

# Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	2	1	3	3	2	1	1
# contigs (>= 5000 bp)	2	2	1	3	3	2	1	1
# contigs (>= 10000 bp)	2	2	1	3	3	2	1	1
# contigs (>= 25000 bp)	0	2	1	3	3	1	1	1
# contigs (>= 50000 bp)	0	2	1	3	2	1	1	0
Total length (>= 1000 bp)	29909	1445497	2884284	1479597	431321	788333	341863	33699
Total length (>= 5000 bp)	29909	1445497	2884284	1479597	431321	788333	341863	33699
Total length (>= 10000 bp)	29909	1445497	2884284	1479597	431321	788333	341863	33699
Total length (>= 25000 bp)	0	1445497	2884284	1479597	431321	764306	341863	33699
Total length (>= 50000 bp)	0	1445497	2884284	1479597	382492	764306	341863	0
# contigs	2	2	1	3	3	2	1	1
Largest contig	17118	764620	2884284	1007761	191246	764306	341863	33699
Total length	29909	1445497	2884284	1479597	431321	788333	341863	33699
Reference length	820	820	820	820	820	820	820	820
GC (%)	36.20	35.43	35.45	35.49	35.63	35.46	35.62	35.43
Reference GC (%)	33.78	33.78	33.78	33.78	33.78	33.78	33.78	33.78
N50	17118	764620	2884284	1007761	191246	764306	341863	33699
NG50	17118	764620	2884284	1007761	191246	764306	341863	33699
N75	12791	680877	2884284	329309	191246	764306	341863	33699
NG75	17118	764620	2884284	1007761	191246	764306	341863	33699
L50	1	1	1	1	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	2	1	2	2	1	1	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	0	0	0	0	0	0
# unaligned contigs	0 + 2 part	0 + 2 part	0 + 1 part	0 + 3 part	0 + 3 part	0 + 2 part	0 + 1 part	0 + 1 part
Unaligned length	28121	1443857	2883464	1477137	428861	786797	341043	32879
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	2.180	2.000	1.000	3.000	3.000	1.873	1.000	1.000
# N's per 100 kbp	494.83	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	0.00	0.00	243.90	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	1463.41	0.00	0.00
Largest alignment	820	820	820	820	820	820	820	820
Total aligned length	1640	1640	820	2460	2460	1536	820	820
NGA50	820	820	820	820	820	820	820	820
NGA75	820	820	820	820	820	820	820	820
LGA50	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1

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

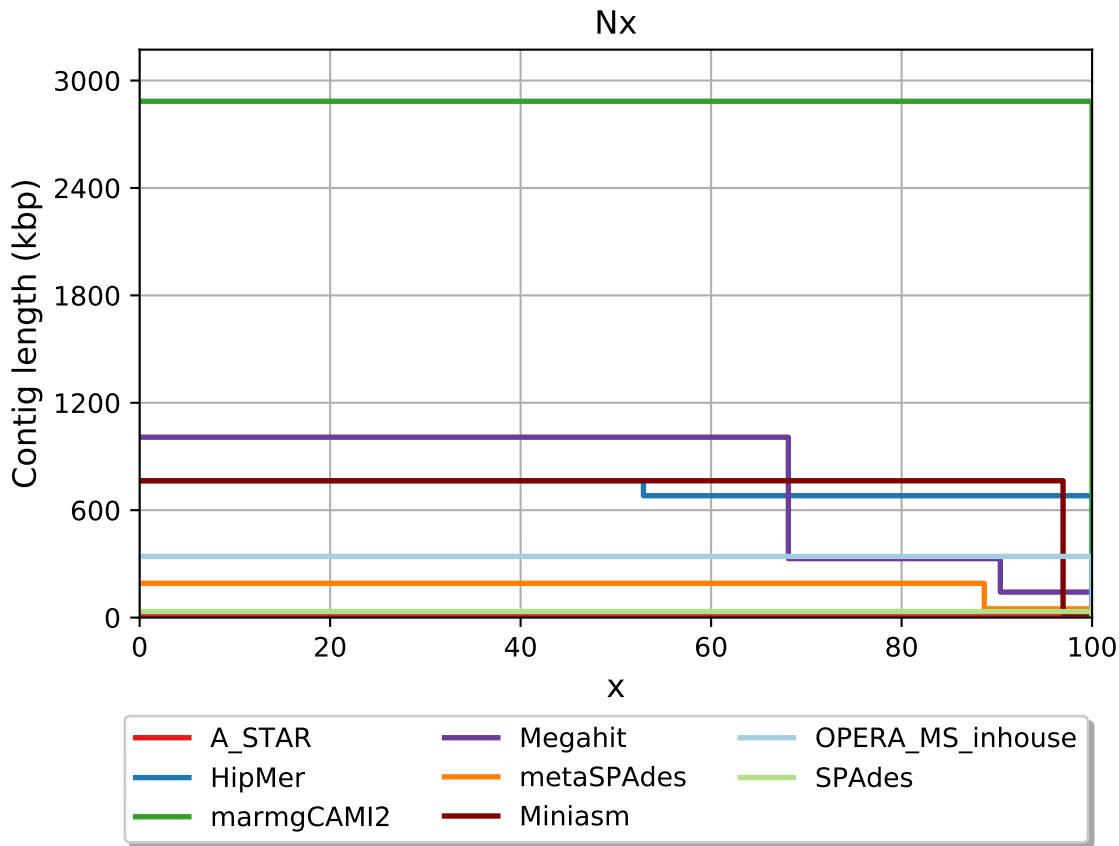
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	1	3	3	2	1	1
# possible misassemblies	4	4	2	6	6	4	2	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	0	0	0	0	0	0
# mismatches	0	0	0	0	0	2	0	0
# indels	0	0	0	0	0	12	0	0
# indels (<= 5 bp)	0	0	0	0	0	12	0	0
# indels (> 5 bp)	0	0	0	0	0	0	0	0
Indels length	0	0	0	0	0	14	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).

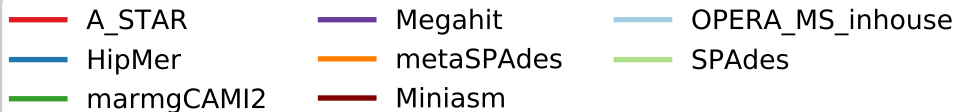
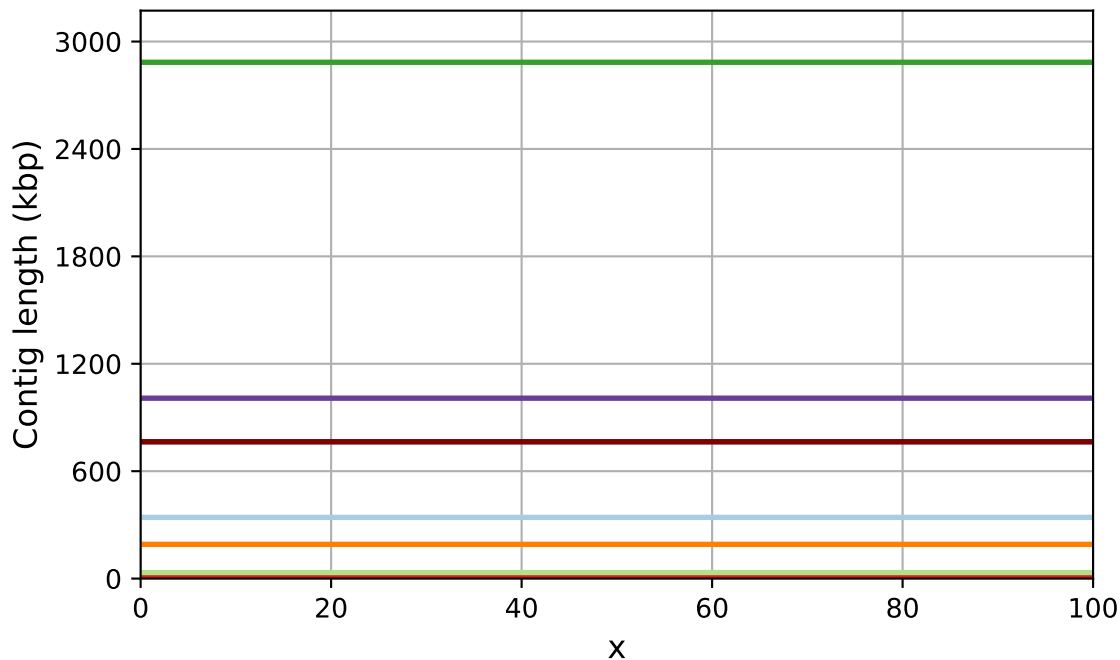
## Unaligned report

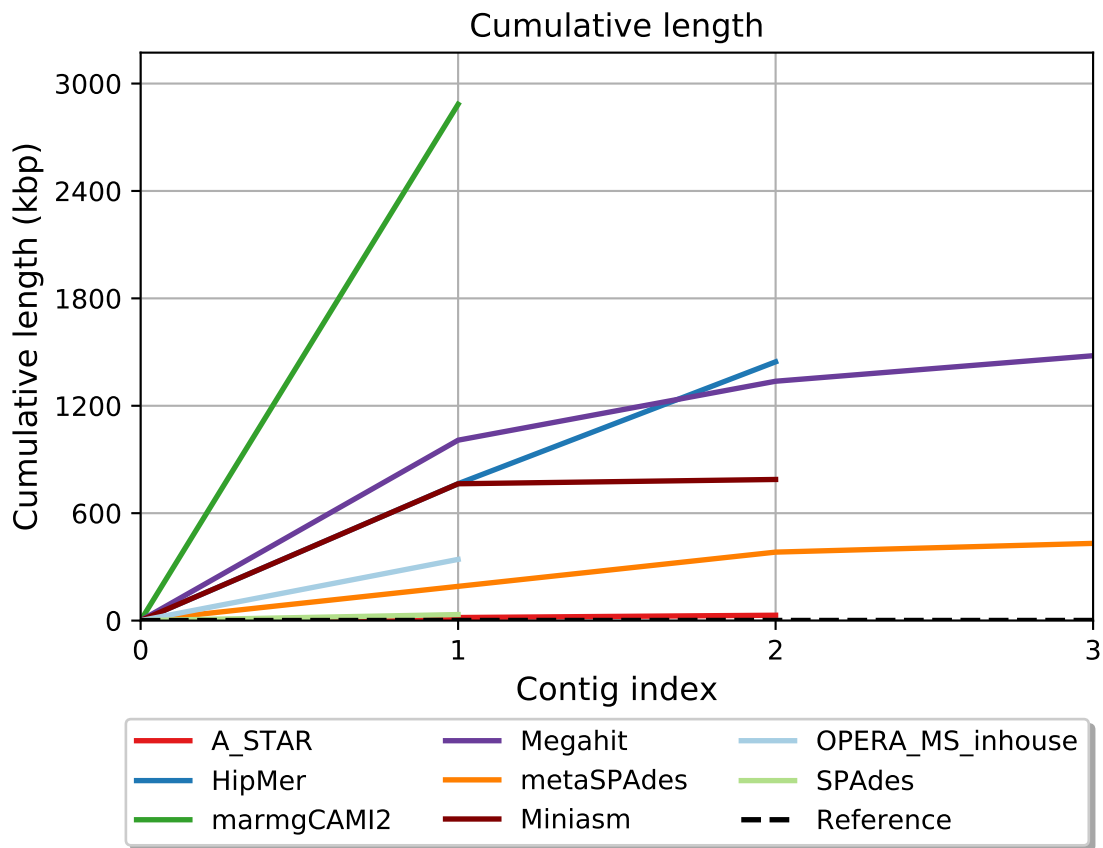
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	2	2	1	3	3	2	1	1
Partially unaligned length	28121	1443857	2883464	1477137	428861	786797	341043	32879
# N's	148	0	0	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).

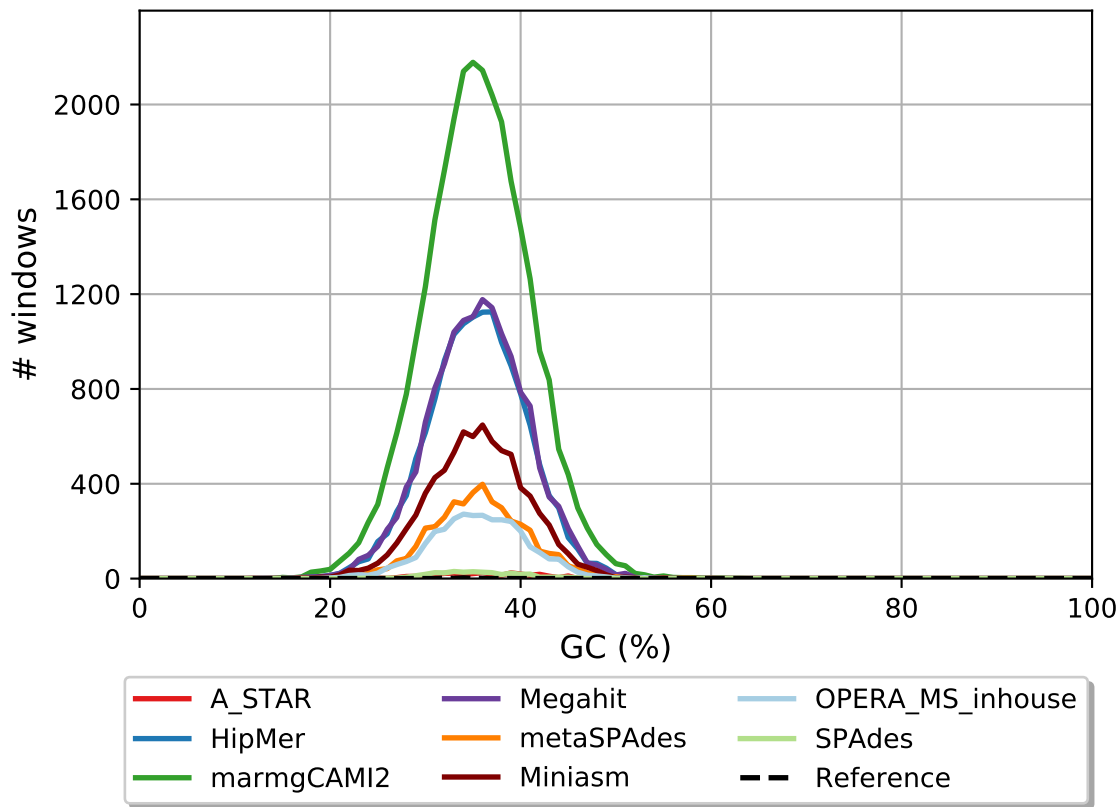


# NGx

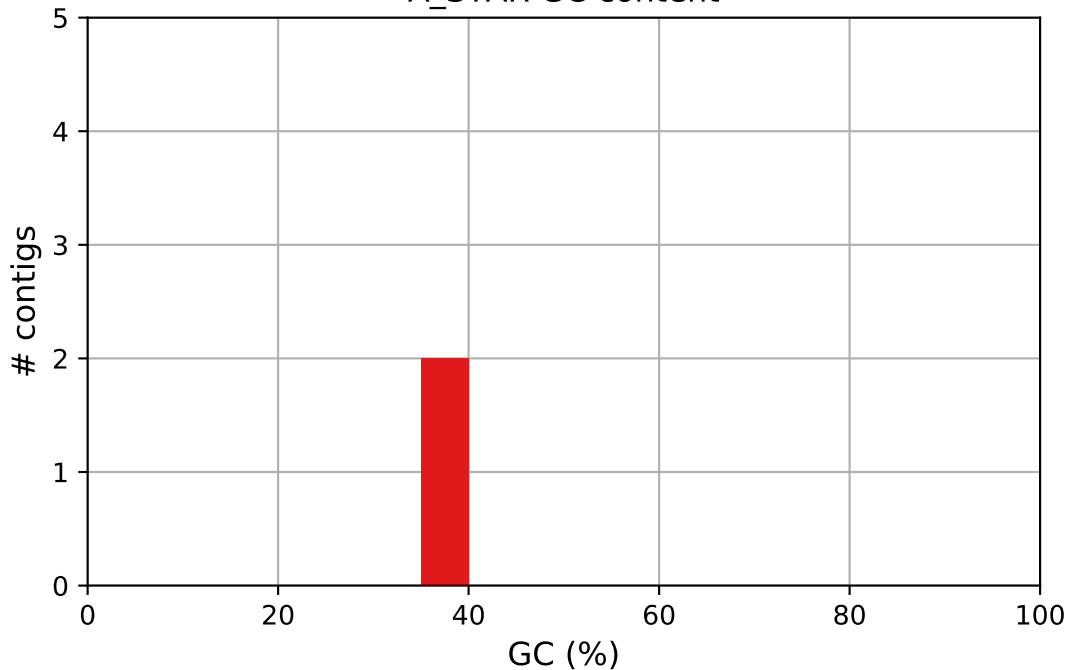




GC content



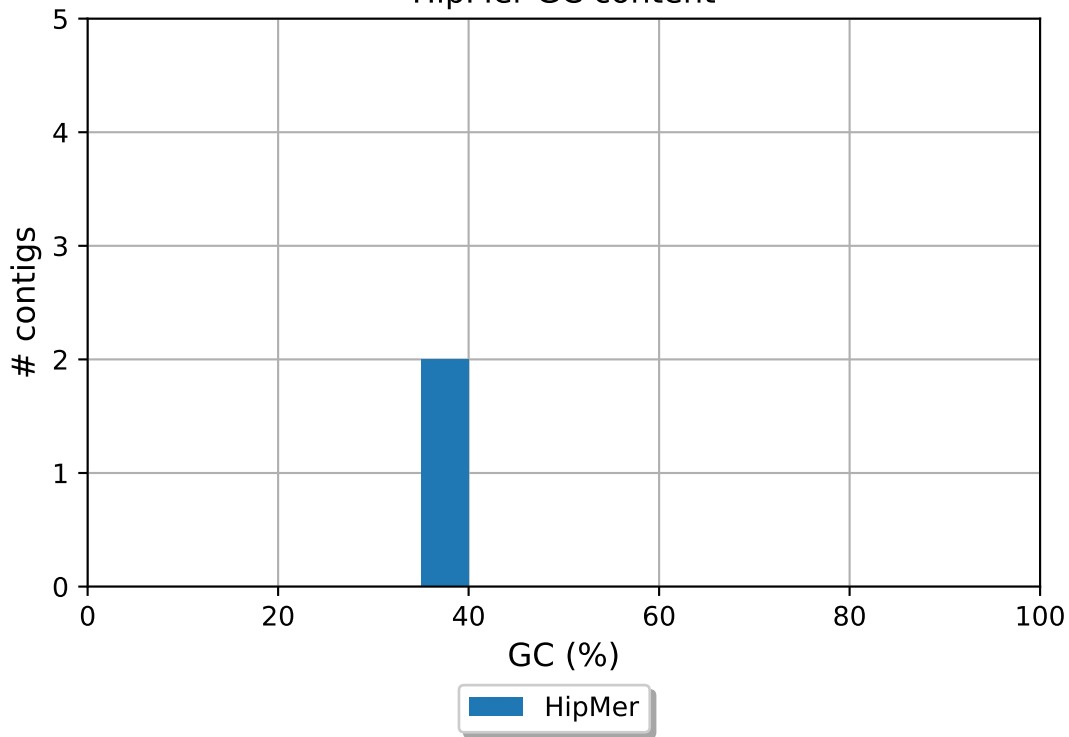
A\_STAR GC content



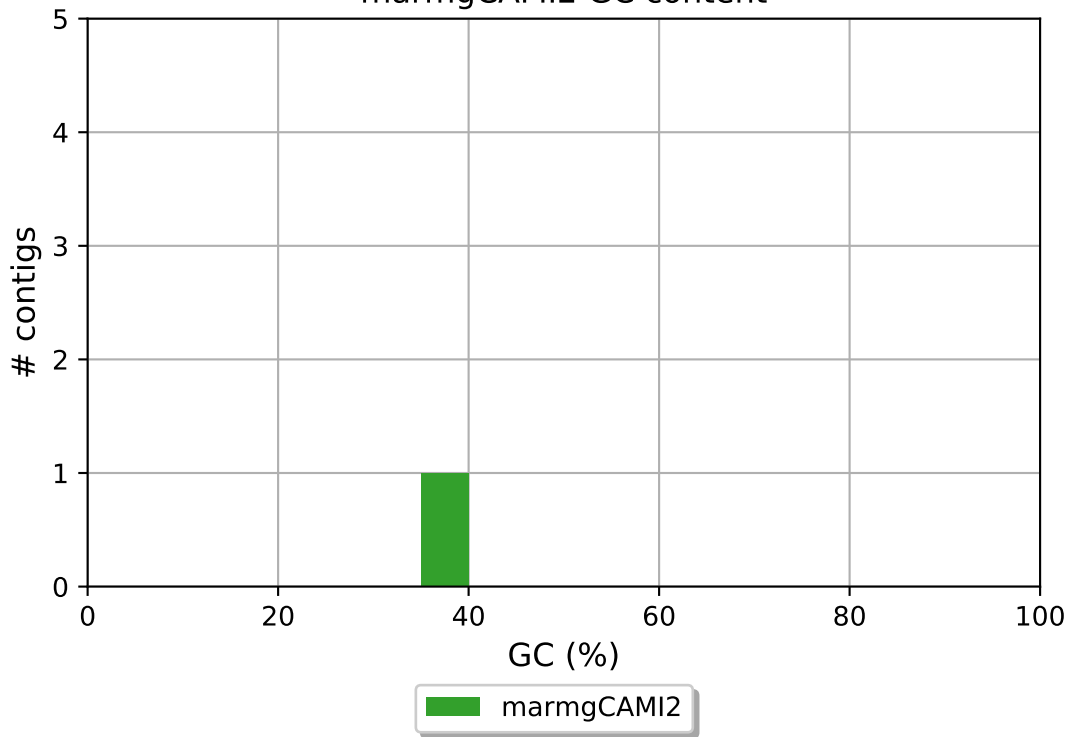
A\_STAR



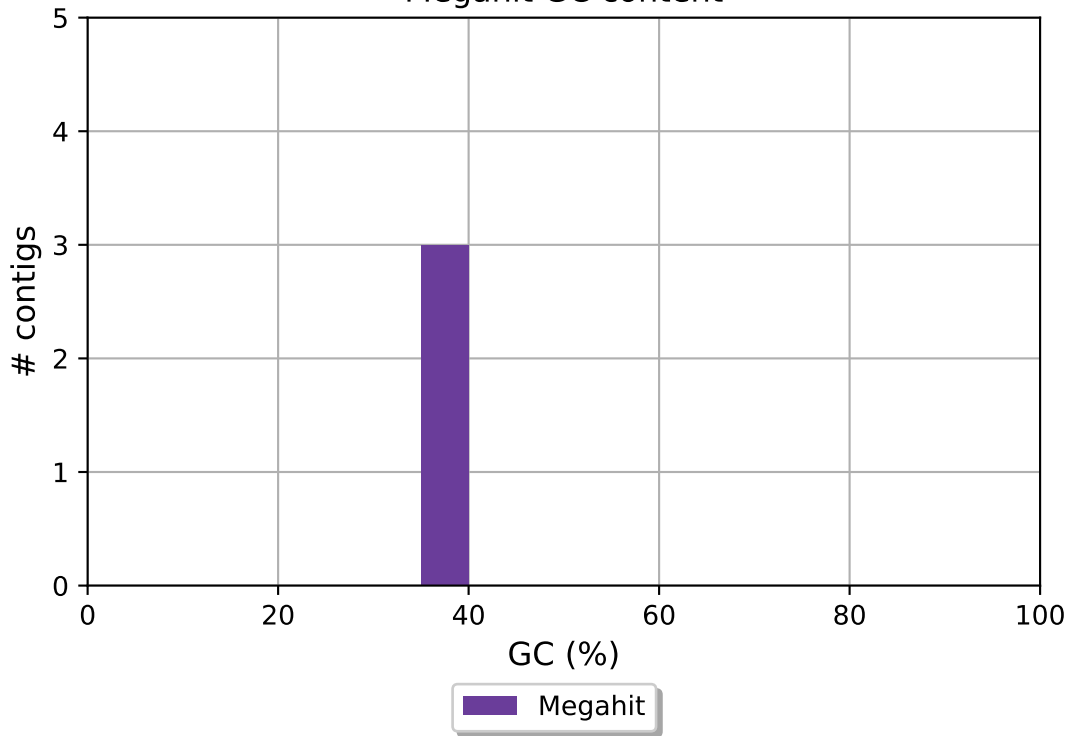
HipMer GC content



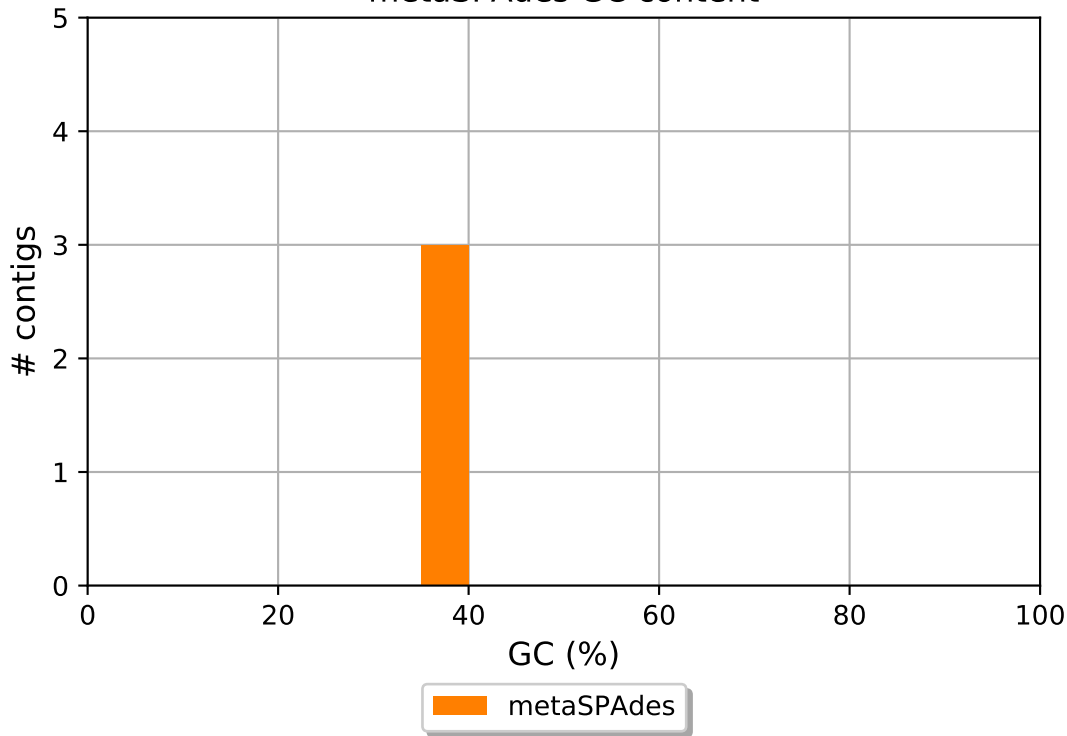
marmgCAMI2 GC content



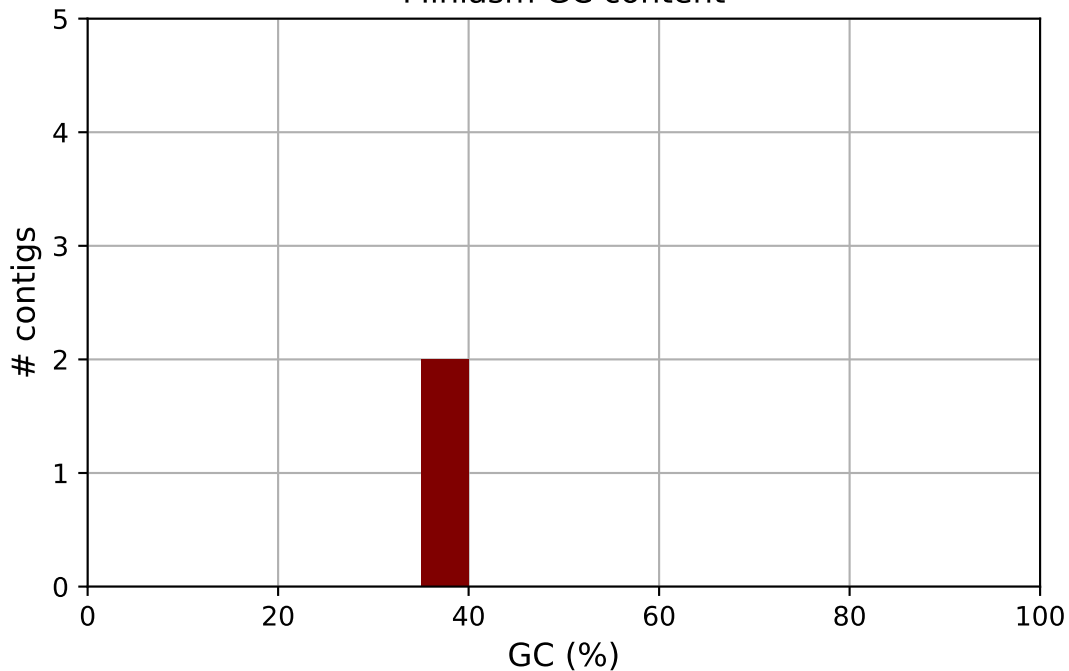
Megahit GC content



metaSPAdes GC content

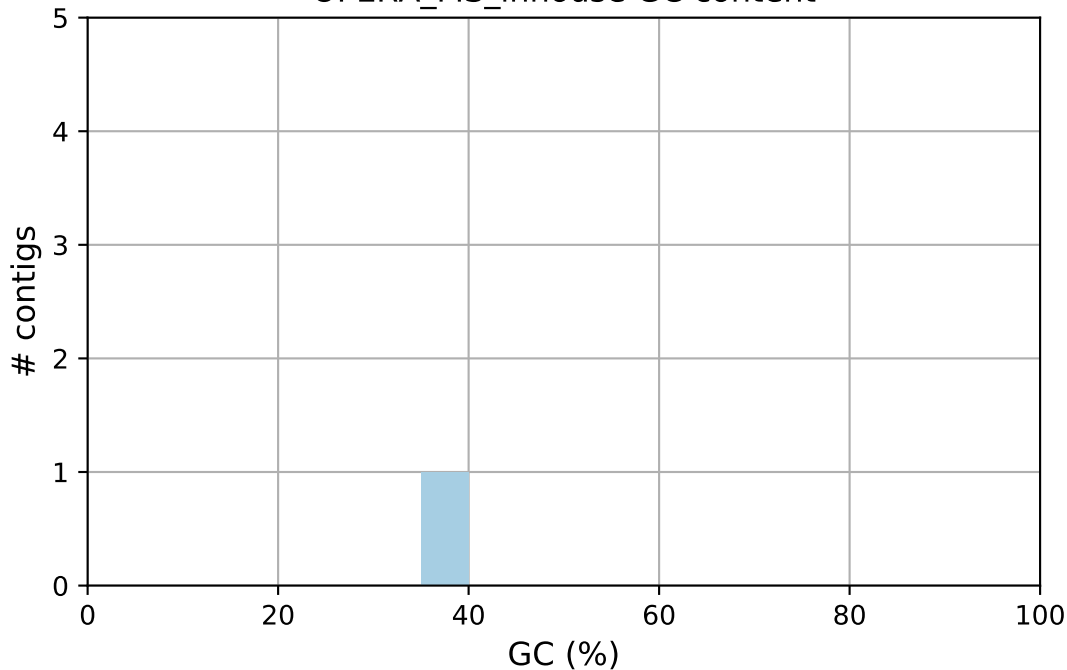


# Miniasm GC content



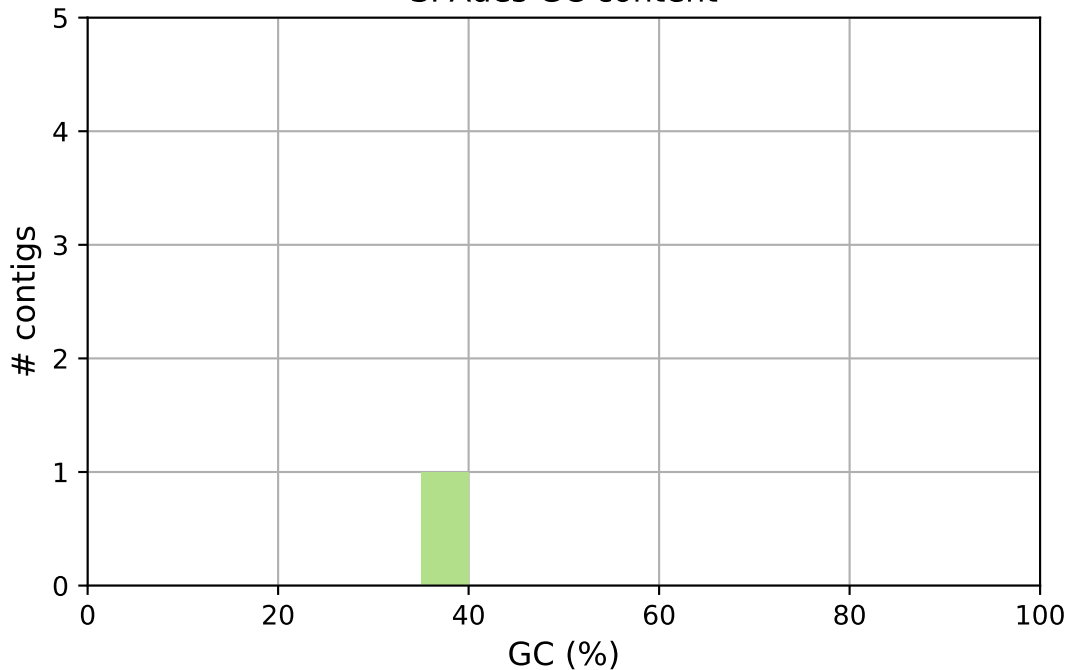
Miniasm

OPERA\_MS\_inhouse GC content



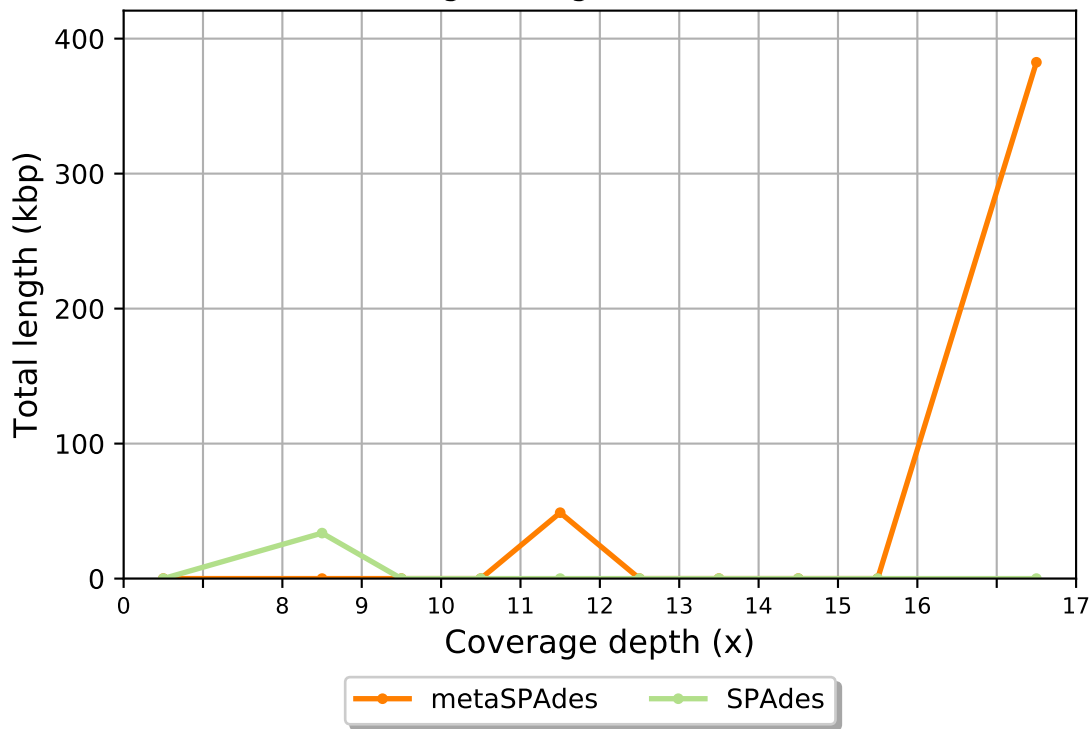
OPERA\_MS\_inhouse

# SPAdes GC content



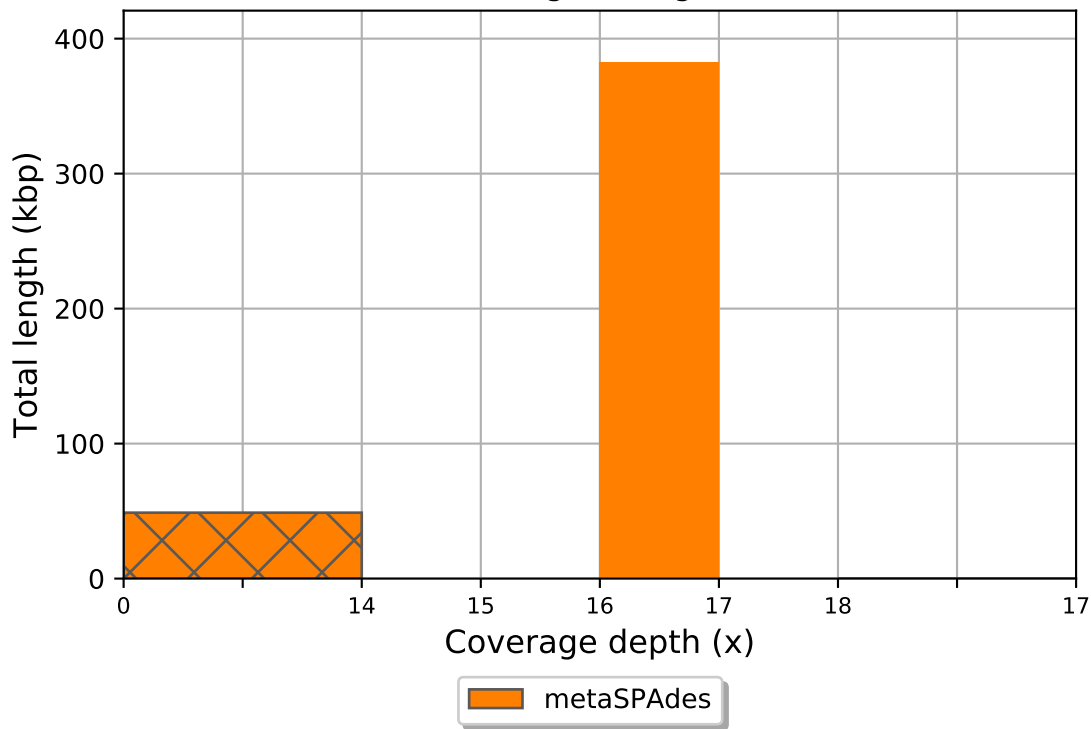
SPAdes

Coverage histogram (bin size: 1x)

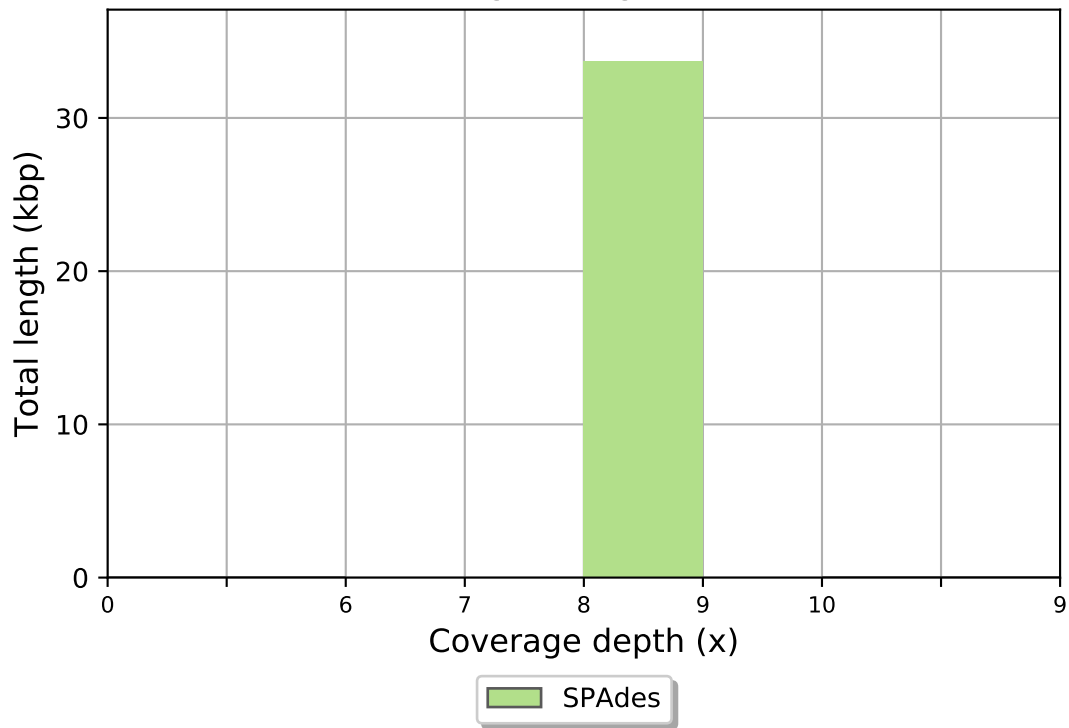




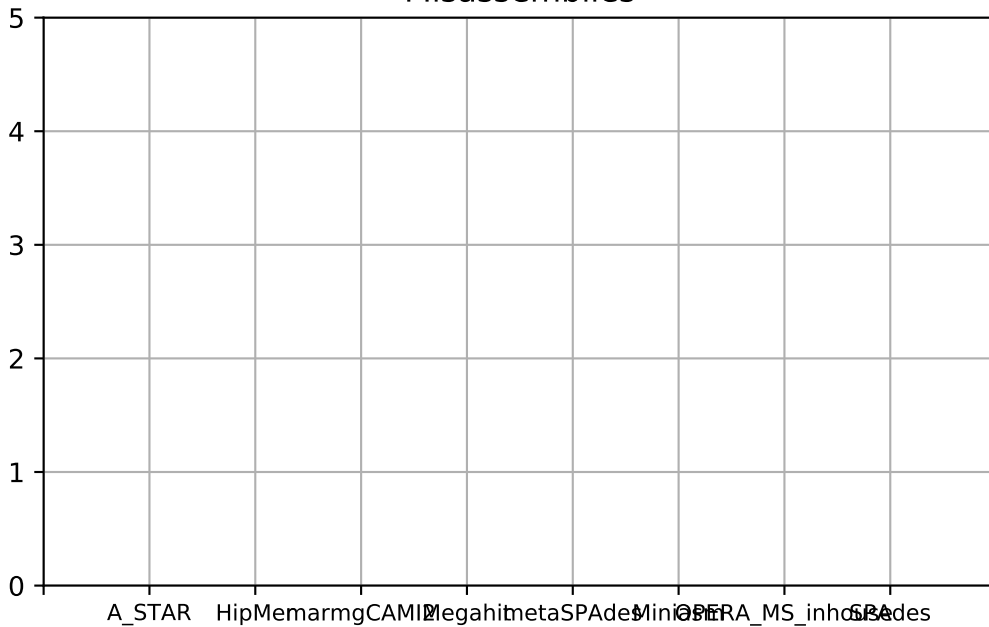
metaSPAdes coverage histogram (bin size: 1x)



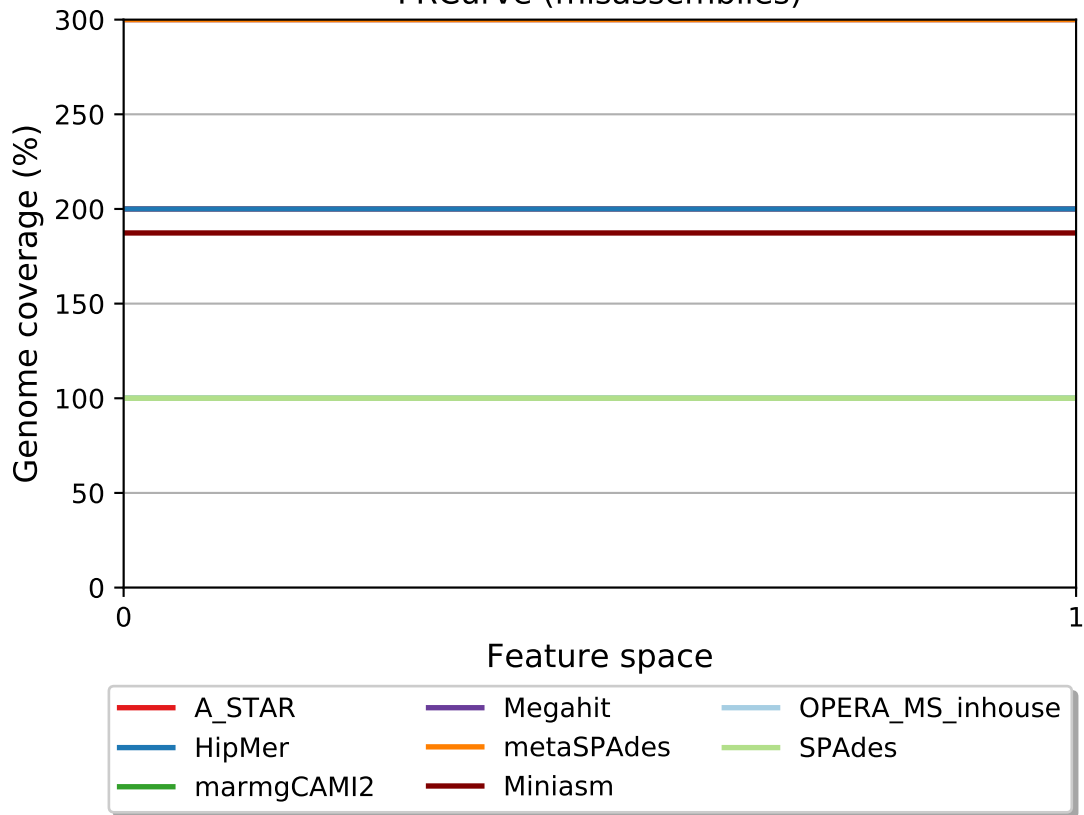
SPAdes coverage histogram (bin size: 1x)



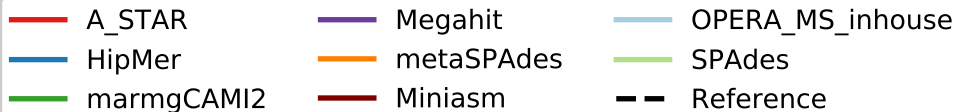
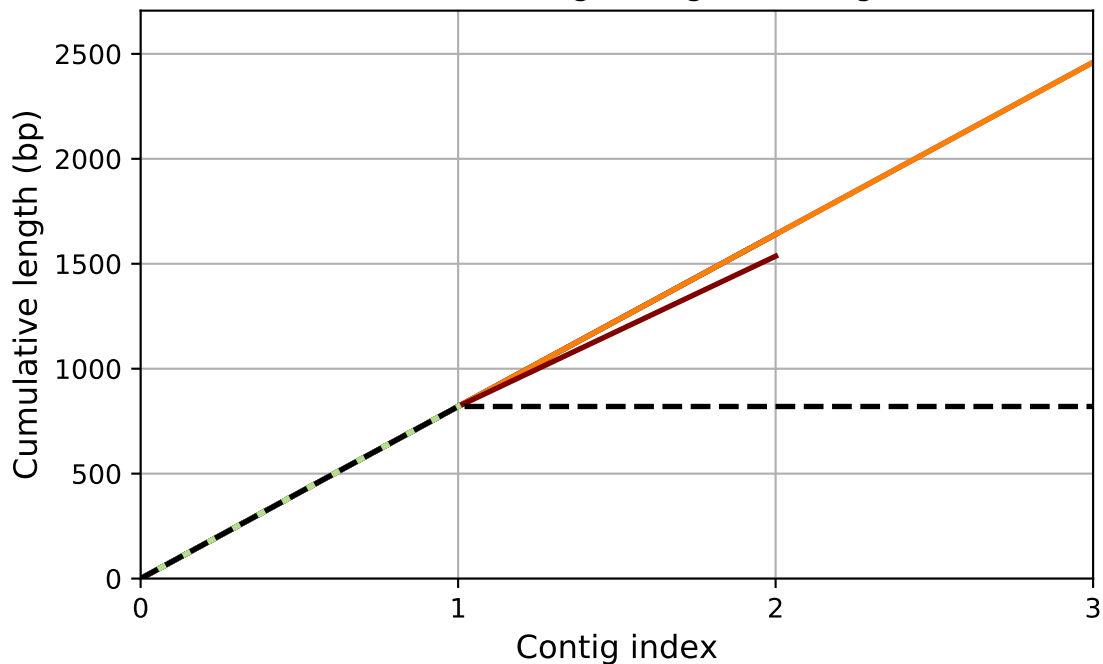
## Misassemblies



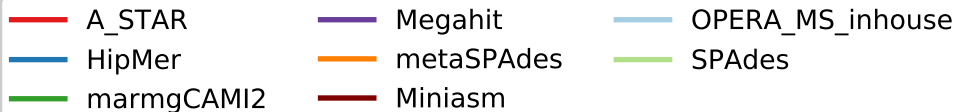
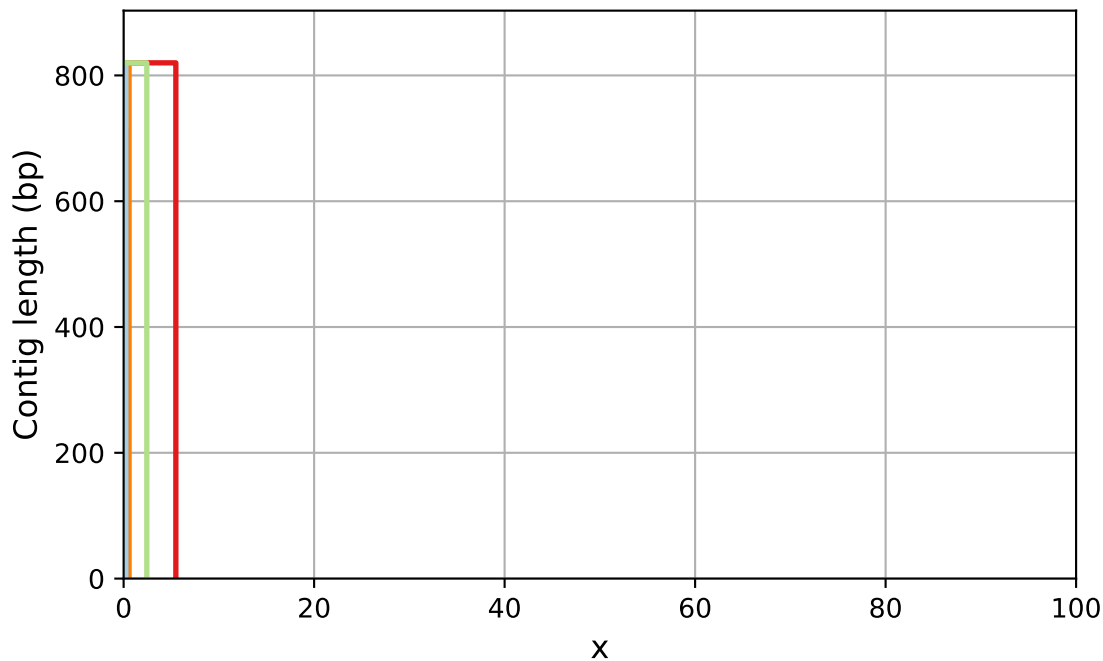
# FRCurve (misassemblies)



Cumulative length (aligned contigs)



## NAX



# NGAx

