

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	4	2	1	6	5	1	2	2
# contigs (>= 5000 bp)	4	2	1	6	5	1	2	2
# contigs (>= 10000 bp)	4	2	1	6	5	1	2	2
# contigs (>= 25000 bp)	4	2	1	6	5	1	2	2
# contigs (>= 50000 bp)	4	2	1	1	3	1	2	1
Total length (>= 1000 bp)	675376	167029	4279149	273657	295252	66341	236292	838805
Total length (>= 5000 bp)	675376	167029	4279149	273657	295252	66341	236292	838805
Total length (>= 10000 bp)	675376	167029	4279149	273657	295252	66341	236292	838805
Total length (>= 25000 bp)	675376	167029	4279149	273657	295252	66341	236292	838805
Total length (>= 50000 bp)	675376	167029	4279149	66508	222120	66341	236292	805128
# contigs	4	2	1	6	5	1	2	3
Largest contig	271443	89078	4279149	66508	77977	66341	169709	805128
Total length	675376	167029	4279149	273657	295252	66341	236292	839311
Reference length	720	720	720	720	720	720	720	720
GC (%)	60.93	60.79	60.22	60.93	60.46	59.83	60.66	60.77
Reference GC (%)	60.97	60.97	60.97	60.97	60.97	60.97	60.97	60.97
N50	271443	89078	4279149	46560	77932	66341	169709	805128
NG50	271443	89078	4279149	66508	77977	66341	169709	805128
N75	271443	77951	4279149	46527	66211	66341	66583	805128
NG75	271443	89078	4279149	66508	77977	66341	169709	805128
L50	2	1	1	3	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	2	1	4	3	1	2	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	1	1	1	0	1	1
# unaligned contigs	0 + 4 part	0 + 2 part	0 + 1 part	0 + 6 part	0 + 5 part	0 + 1 part	0 + 2 part	0 + 2 part
Unaligned length	674522	166556	4278057	271828	293238	66208	235757	838134
Genome fraction (%)	42.778	29.861	100.000	78.333	100.000	18.472	68.750	82.500
Duplication ratio	2.773	2.200	1.517	3.243	2.797	1.000	1.081	1.981
# N's per 100 kbp	0.00	25.74	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	3896.10	0.00	3194.44	7978.72	5416.67	1503.76	1212.12	3703.70
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	308	215	720	304	720	133	274	506
Total aligned length	854	430	1244	1829	2166	133	535	1177
NGA50	308	215	720	294	720	-	111	506
NGA75	308	-	720	294	720	-	-	294
LGA50	2	2	1	2	1	-	2	1
LGA75	2	-	1	2	1	-	-	2

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

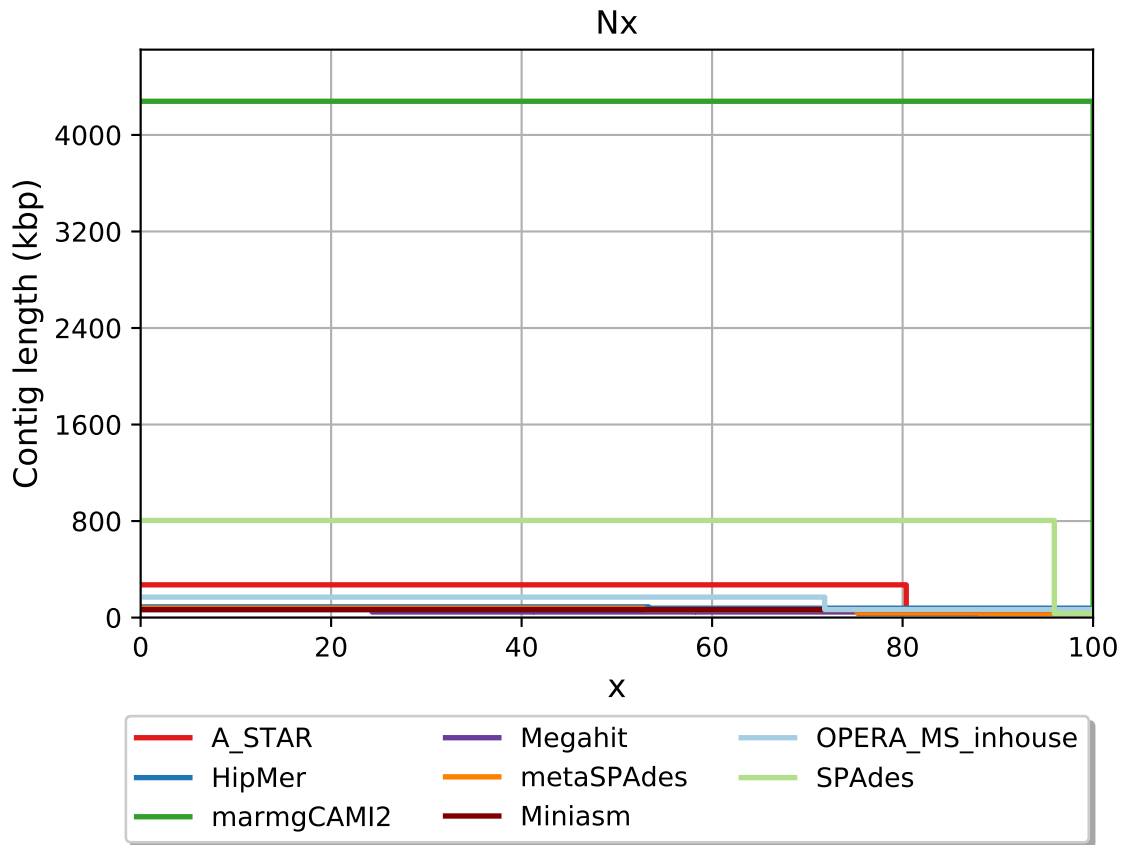
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	0	5	4	1	1	1
# possible misassemblies	2	2	0	5	4	1	1	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	1	1	1	0	1	1
# mismatches	12	0	23	45	39	2	6	22
# 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).

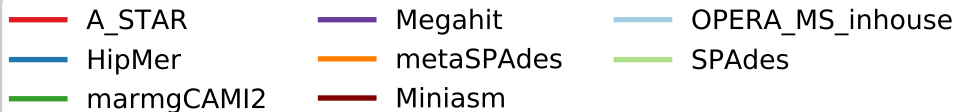
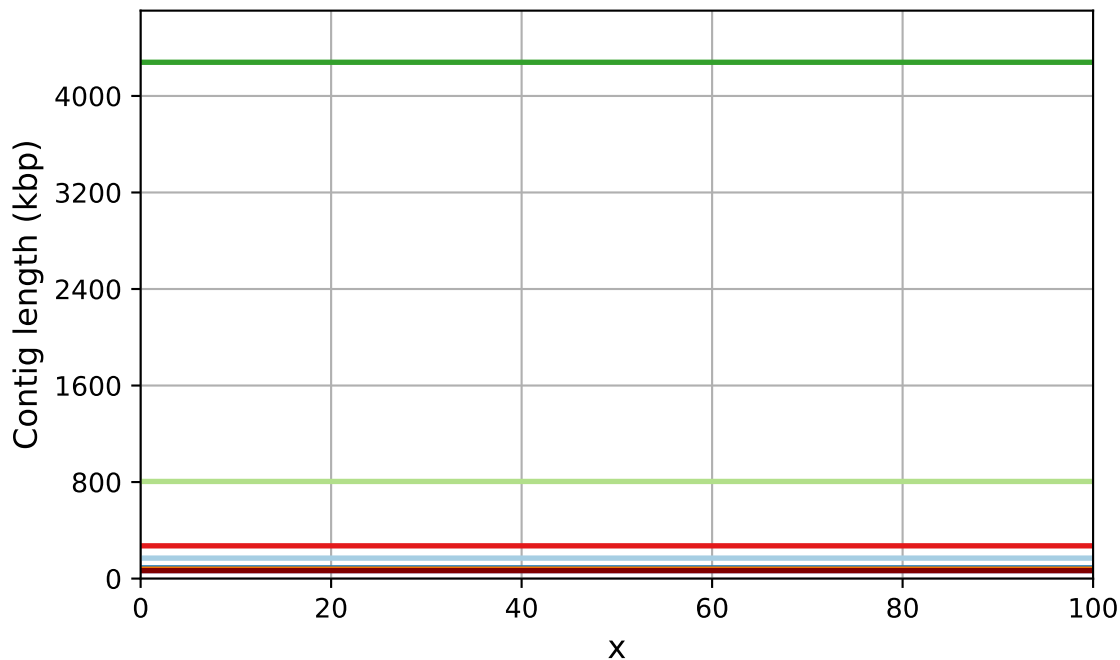
Unaligned report

	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	4	2	1	6	5	1	2	2
Partially unaligned length	674522	166556	4278057	271828	293238	66208	235757	838134
# N's	0	43	0	0	0	0	0	0

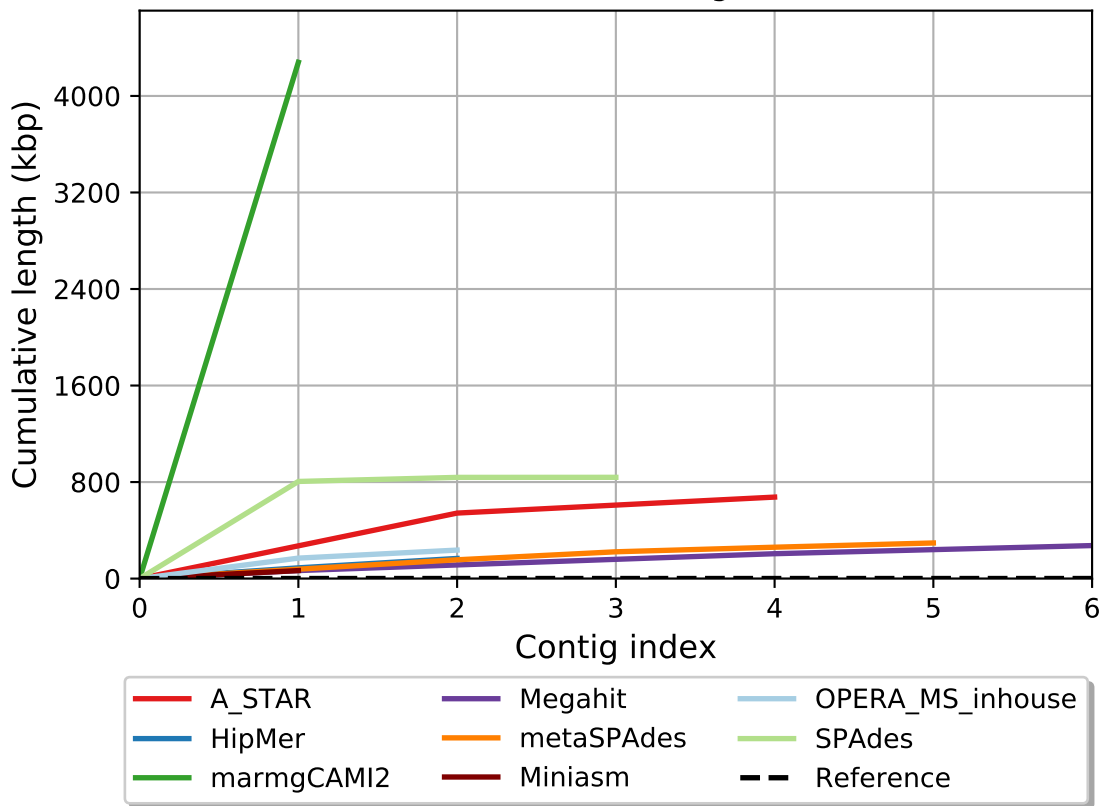
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



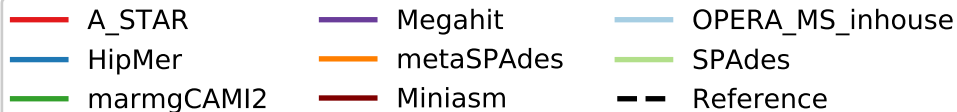
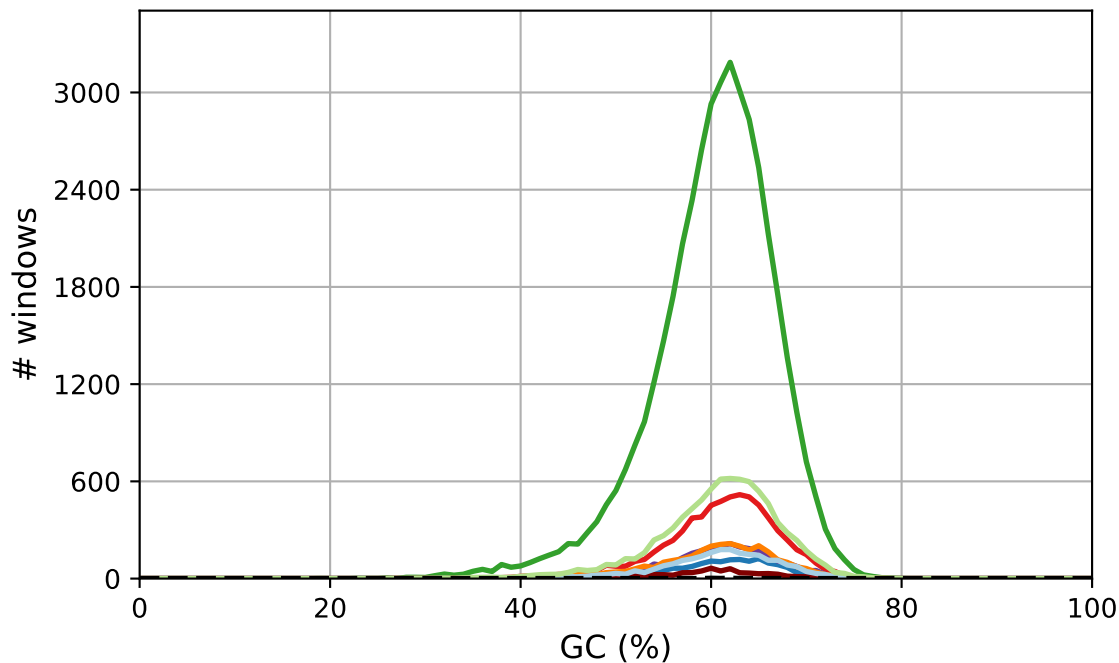
NGx



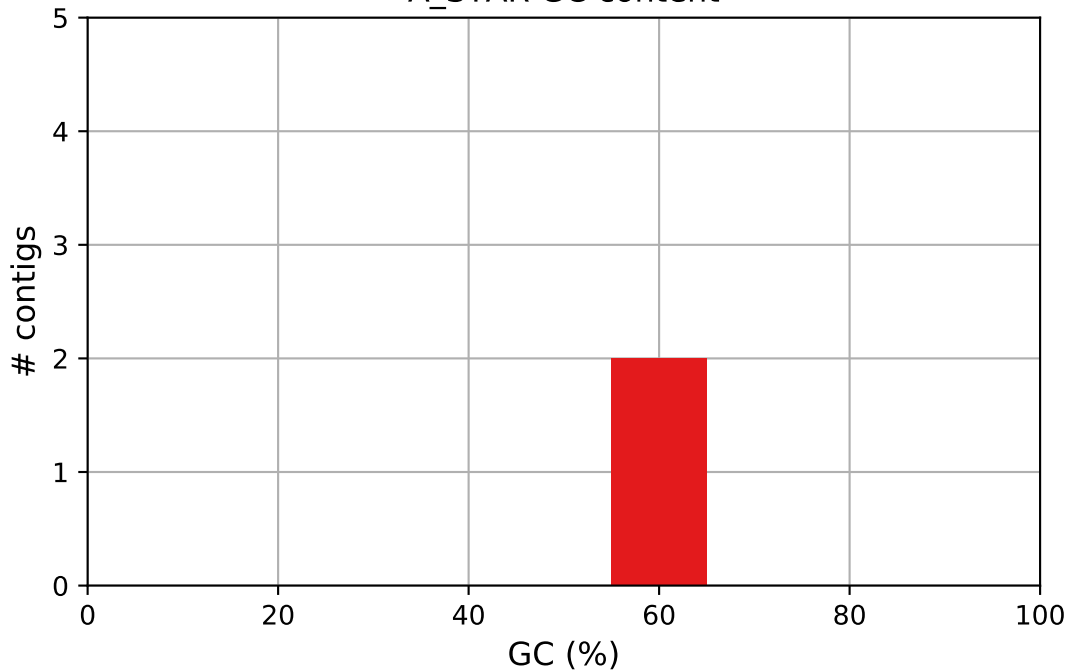
Cumulative length



GC content

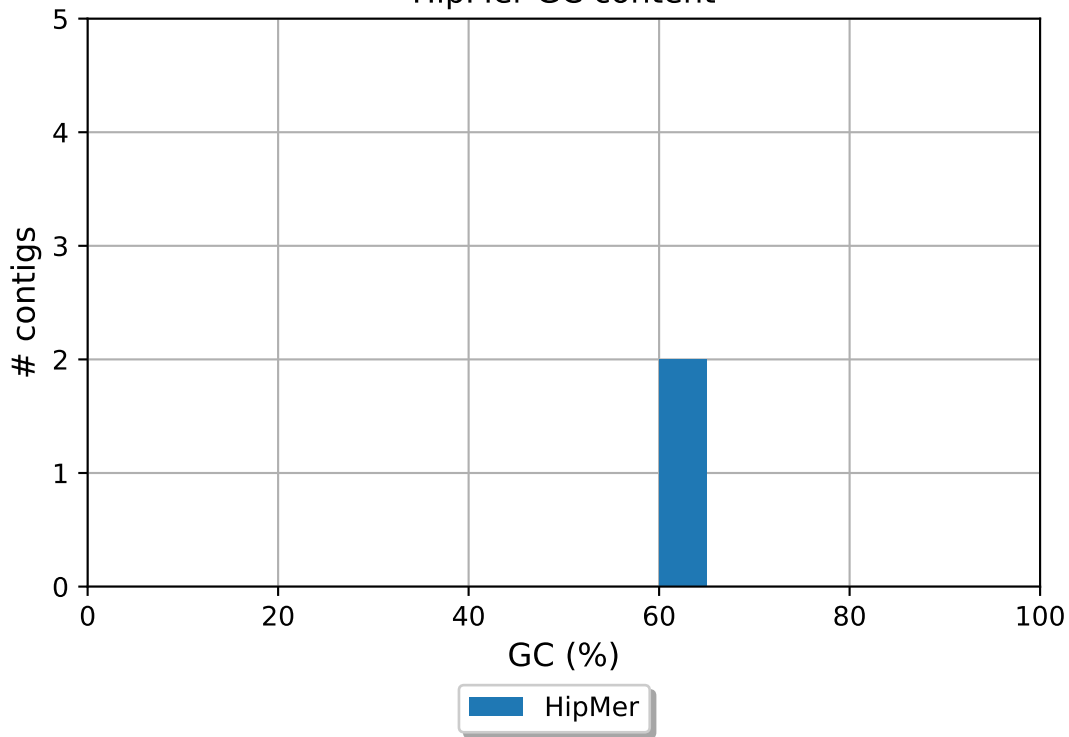


A_STAR GC content

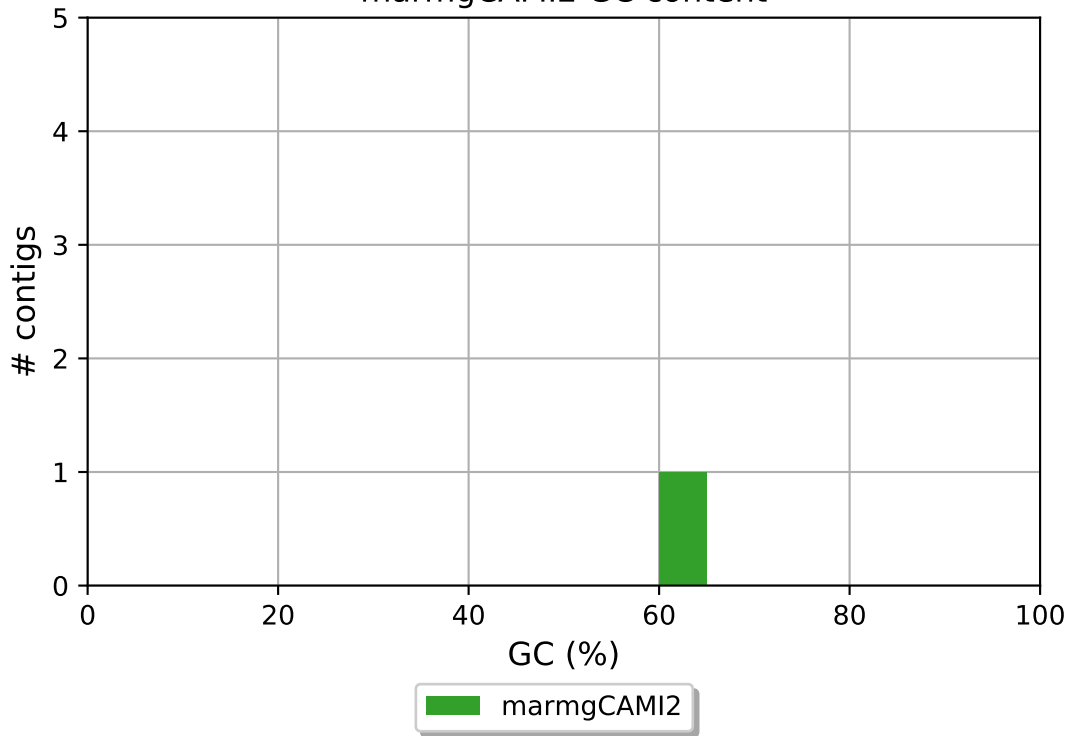


A_STAR

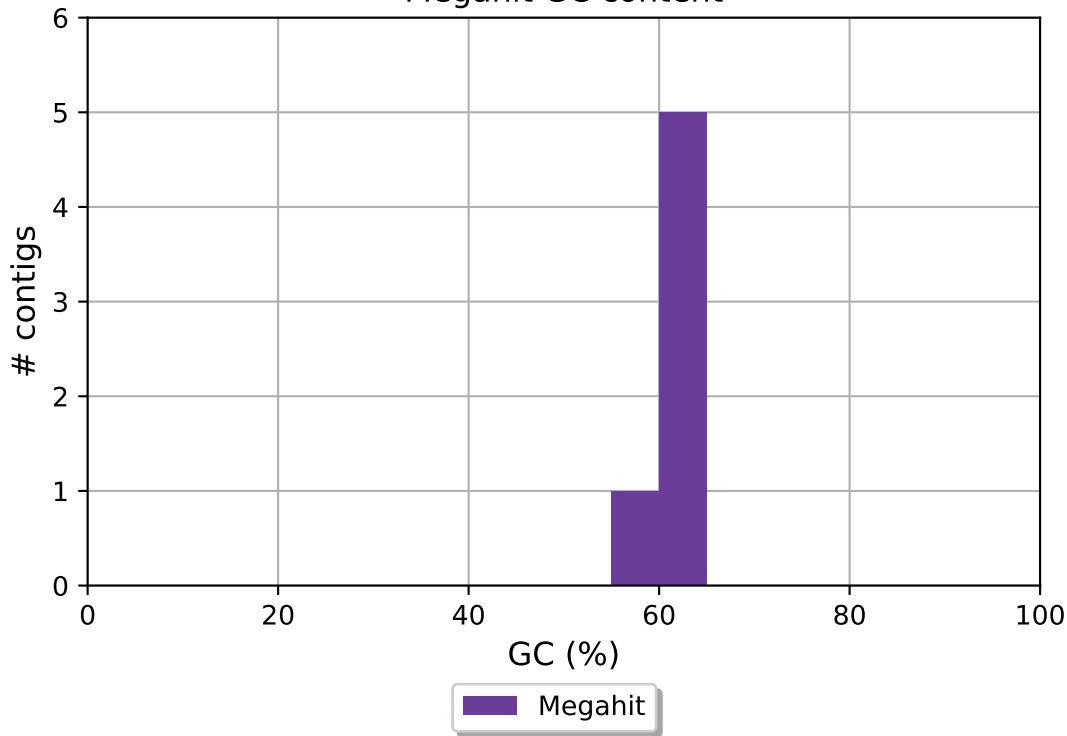
HipMer GC content



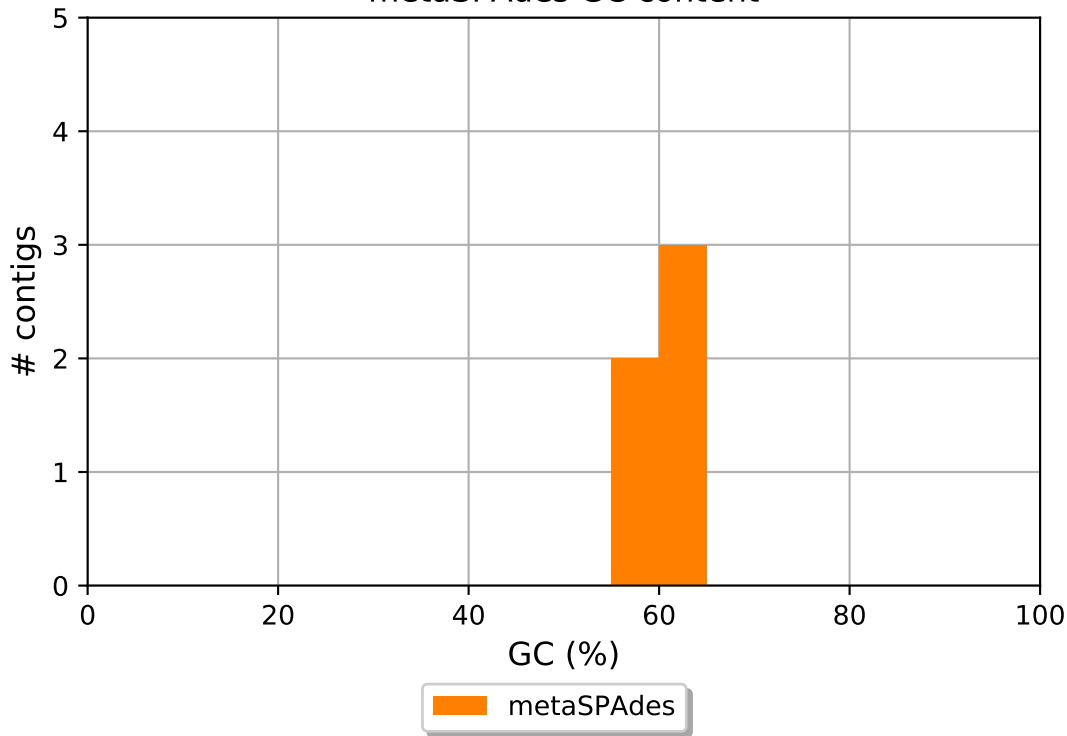
marmgCAMI2 GC content



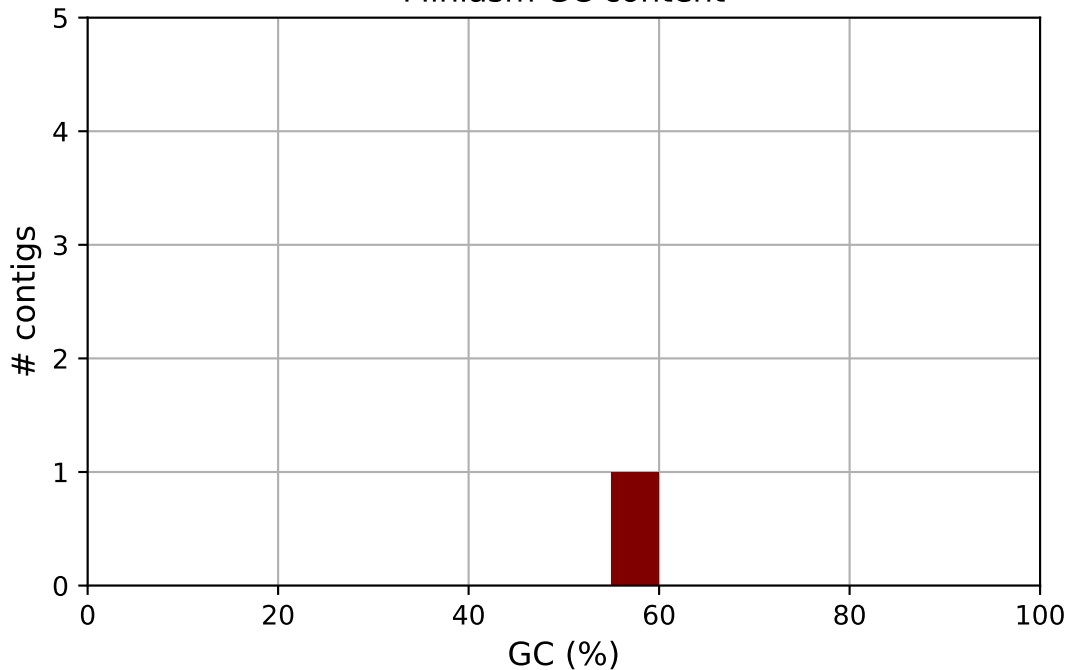
Megahit GC content



metaSPAdes GC content

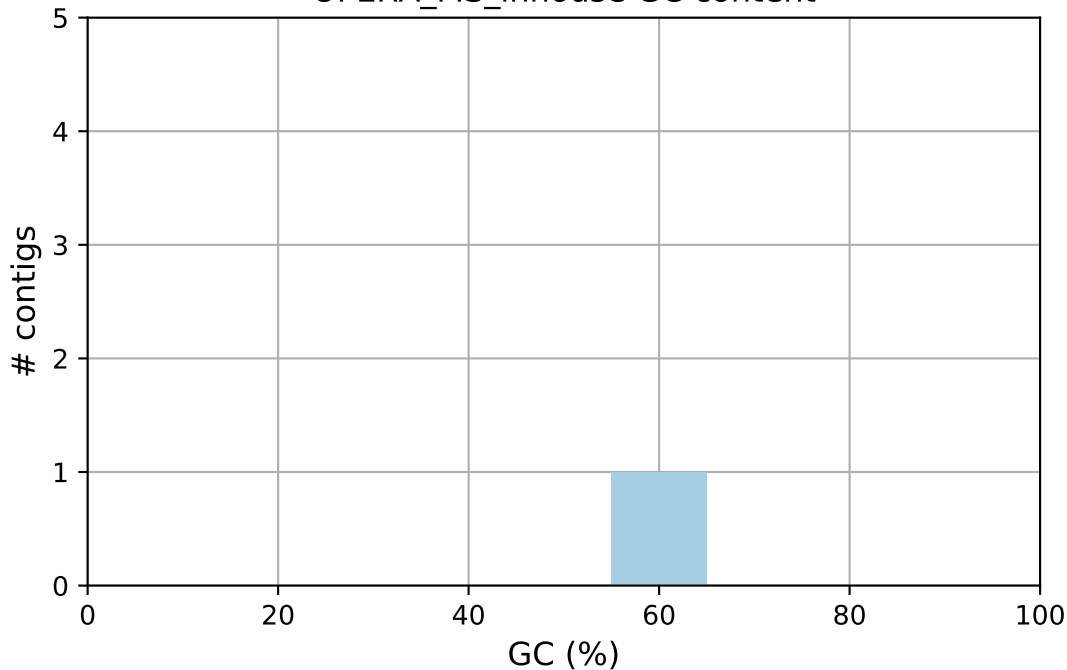


Miniasm GC content



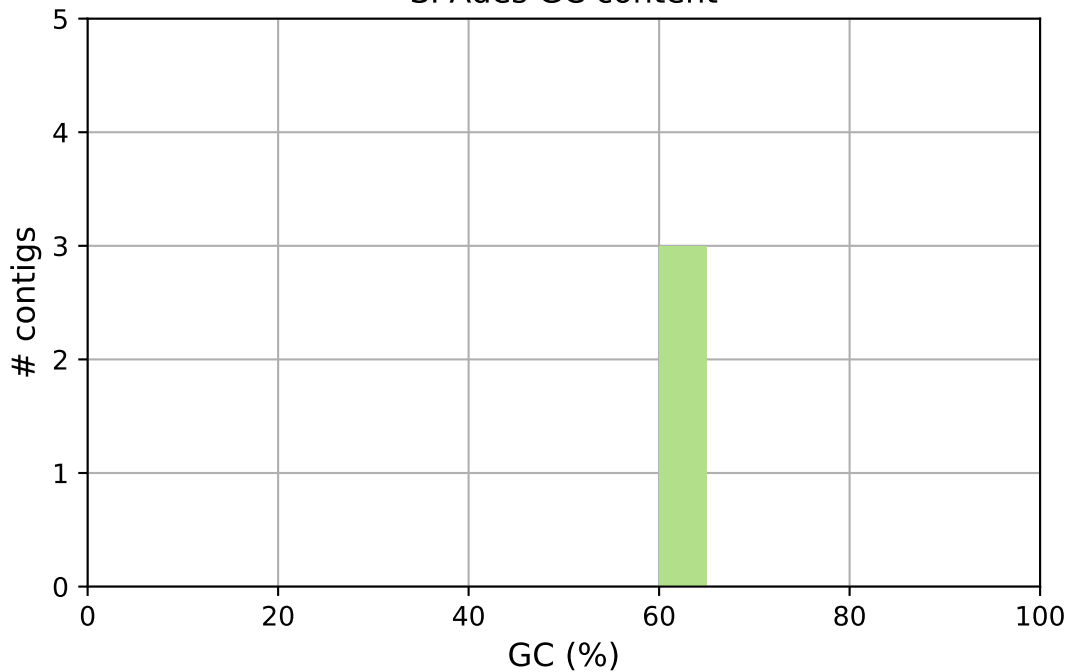
Miniasm

OPERA_MS_inhouse GC content



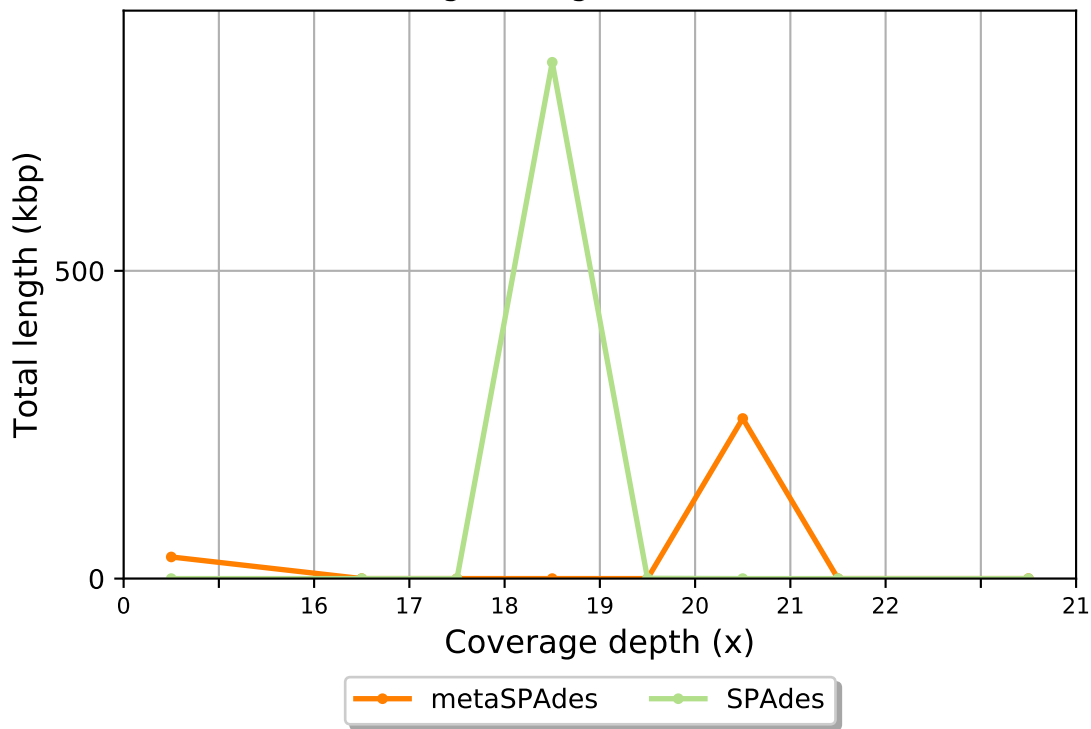
OPERA_MS_inhouse

SPAdes GC content

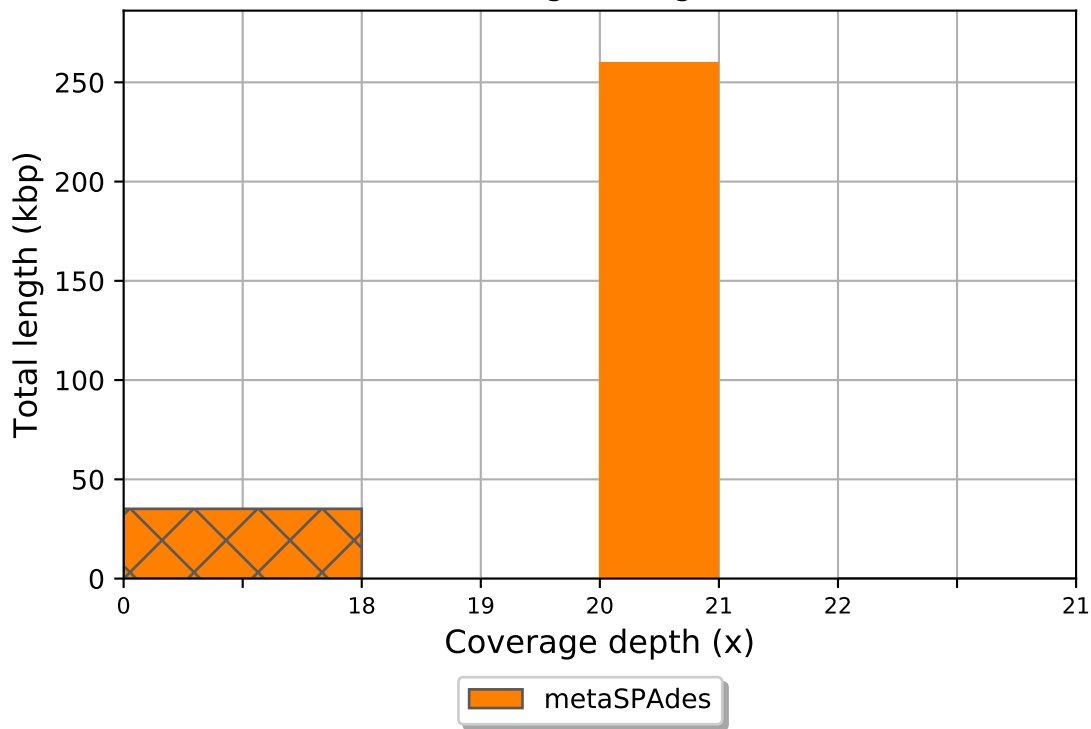


SPAdes

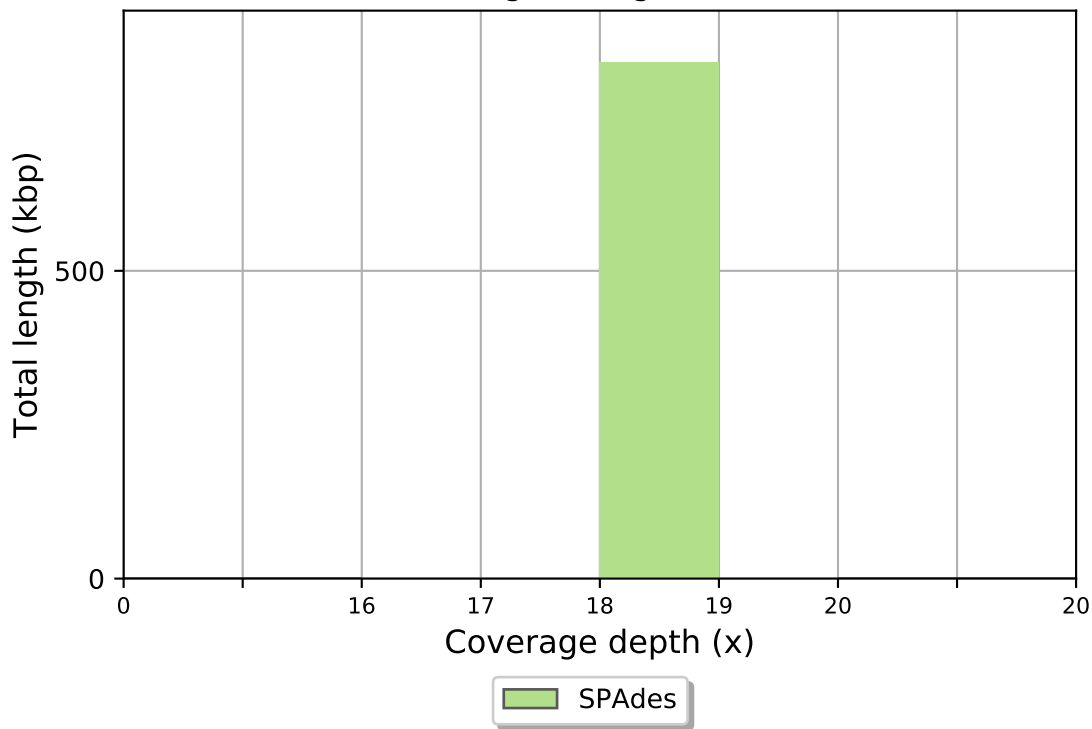
Coverage histogram (bin size: 1x)



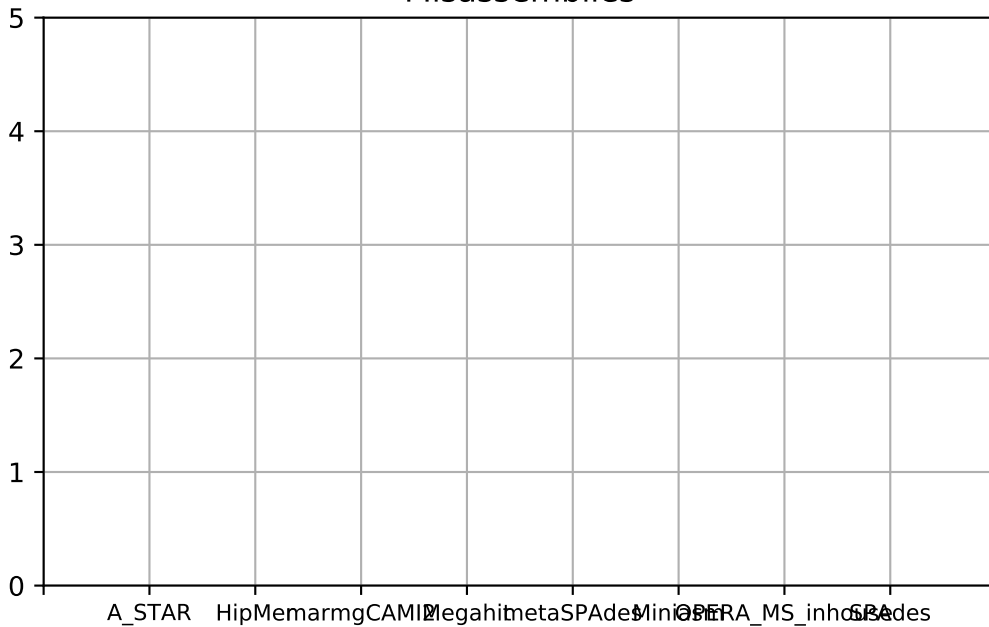
metaSPAdes coverage histogram (bin size: 1x)



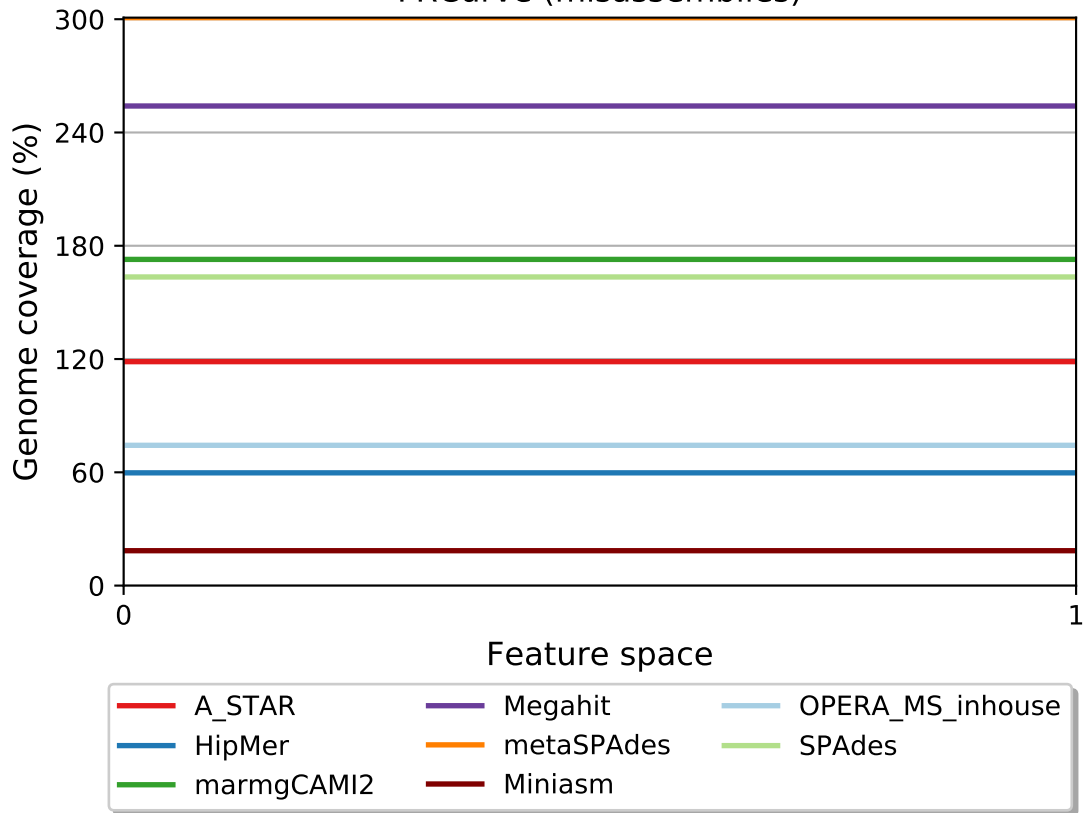
SPAdes coverage histogram (bin size: 1x)



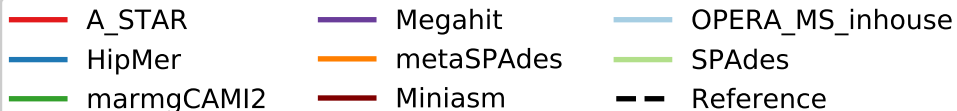
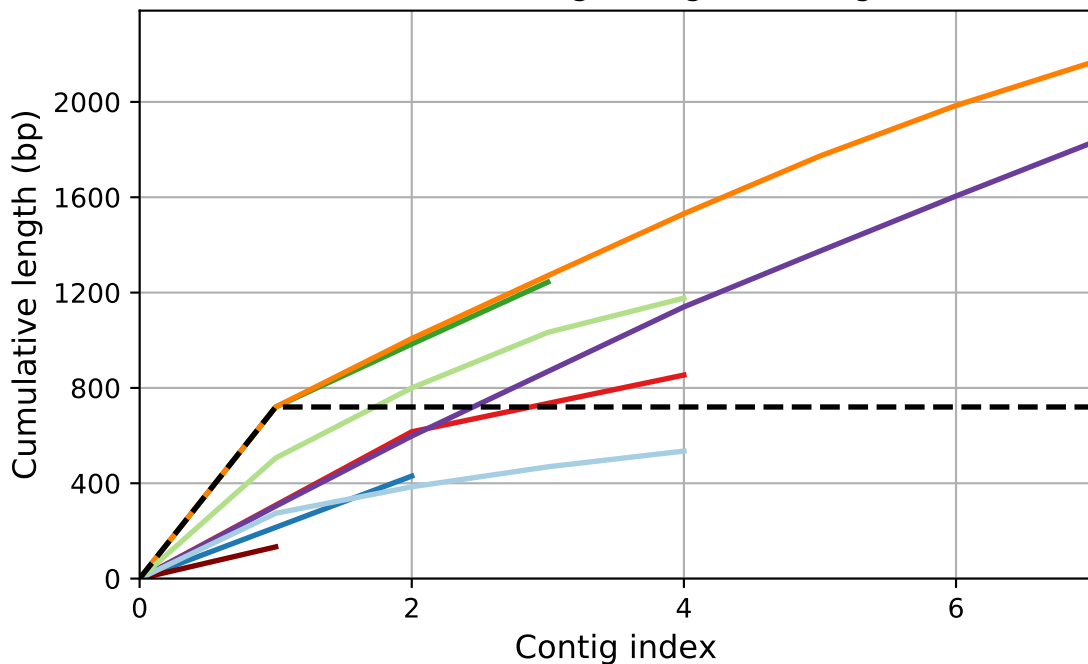
Misassemblies



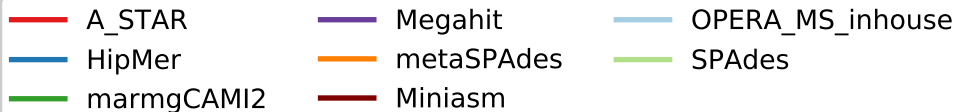
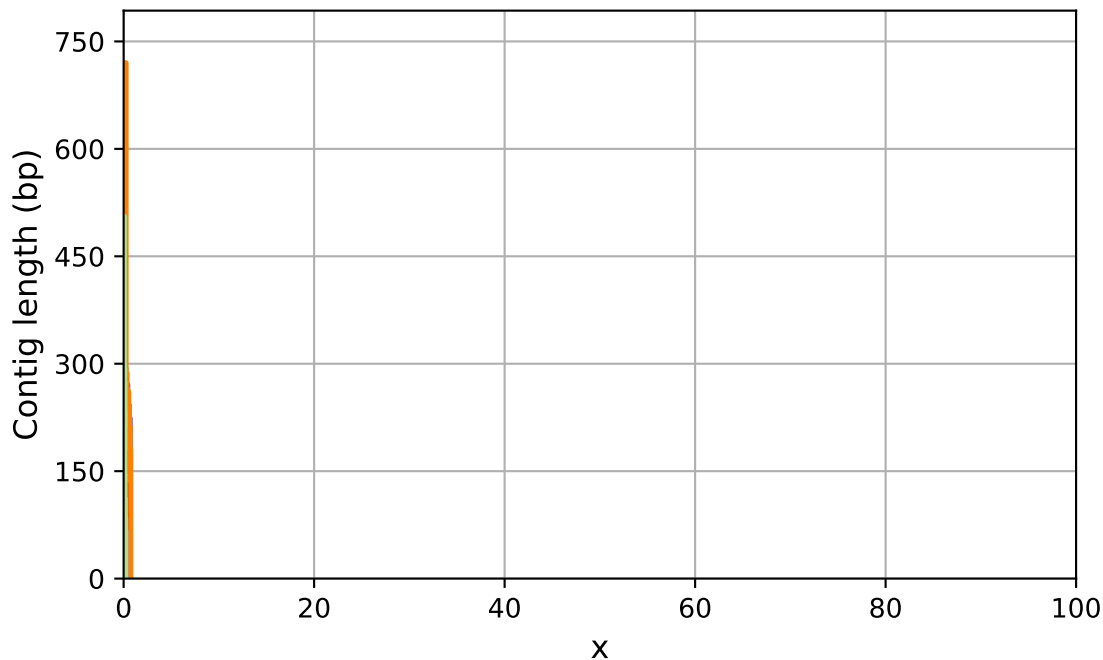
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

