

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	8	11	1	13	13	3	4	2
# contigs (>= 5000 bp)	8	11	1	11	13	3	4	0
# contigs (>= 10000 bp)	8	9	1	8	13	3	4	0
# contigs (>= 25000 bp)	6	7	1	5	3	1	1	0
# contigs (>= 50000 bp)	2	2	1	4	3	1	0	0
Total length (>= 1000 bp)	270066	393210	1595975	436339	352463	142720	90829	4099
Total length (>= 5000 bp)	270066	393210	1595975	429692	352463	142720	90829	0
Total length (>= 10000 bp)	270066	377478	1595975	407749	352463	142720	90829	0
Total length (>= 25000 bp)	226182	339613	1595975	348329	203734	108667	37923	0
Total length (>= 50000 bp)	101484	122467	1595975	307639	203734	108667	0	0
# contigs	10	11	1	13	13	3	4	8
Largest contig	50742	72353	1595975	114356	71834	108667	37923	2717
Total length	272000	393210	1595975	436339	352463	142720	90829	8648
Reference length	4642	4642	4642	4642	4642	4642	4642	4642
GC (%)	54.83	56.97	56.73	55.68	56.45	55.37	56.07	50.87
Reference GC (%)	49.33	49.33	49.33	49.33	49.33	49.33	49.33	49.33
N50	31879	48472	1595975	56467	60066	108667	21739	976
NG50	50742	72353	1595975	114356	71834	108667	37923	2717
N75	30470	46255	1595975	40690	18615	108667	15970	896
NG75	50742	72353	1595975	114356	71834	108667	37923	1382
L50	4	4	1	3	3	1	2	3
LG50	1	1	1	1	1	1	1	1
L75	6	6	1	5	7	1	3	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	0	1	1	0	1	0	0
# unaligned contigs	0 + 8 part	0 + 11 part	0 + 1 part	0 + 13 part	0 + 13 part	0 + 3 part	0 + 4 part	0 + 3 part
Unaligned length	262876	384147	1591548	422154	338417	138078	86189	4216
Genome fraction (%)	98.040	99.698	95.368	100.000	100.000	100.000	99.957	78.479
Duplication ratio	2.005	1.958	1.000	3.056	3.026	1.000	1.000	1.217
# 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	395.52	0.00	0.00	775.53	43.08	21.54	129.31	713.70
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	1199	1953	2188	2188	2188	2188	2188	907
Total aligned length	9200	9063	4427	14185	14046	4642	4640	3995
NGA50	1199	1947	1199	2188	2188	1199	1199	727
NGA75	1040	1947	1040	2188	2188	1040	1040	215
LGA50	2	2	2	2	2	2	2	3
LGA75	4	2	3	2	2	3	3	6

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

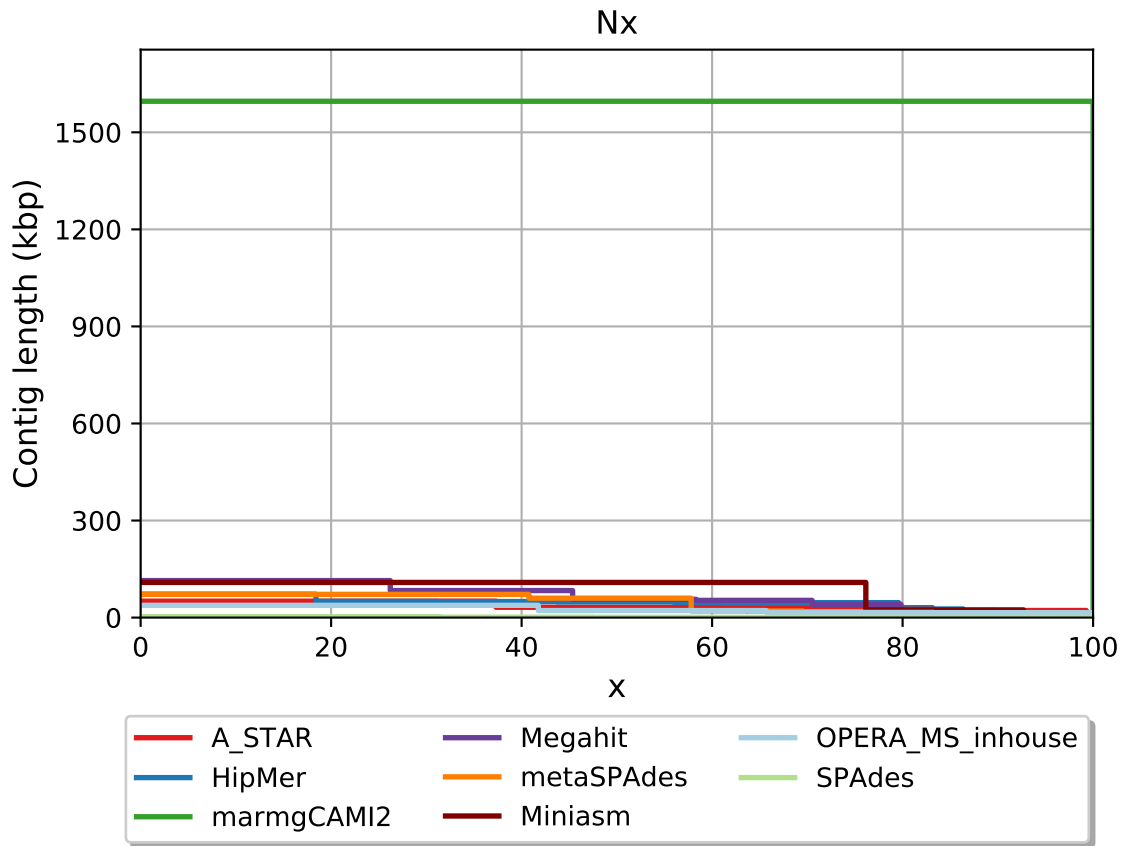
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	6	11	0	12	13	2	4	3
# possible misassemblies	6	13	0	14	15	2	5	3
# 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	0	1	1	0	1	0	0
# mismatches	18	0	0	36	2	1	6	26
# 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).

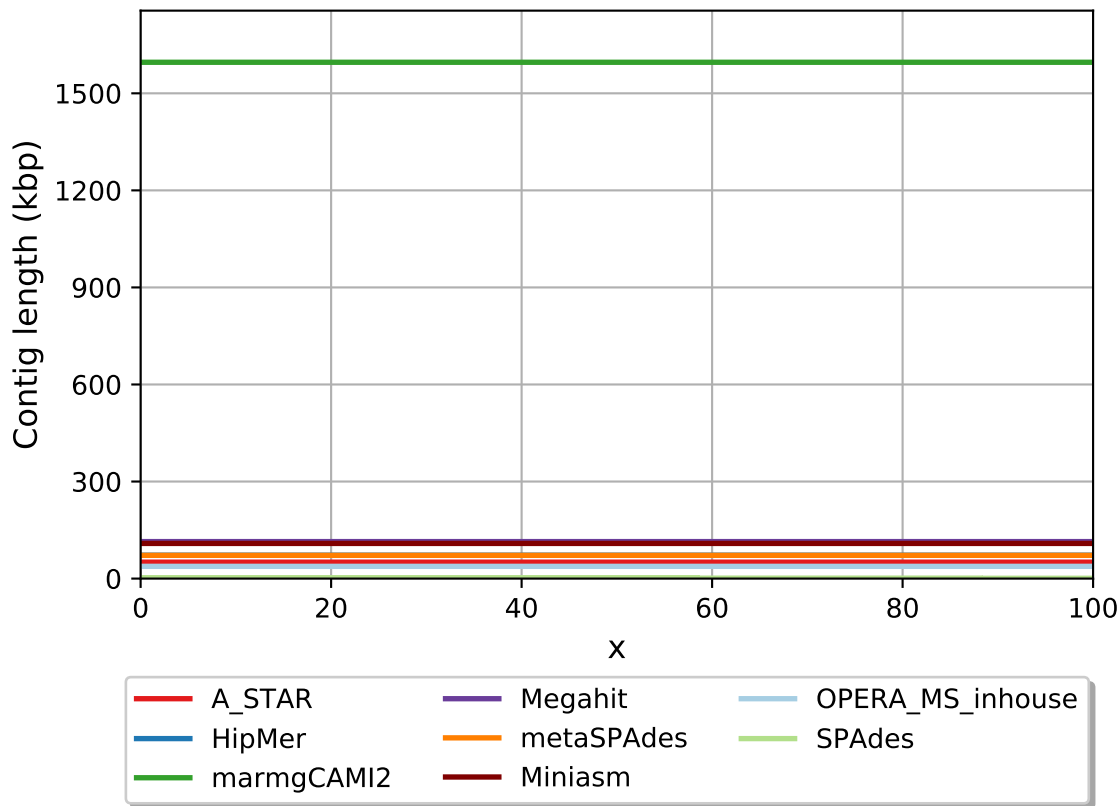
Unaligned report

	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	8	11	1	13	13	3	4	3
Partially unaligned length	262876	384147	1591548	422154	338417	138078	86189	4216
# N's	0	0	0	0	0	0	0	0

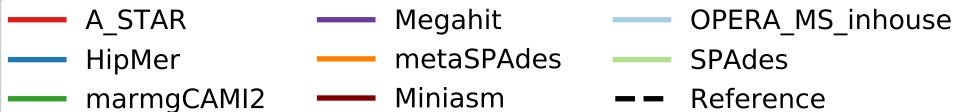
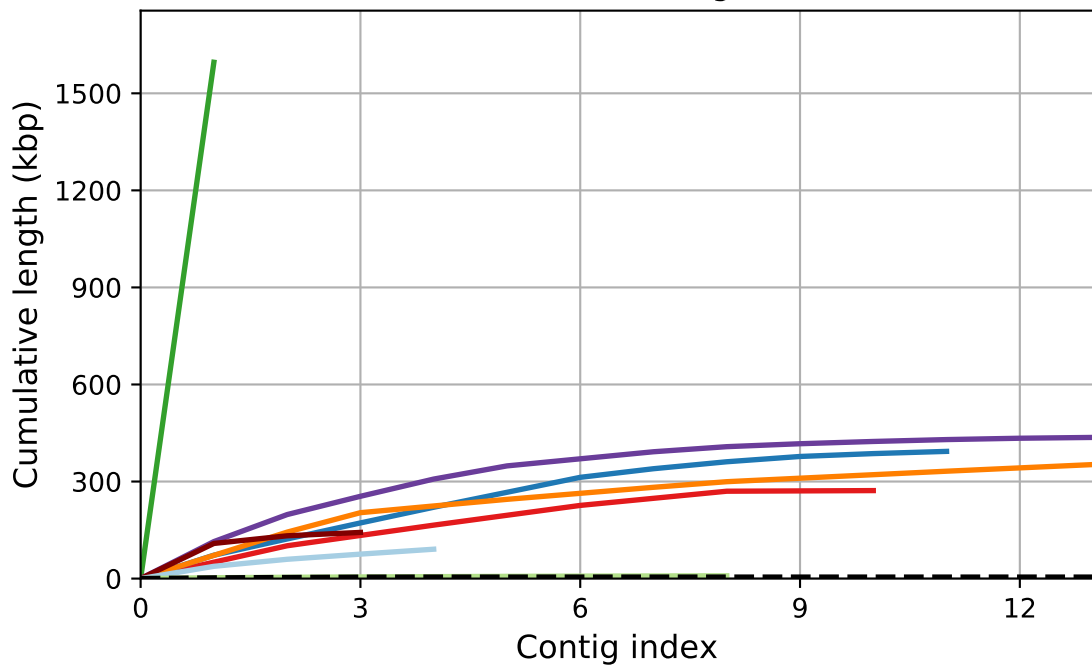
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



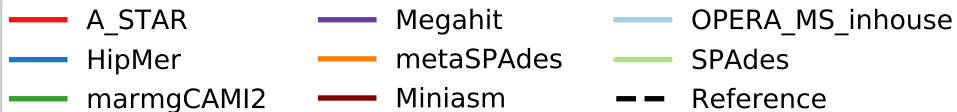
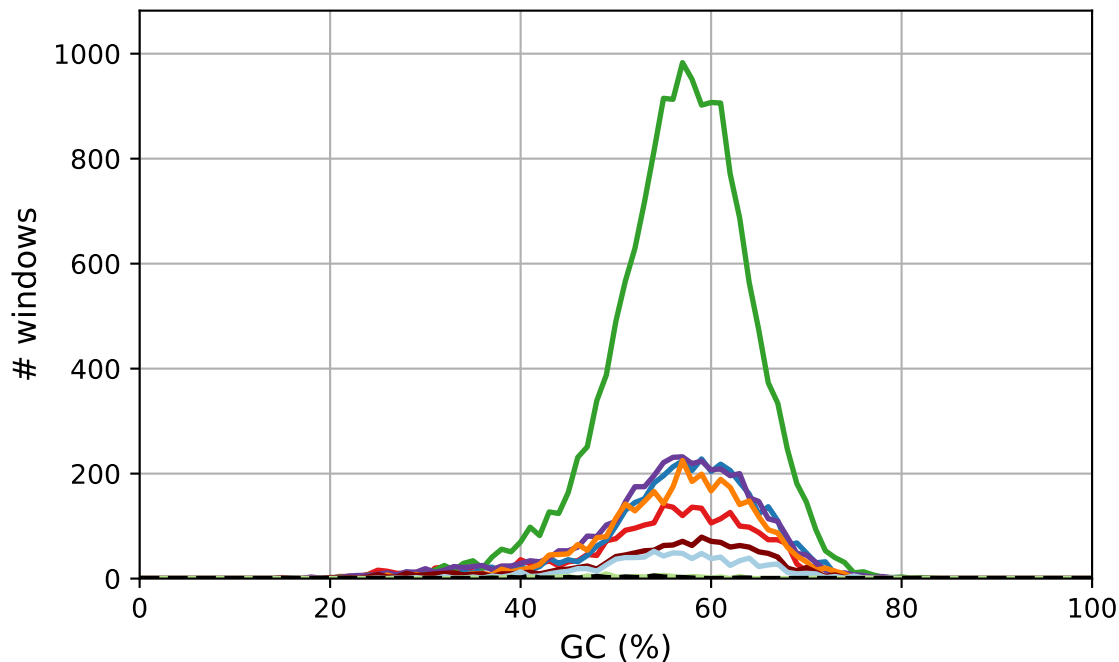
NGx



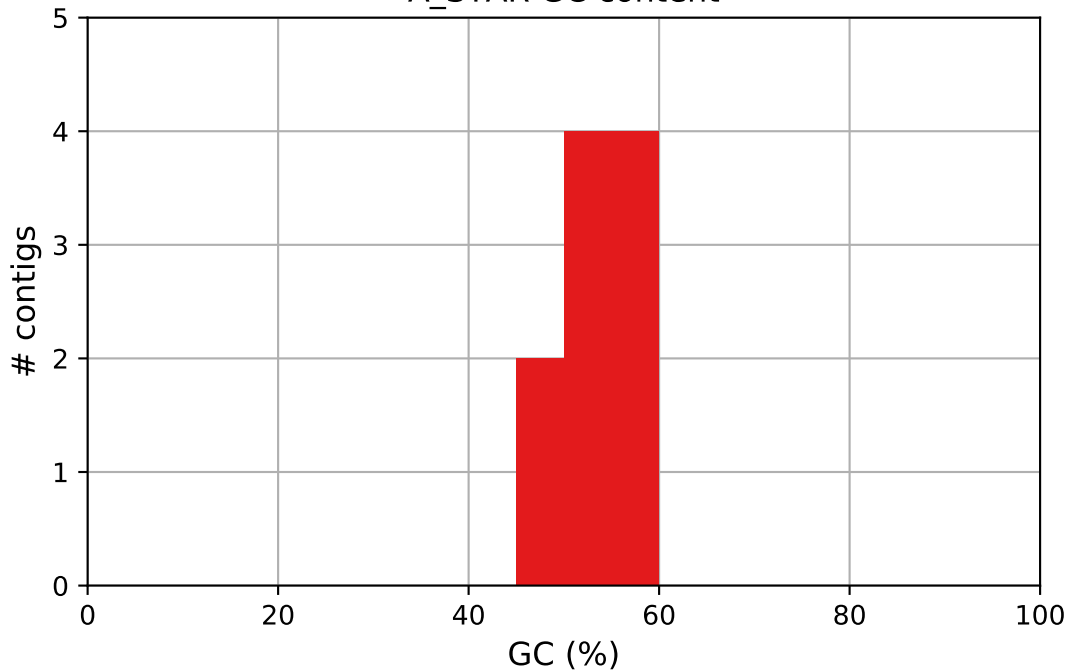
Cumulative length



GC content

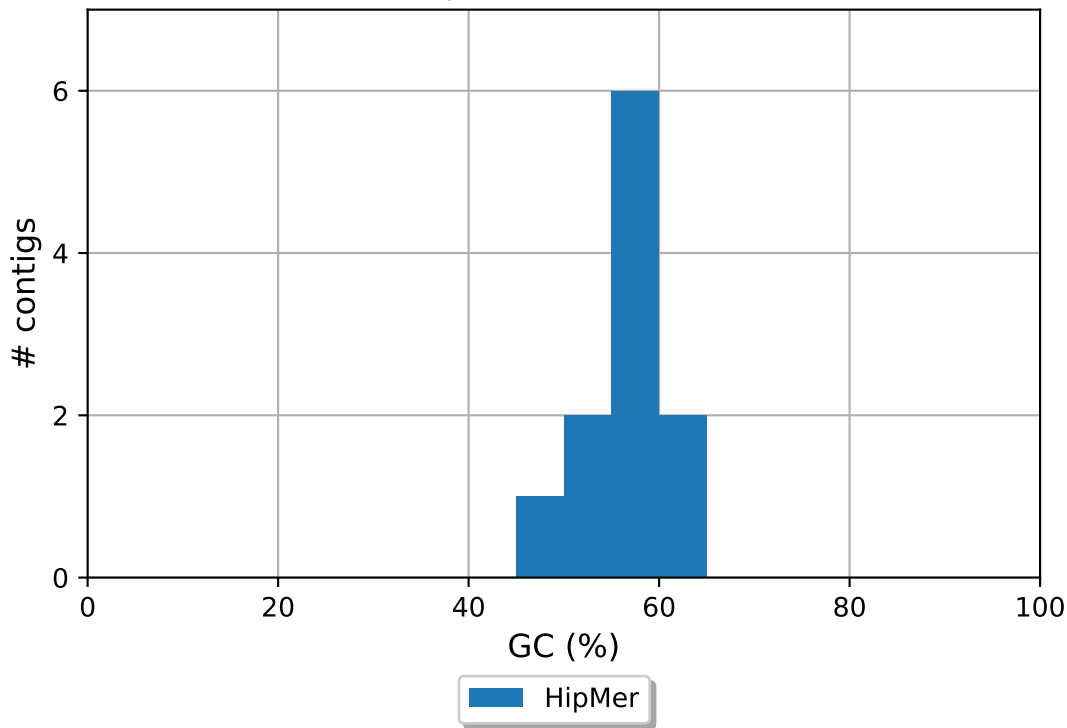


A_STAR GC content

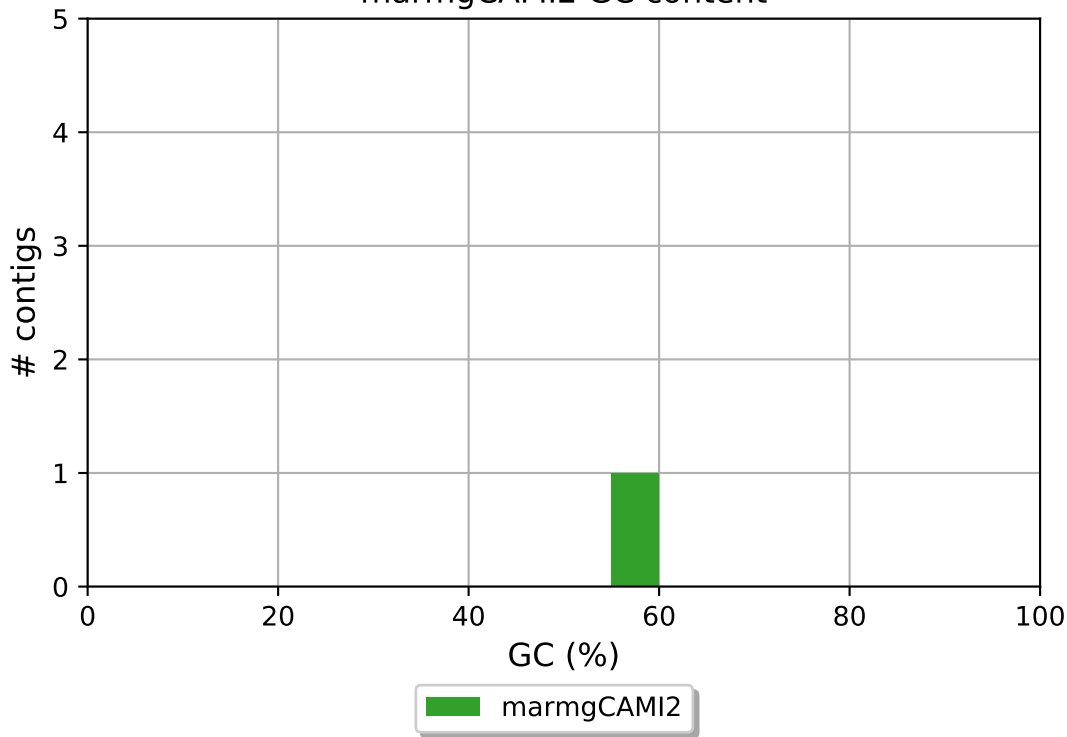


A_STAR

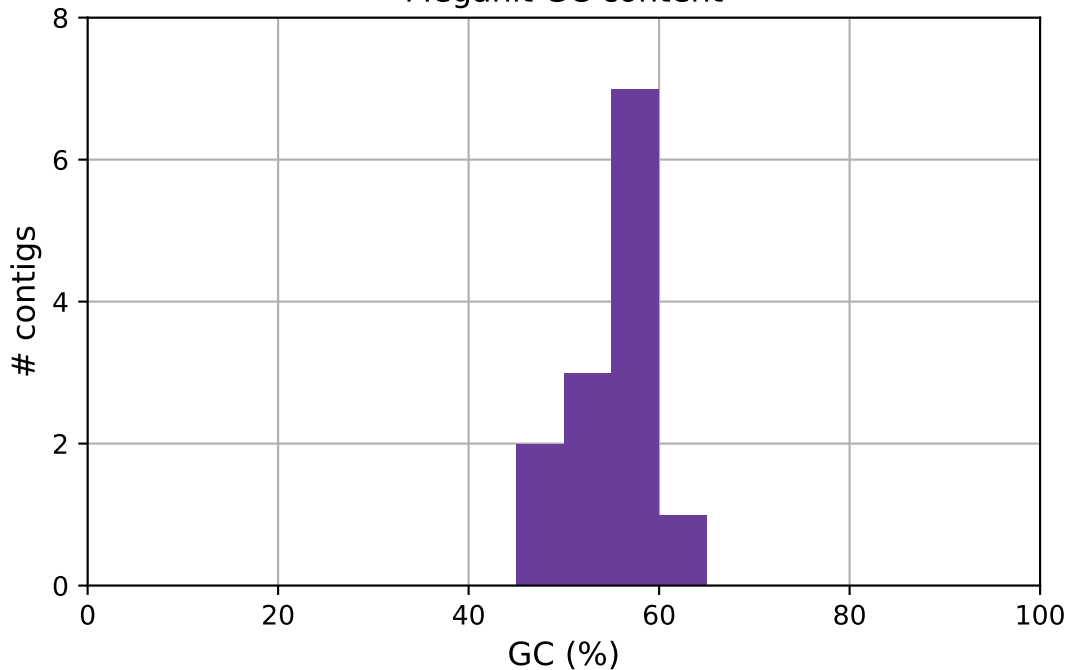
HipMer GC content



marmgCAMI2 GC content

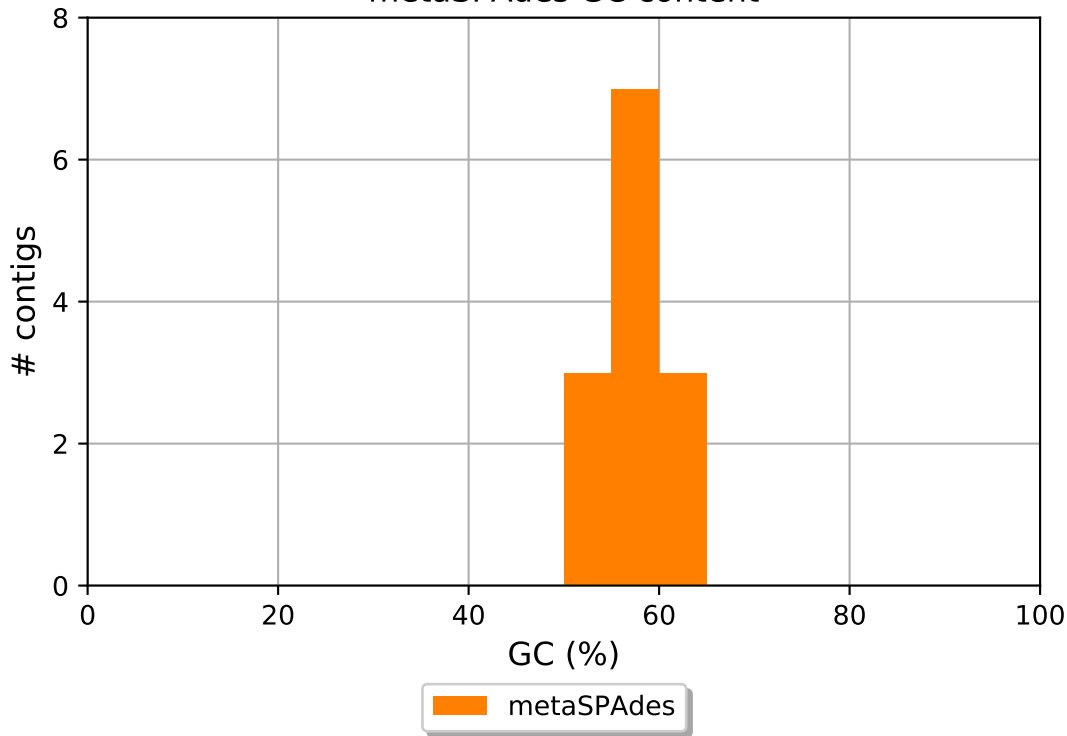


Megahit GC content

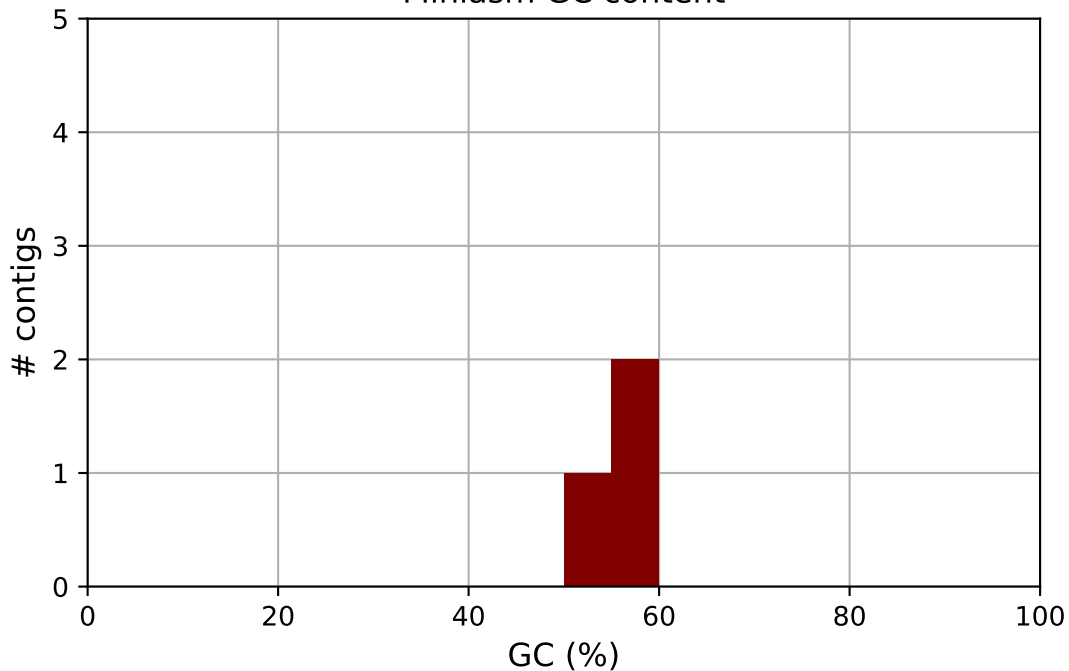


Megahit

metaSPAdes GC content

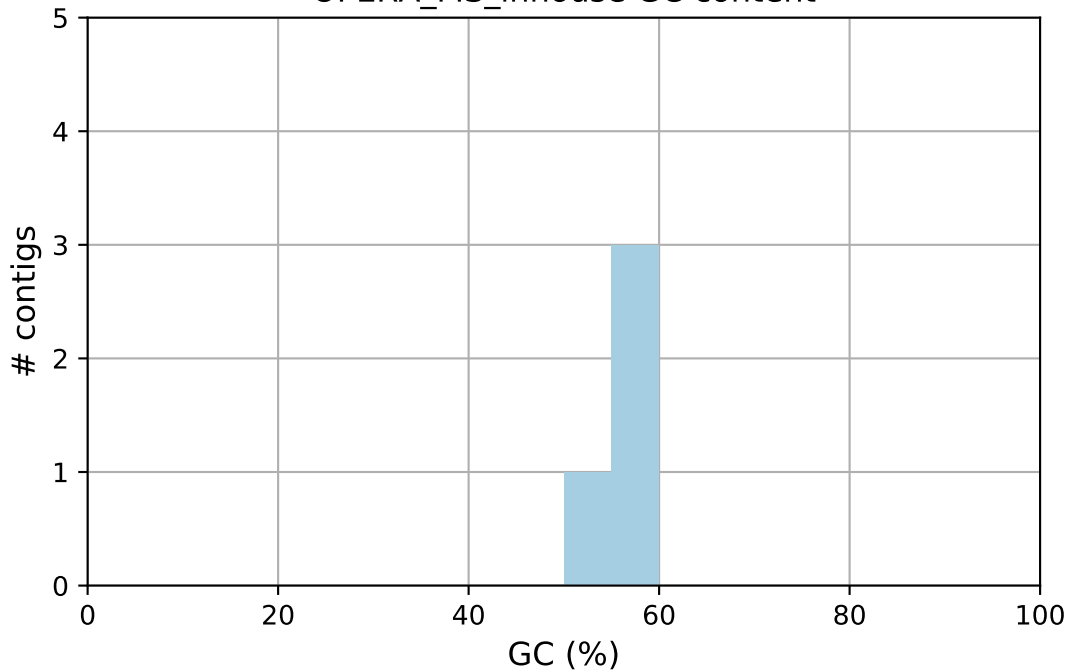


Miniasm GC content



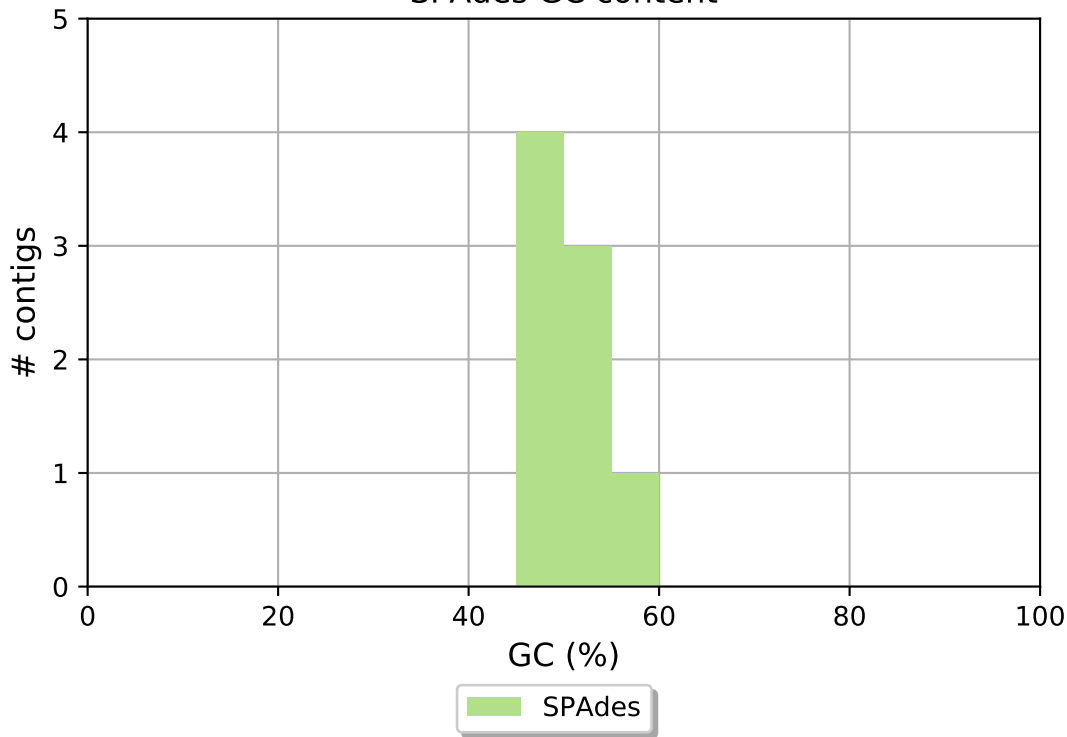
Miniasm

OPERA_MS_inhouse GC content

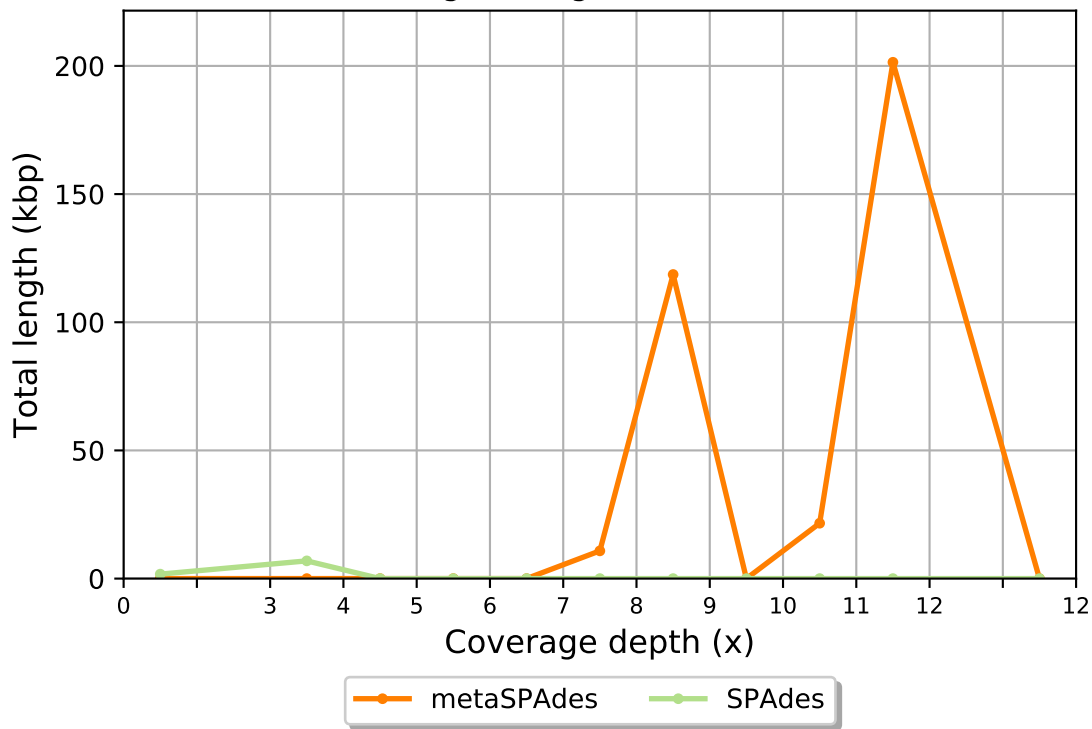


OPERA_MS_inhouse

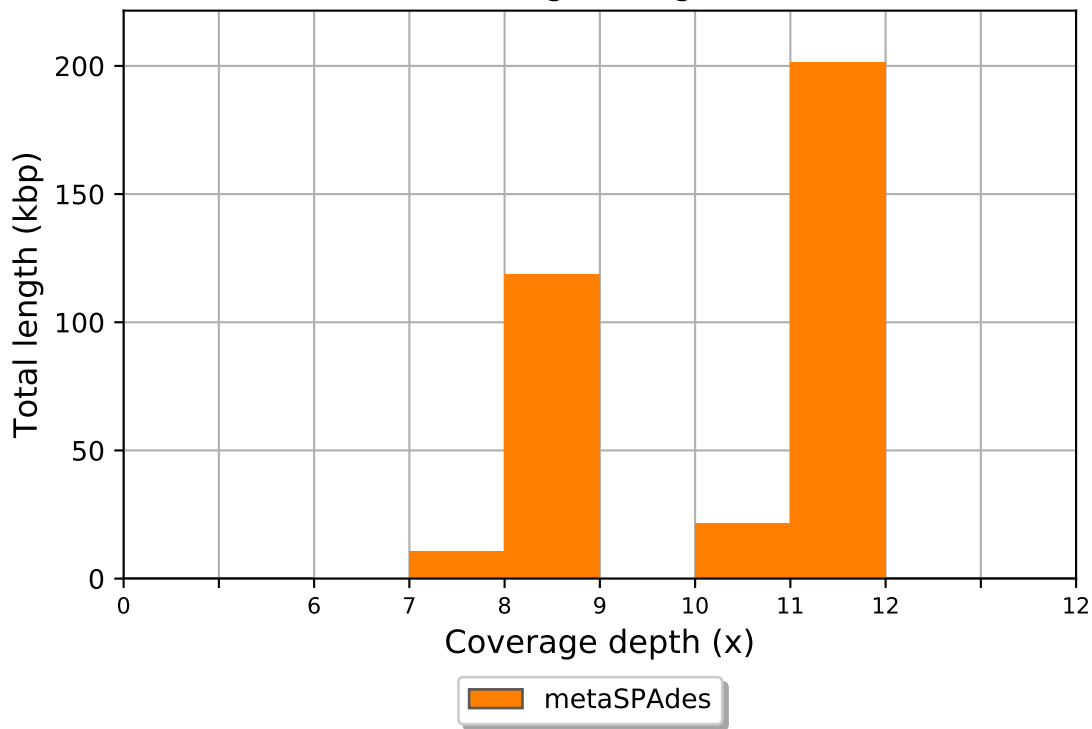
SPAdes GC content



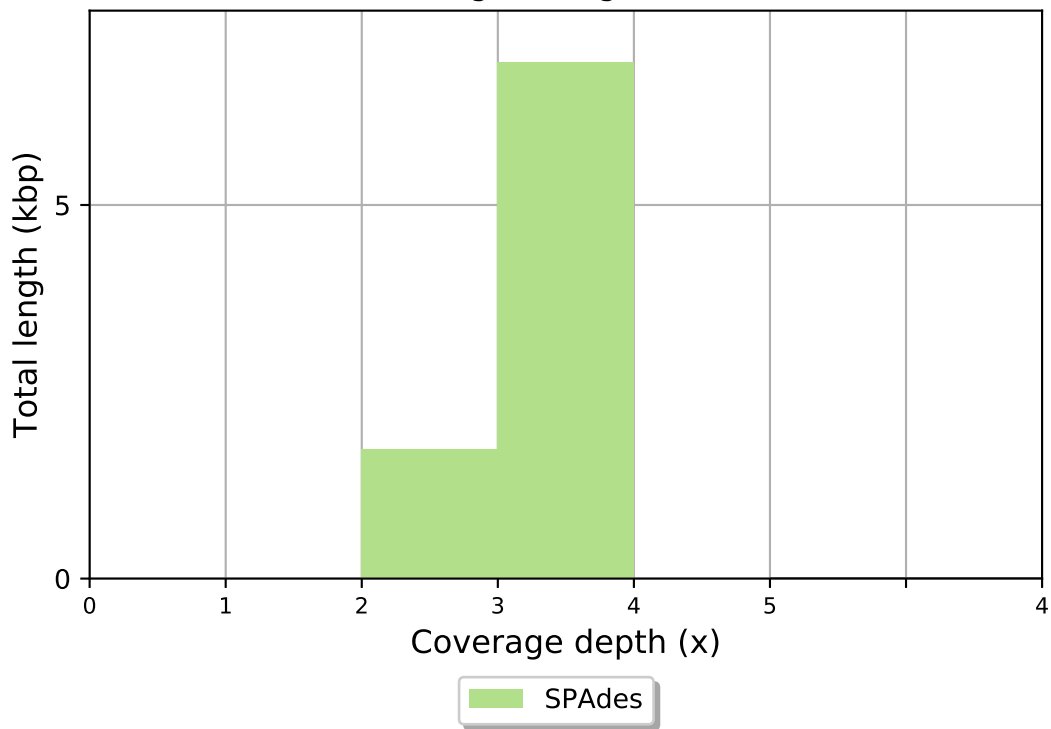
Coverage histogram (bin size: 1x)



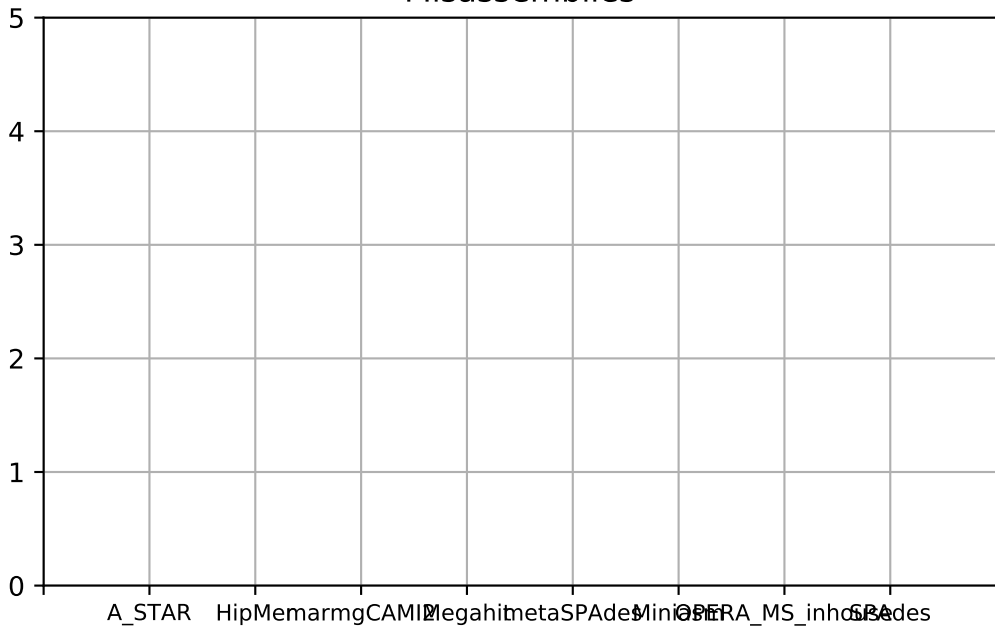
metaSPAdes coverage histogram (bin size: 1x)



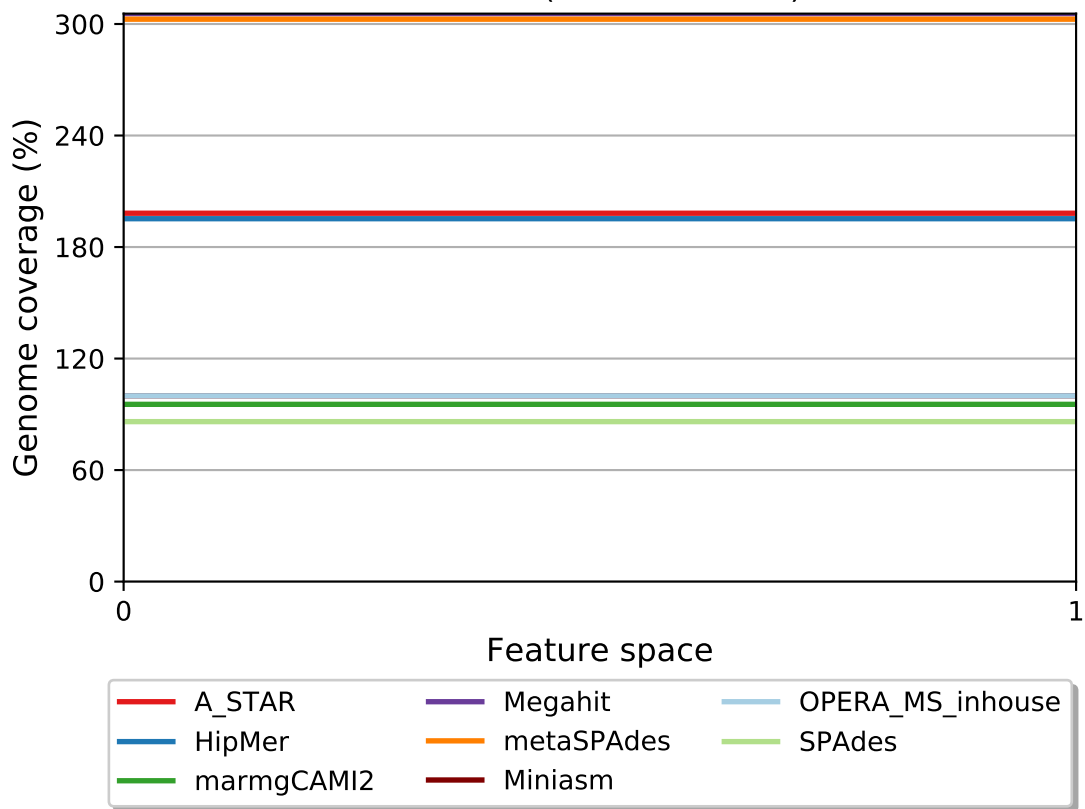
SPAdes coverage histogram (bin size: 1x)



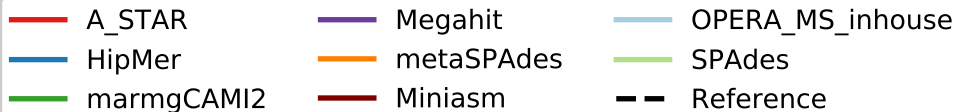
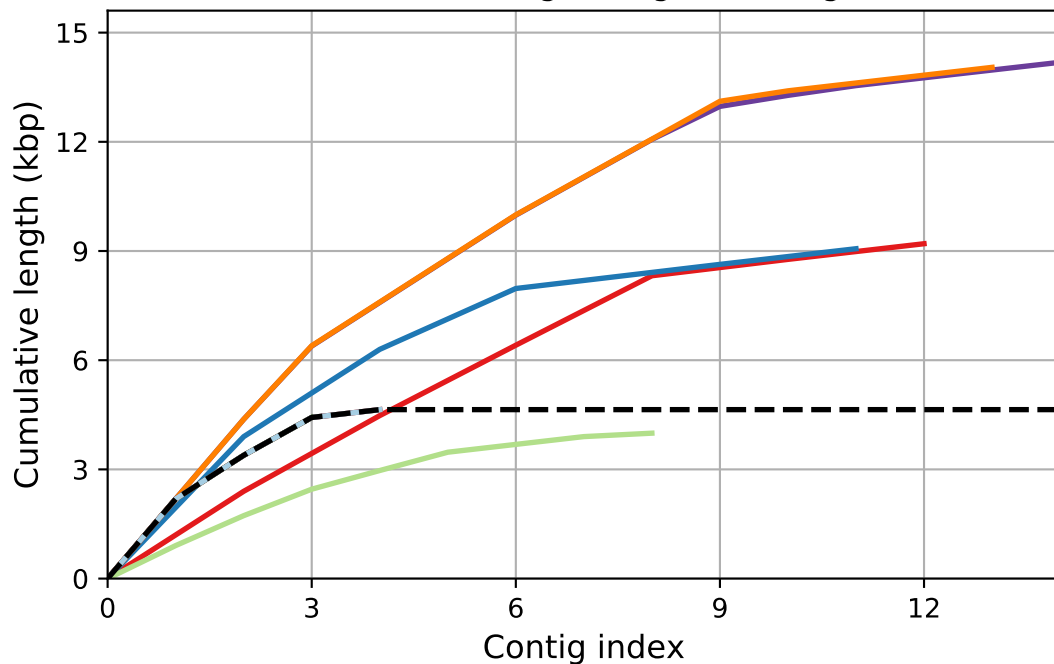
Misassemblies



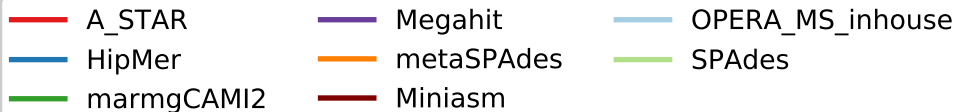
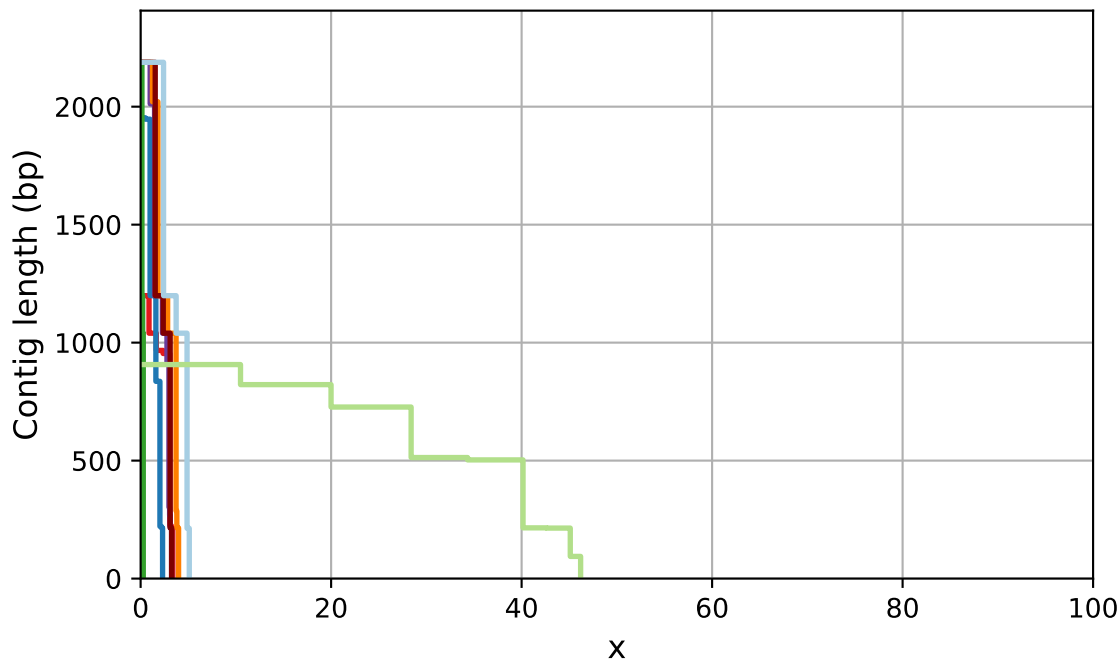
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

