

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	8	1	11	3	2	2	3
# contigs (>= 5000 bp)	0	4	1	6	3	2	2	2
# contigs (>= 10000 bp)	0	4	1	6	3	2	2	1
# contigs (>= 25000 bp)	0	1	1	1	3	2	2	0
# contigs (>= 50000 bp)	0	1	1	1	3	0	2	0
Total length (>= 1000 bp)	4850	153096	4719539	191479	267623	83507	187862	22876
Total length (>= 5000 bp)	0	140036	4719539	180720	267623	83507	187862	19823
Total length (>= 10000 bp)	0	140036	4719539	180720	267623	83507	187862	12914
Total length (>= 25000 bp)	0	78316	4719539	82451	267623	83507	187862	0
Total length (>= 50000 bp)	0	78316	4719539	82451	267623	0	187862	0
# contigs	4	8	1	13	3	2	2	3
Largest contig	2425	78316	4719539	82451	106950	45687	120652	12914
Total length	6772	153096	4719539	192603	267623	83507	187862	22876
Reference length	9260	9260	9260	9260	9260	9260	9260	9260
GC (%)	54.25	53.21	54.17	52.80	53.33	52.94	53.85	55.04
Reference GC (%)	57.72	57.72	57.72	57.72	57.72	57.72	57.72	57.72
N50	2425	78316	4719539	20722	106950	45687	120652	12914
NG50	2425	78316	4719539	82451	106950	45687	120652	12914
N75	961	22298	4719539	18864	106950	37820	67210	6909
NG75	-	78316	4719539	82451	106950	45687	120652	12914
L50	2	1	1	2	2	1	1	1
LG50	2	1	1	1	1	1	1	1
L75	3	3	1	5	2	2	2	2
LG75	-	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 + 6 part	0 + 3 part	0 + 2 part	0 + 2 part	0 + 2 part
Unaligned length	3058	134458	4710279	173000	239843	74174	178925	13330
Genome fraction (%)	15.065	99.374	100.000	100.000	100.000	100.000	96.512	100.000
Duplication ratio	2.662	2.025	1.000	2.117	3.000	1.008	1.000	1.031
# 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	1371.49	0.00	0.00	268.55	205.18
# indels per 100 kbp	0.00	0.00	0.00	10.80	0.00	0.00	0.00	0.00
Largest alignment	896	4153	9260	4327	9260	9260	4759	5784
Total aligned length	2790	18540	9260	19146	27780	9333	8937	9536
NGA50	-	4153	9260	2919	9260	9260	4759	5784
NGA75	-	4153	9260	2919	9260	9260	4178	3043
LGA50	-	2	1	2	1	1	1	1
LGA75	-	2	1	2	1	1	2	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

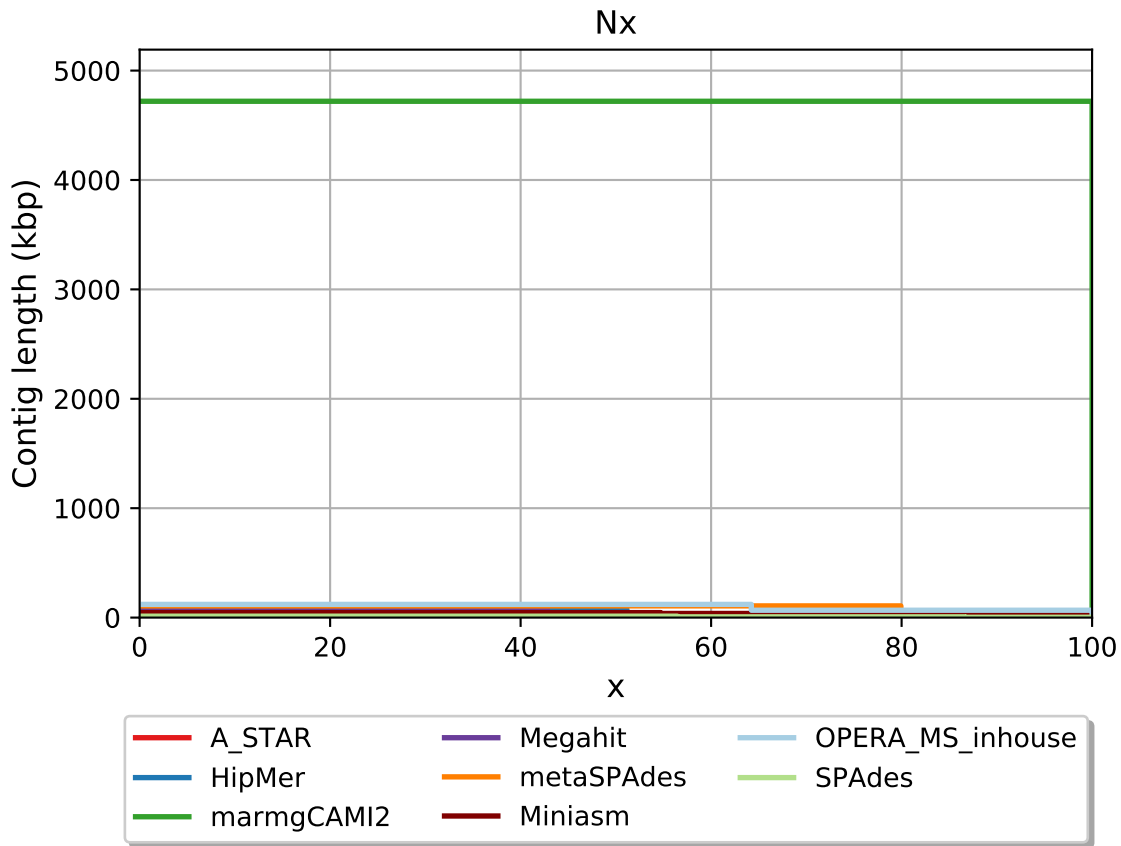
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	4	1	6	3	2	2	2
# possible misassemblies	2	4	2	6	6	3	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	127	0	0	24	19
# indels	0	0	0	1	0	0	0	0
# indels (<= 5 bp)	0	0	0	0	0	0	0	0
# indels (> 5 bp)	0	0	0	1	0	0	0	0
Indels length	0	0	0	69	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).

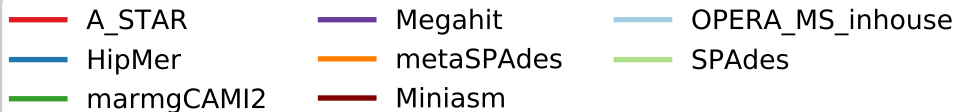
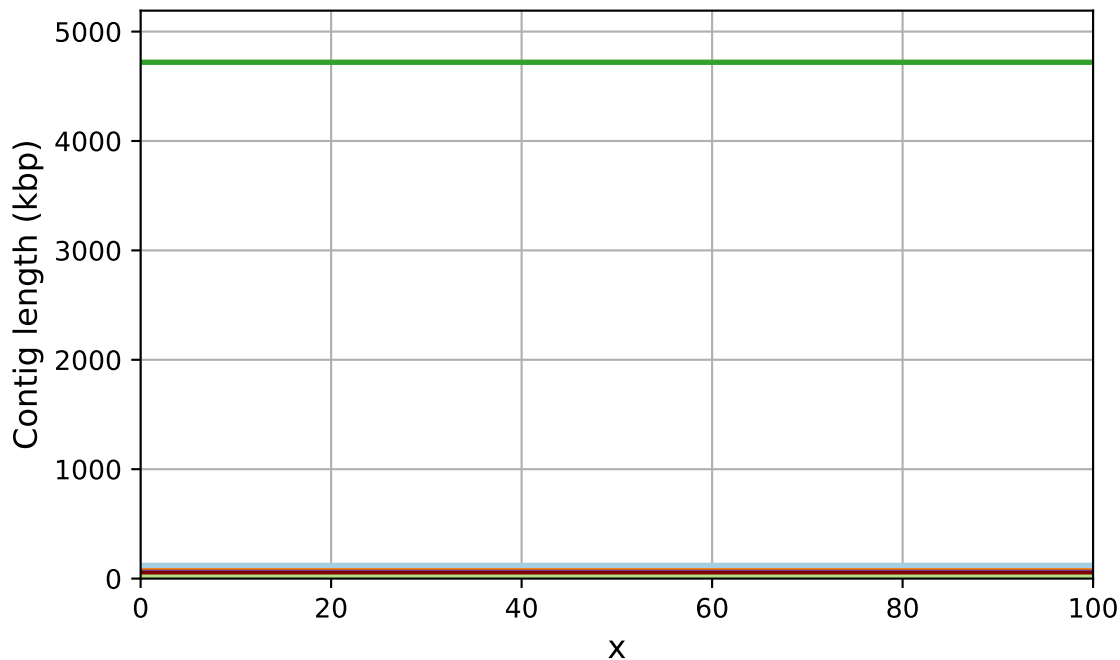
Unaligned report

	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	6	3	2	2	2
Partially unaligned length	3058	134458	4710279	173000	239843	74174	178925	13330
# N's	0	0	0	0	0	0	0	0

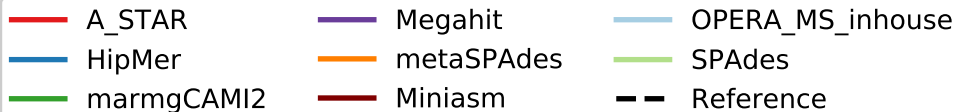
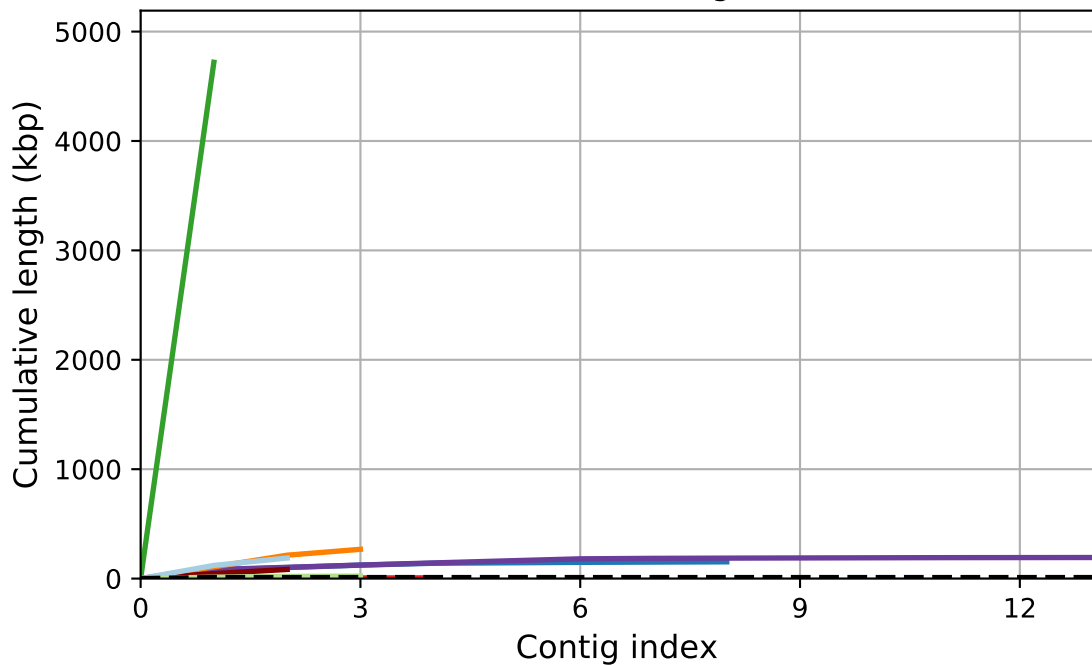
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



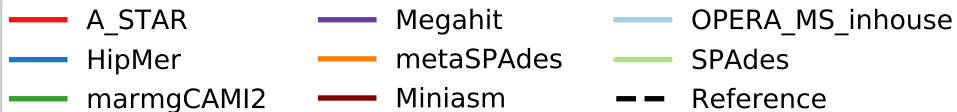
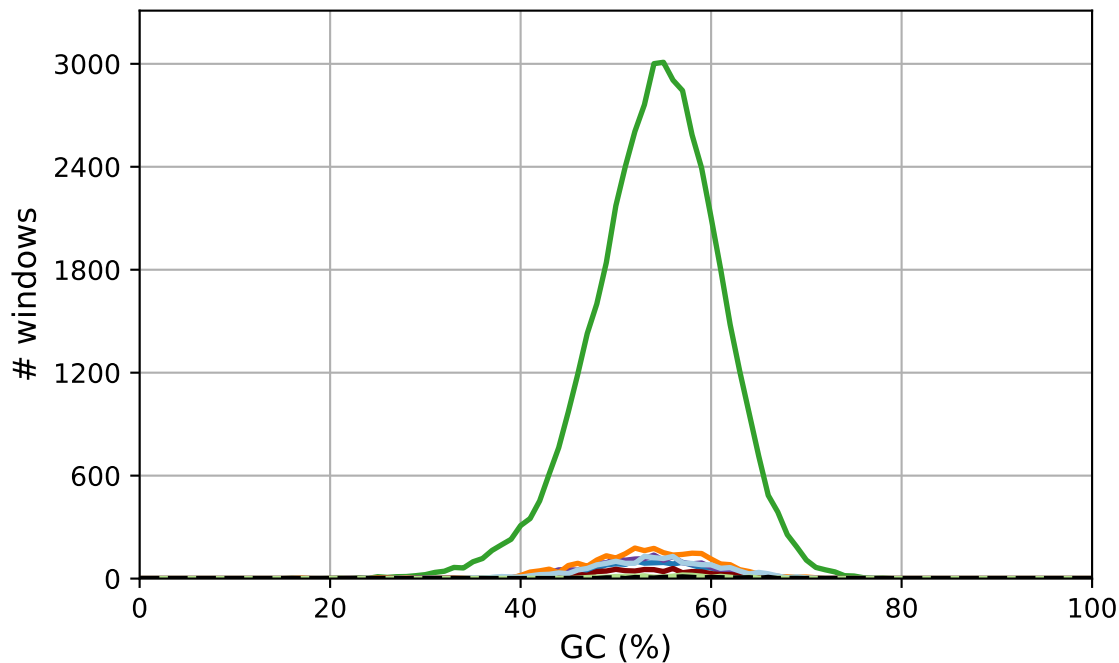
NGx



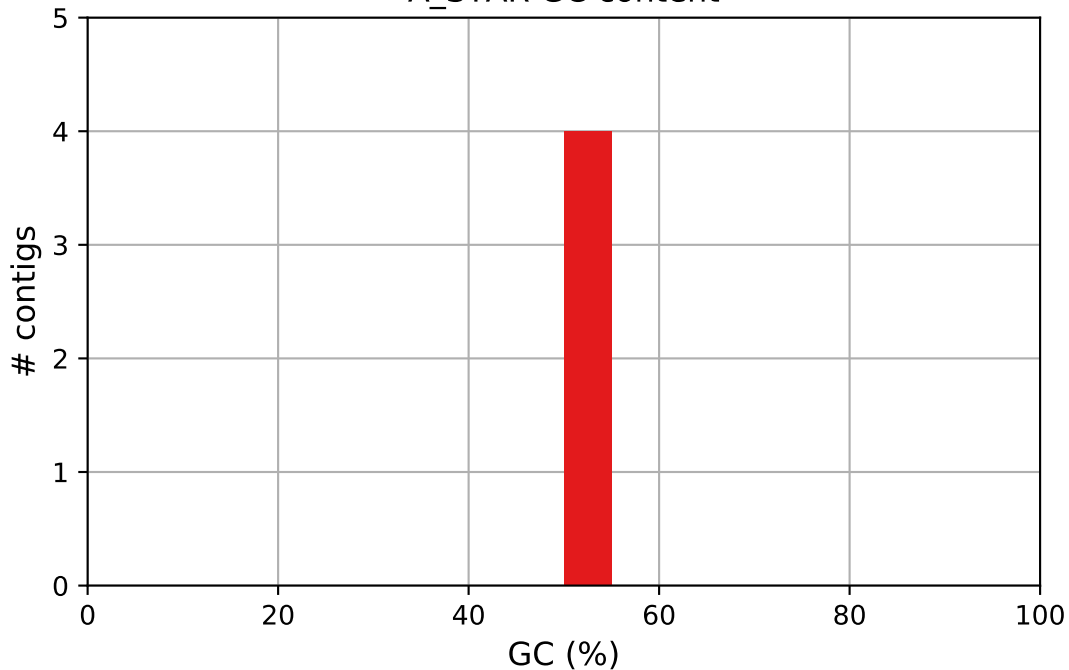
Cumulative length



GC content

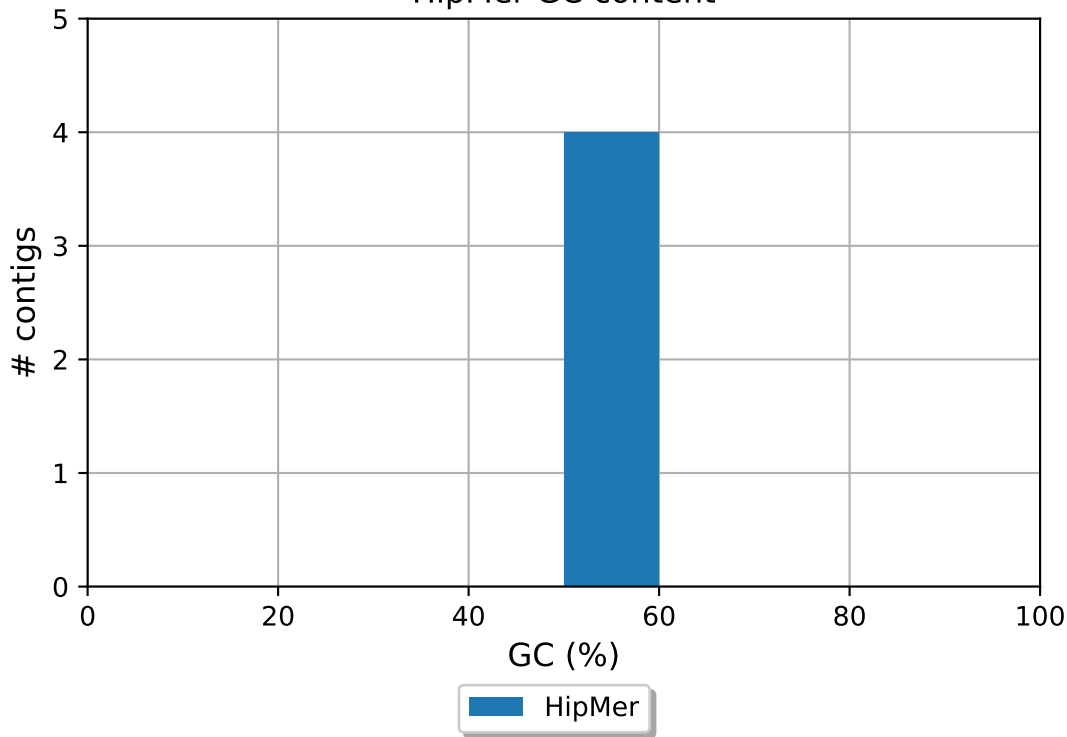


A_STAR GC content

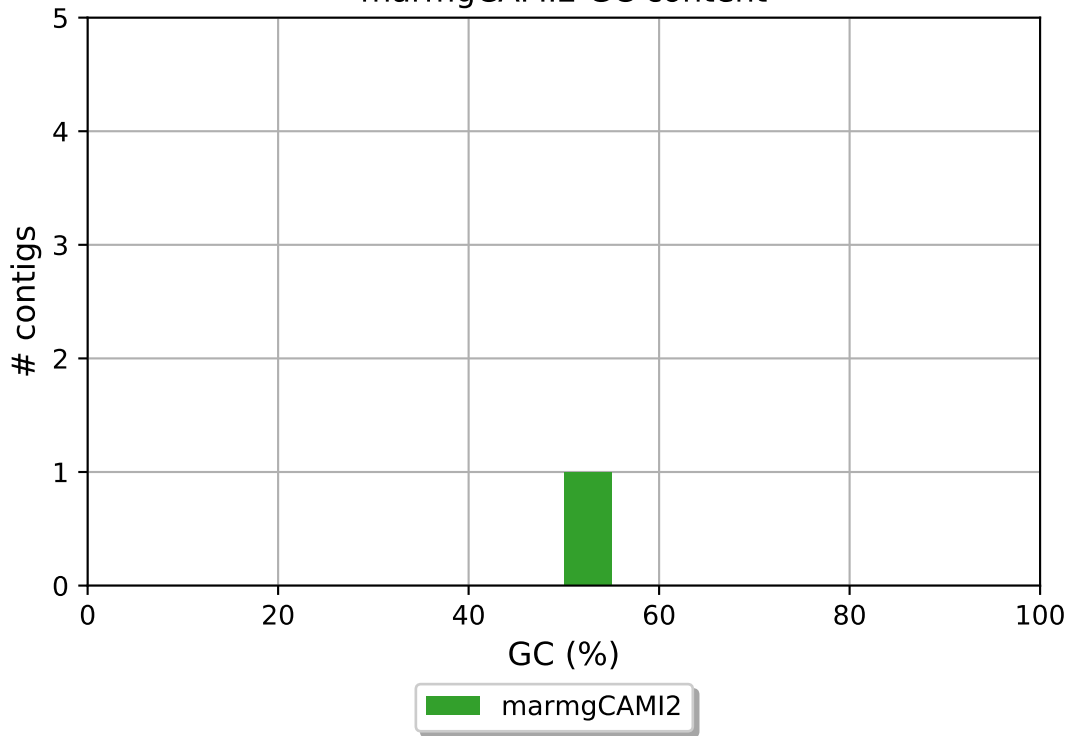


A_STAR

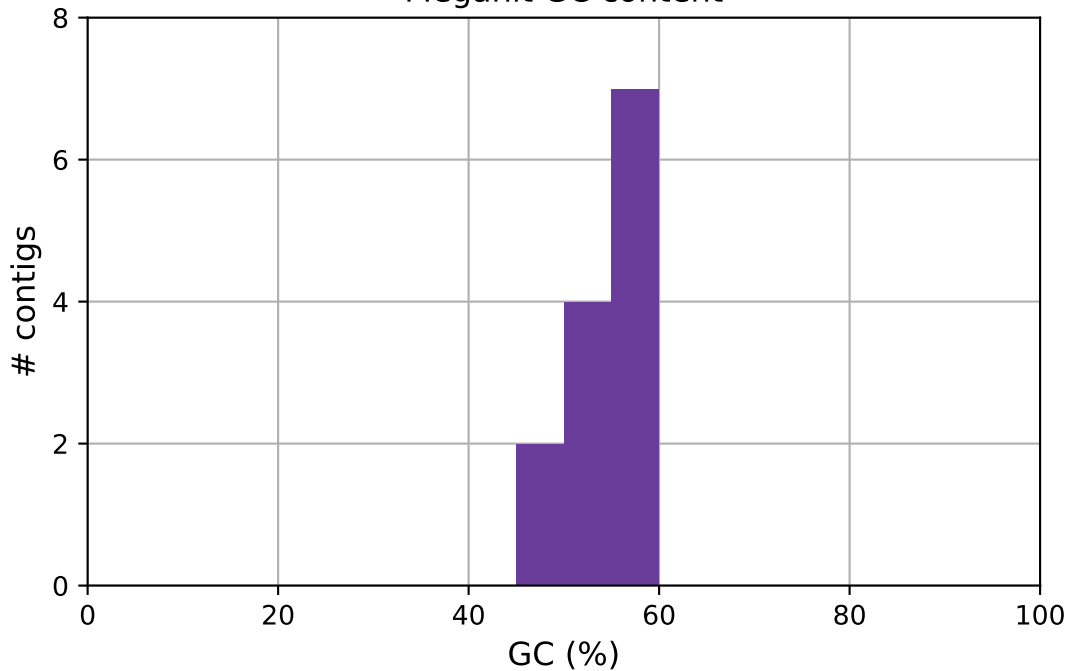
HipMer GC content



marmgCAMI2 GC content

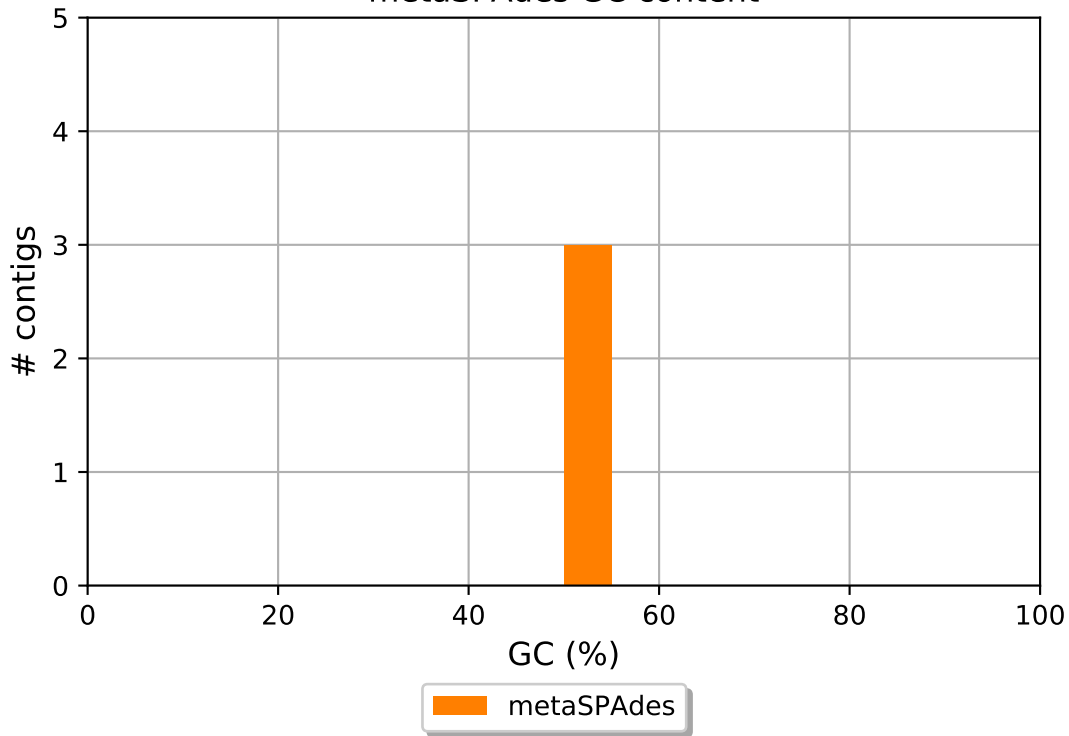


Megahit GC content

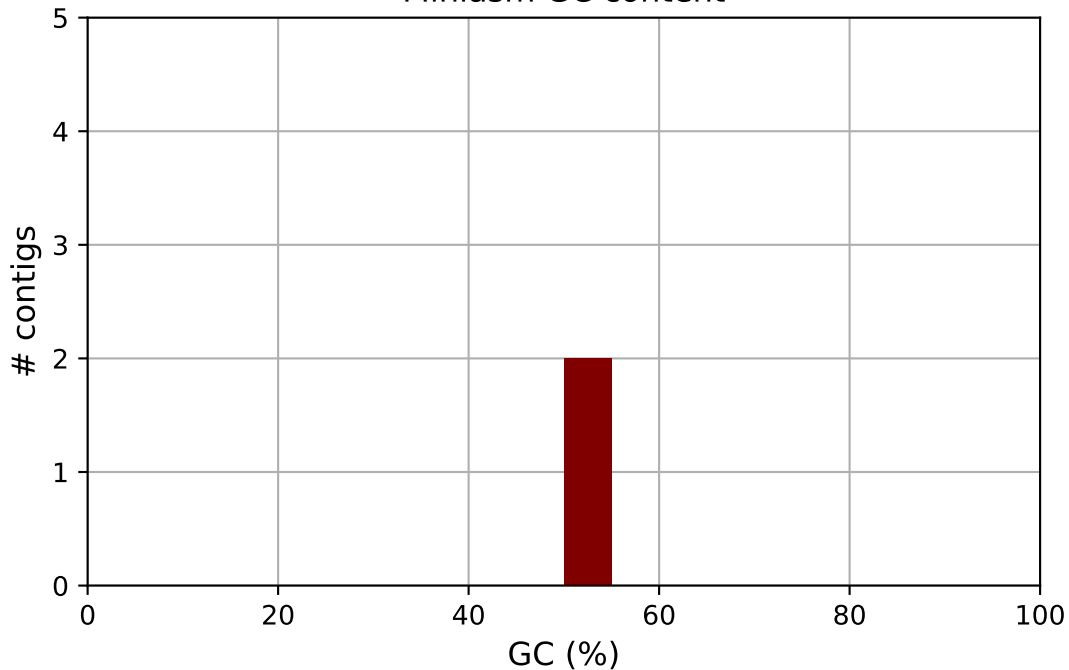


Megahit

metaSPAdes GC content

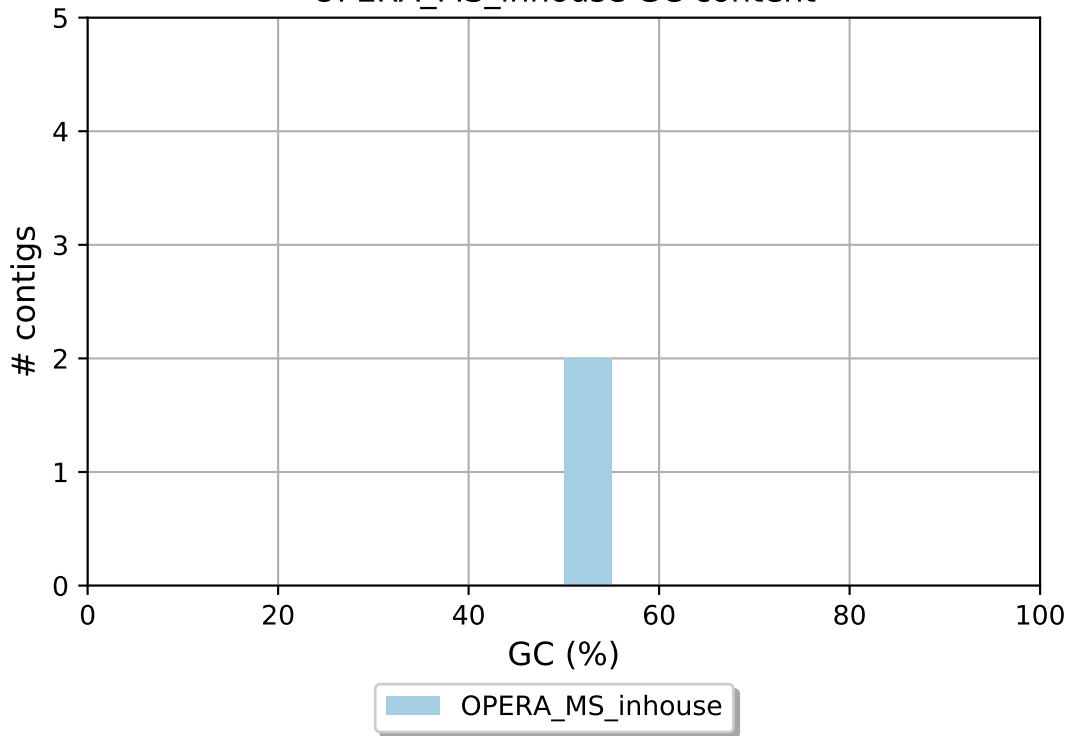


Miniasm GC content

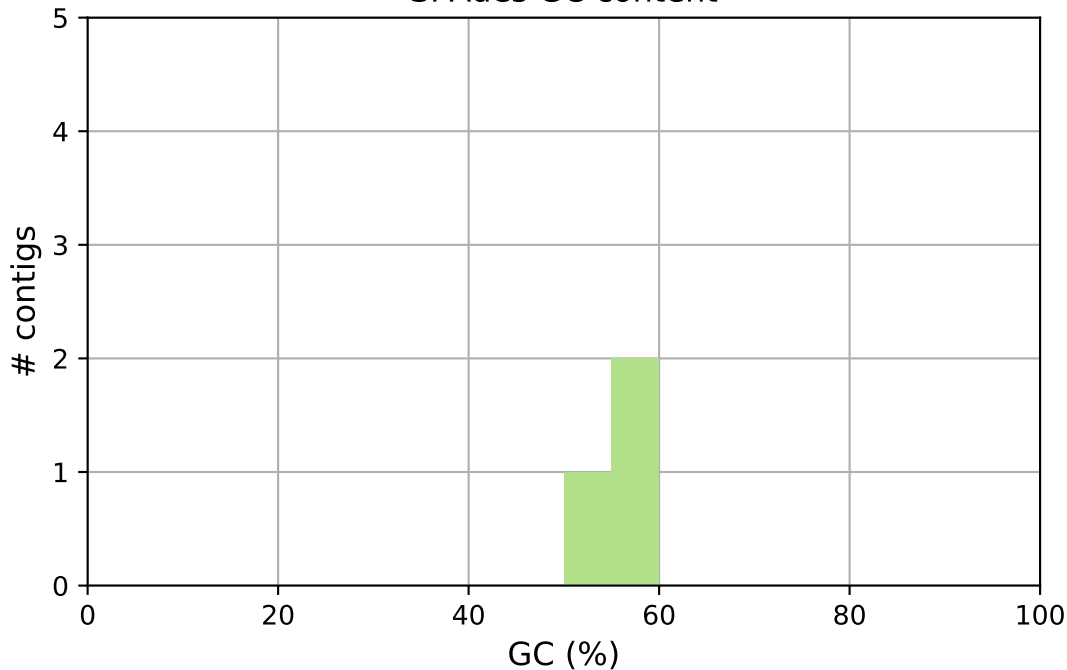


Miniasm

OPERA_MS_inhouse GC content

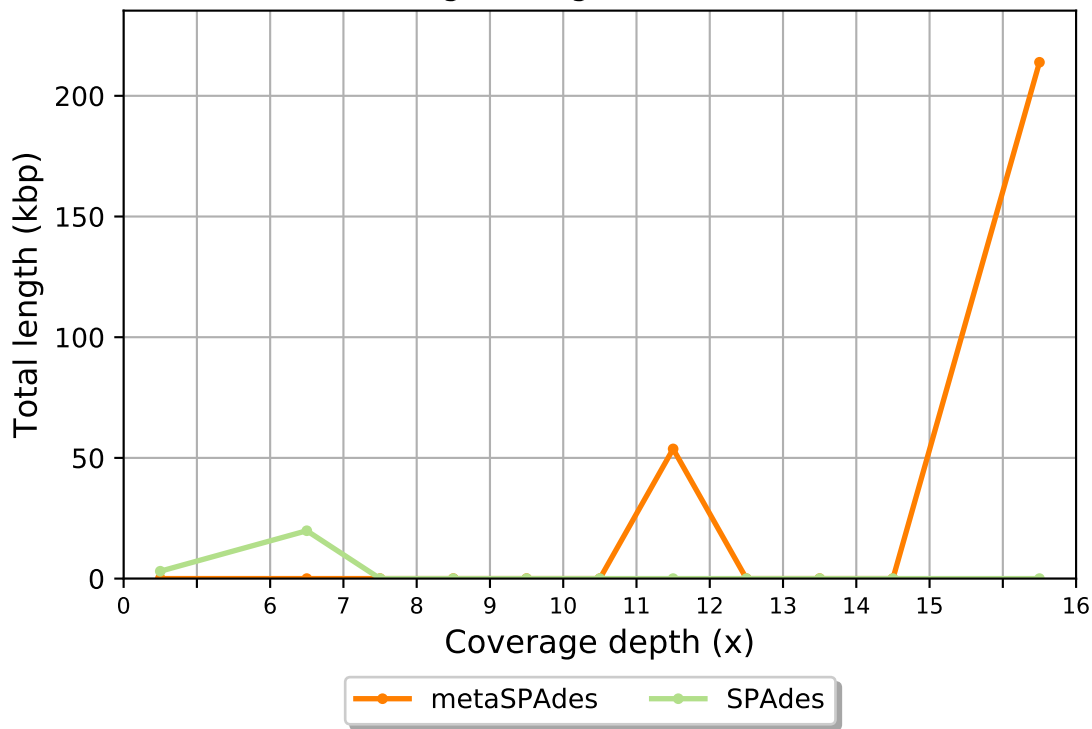


SPAdes GC content

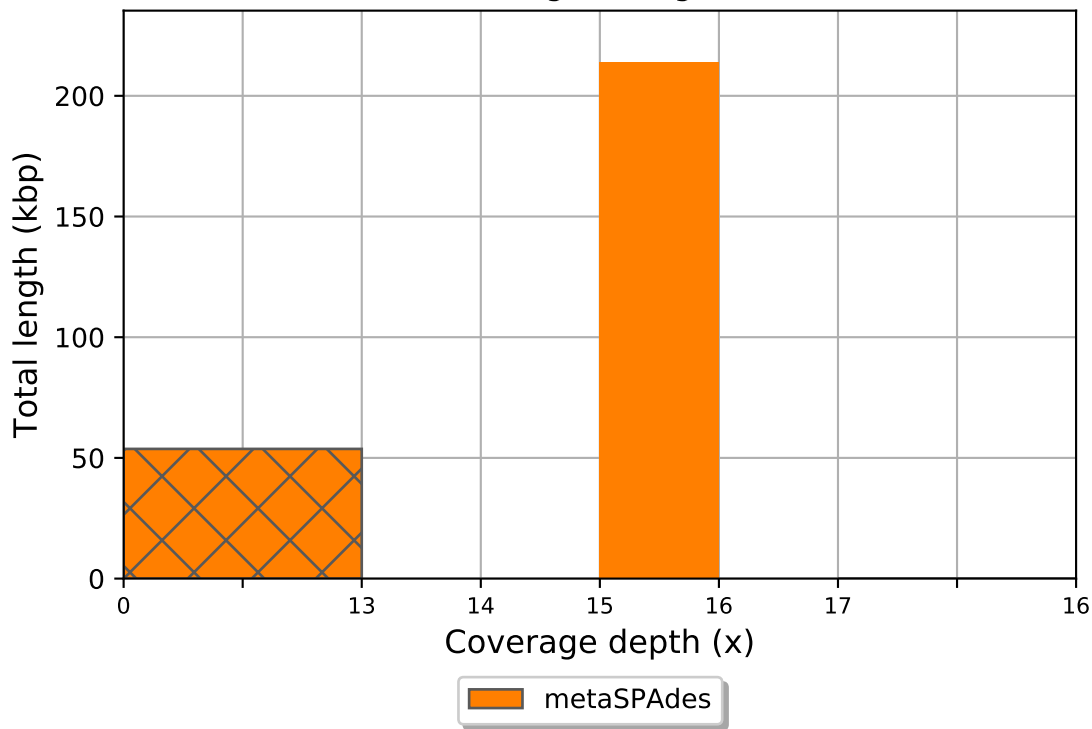


SPAdes

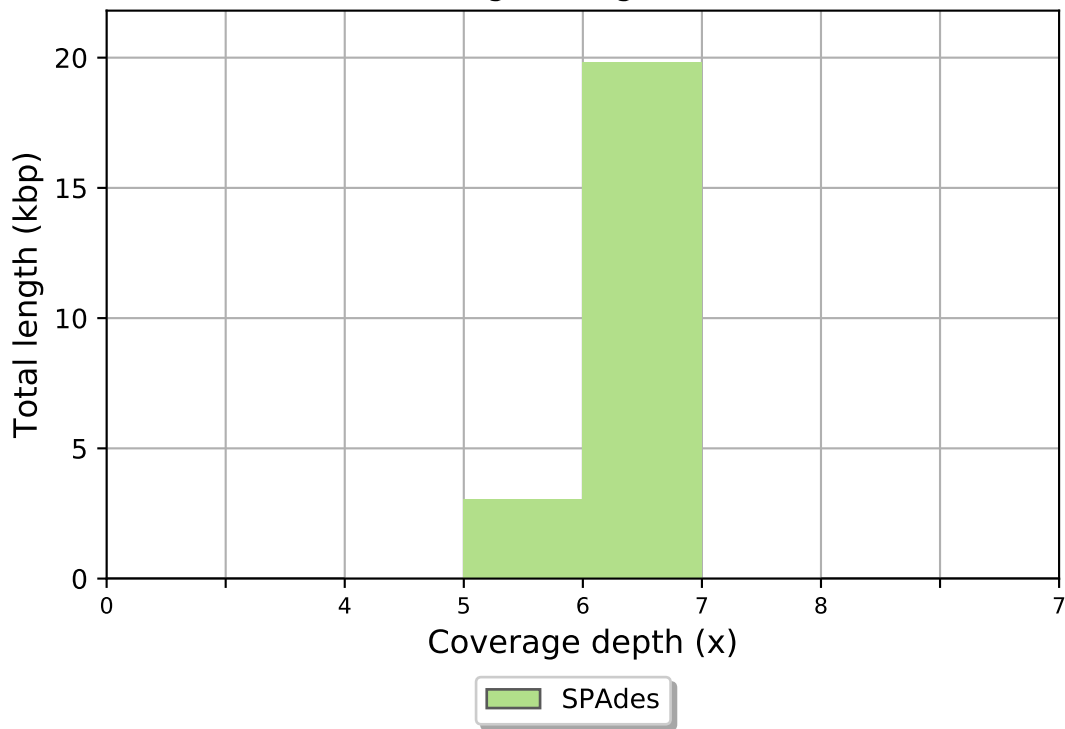
Coverage histogram (bin size: 1x)



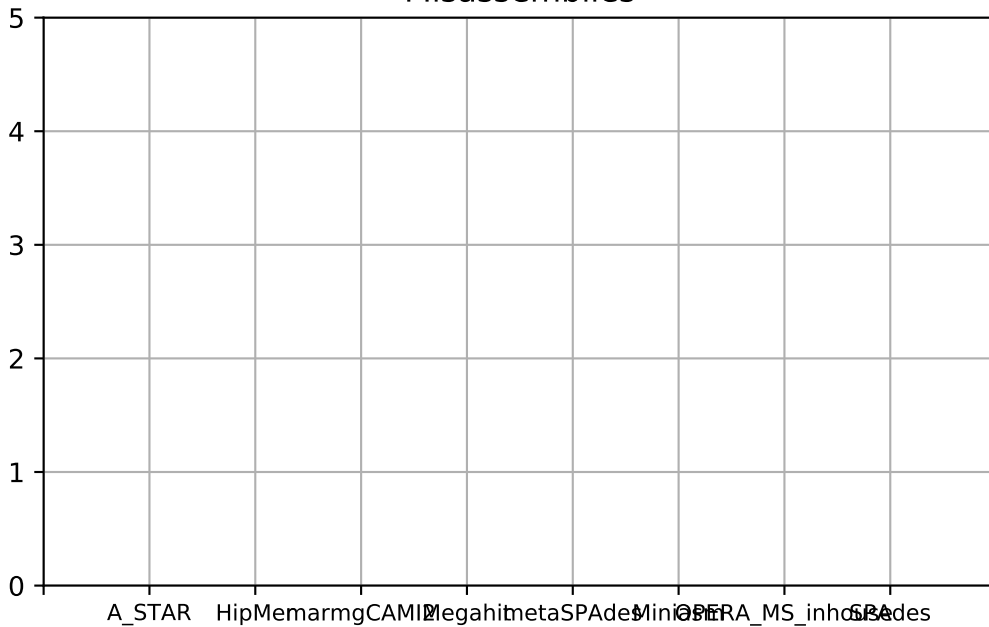
metaSPAdes coverage histogram (bin size: 1x)



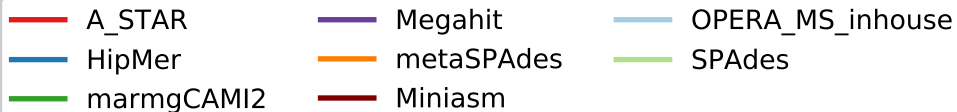
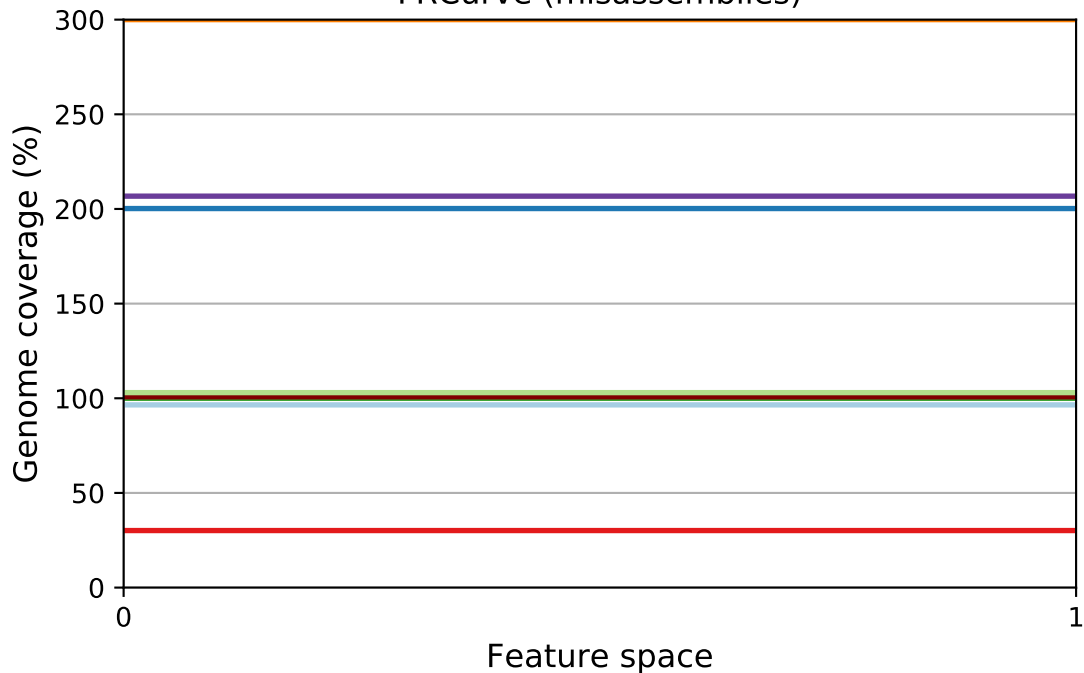
SPAdes coverage histogram (bin size: 1x)



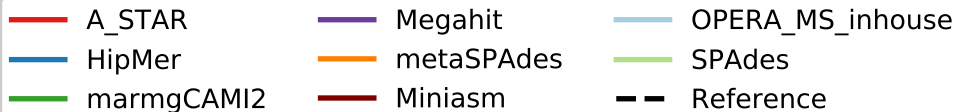
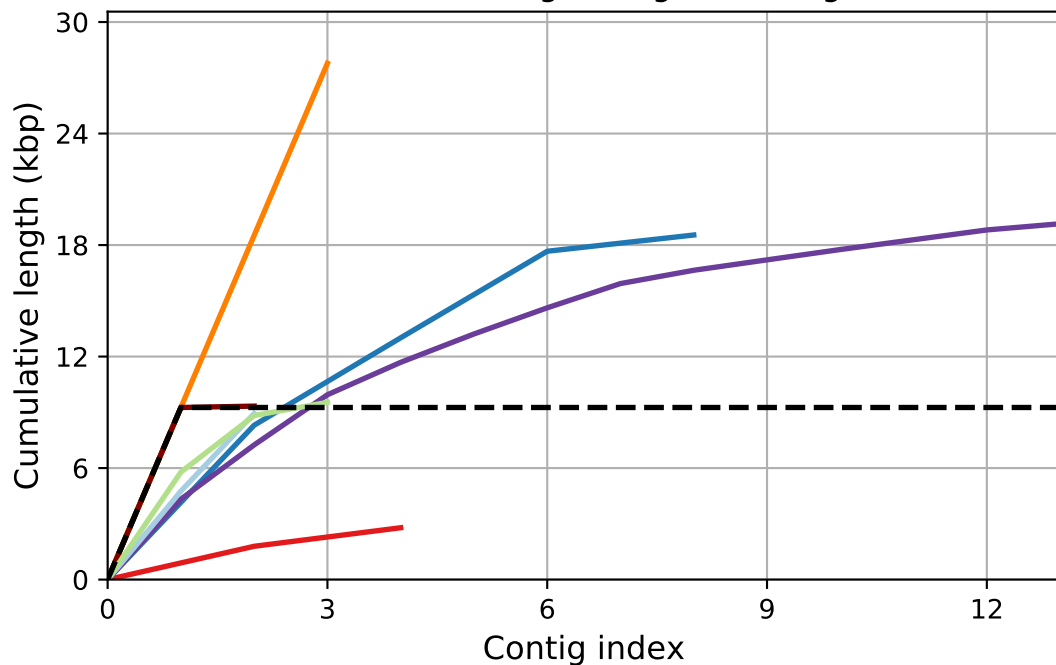
Misassemblies



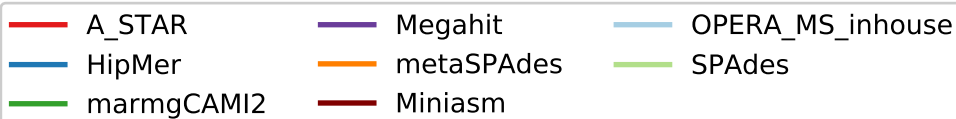
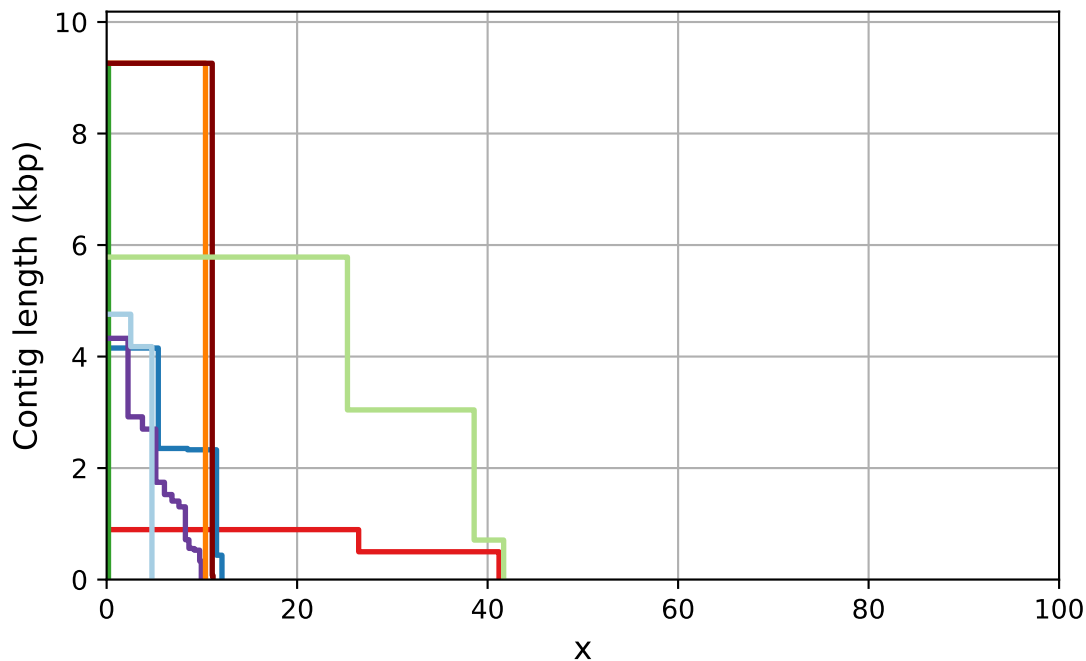
FRCurve (misassemblies)



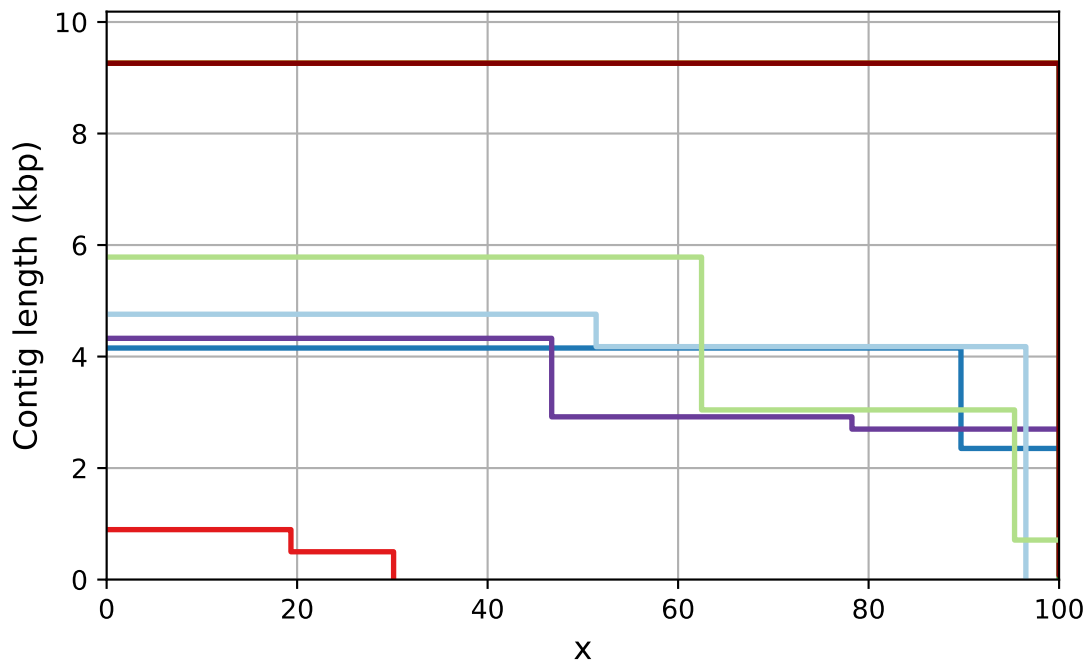
Cumulative length (aligned contigs)



NAx



NGAx



- | | | |
|---|--|---|
| — A_STAR | — Megahit | — OPERA_MS_inhouse |
| — HipMer | — metaSPAdes | — SPAdes |
| — marmgCAMI2 | — Miniasm | |

