

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	14	16	1	20	13	4	4	6
# contigs (>= 5000 bp)	5	4	1	11	11	4	4	0
# contigs (>= 10000 bp)	4	1	1	8	8	4	3	0
# contigs (>= 25000 bp)	1	0	1	5	2	2	2	0
# contigs (>= 50000 bp)	0	0	1	0	0	0	2	0
Total length (>= 1000 bp)	111613	64486	2011287	283625	176690	132269	156983	14548
Total length (>= 5000 bp)	90015	40152	2011287	254713	168141	132269	156983	0
Total length (>= 10000 bp)	82694	21427	2011287	235326	146679	132269	150818	0
Total length (>= 25000 bp)	34316	0	2011287	175394	63344	85321	136325	0
Total length (>= 50000 bp)	0	0	2011287	0	0	0	136325	0
# contigs	17	17	1	21	13	4	4	7
Largest contig	34316	21427	2011287	39210	31672	44078	71756	3432
Total length	113561	65003	2011287	284527	176690	132269	156983	15136
Reference length	7907	7907	7907	7907	7907	7907	7907	7907
GC (%)	55.19	52.89	56.08	54.95	54.40	55.19	55.57	50.13
Reference GC (%)	48.01	48.01	48.01	48.01	48.01	48.01	48.01	48.01
N50	19019	6075	2011287	32814	19409	41243	64569	2729
NG50	34316	21427	2011287	39210	31672	44078	71756	2894
N75	7321	2592	2011287	19879	10684	24463	64569	1957
NG75	34316	21427	2011287	39210	31672	44078	71756	2894
L50	3	3	1	4	4	2	2	3
LG50	1	1	1	1	1	1	1	2
L75	5	8	1	7	7	3	2	5
LG75	1	1	1	1	1	1	1	2
# 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	2	2	1	2	3	1	1	0
# unaligned contigs	0 + 12 part	0 + 11 part	0 + 1 part	0 + 19 part	0 + 13 part	0 + 4 part	0 + 4 part	0 + 5 part
Unaligned length	96501	48281	2003380	263571	153072	124362	149134	7165
Genome fraction (%)	58.821	98.191	100.000	100.000	100.000	100.000	100.000	90.135
Duplication ratio	3.668	2.154	1.000	2.650	2.987	1.000	0.993	1.118
# N's per 100 kbp	5055.43	0.00	0.00	0.00	0.00	0.00	0.64	0.00
# mismatches per 100 kbp	86.00	0.00	0.00	1783.23	75.88	0.00	417.35	631.40
# indels per 100 kbp	0.00	0.00	0.00	25.29	0.00	0.00	189.71	238.53
Largest alignment	779	1986	2558	2558	2558	2558	2564	2040
Total aligned length	9561	15750	7907	20818	23618	7907	7848	7346
NGA50	569	1591	2041	1976	2558	2041	1976	1291
NGA75	438	1151	1777	1976	2041	1777	1777	760
LGA50	6	3	2	2	2	2	2	3
LGA75	10	4	3	3	3	3	3	5

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

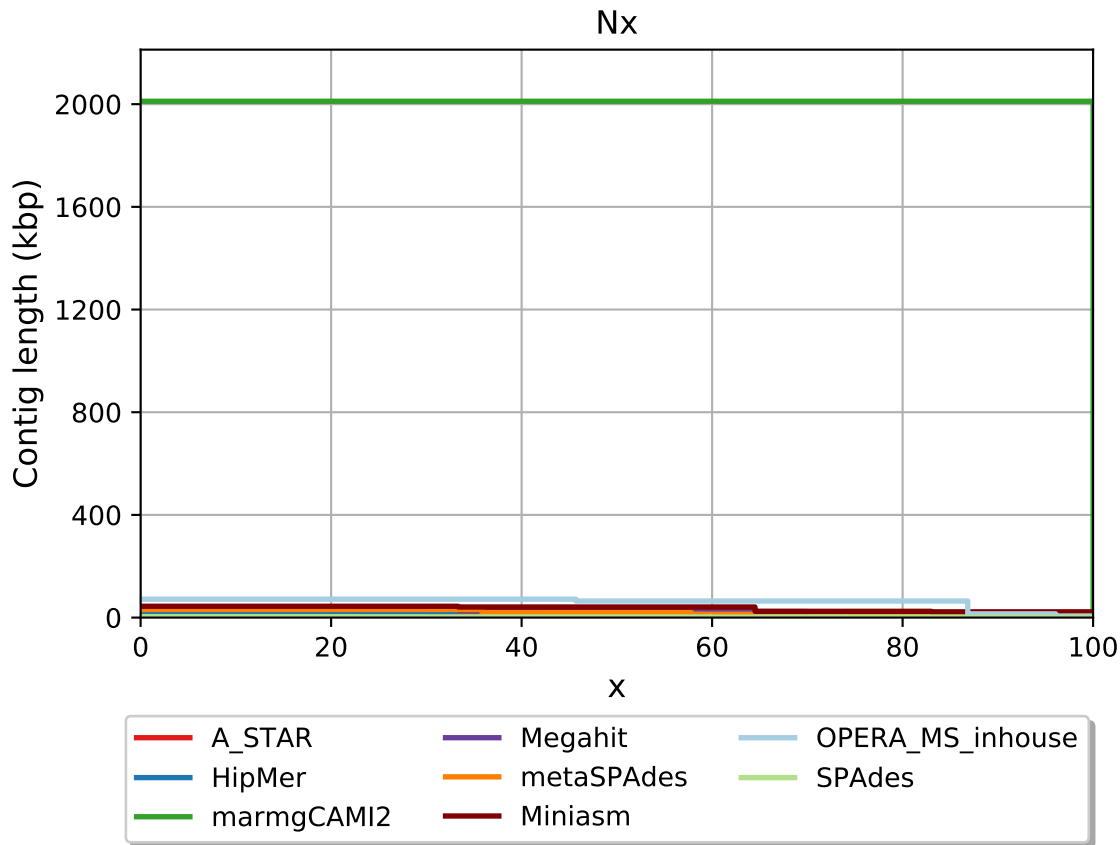
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	10	9	0	17	10	3	3	5
# possible misassemblies	10	11	0	24	16	6	6	5
# 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	2	1	2	3	1	1	0
# mismatches	4	0	0	141	6	0	33	45
# indels	0	0	0	2	0	0	15	17
# indels (<= 5 bp)	0	0	0	0	0	0	14	15
# indels (> 5 bp)	0	0	0	2	0	0	1	2
Indels length	0	0	0	130	0	0	83	29

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).

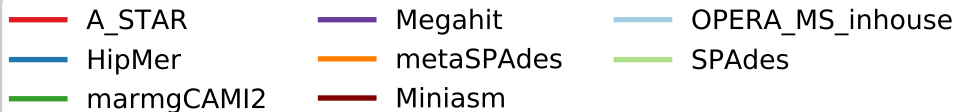
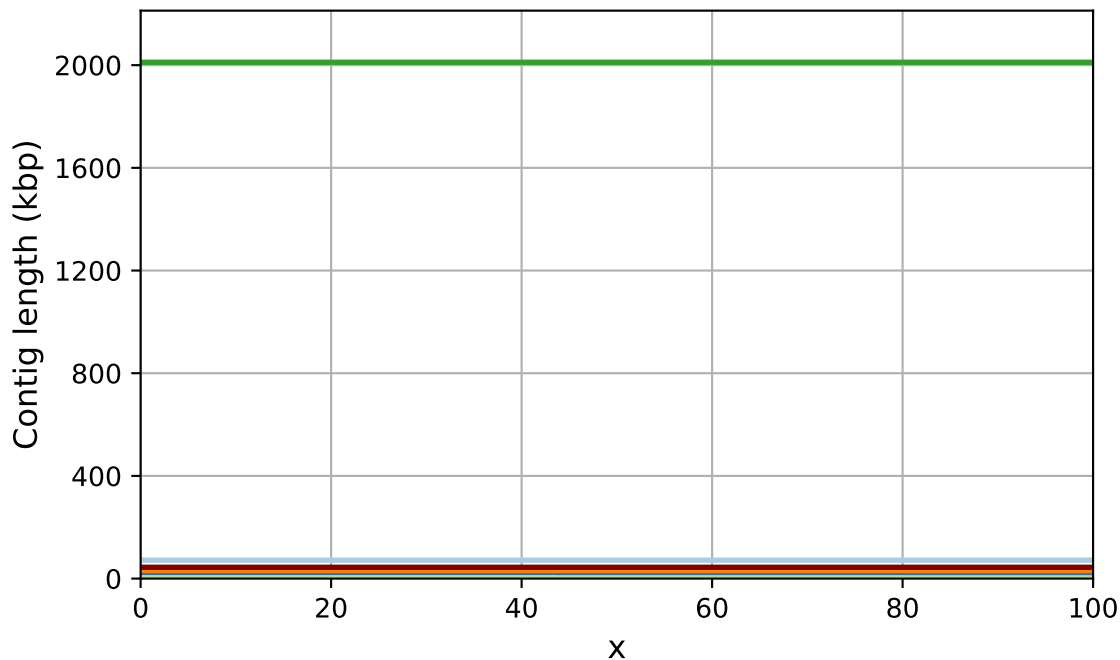
Unaligned report

	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	12	11	1	19	13	4	4	5
Partially unaligned length	96501	48281	2003380	263571	153072	124362	149134	7165
# N's	5741	0	0	0	0	0	1	0

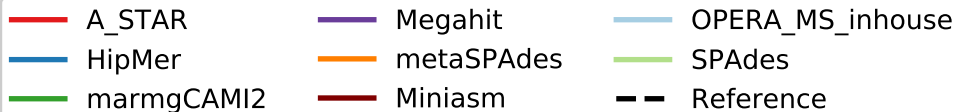
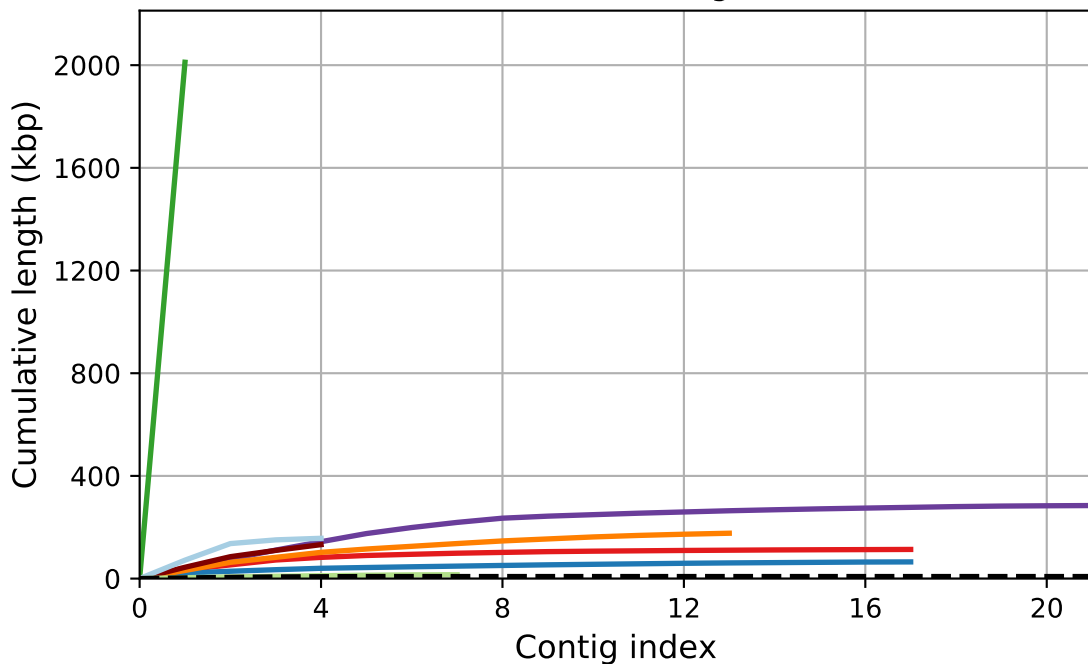
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



NGx

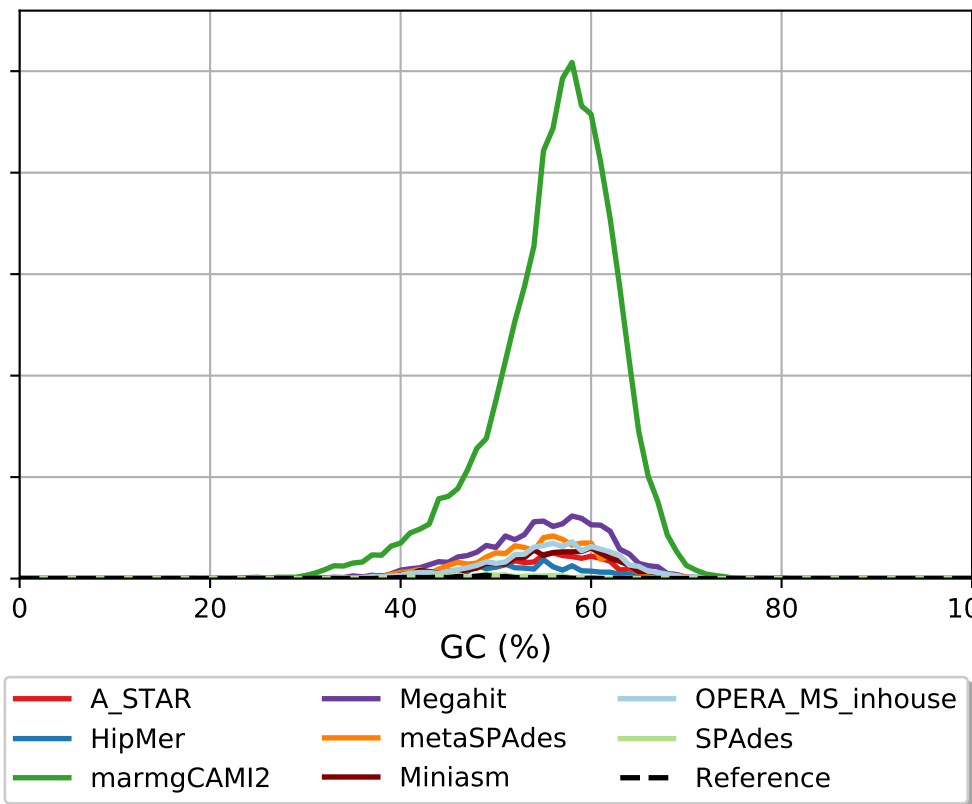


Cumulative length

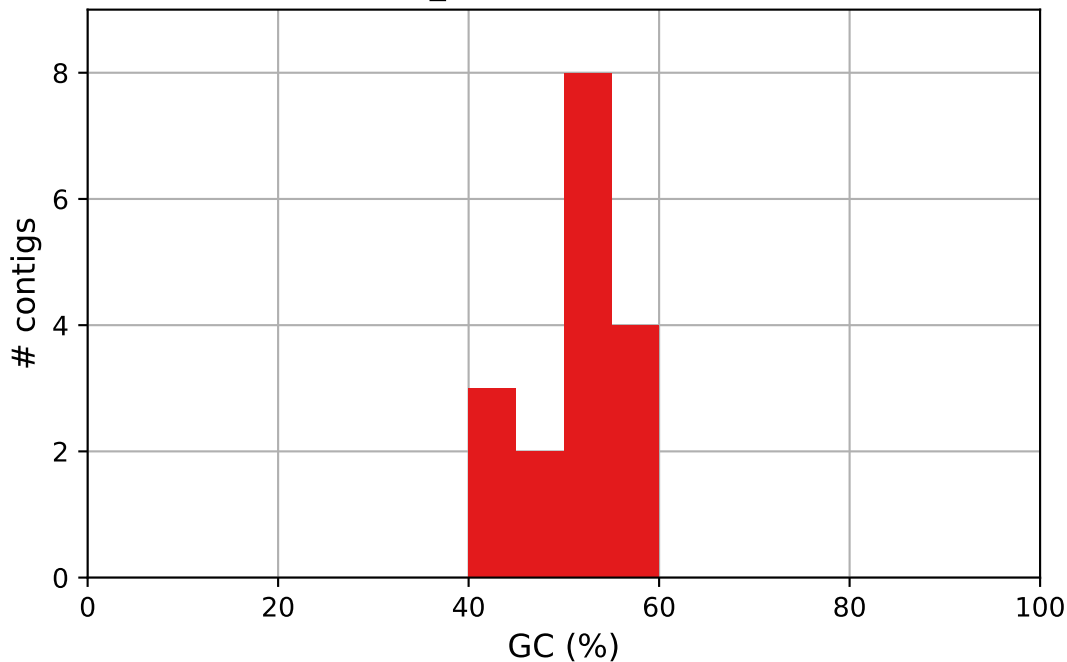


The figure displays the GC content distribution for several genome assembly methods. The x-axis represents GC percentage from 0 to 100, and the y-axis represents frequency. A dashed black line indicates the reference distribution, which is centered around 50% GC. Most assemblers show a peak between 50% and 60% GC, with marmgCAMI2 having the highest and narrowest peak.

Assembler	Approximate Peak GC (%)	Relative Peak Height
A_STAR	~58	Low
HipMer	~55	Low
marmgCAMI2	~58	High
Megahit	~58	Medium-High
metaSPAdes	~55	Medium-Low
OPERA_MS_inhouse	~55	Low
SPAdes	~55	Low
Miniasm	~55	Low
Reference	~50	Baseline

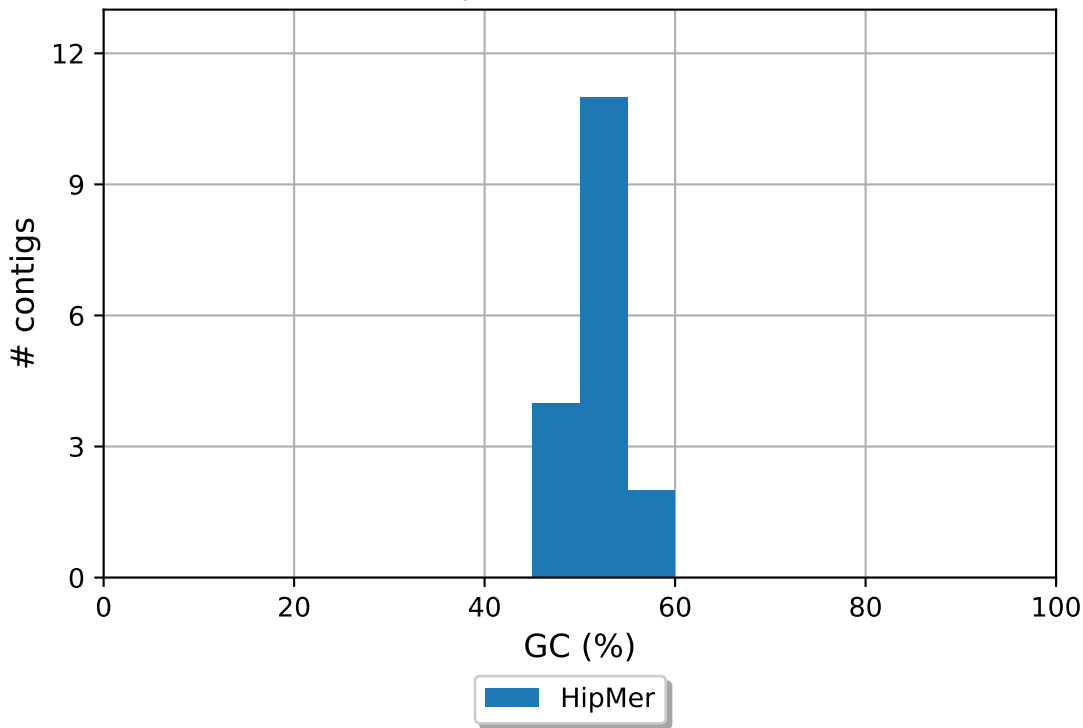


A_STAR GC content

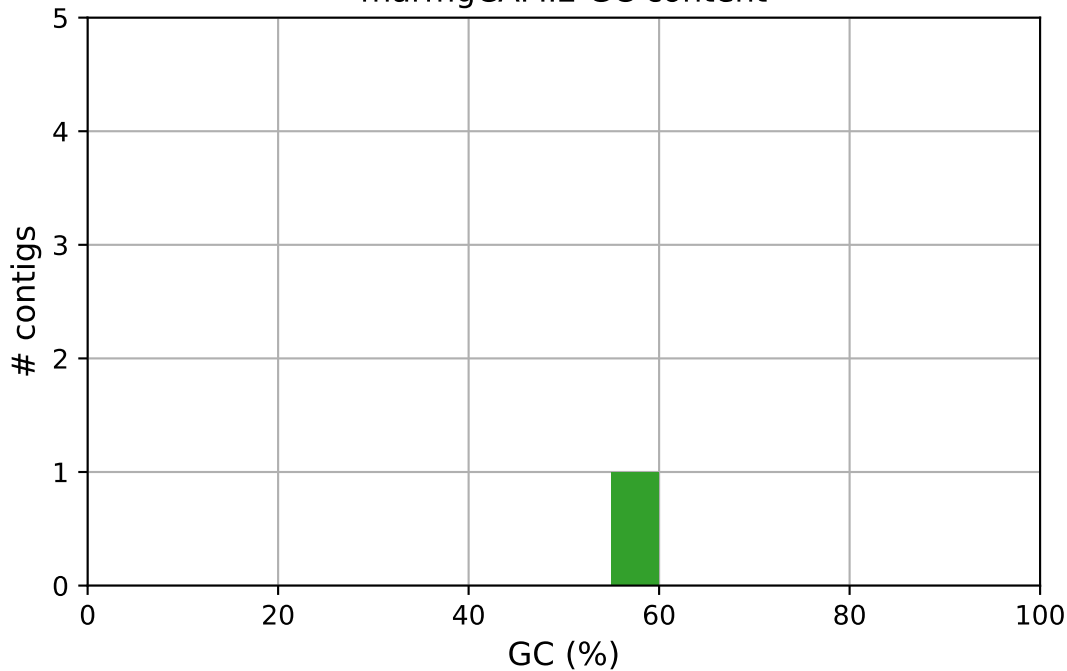


A_STAR

HipMer GC content

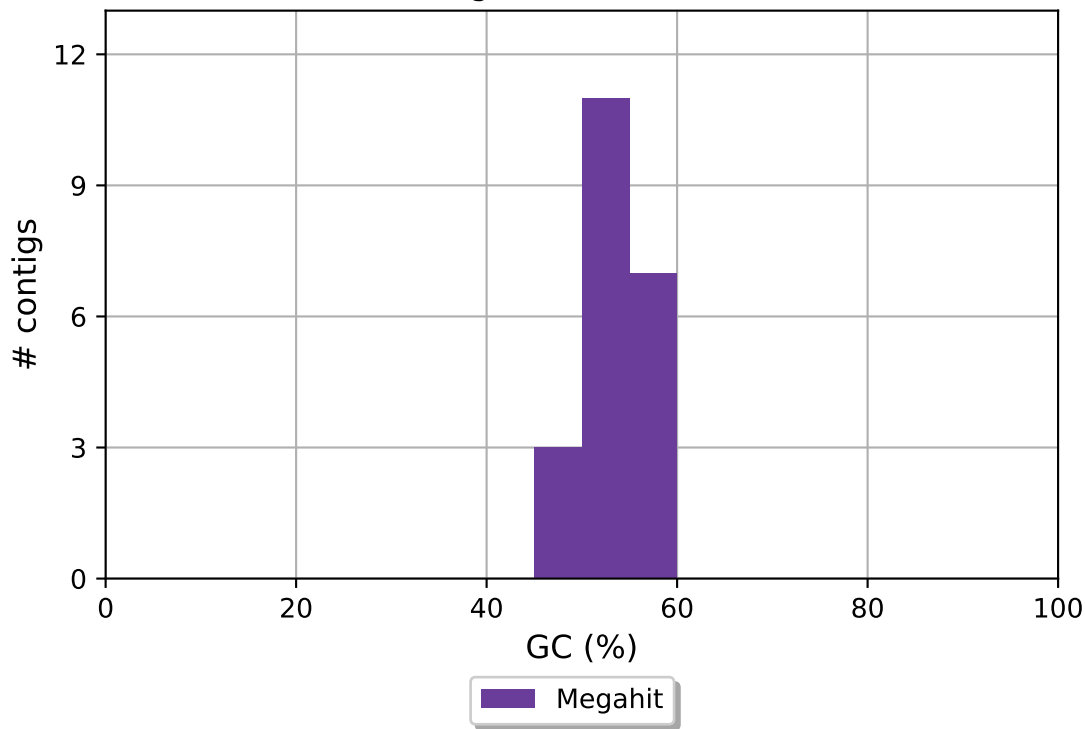


marmgCAMI2 GC content

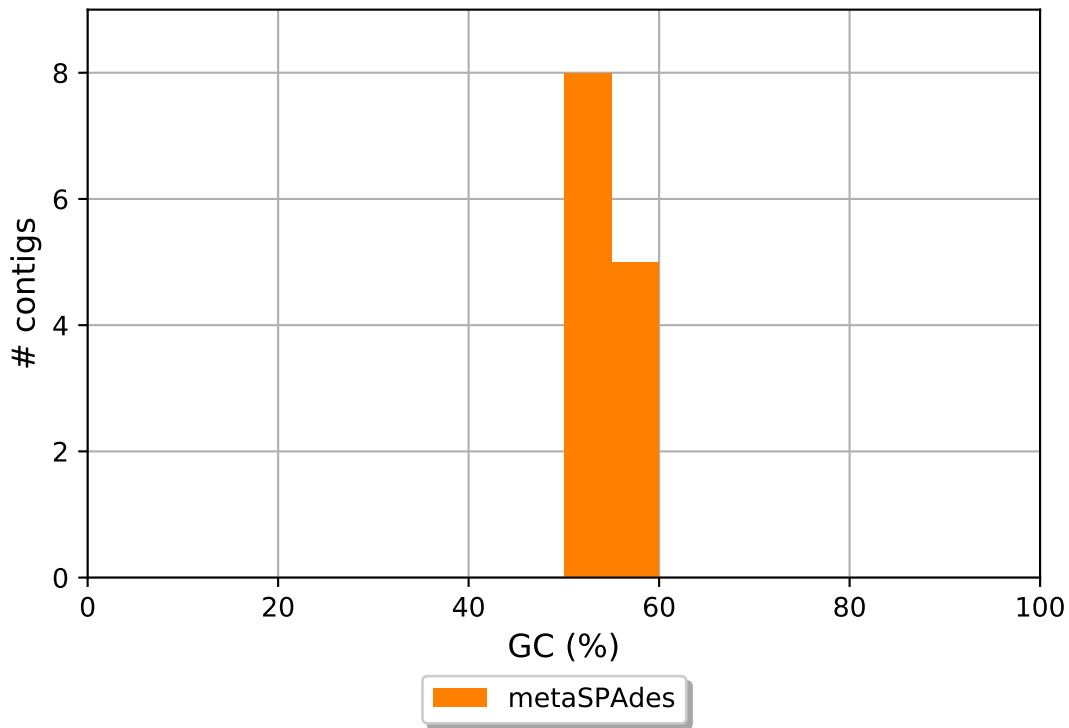


marmgCAMI2

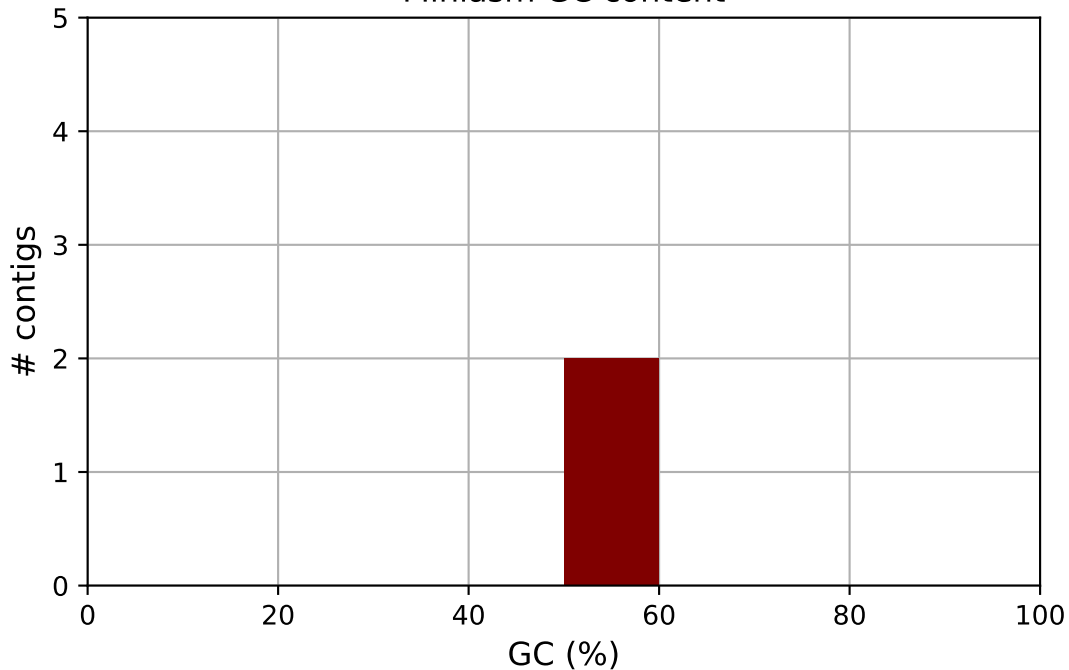
Megahit GC content



metaSPAdes GC content

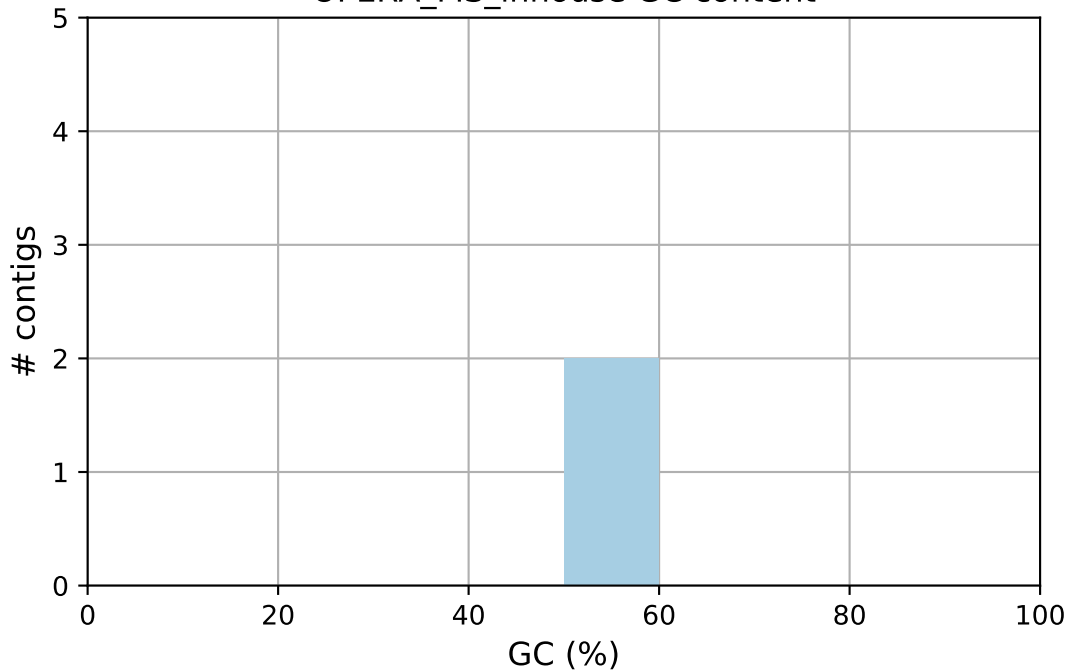


Miniasm GC content



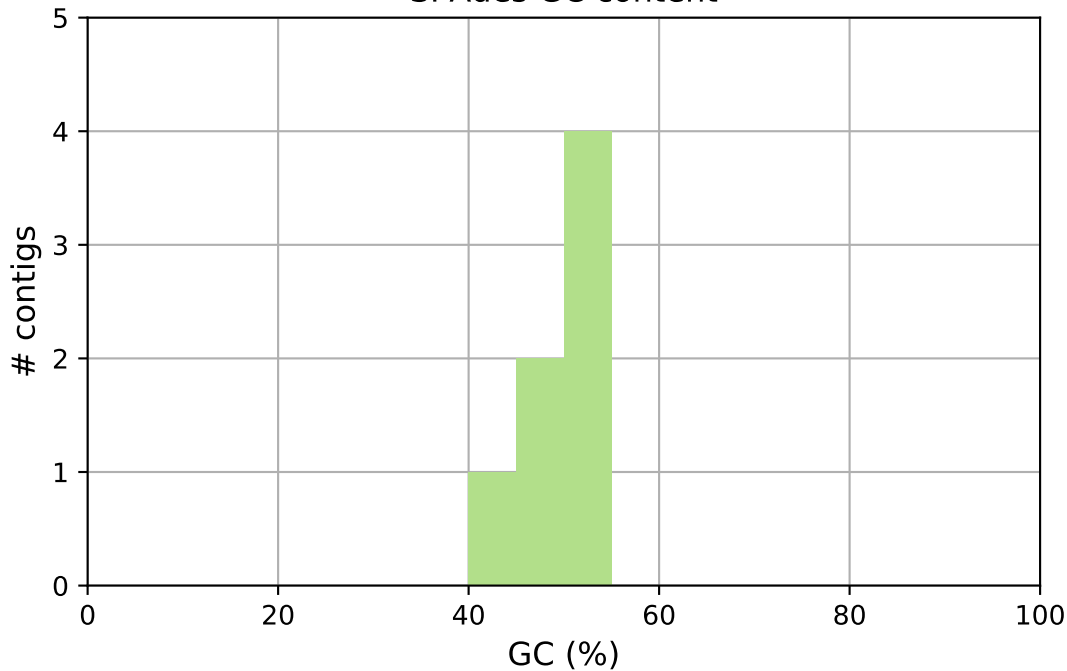
Miniasm

OPERA_MS_inhouse GC content



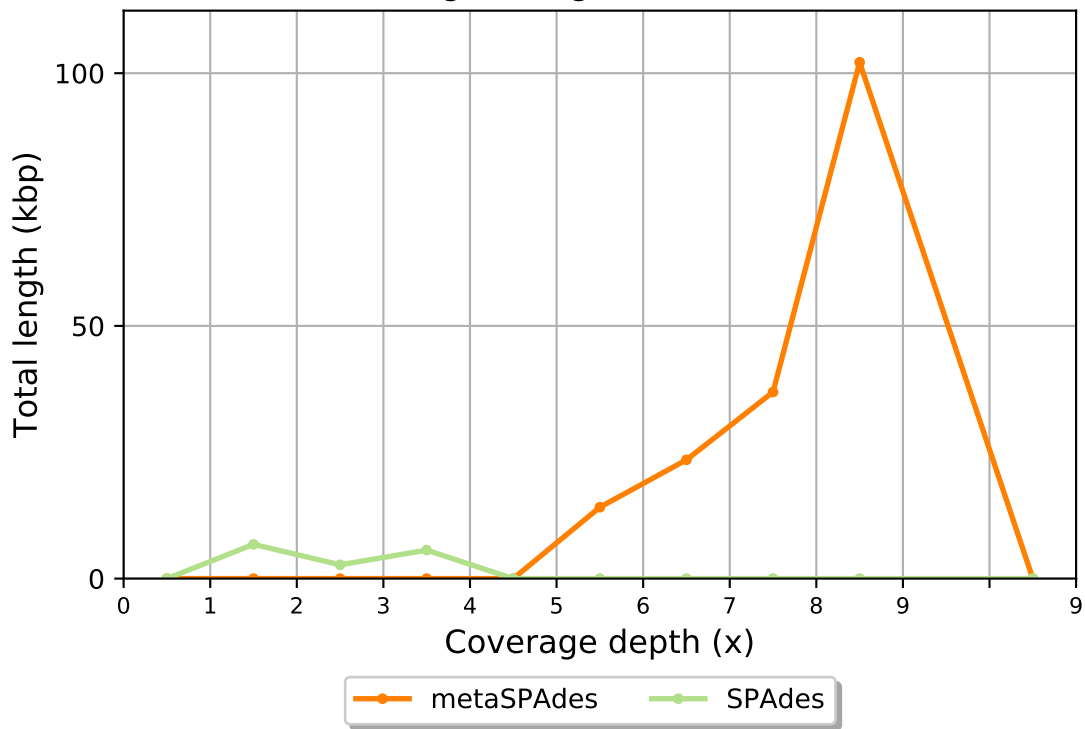
OPERA_MS_inhouse

SPAdes GC content

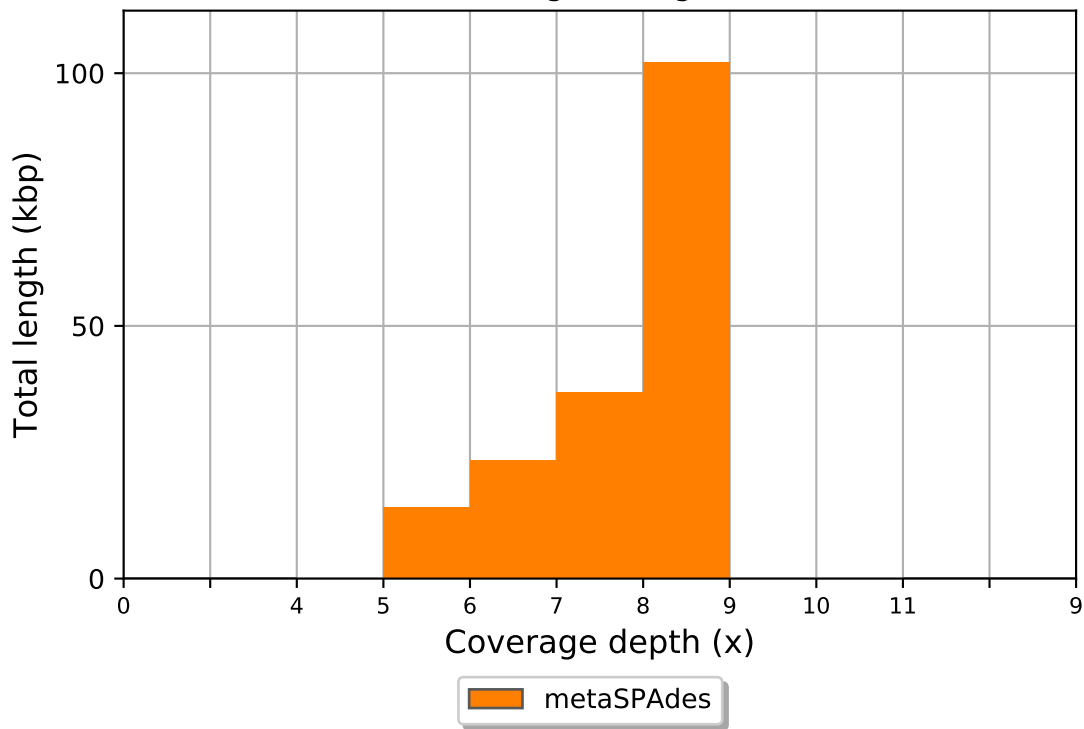


SPAdes

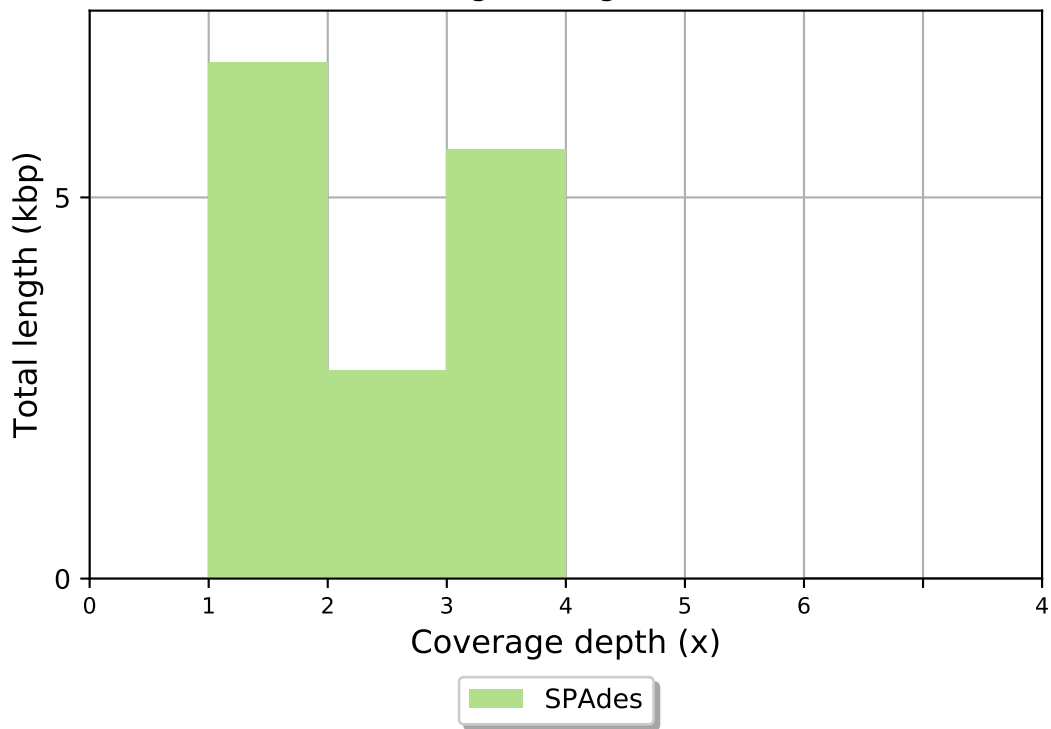
Coverage histogram (bin size: 1x)



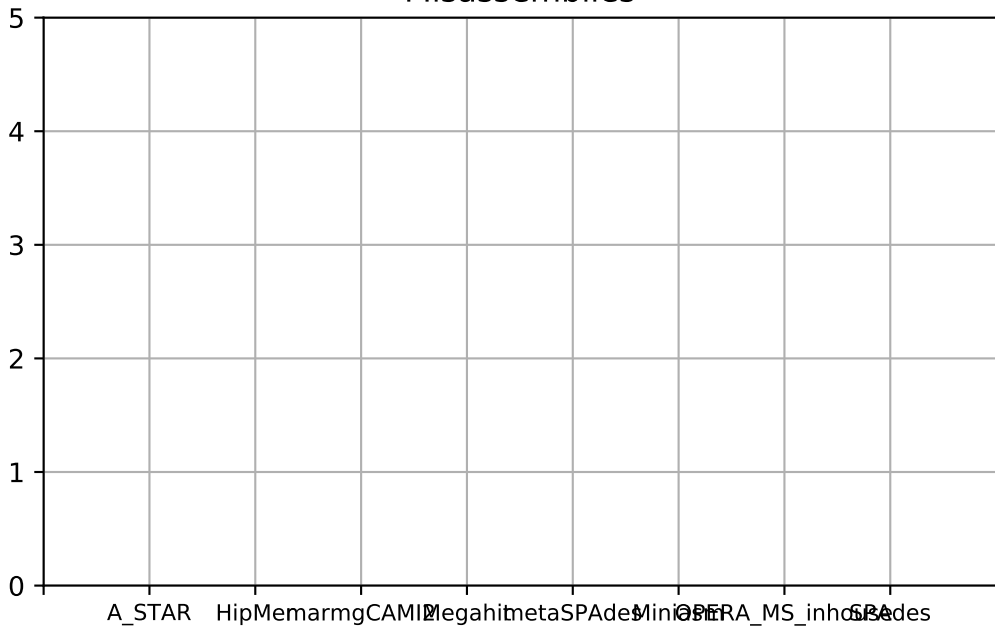
metaSPAdes coverage histogram (bin size: 1x)



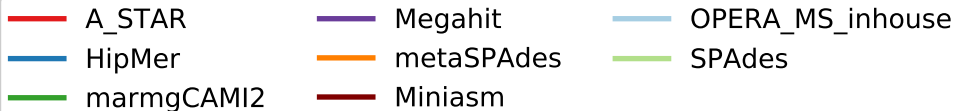
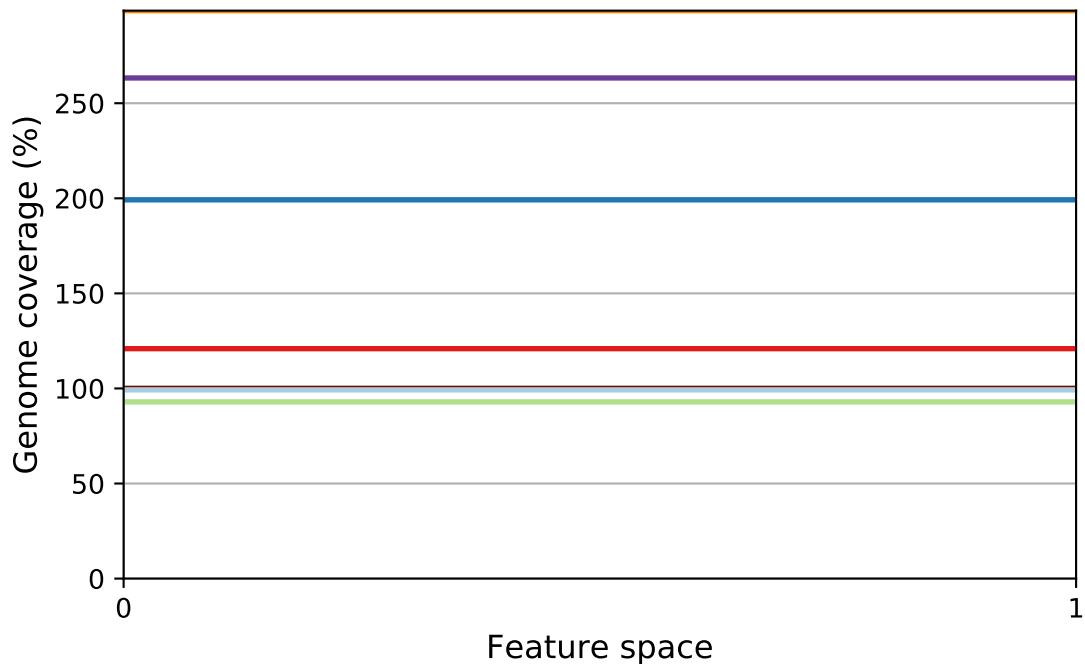
SPAdes coverage histogram (bin size: 1x)



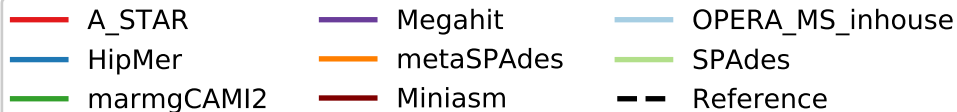
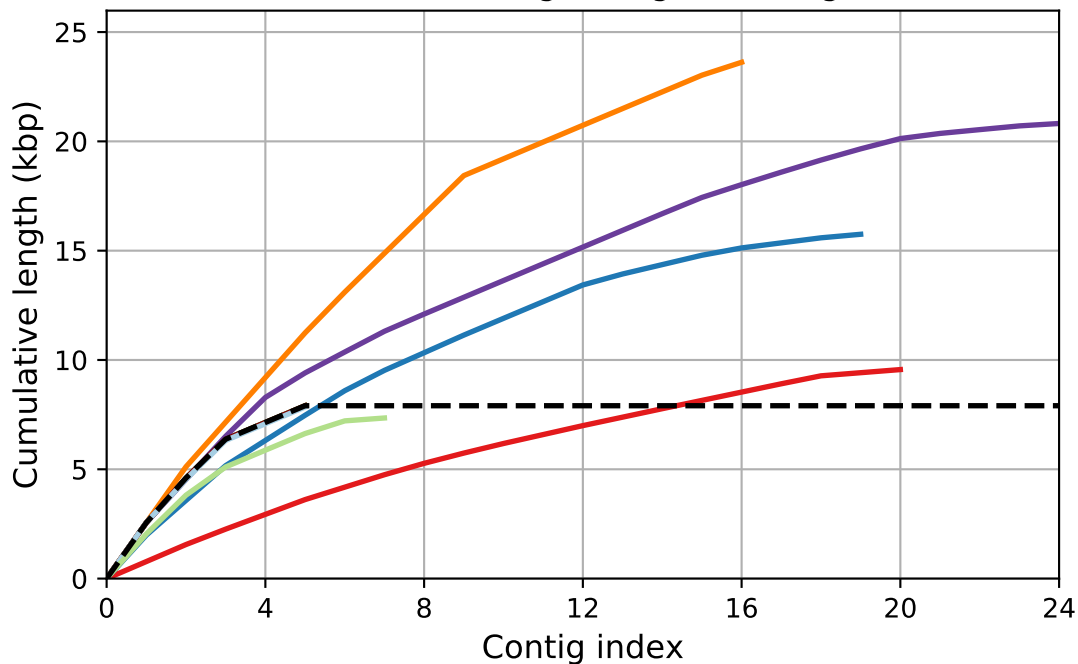
Misassemblies



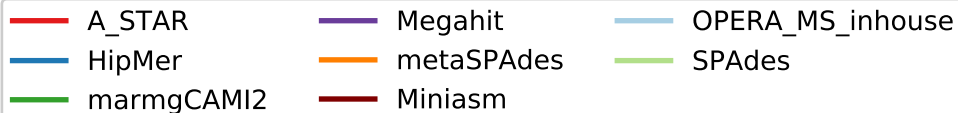
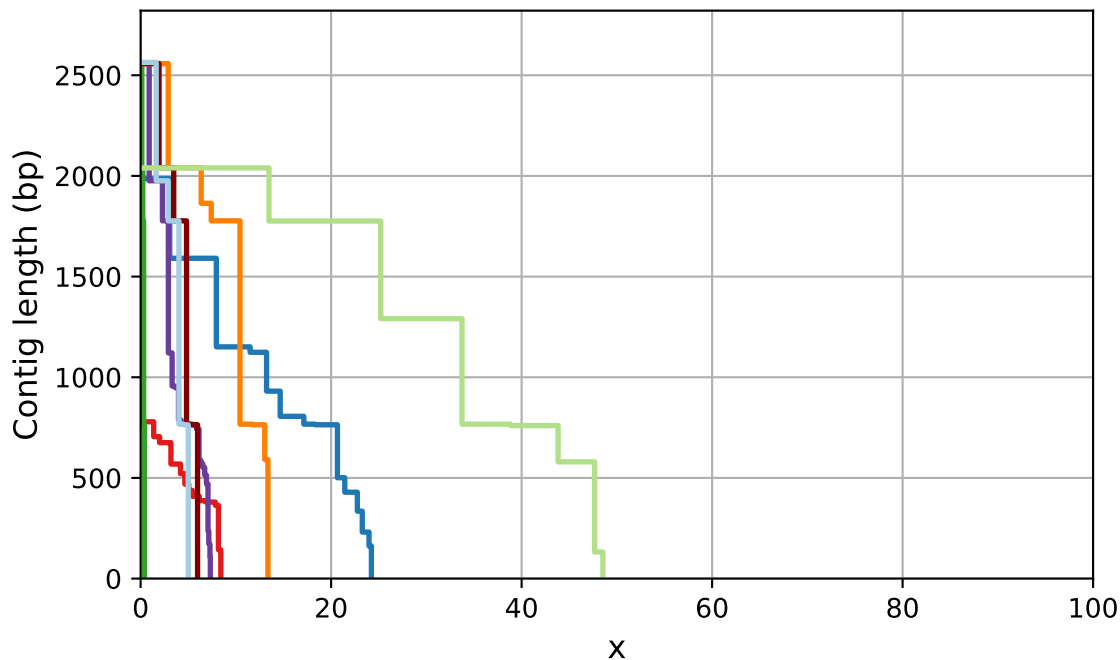
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

