Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	4	1	8	6	2	1	3
# contigs (>= 5000 bp)	2	4	1	6	6	2	1	1
# contigs (>= 10000 bp)	2	2	1	6	5	2	1	1
# contigs (>= 25000 bp)	2	0	1	1	0	1	1	0
# contigs (>= 50000 bp)	2	0	1	0	0	1	1	0
Total length (>= 1000 bp)	109606	59761	5183322	132706	111651	66150	57927	22257
Total length (>= 5000 bp)	109606	59761	5183322	127934	111651	66150	57927	15693
Total length (>= 10000 bp)	109606	42361	5183322	127934	103141	66150	57927	15693
Total length (>= 25000 bp)	109606	0	5183322	41123	0	52601	57927	0
Total length (>= 50000 bp)	109606	0	5183322	0	0	52601	57927	0
# contigs	2	4	1	10	6	2	1	3
Largest contig	54803	21366	5183322	41123	22718	52601	57927	15693
Total length	109606	59761	5183322	133976	111651	66150	57927	22257
Reference length	1853	1853	1853	1853	1853	1853	1853	1853
GC (%)	68.05	67.74	69.46	68.33	68.49	68.19	68.27	67.81
Reference GC (%)	66.16	66.16	66.16	66.16	66.16	66.16	66.16	66.16
N50	54803	20995	5183322	22853	21857	52601	57927	15693
NG50	54803	21366	5183322	41123	22718	52601	57927	15693
N75	54803	8700	5183322	19325	21857	52601	57927	4836
NG75	54803	21366	5183322	41123	22718	52601	57927	15693
L50	1	2	1	3	3	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	3	1	4	4	1	1	2
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	2	0	0	0	0	0	0	0
# unaligned contigs	0 + 2 part	0 + 4 part	0 + 1 part	0 + 7 part	0 + 6 part	0 + 2 part	0 + 1 part	0 + 3 part
Unaligned length	108024	56055	5181698	128589	106092	64430	56303	20379
Genome fraction (%)	42.688	100.000	87.642	100.000	100.000	87.642	87.642	100.000
Duplication ratio	2.000	2.000	1.000	2.907	3.000	1.059	1.000	1.013
# 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	252.84	0.00	0.00	1726.93	0.00	0.00	431.03	269.83
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	480	1624	1624	943	1624	957	1624	877
Total aligned length	1582	3706	1624	5200	5559	1720	1624	1878
NGA50	480	1624	1624	943	1624	957	1624	772
NGA75	311	1624	1624	751	1624	763	1624	772
LGA50	2	1	1	1	1	1	1	2
LGA75	4	1	1	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	0	4	1	7	6	2	1	3
# possible misassemblies	0	8	2	10	12	2	2	4
# 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	0	0	0	0	0	0
# mismatches	2	0	0	32	0	0	7	5
# 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	2	4	1	7	6	2	1	3
Partially unaligned length	108024	56055	5181698	128589	106092	64430	56303	20379
# 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).

Nx
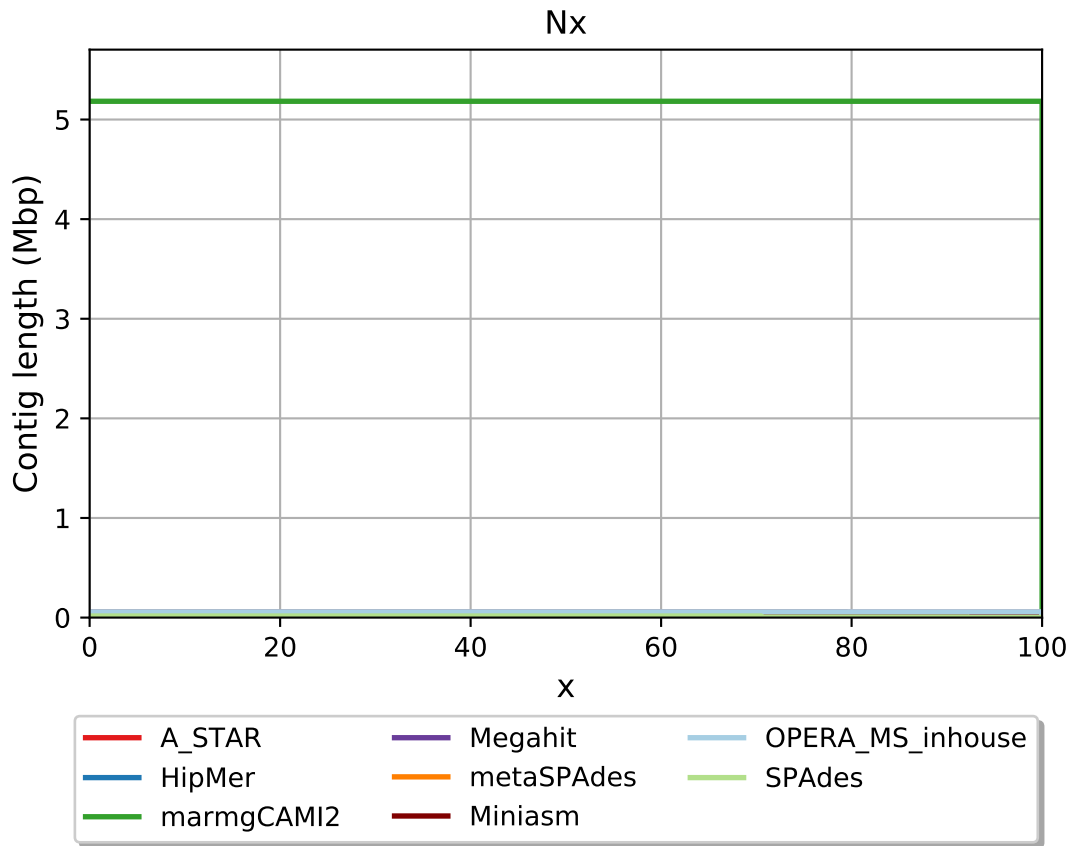
NGx
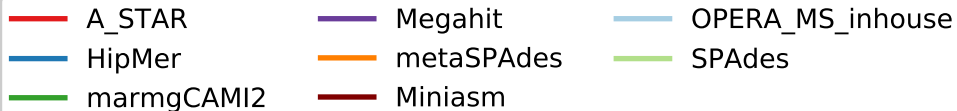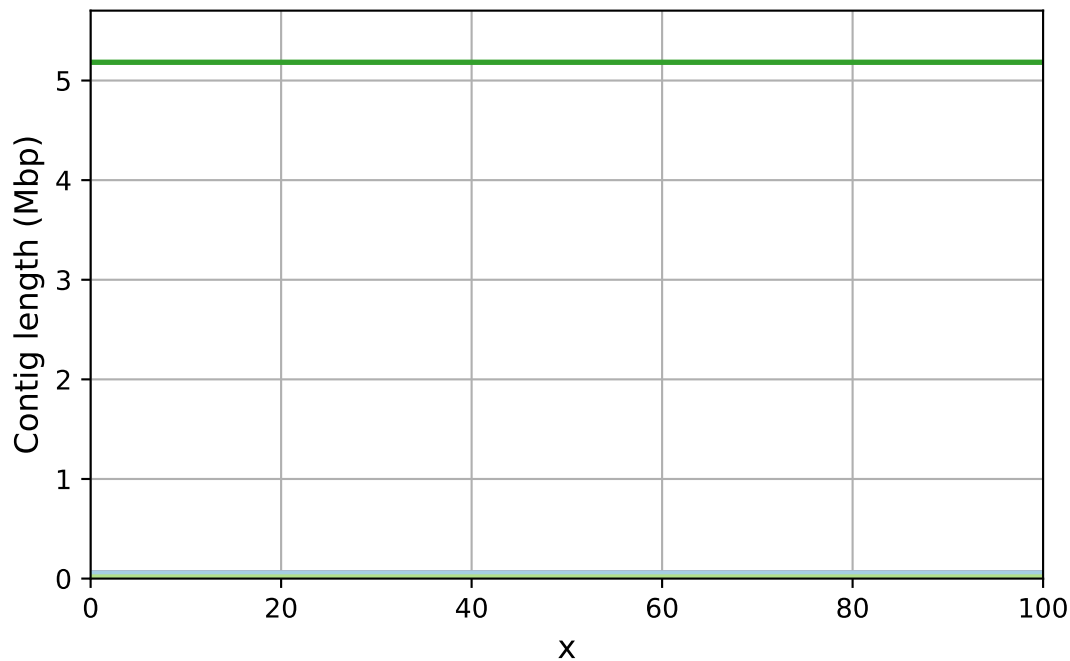
Cumulative length
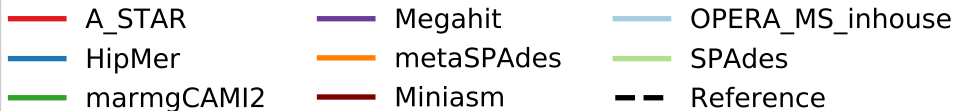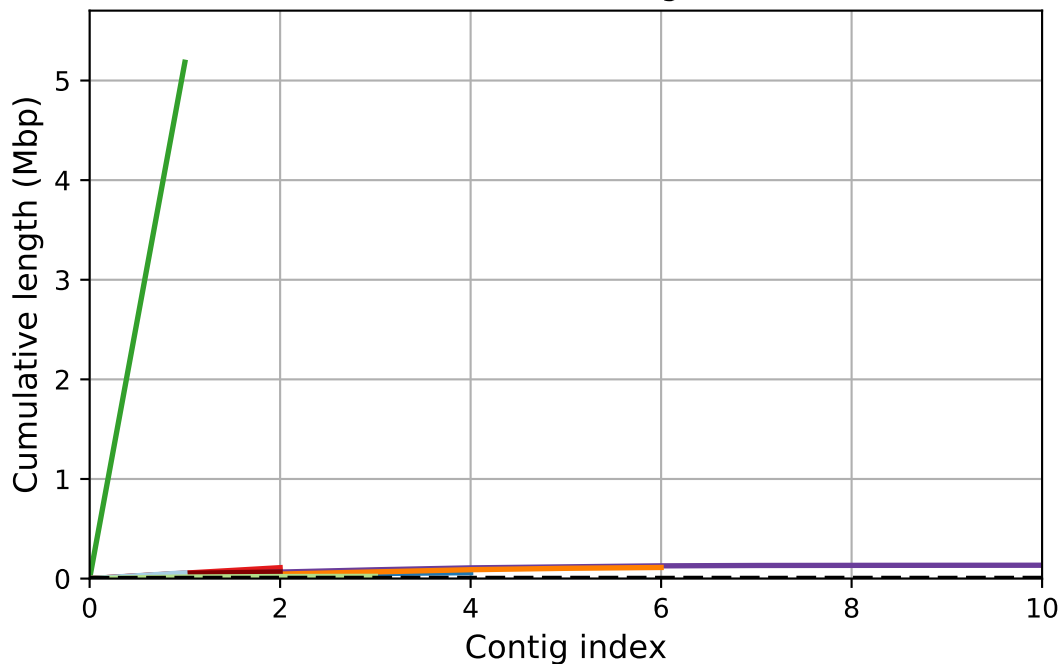
GC content
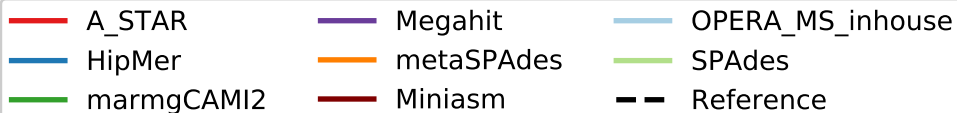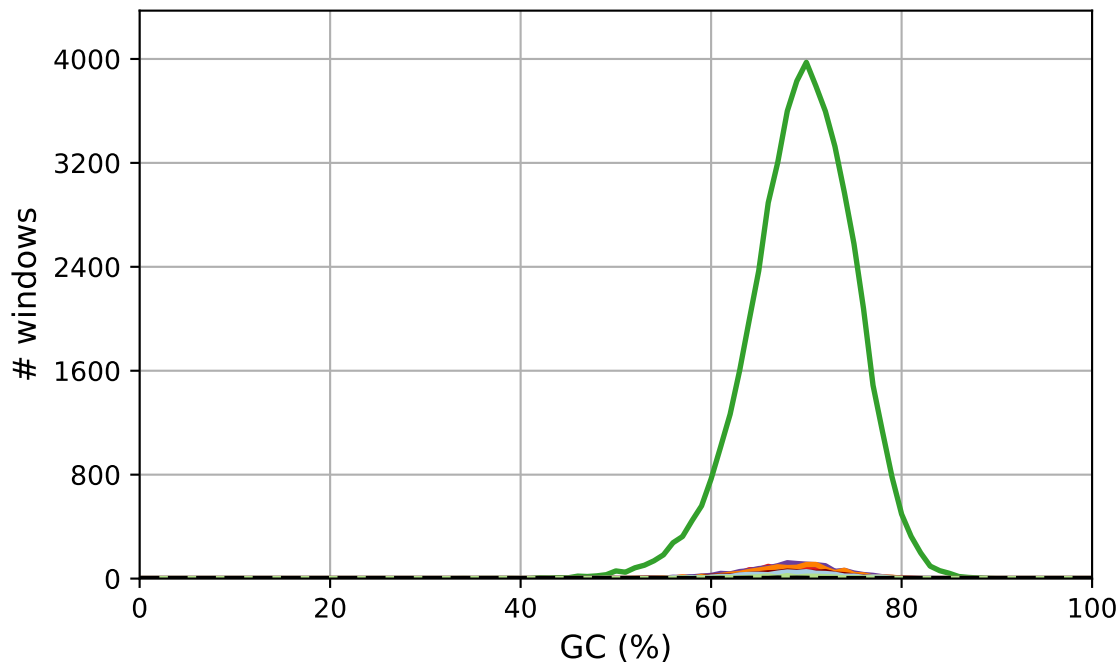
A_STAR GC content
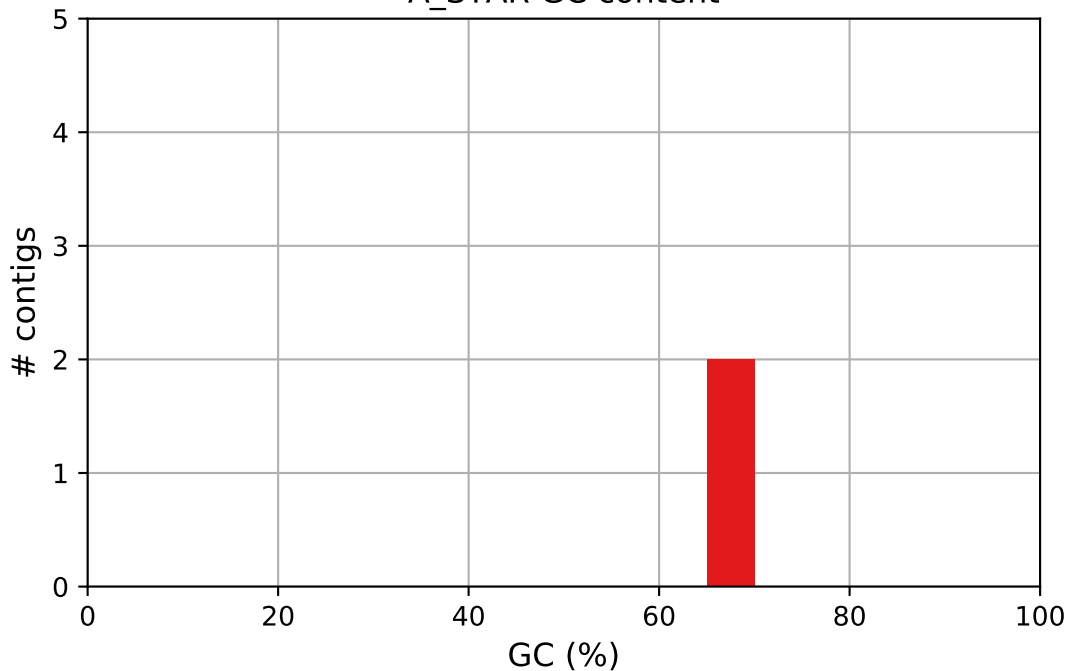
HipMer GC content
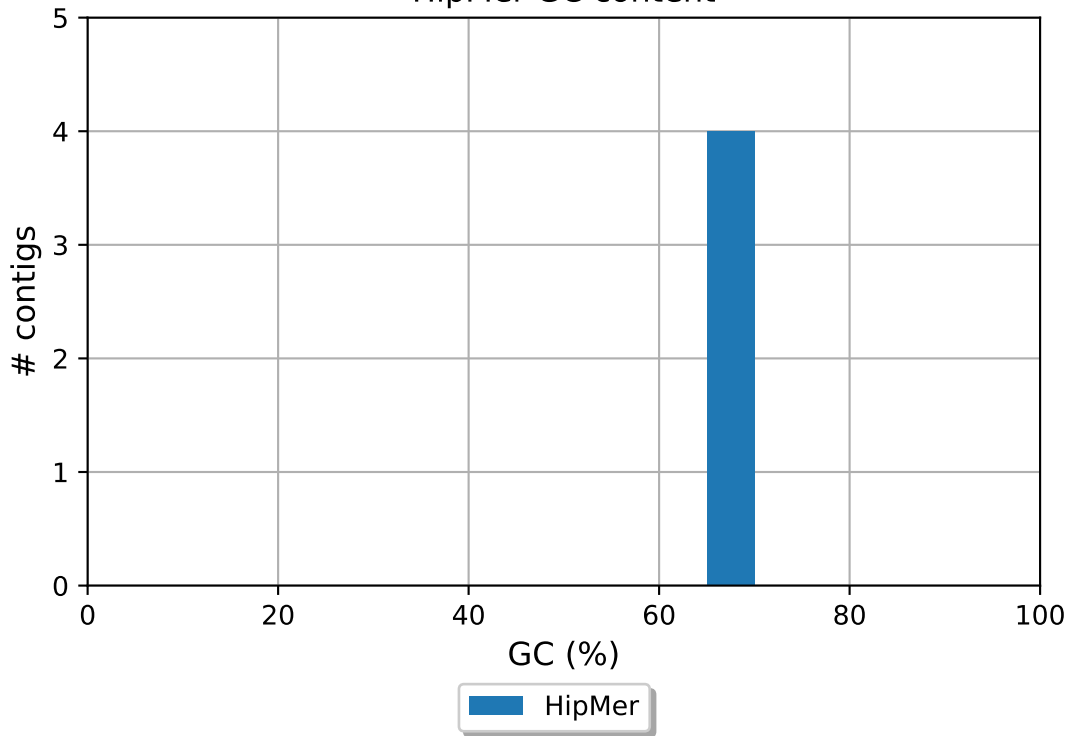
marmgCAMI2 GC content
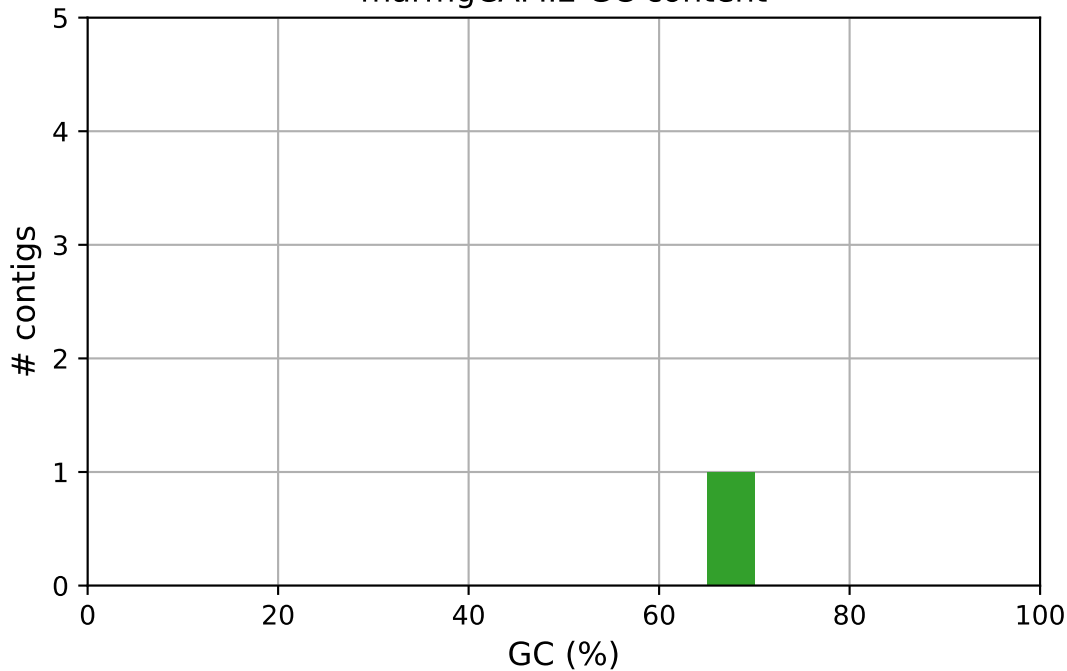
Megahit GC content

contigs (y-axis)

GC (%) (x-axis)

Megahit
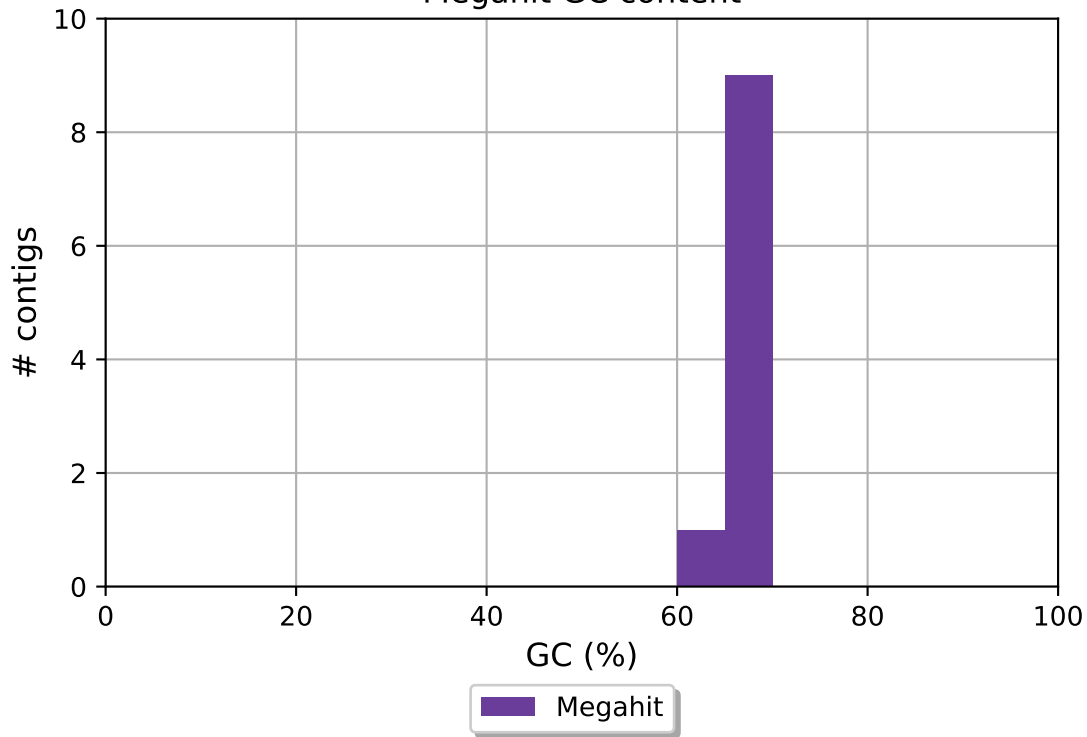
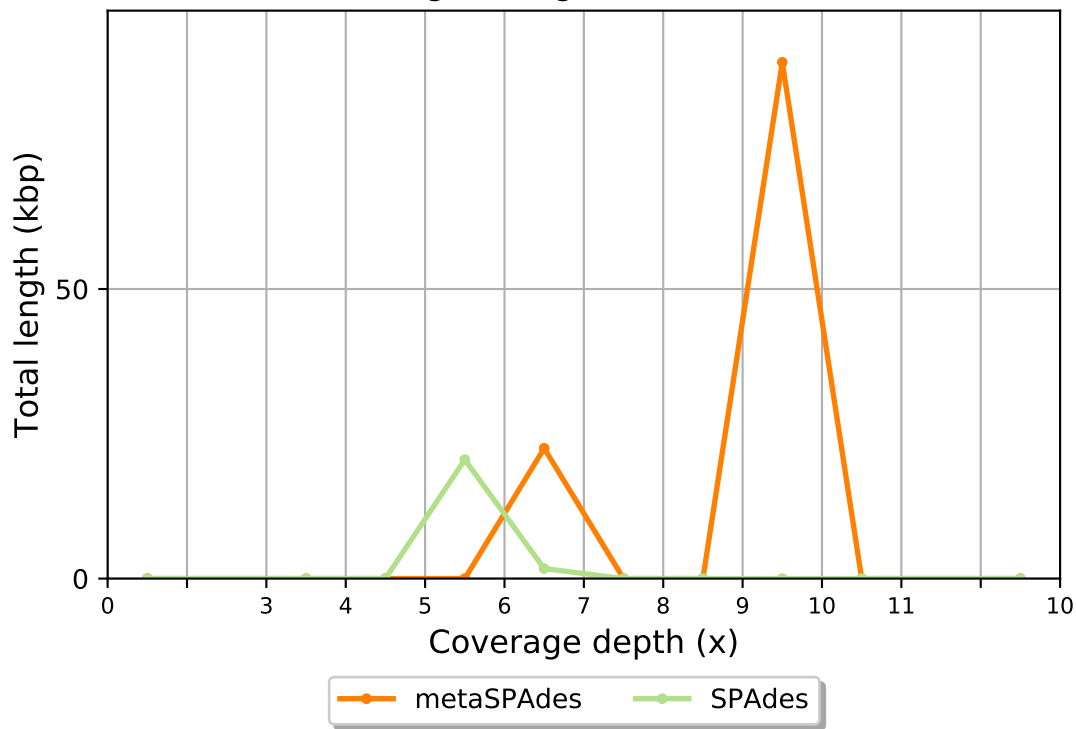metaSPAdes GC content
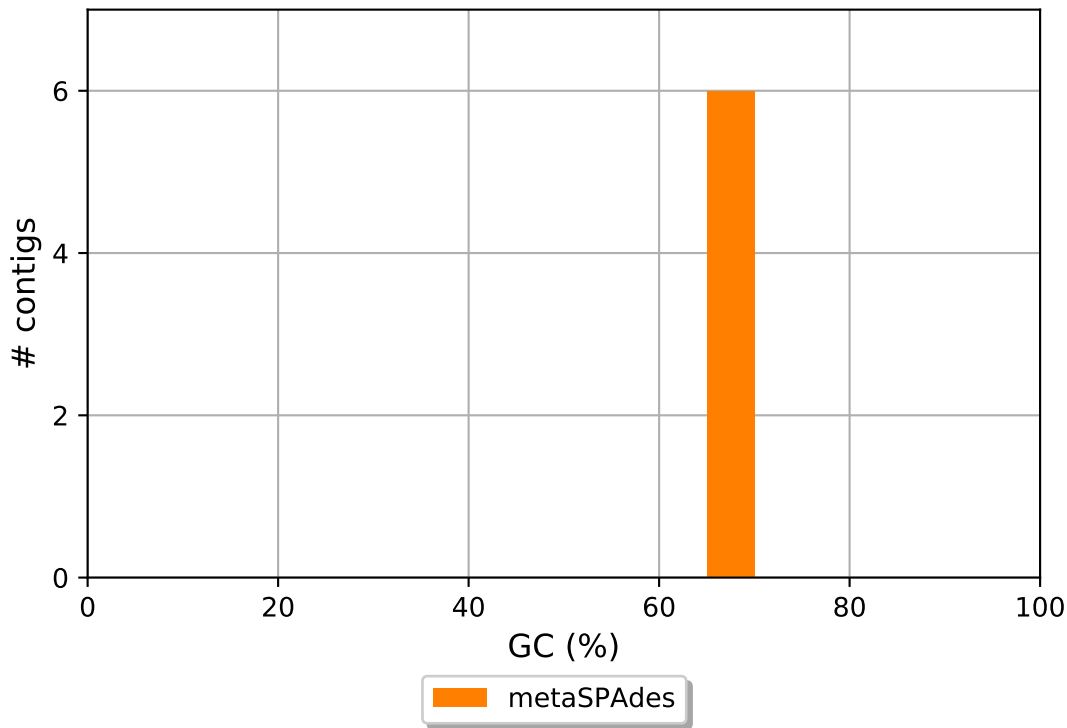
Miniasm GC content
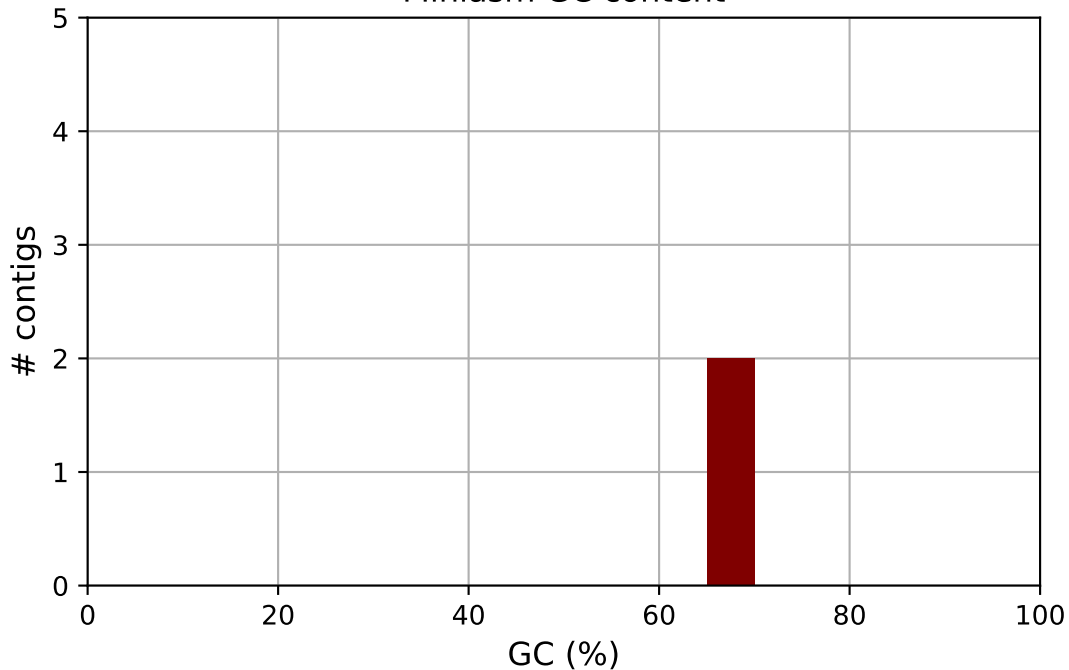
OPERA_MS_inhouse GC content
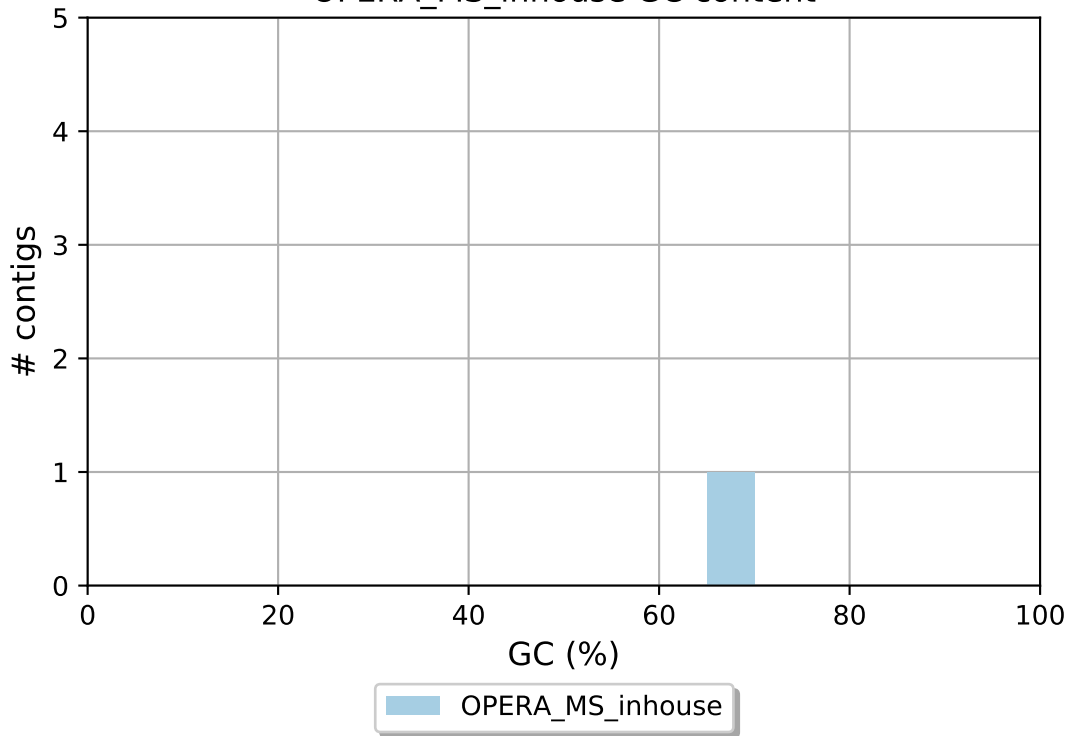
SPAdes GC content
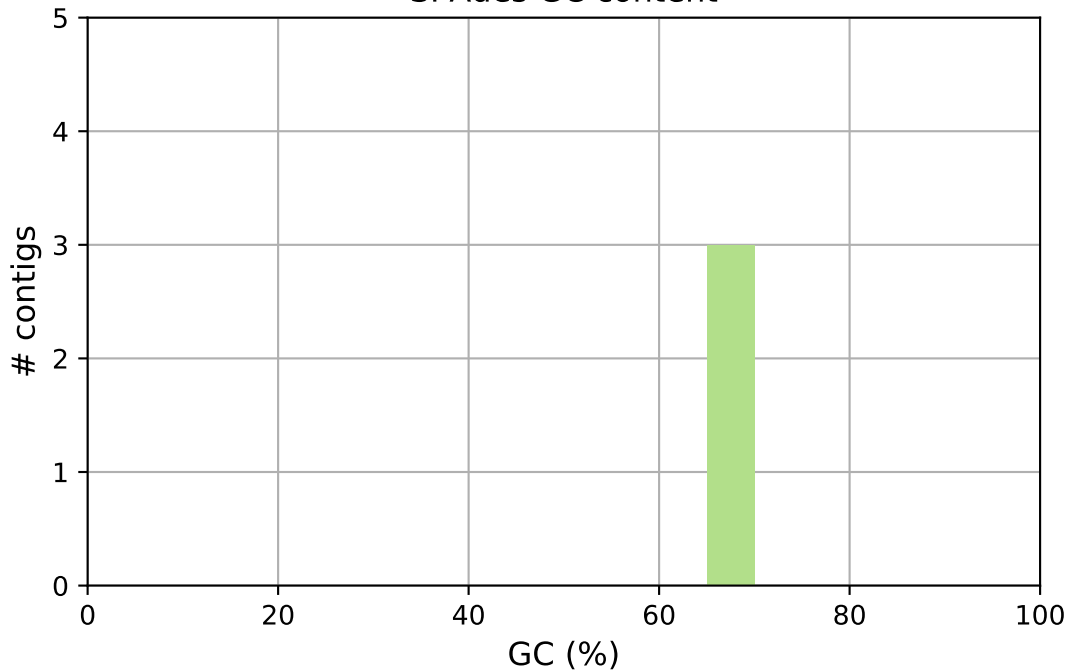
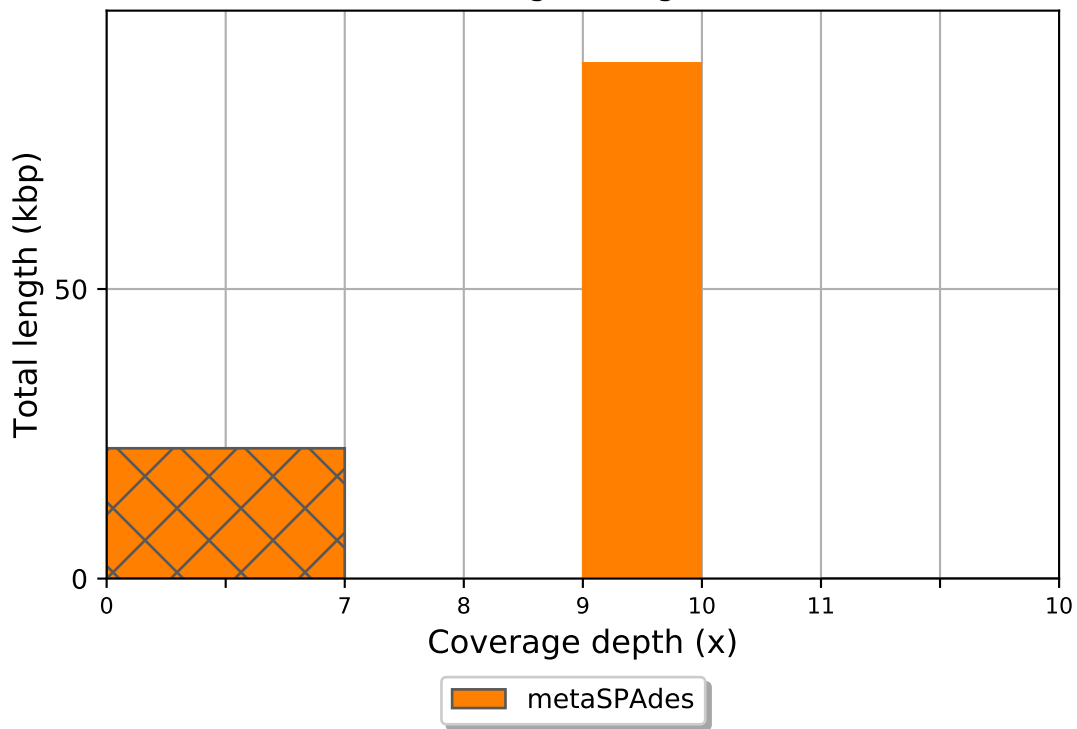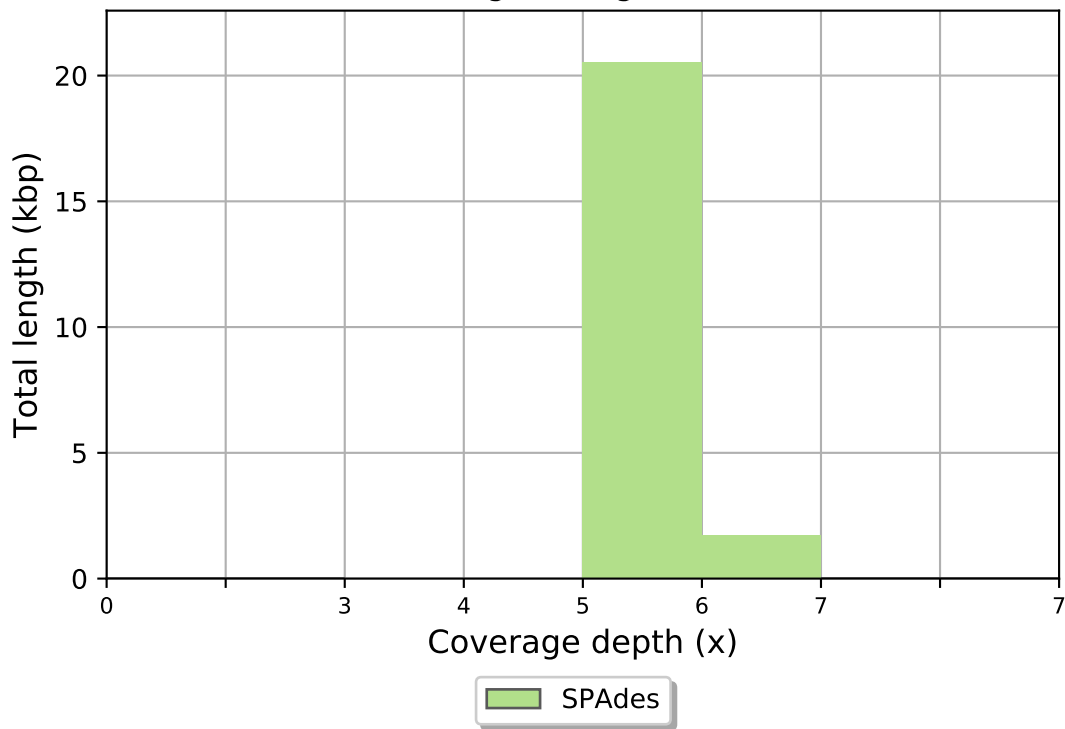Coverage histogram (bin size: 1x)

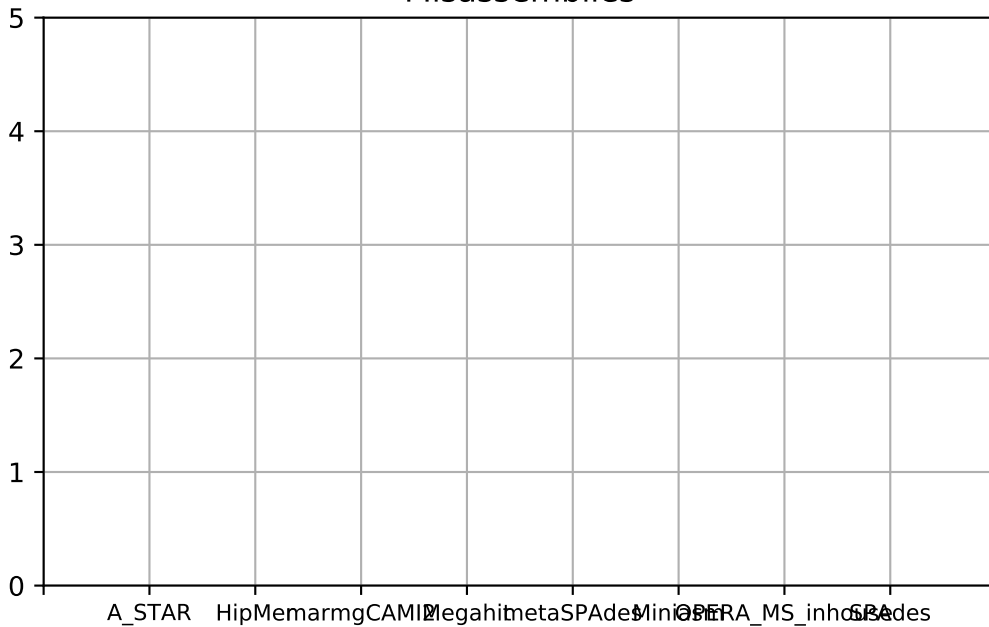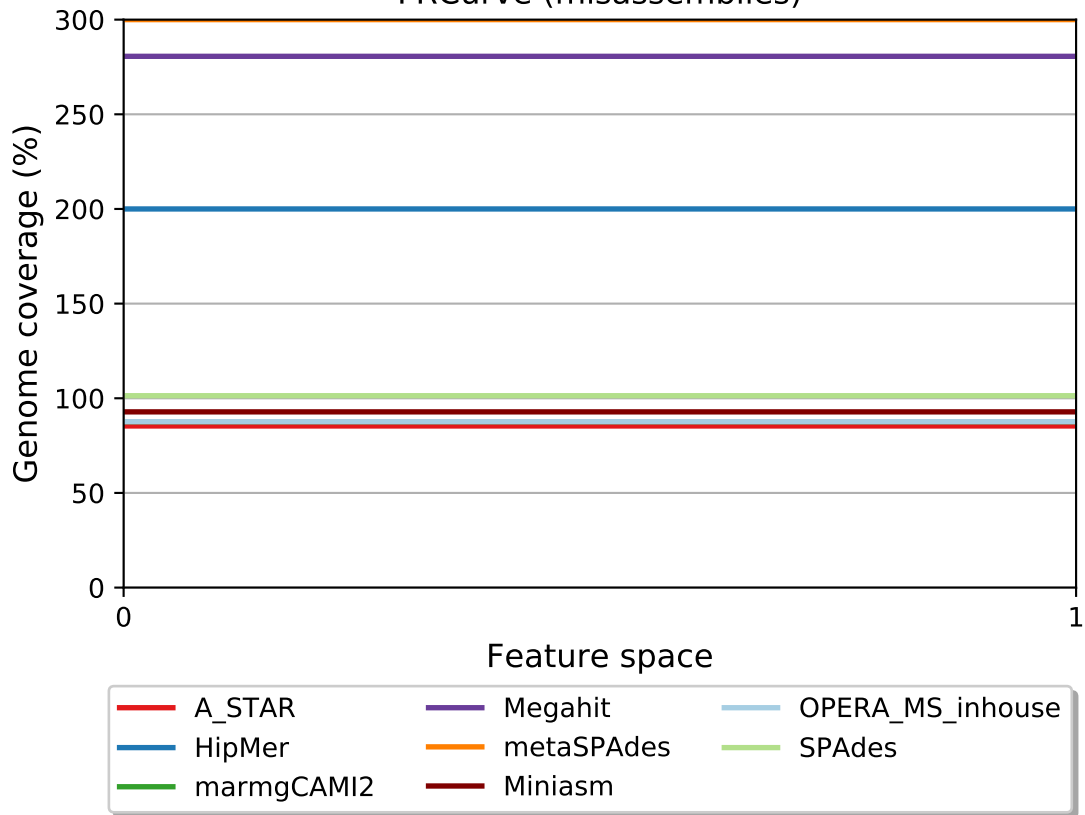metaSPAdes coverage histogram (bin size: 1x)

SPAdes coverage histogram (bin size: 1x)

Misassemblies

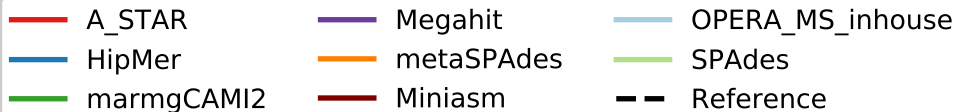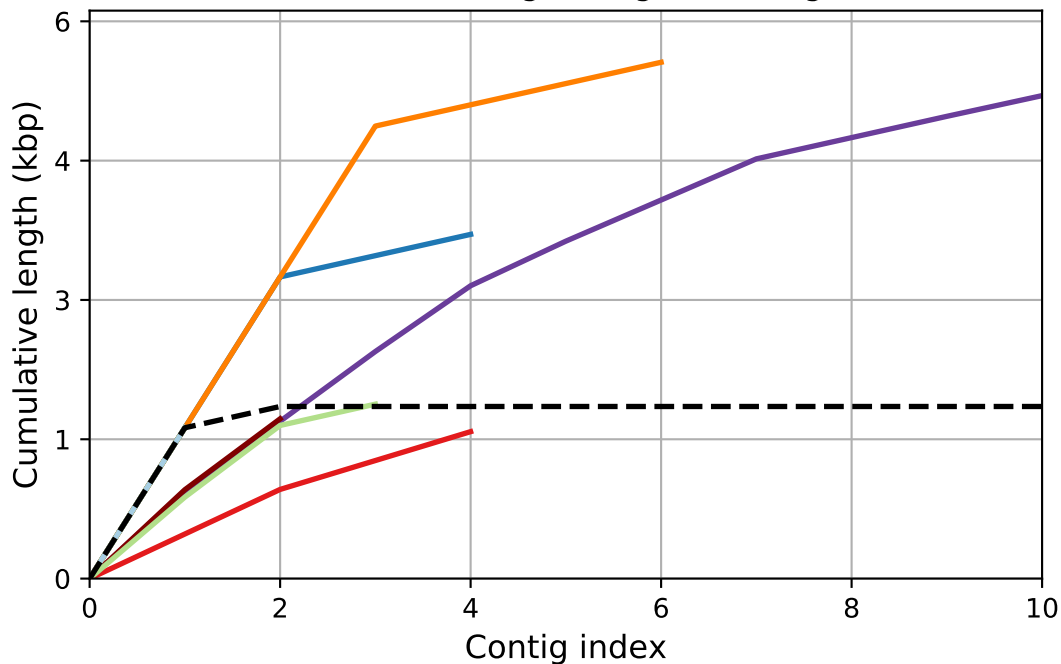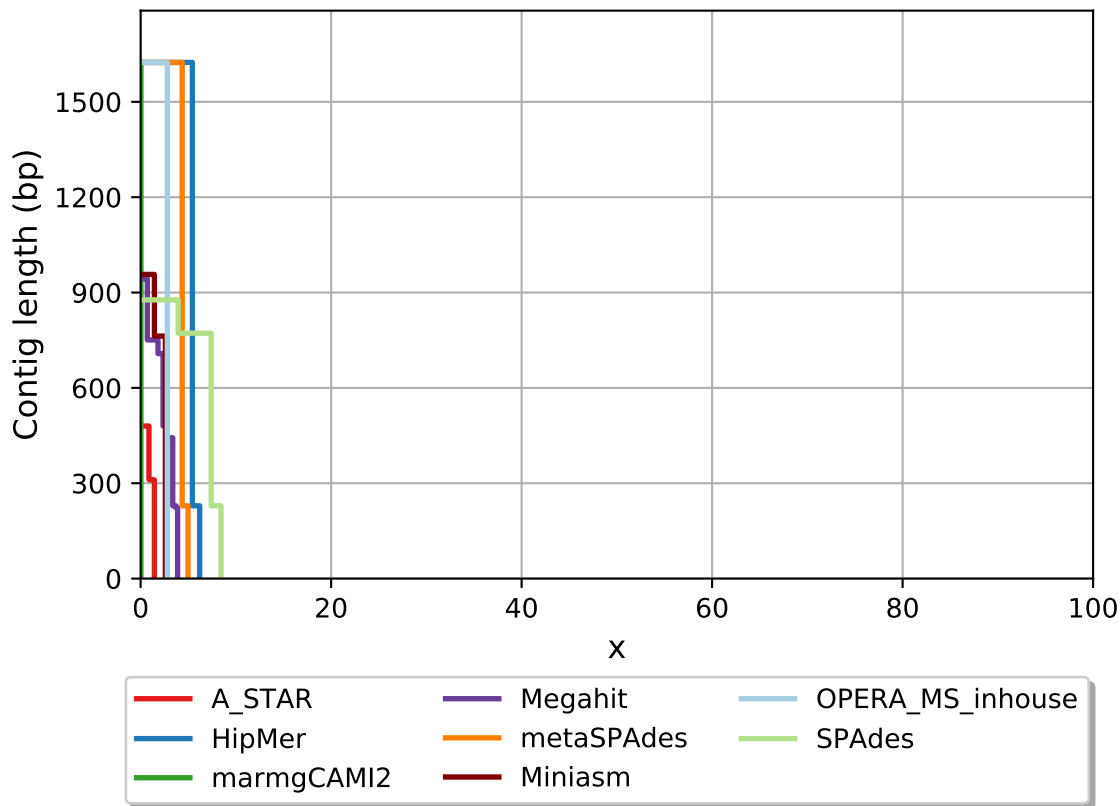A_STAR HipMer armg CAMISADA Megahit metaSPAdes Miniasm OPERA_MS_inhouse SPAdes

FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx

Genome fraction, %