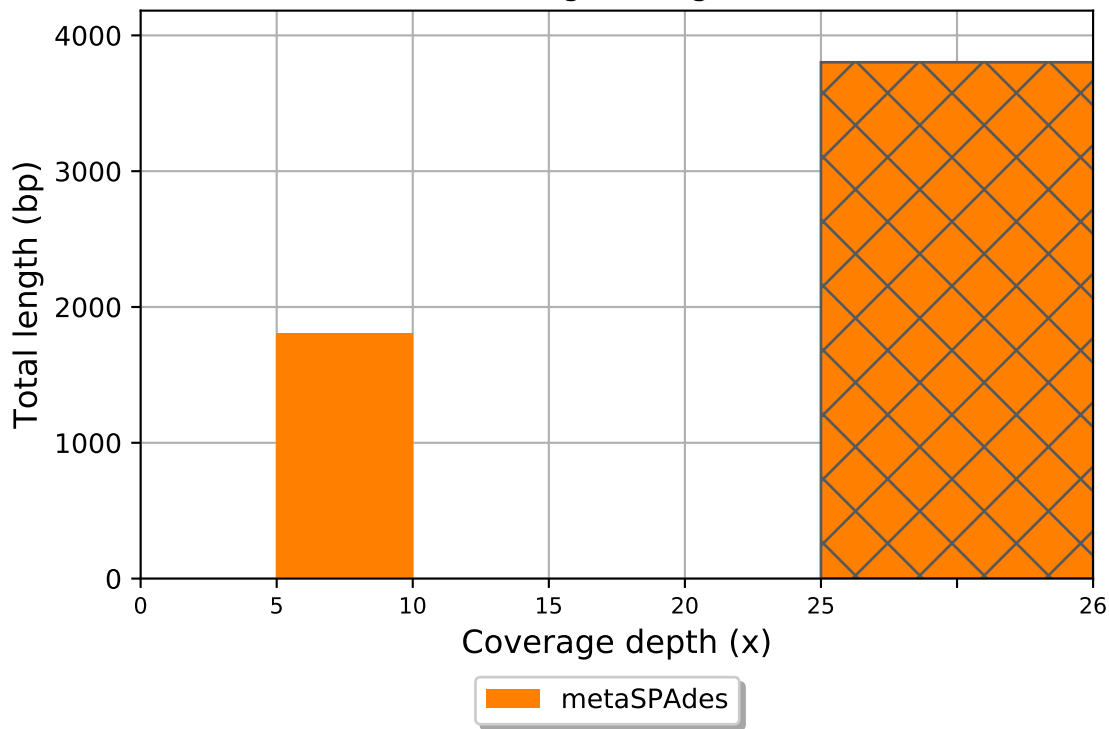


SPAdes

Coverage histogram (bin size: 1x)

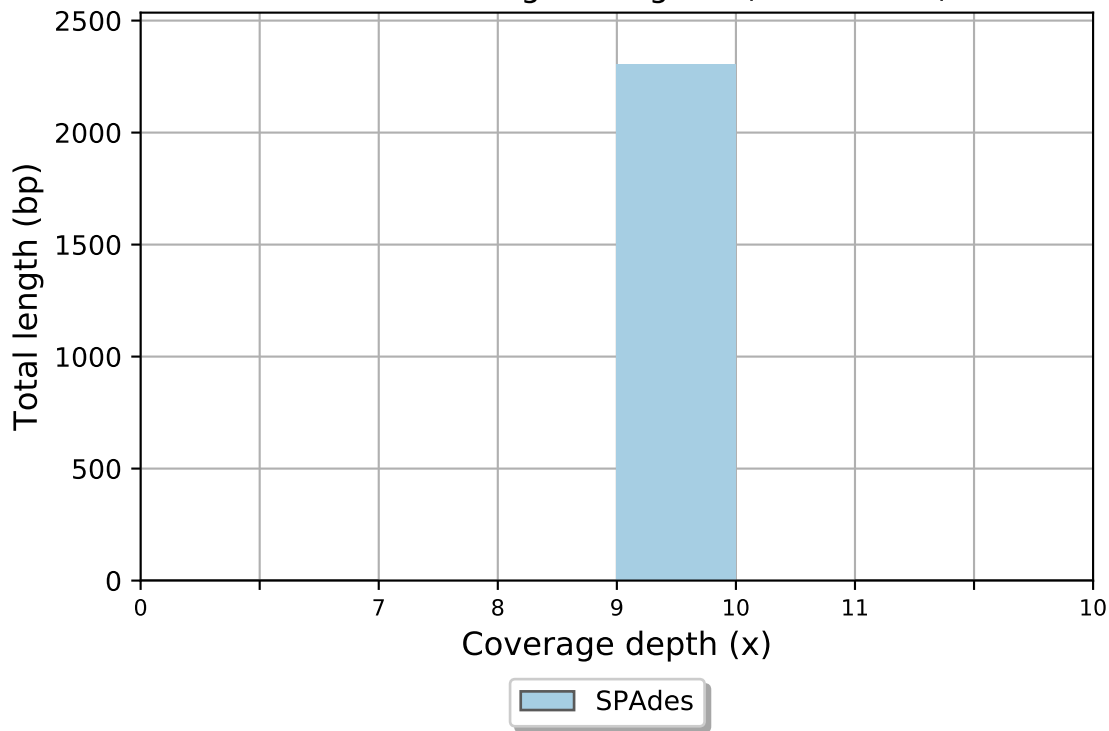


metaSPAdes coverage histogram (bin size: 5x)

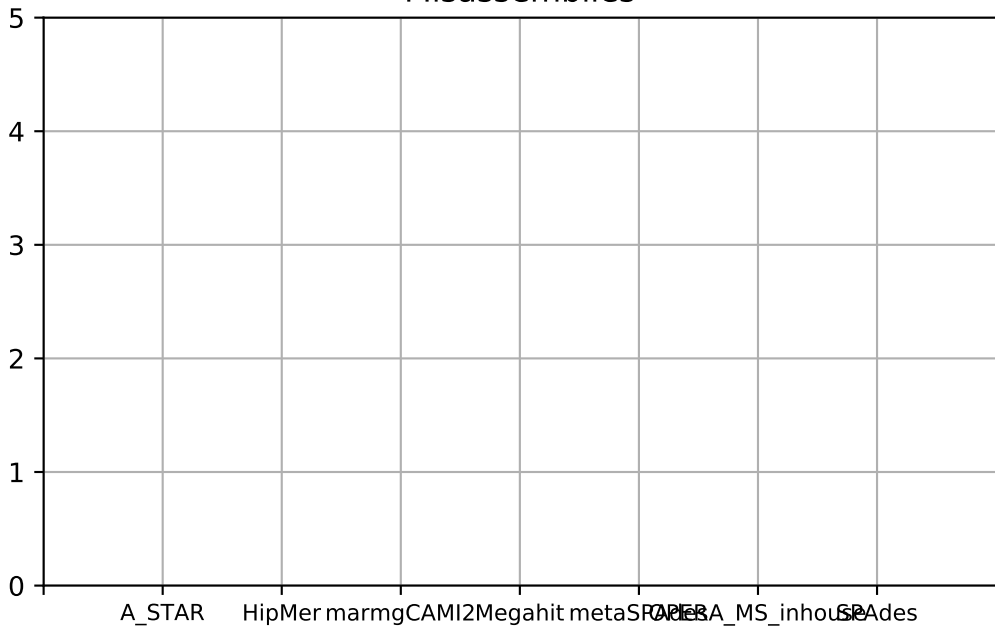




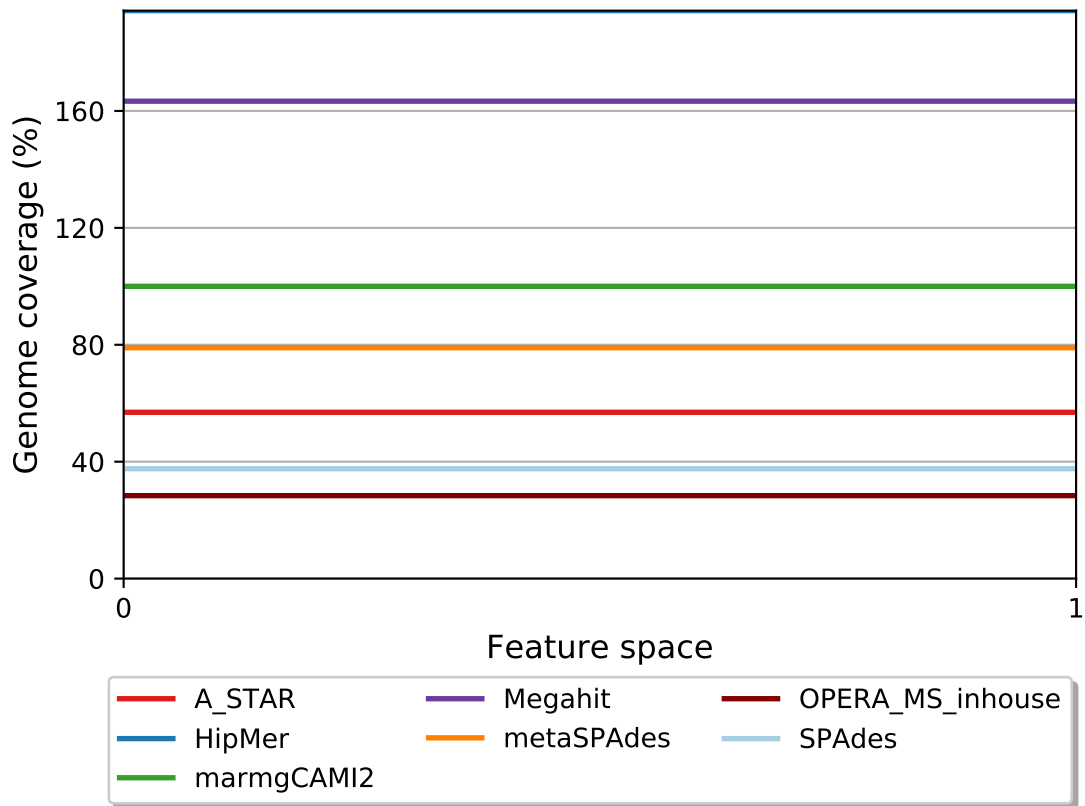
SPAdes coverage histogram (bin size: 1x)



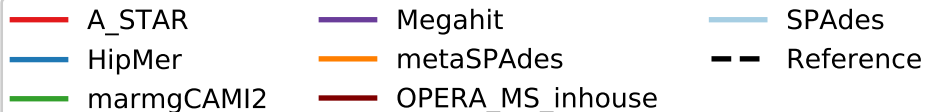
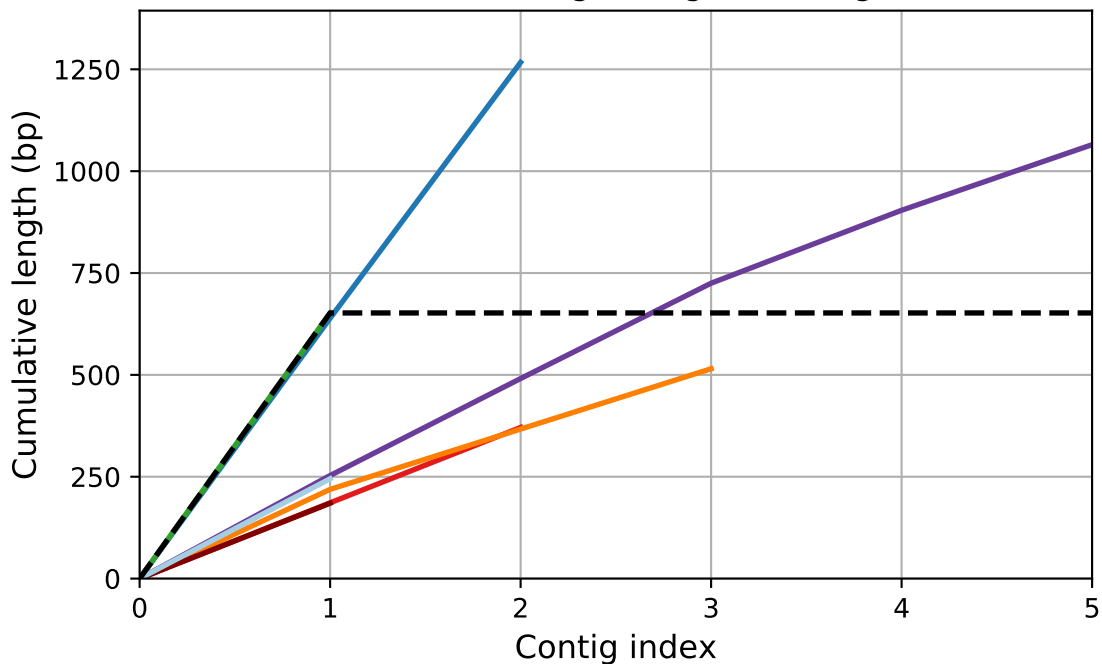
## Misassemblies



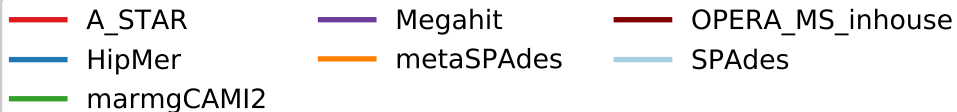
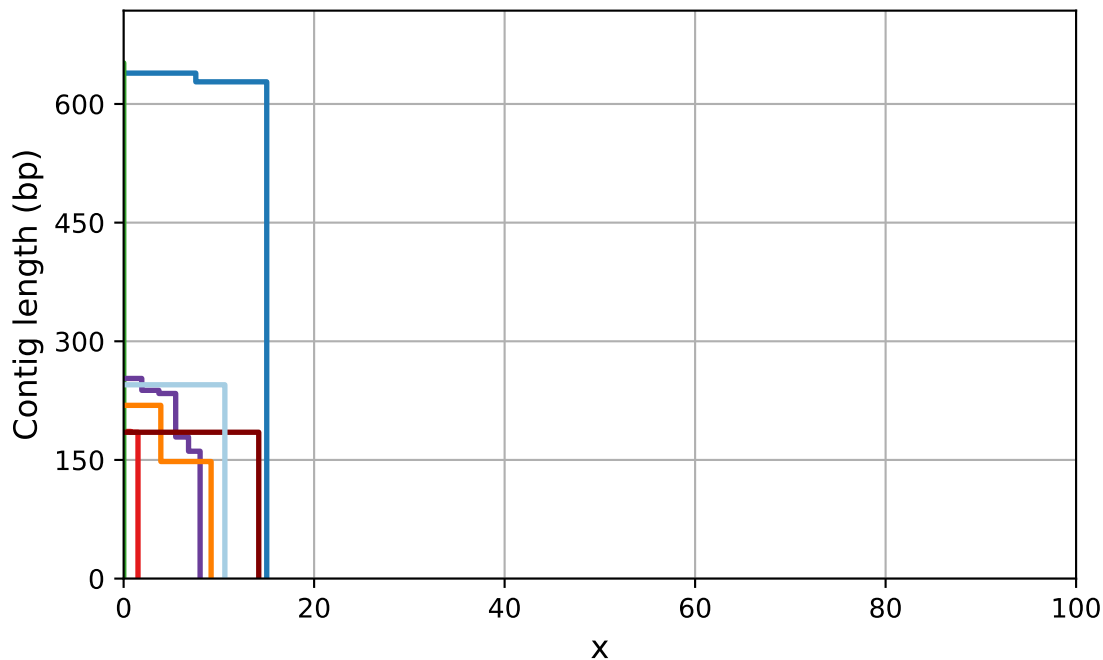
FRCurve (misassemblies)



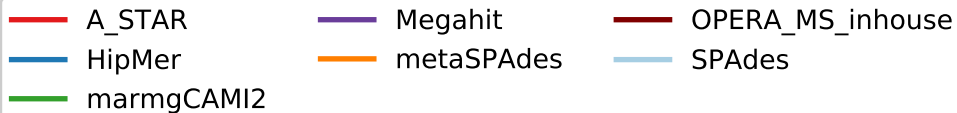
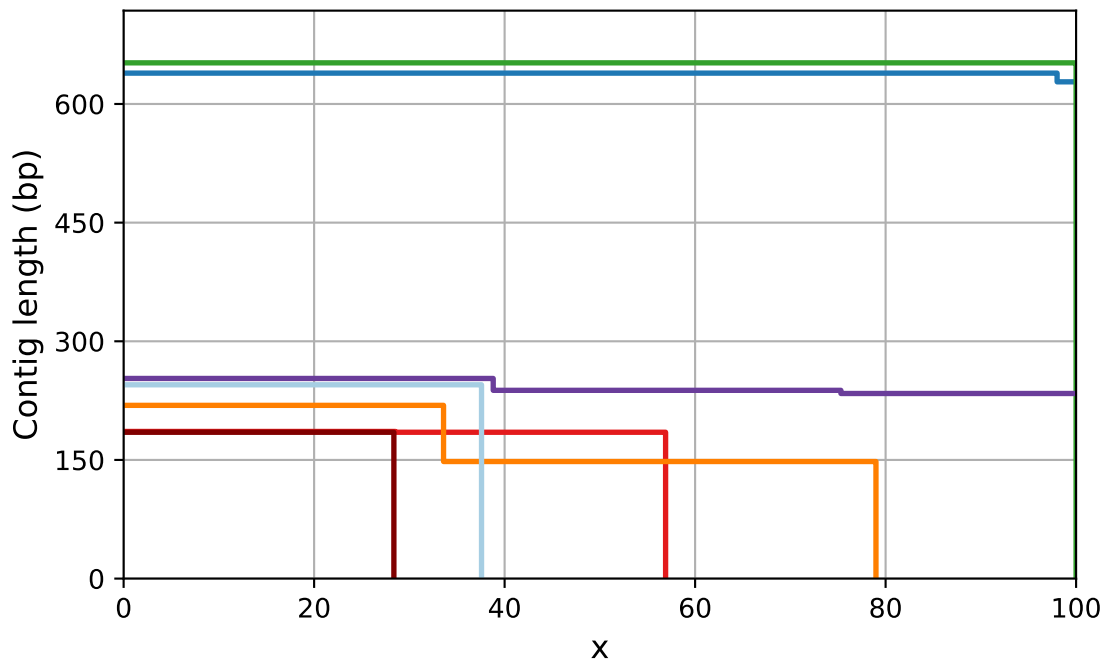
Cumulative length (aligned contigs)

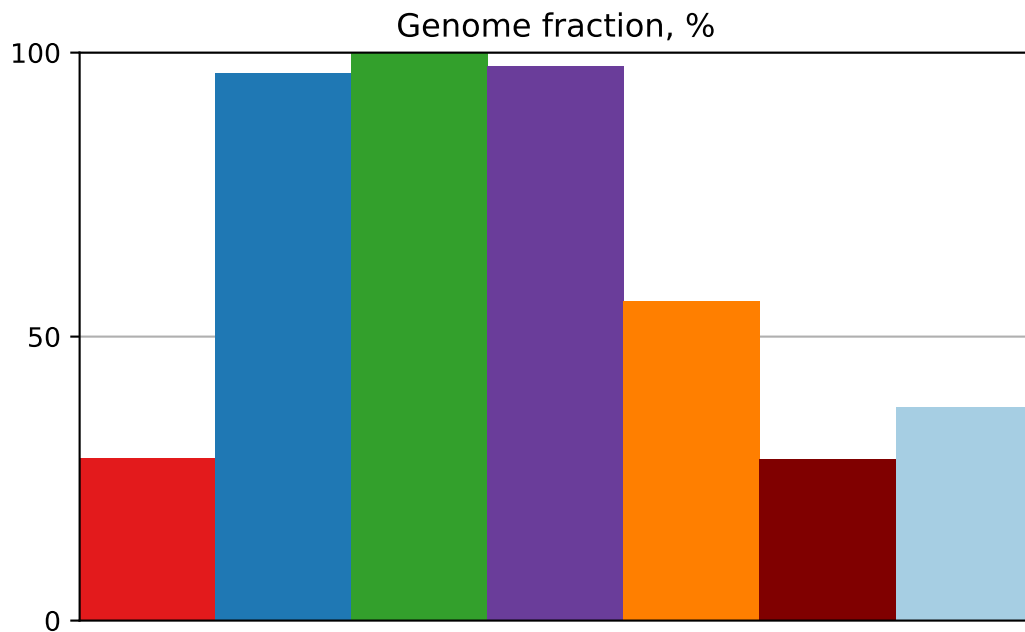


# NAx



# NGAx





A\_STAR

HipMer

marmgCAMI2

Megahit

metaSPAdes

OPERA\_MS\_inhouse

SPAdes