

# Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	2	1	3	3	1	1	1
# contigs (>= 5000 bp)	2	2	1	3	3	1	1	0
# contigs (>= 10000 bp)	2	2	1	3	3	1	1	0
# contigs (>= 25000 bp)	2	2	1	3	2	1	1	0
# contigs (>= 50000 bp)	2	2	1	2	2	1	1	0
Total length (>= 1000 bp)	109800	111634	3555091	161307	152916	191257	106155	3556
Total length (>= 5000 bp)	109800	111634	3555091	161307	152916	191257	106155	0
Total length (>= 10000 bp)	109800	111634	3555091	161307	152916	191257	106155	0
Total length (>= 25000 bp)	109800	111634	3555091	161307	128288	191257	106155	0
Total length (>= 50000 bp)	109800	111634	3555091	127600	128288	191257	106155	0
# contigs	2	2	1	3	3	1	1	1
Largest contig	54900	55817	3555091	66999	64144	191257	106155	3556
Total length	109800	111634	3555091	161307	152916	191257	106155	3556
Reference length	590	590	590	590	590	590	590	590
GC (%)	64.10	64.18	65.74	62.40	63.81	64.73	63.13	62.63
Reference GC (%)	64.75	64.75	64.75	64.75	64.75	64.75	64.75	64.75
N50	54900	55817	3555091	60601	64144	191257	106155	3556
NG50	54900	55817	3555091	66999	64144	191257	106155	3556
N75	54900	55817	3555091	60601	64144	191257	106155	3556
NG75	54900	55817	3555091	66999	64144	191257	106155	3556
L50	1	1	1	2	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 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	108620	110454	3554501	159537	151146	190667	105565	2966
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	2.000	2.000	1.000	3.000	3.000	1.000	1.000	1.000
# 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	677.97	0.00	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	590	590	590	590	590	590	590	590
Total aligned length	1180	1180	590	1770	1770	590	590	590
NGA50	590	590	590	590	590	590	590	590
NGA75	590	590	590	590	590	590	590	590
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

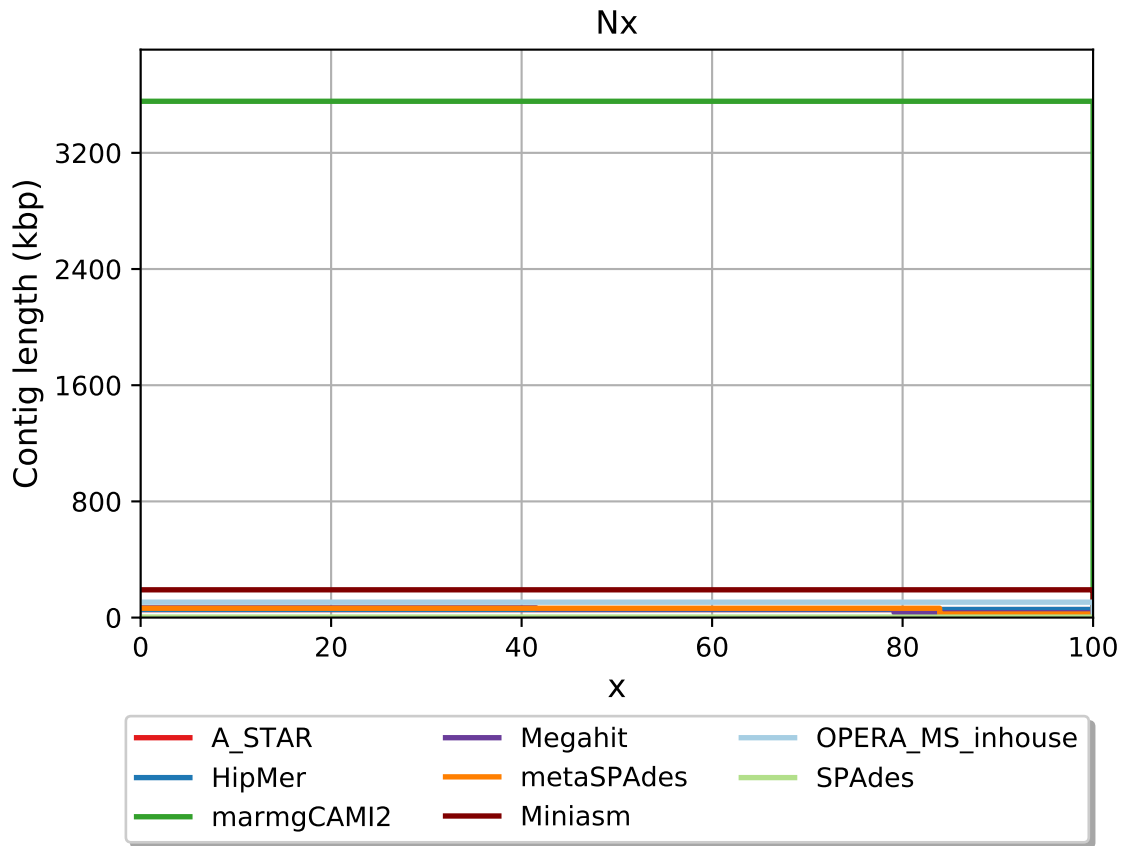
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	1	1	1
# possible misassemblies	4	4	2	6	6	2	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	4	0	0	0	0
# 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  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

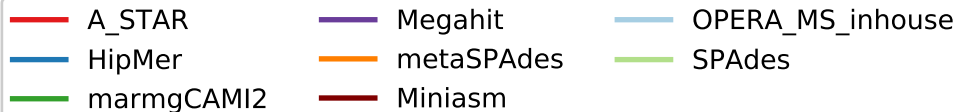
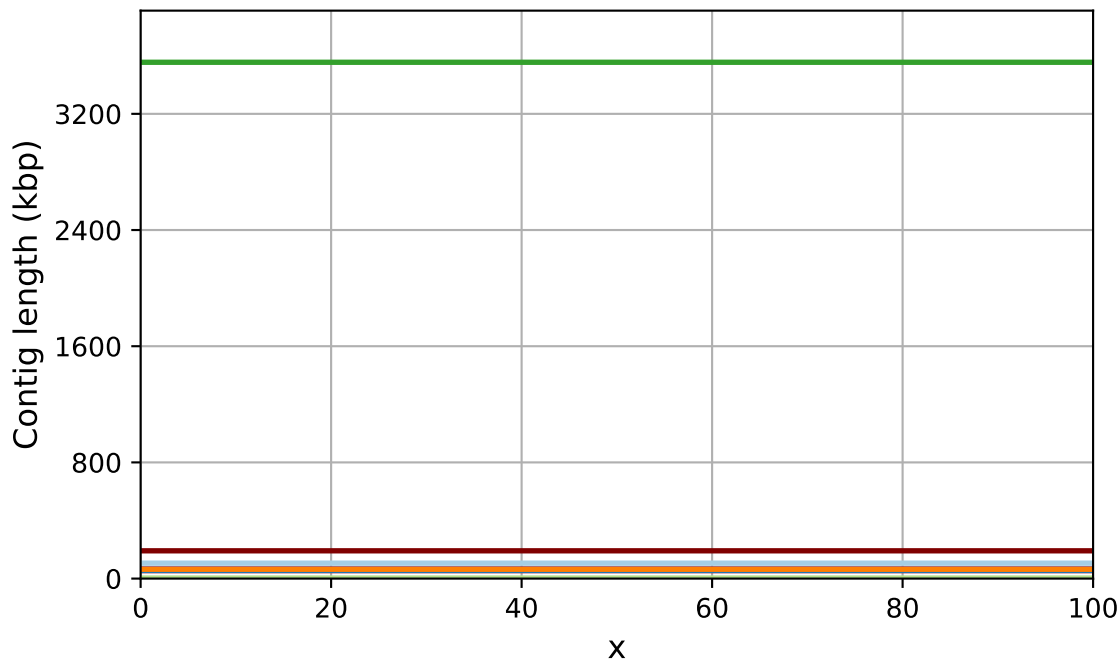
## Unaligned report

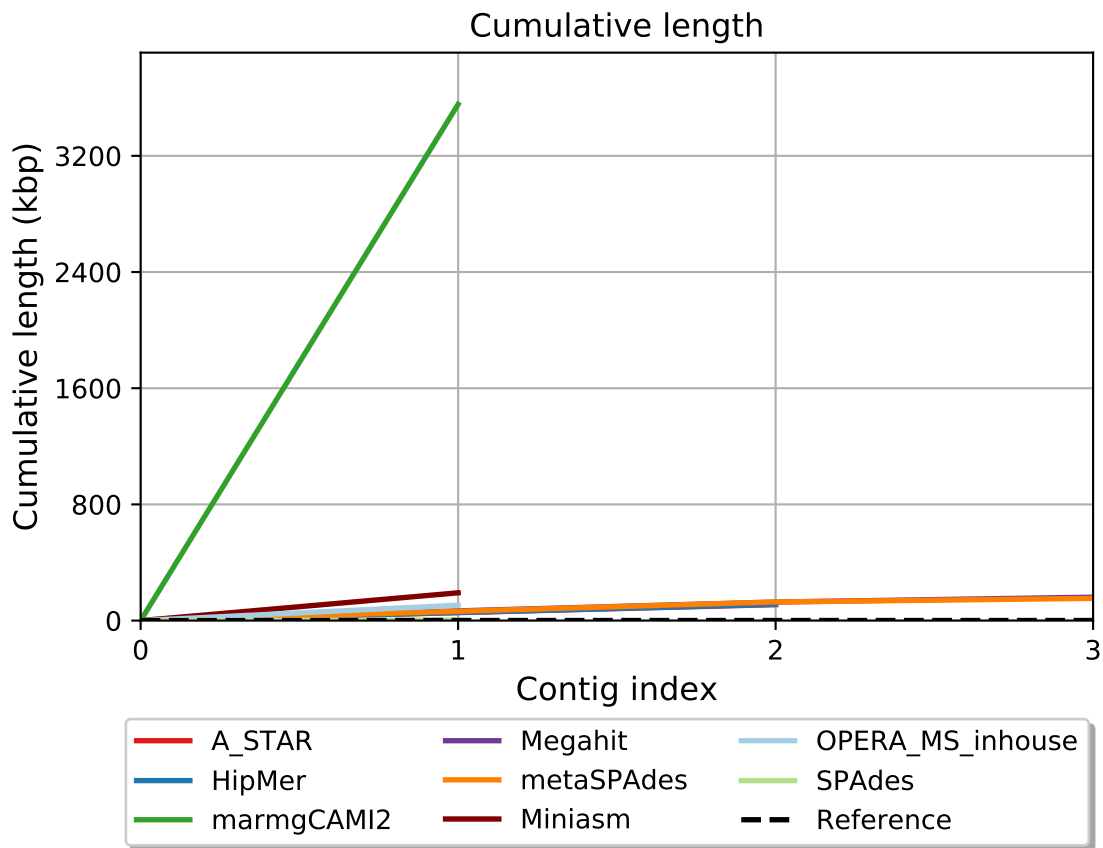
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	2	2	1	3	3	1	1	1
Partially unaligned length	108620	110454	3554501	159537	151146	190667	105565	2966
# N's	0	0	0	0	0	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

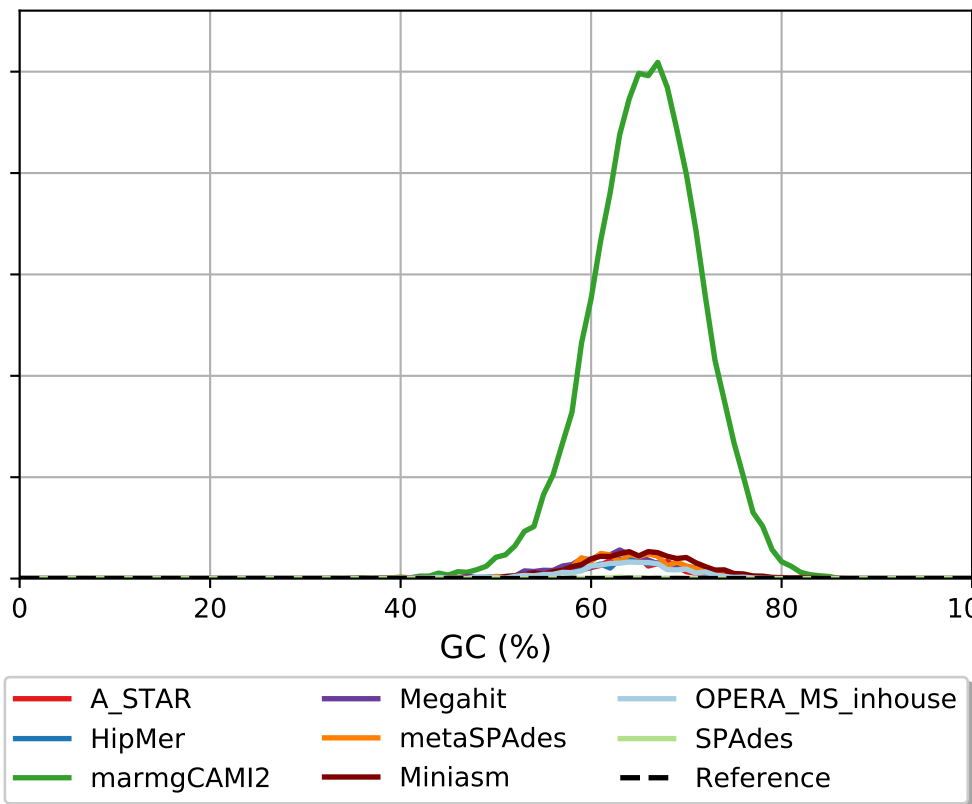




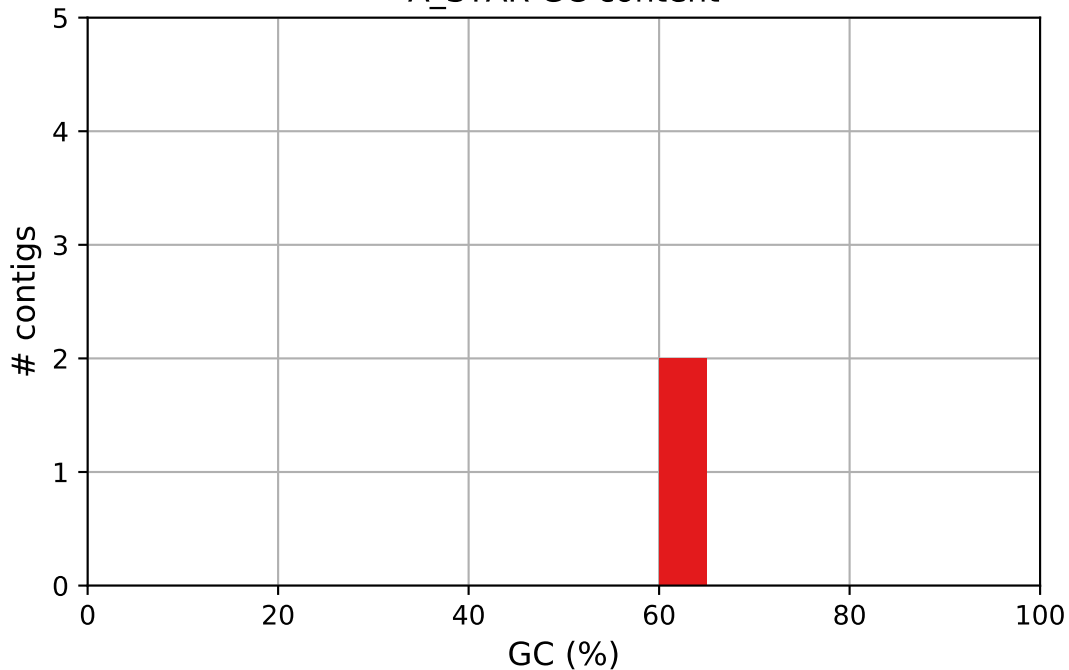
GC (%)

Legend:

- A\_STAR
- HipMer
- marmgCAMI2
- Megahit
- metaSPAdes
- Miniasm
- OPERA\_MS\_inhouse
- SPAdes
- Reference



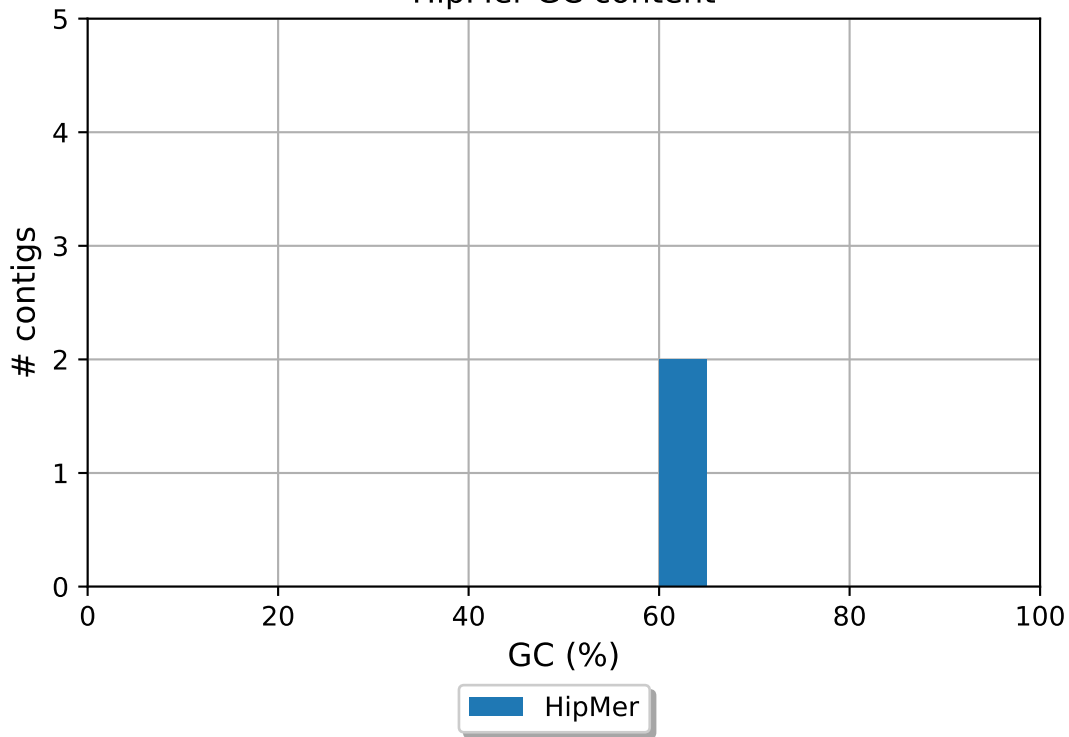
# A\_STAR GC content



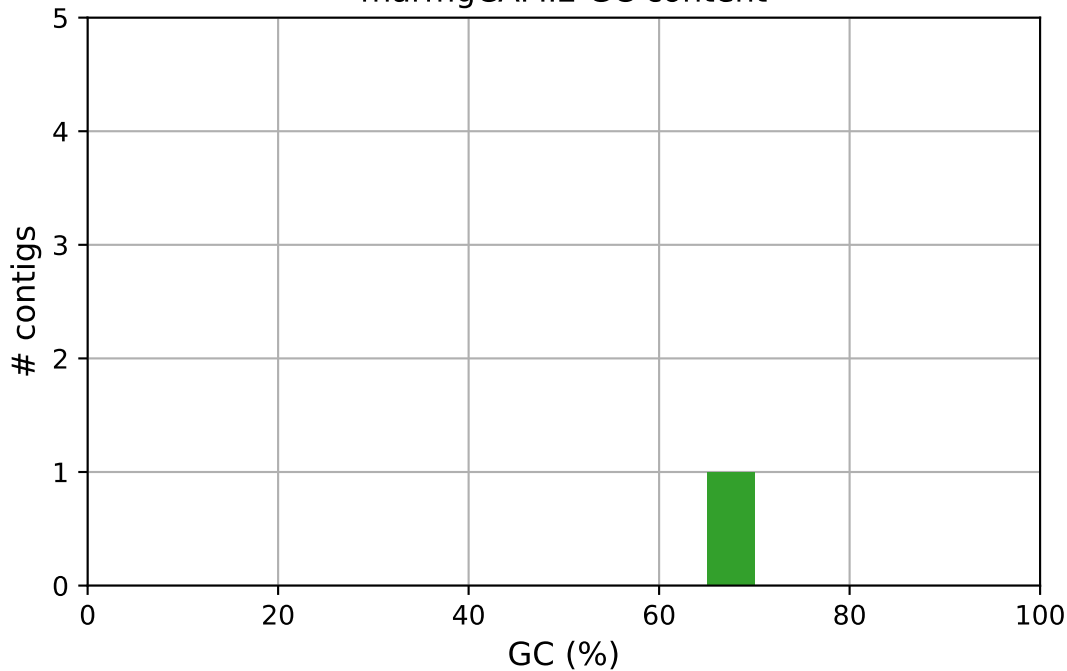
A\_STAR



# HipMer GC content

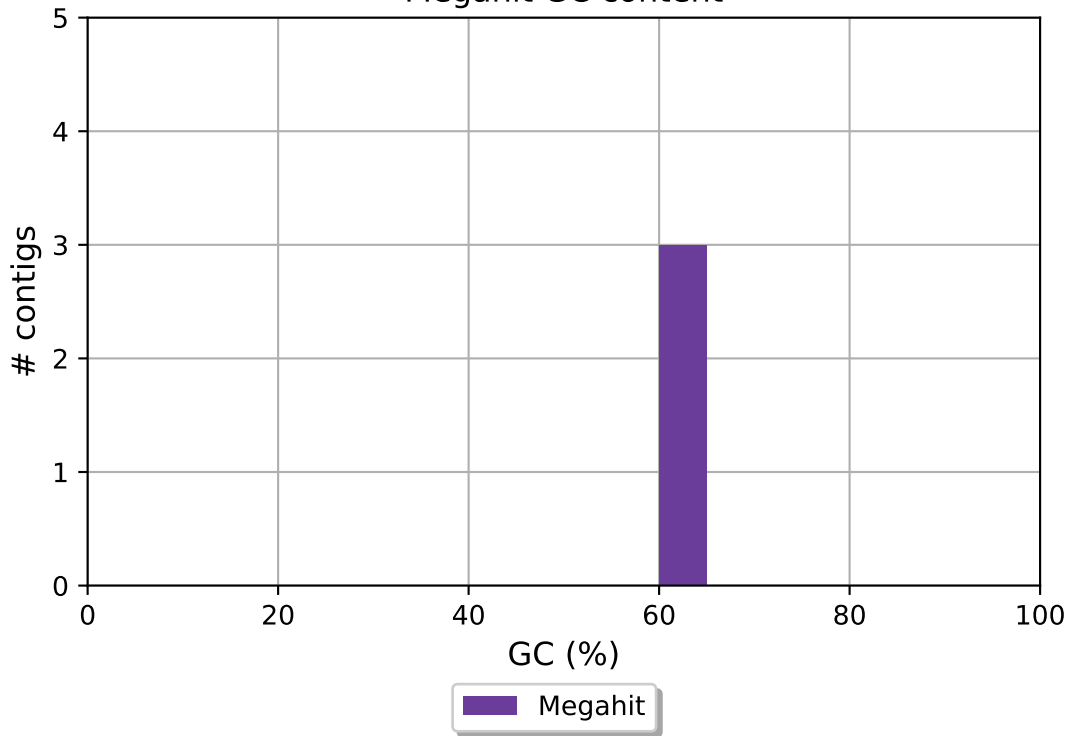


marmgCAMI2 GC content

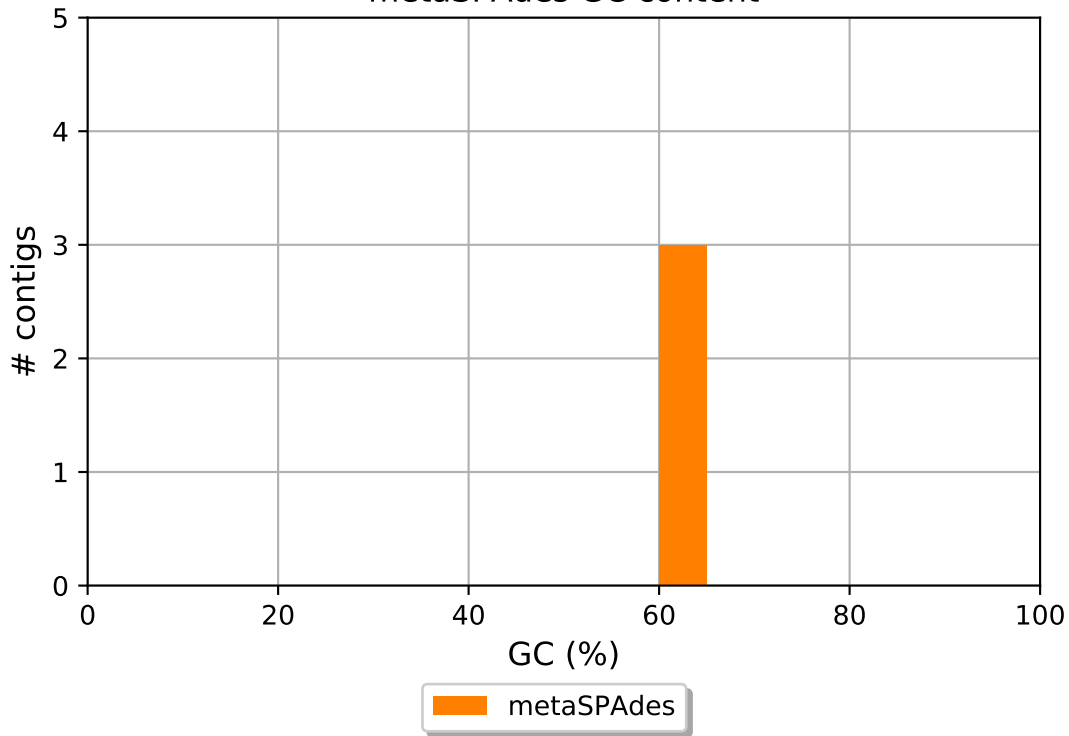


marmgCAMI2

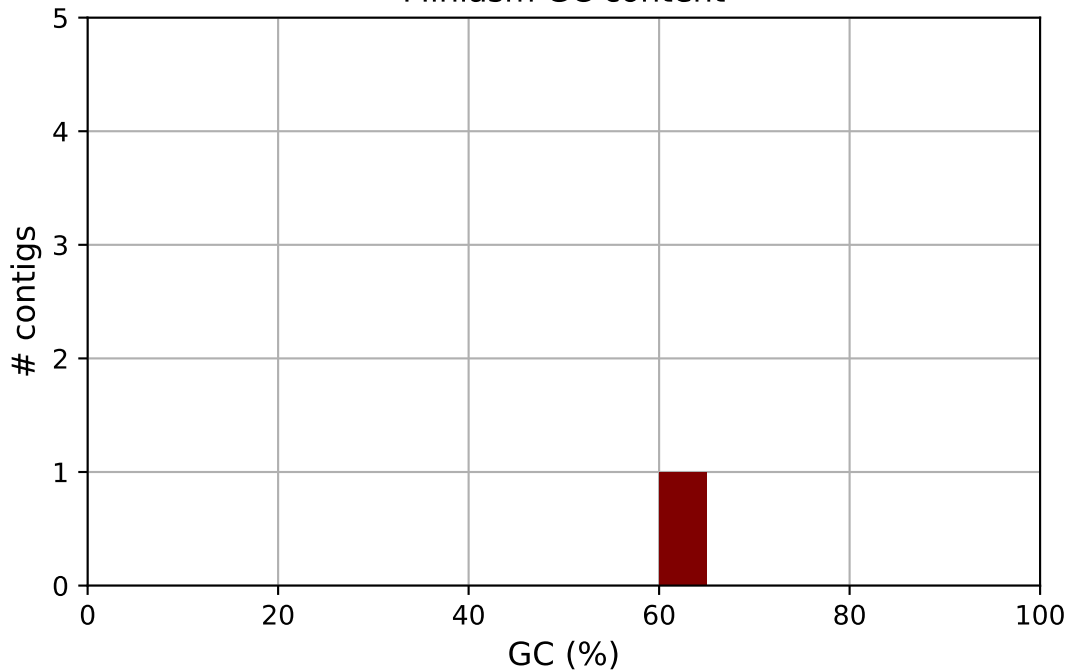
Megahit GC content



metaSPAdes GC content

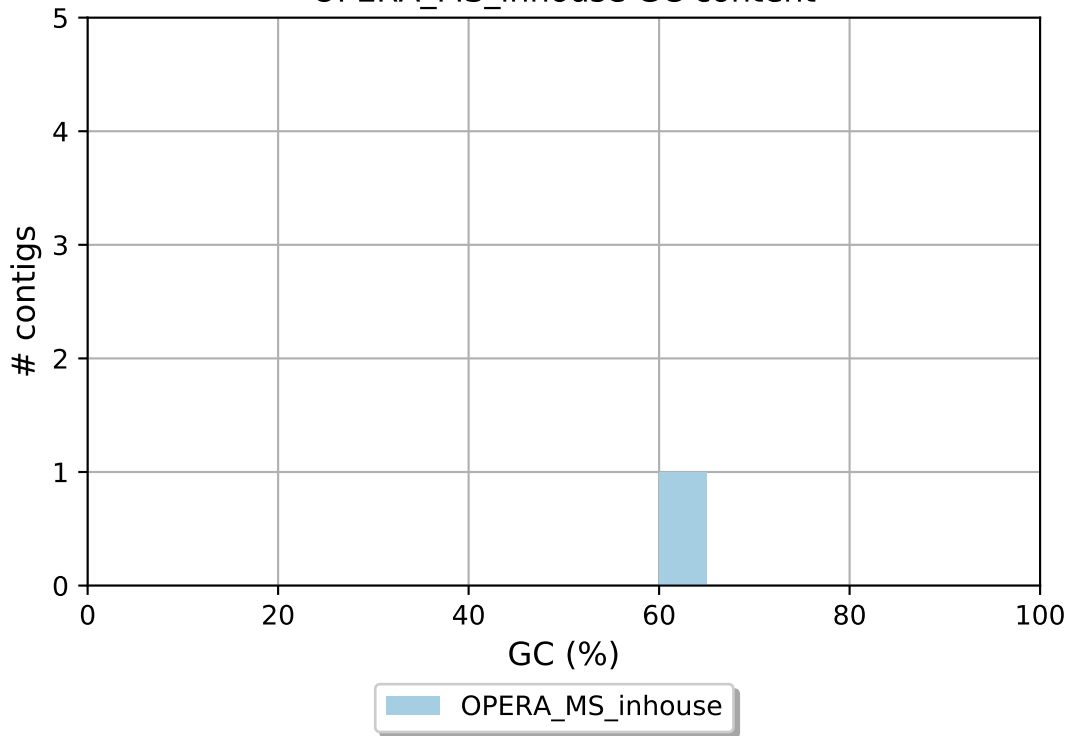


# Miniasm GC content

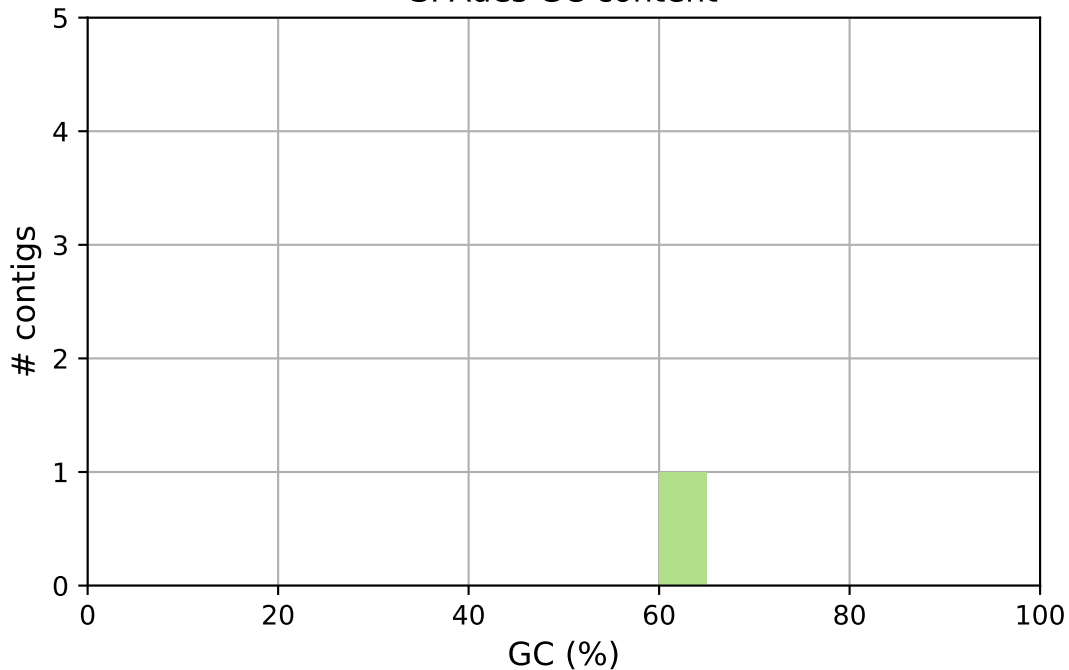


Miniasm

OPERA\_MS\_inhouse GC content

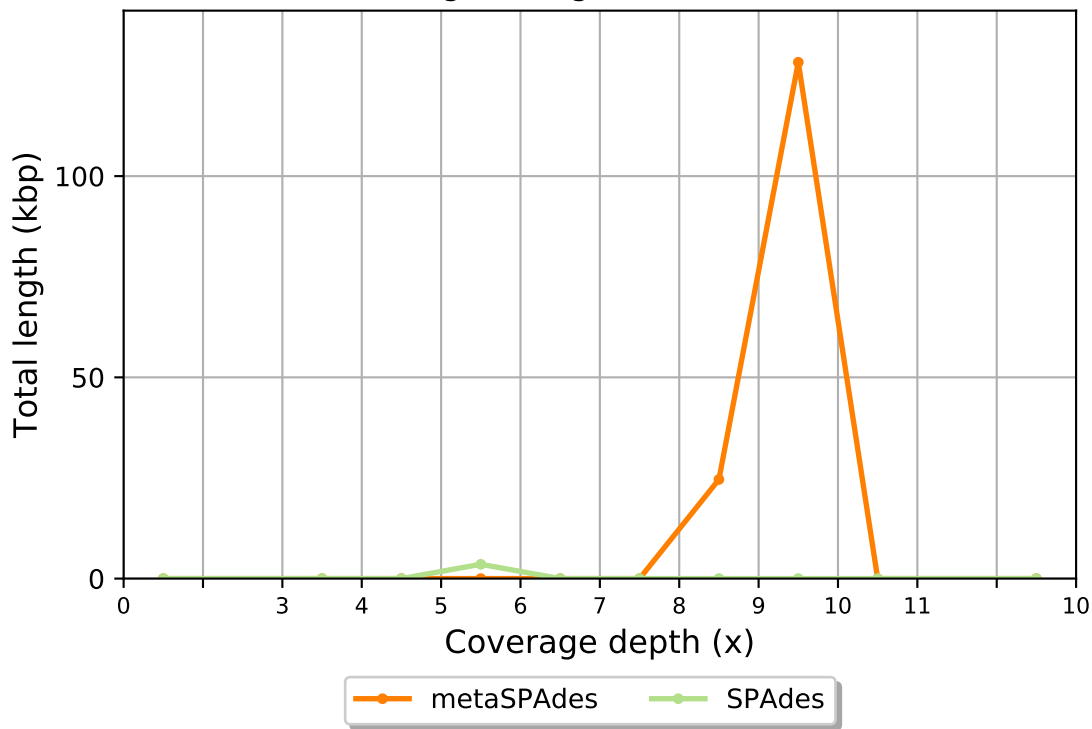


# SPAdes GC content



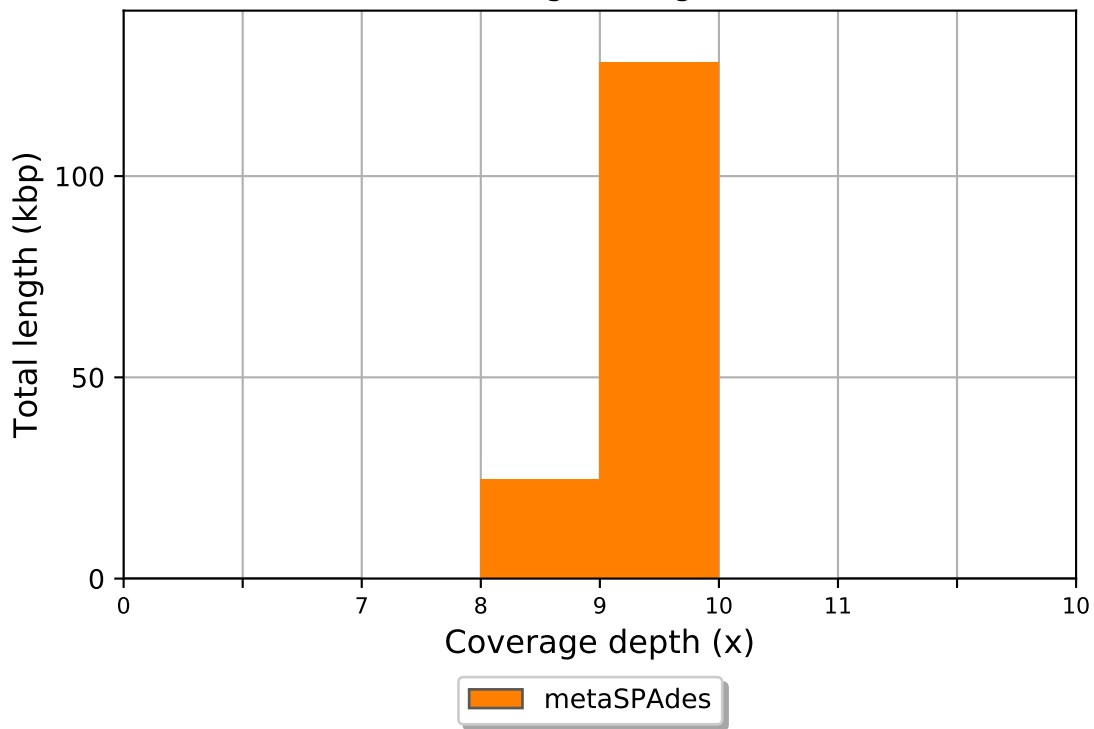
SPAdes

Coverage histogram (bin size: 1x)

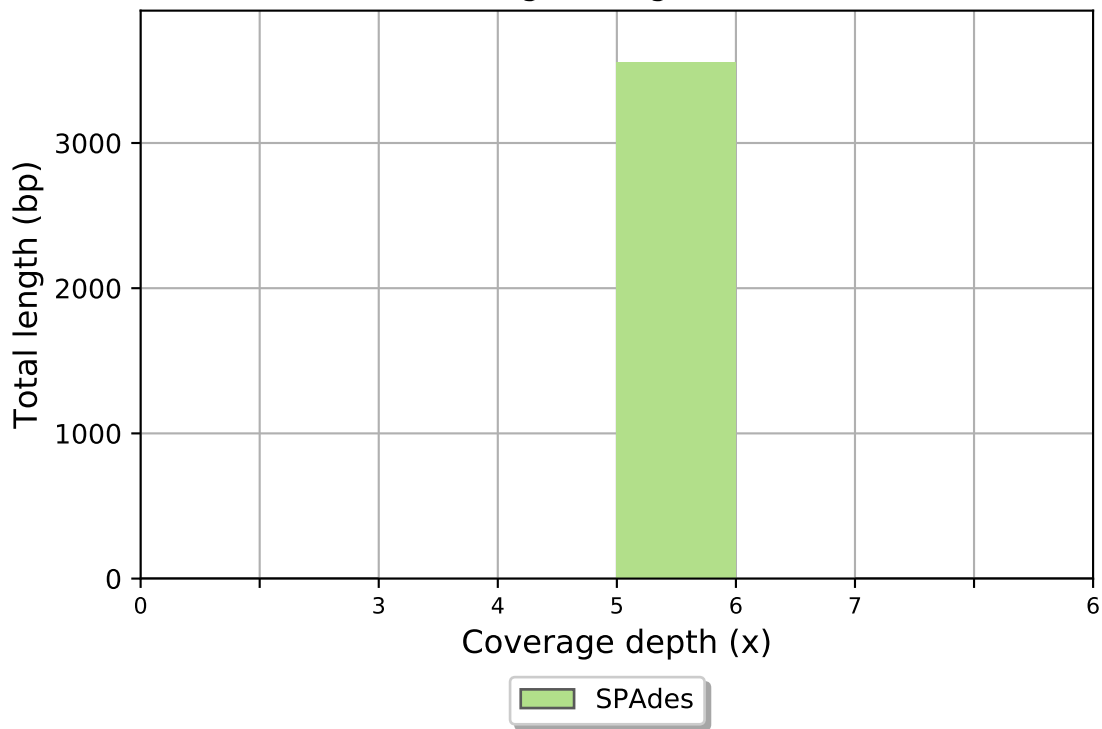




metaSPAdes coverage histogram (bin size: 1x)



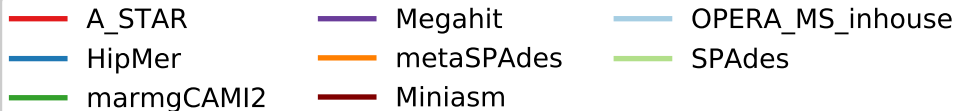
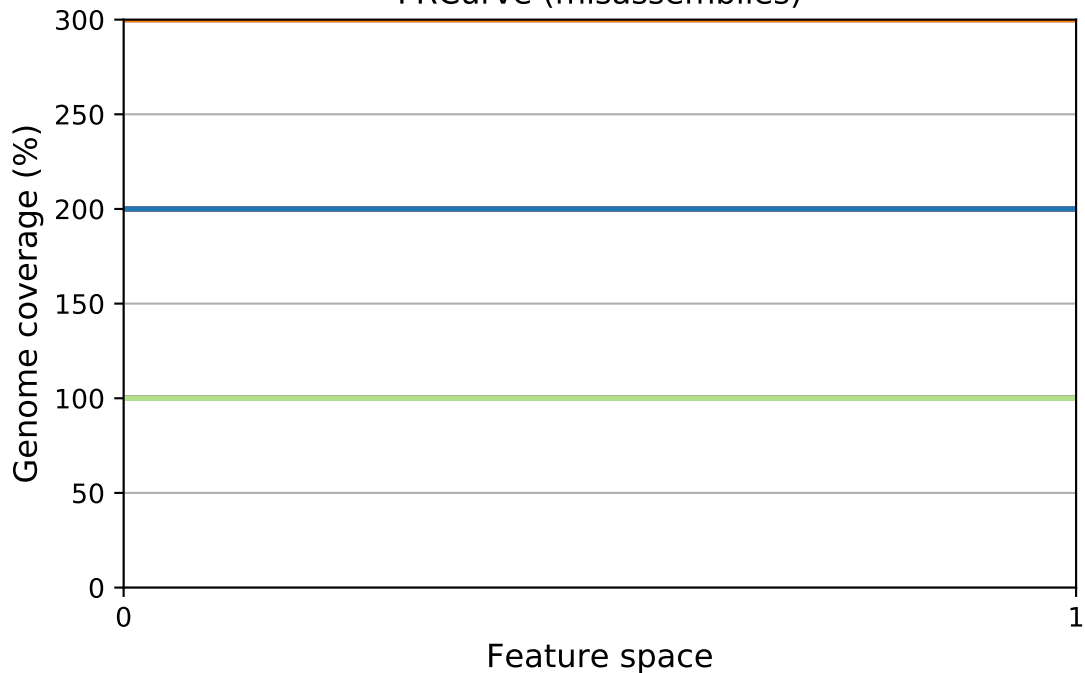
SPAdes coverage histogram (bin size: 1x)



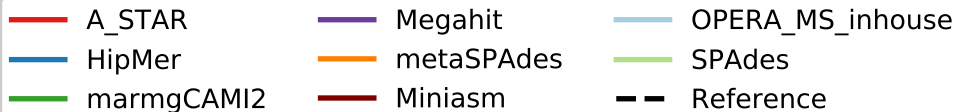
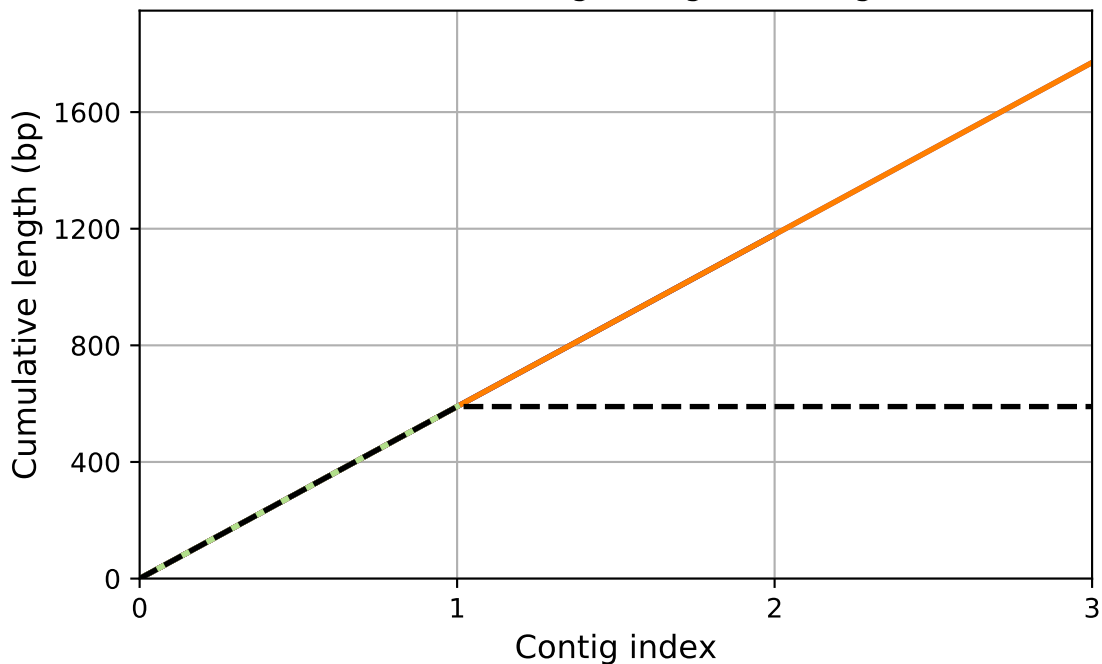
## Misassemblies



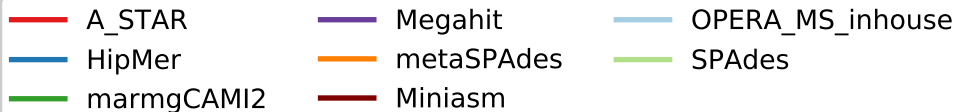
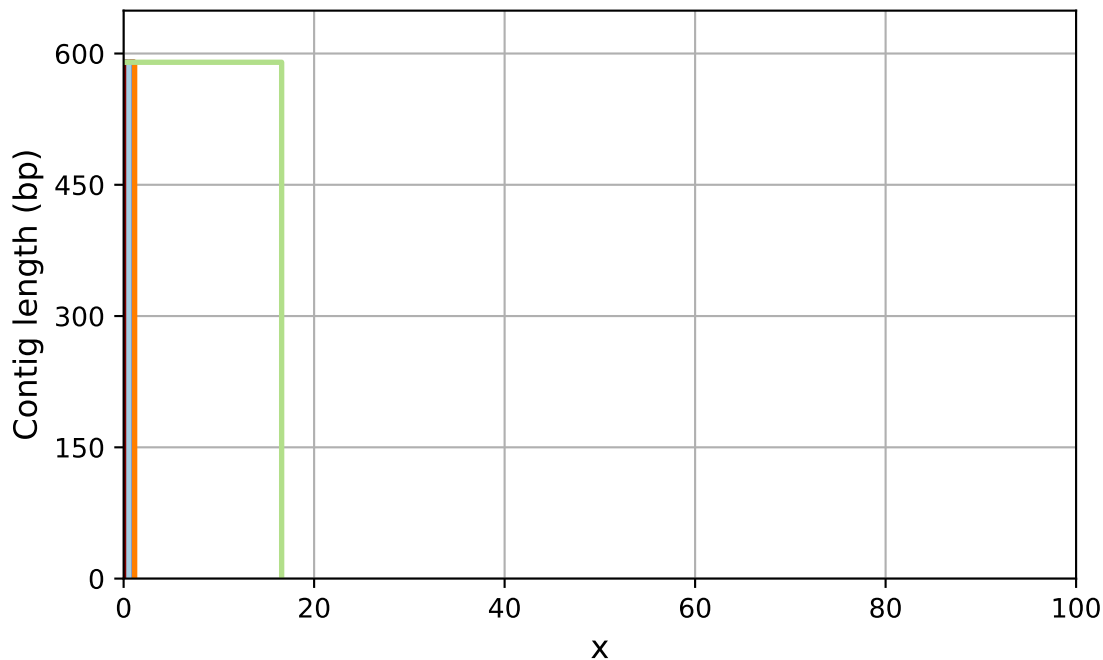
# FRCurve (misassemblies)



Cumulative length (aligned contigs)



# NAx



# NGAx

