Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	4	8	1	14	6	3	1	3
# contigs (>= 5000 bp)	2	2	1	7	5	3	1	0
# contigs (>= 10000 bp)	2	0	1	5	5	2	1	0
# contigs (>= 25000 bp)	2	0	1	1	0	1	1	0
# contigs (>= 50000 bp)	2	0	1	1	0	1	1	0
Total length (>= 1000 bp)	149898	24577	7215228	142338	91586	179417	95253	8237
Total length (>= 5000 bp)	145864	13026	7215228	130299	88747	179417	95253	0
Total length (>= 10000 bp)	145864	0	7215228	111778	88747	170201	95253	0
Total length (>= 25000 bp)	145864	0	7215228	60780	0	156385	95253	0
Total length (>= 50000 bp)	145864	0	7215228	60780	0	156385	95253	0
# contigs	4	12	1	20	6	3	1	4
Largest contig	72932	6513	7215228	60780	20510	156385	95253	3422
Total length	149898	27989	7215228	146857	91586	179417	95253	9219
Reference length	5818	5818	5818	5818	5818	5818	5818	5818
GC (%)	53.68	55.15	53.87	53.01	53.75	51.22	53.34	55.70
Reference GC (%)	57.00	57.00	57.00	57.00	57.00	57.00	57.00	57.00
N50	72932	2515	7215228	18016	20325	156385	95253	2897
NG50	72932	6513	7215228	60780	20510	156385	95253	3422
N75	72932	2026	7215228	10841	13701	156385	95253	1918
NG75	72932	6513	7215228	60780	20510	156385	95253	2897
L50	2	3	1	2	3	1	1	2
LG50	1	1	1	1	1	1	1	1
L75	2	6	1	5	4	1	1	3
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	2
# 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	2	0	0	1	1
# unaligned contigs	0 + 4 part	0 + 6 part	0 + 1 part	0 + 11 part	0 + 6 part	1 + 2 part	0 + 1 part	0 + 3 part
Unaligned length	145506	16294	7209410	132466	74132	173665	89493	3550
Genome fraction (%)	37.745	99.897	100.000	99.862	100.000	100.000	100.000	92.454
Duplication ratio	2.000	2.012	1.000	2.477	3.000	0.989	0.990	1.054
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	1.05	0.00
# mismatches per 100 kbp	0.00	17.21	0.00	1876.08	0.00	0.00	326.57	687.86
# indels per 100 kbp	0.00	0.00	0.00	17.21	0.00	17.19	395.32	18.59
Largest alignment	898	2492	3670	1481	3670	3604	3608	2425
Total aligned length	4392	11441	5818	13783	17454	5752	5759	5554
NA50	-	-	-	-	-	-	-	867
NGA50	829	2025	3670	1199	3670	3604	3608	1342
NGA75	469	2025	2148	1181	3670	2148	2151	867
LA50	-	-	-	-	-	-	-	3
LGA50	4	2	1	3	1	1	1	2
LGA75	6	2	2	4	2	2	2	3

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

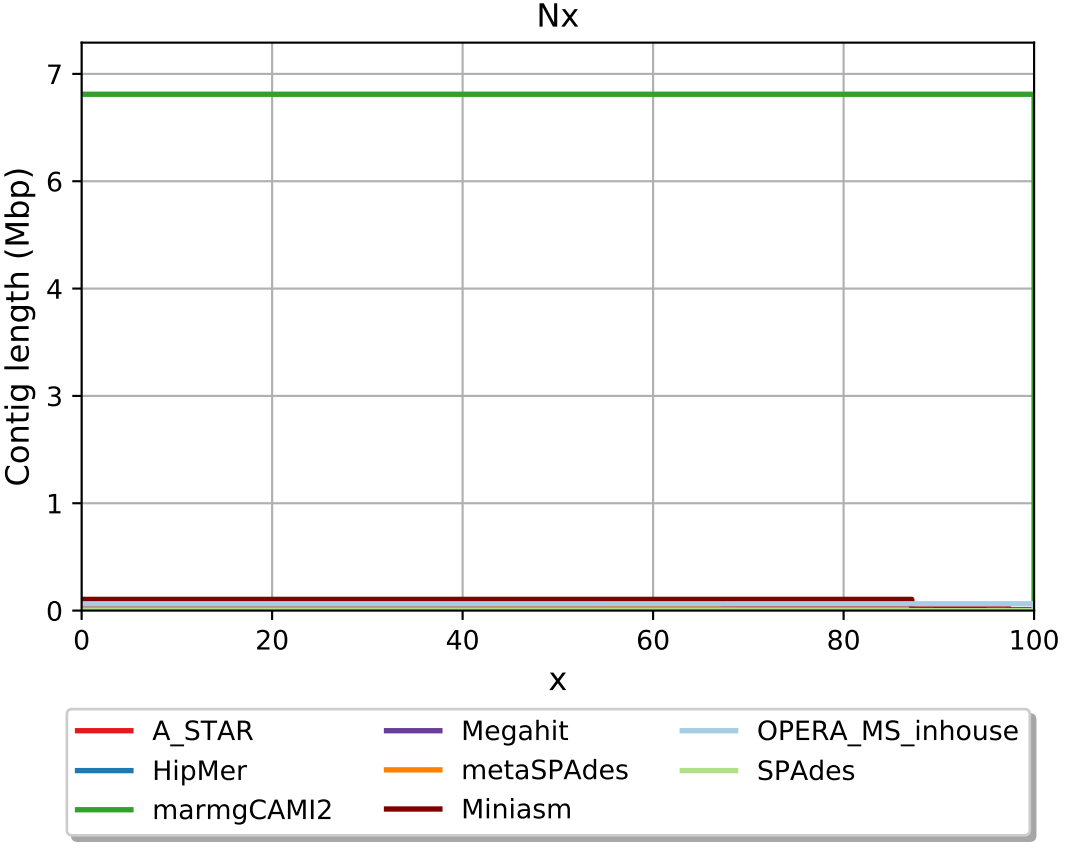
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	6	0	8	6	3	0	2
# possible misassemblies	2	6	0	8	7	4	0	3
# local misassemblies	0	0	0	0	0	0	0	2
# 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	2	0	0	1	1
# mismatches	0	1	0	109	0	0	19	37
# indels	0	0	0	1	0	1	23	1
# indels (<= 5 bp)	0	0	0	0	0	0	22	1
# indels (> 5 bp)	0	0	0	1	0	1	1	0
Indels length	0	0	0	66	0	66	95	1

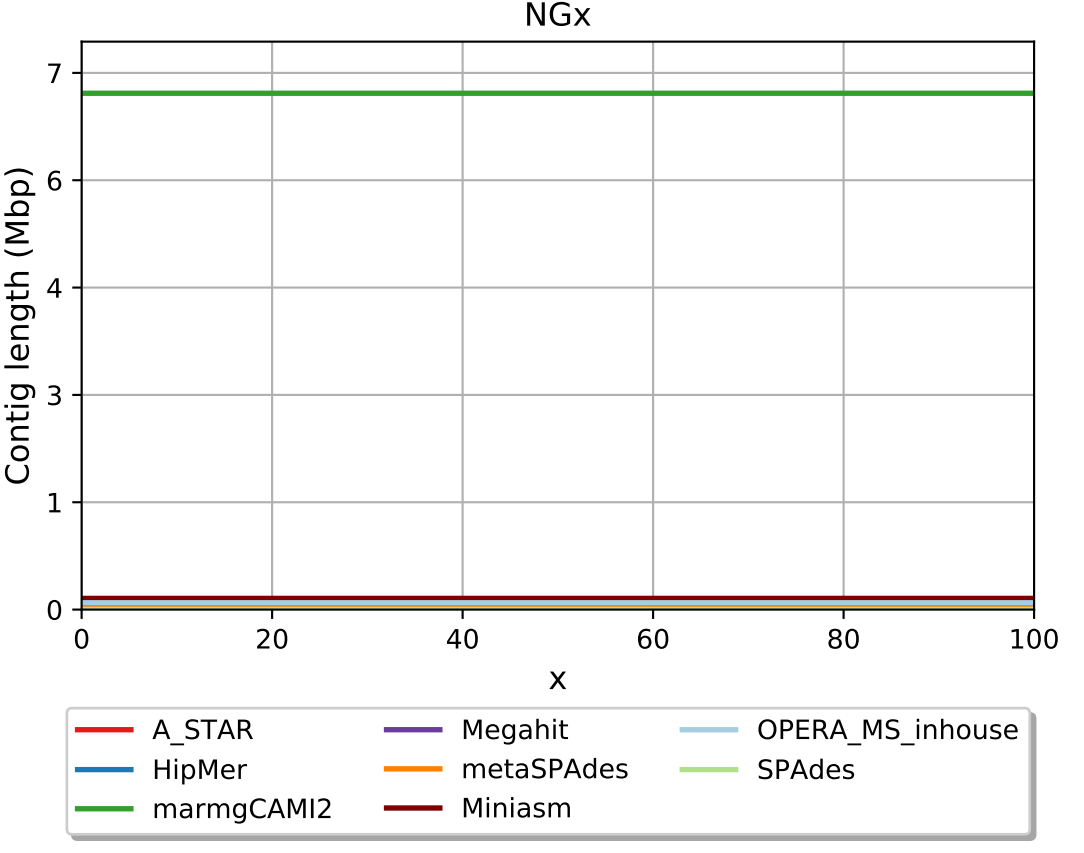
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

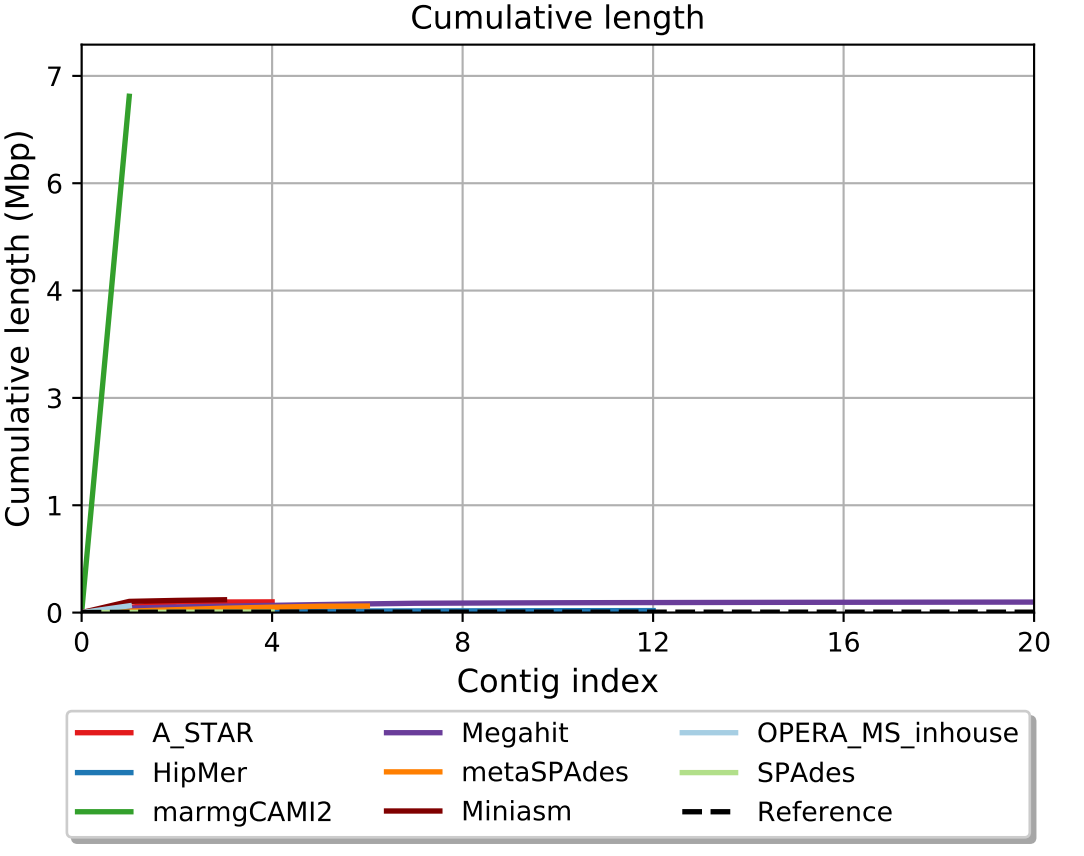
Unaligned report

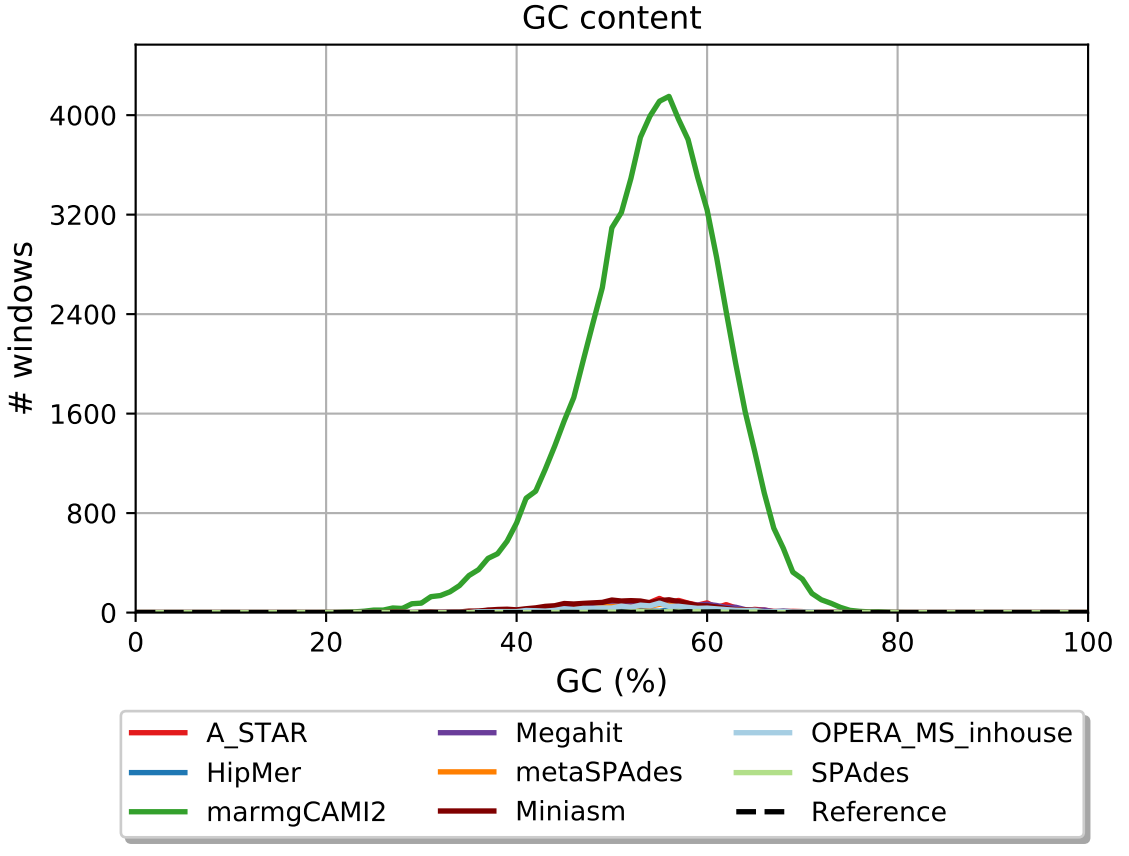
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	1	0	0
Fully unaligned length	0	0	0	0	0	9216	0	0
# partially unaligned contigs	4	6	1	11	6	2	1	3
Partially unaligned length	145506	16294	7209410	132466	74132	164449	89493	3550
# N's	0	0	0	0	0	0	1	0

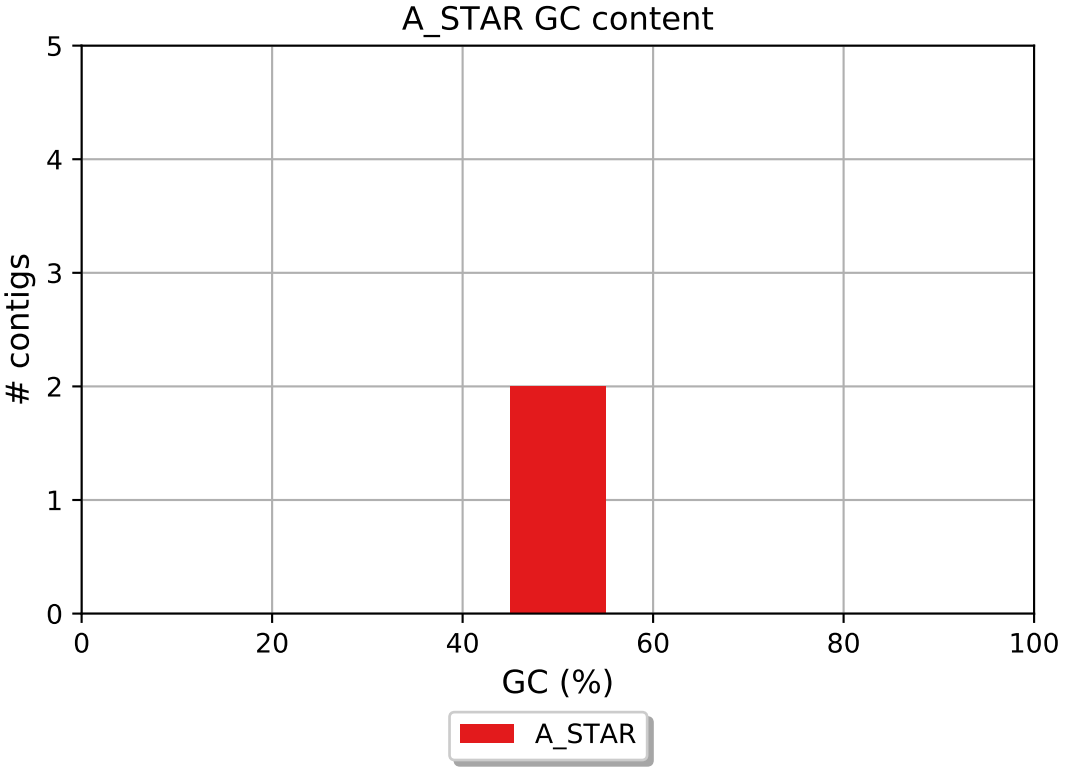
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

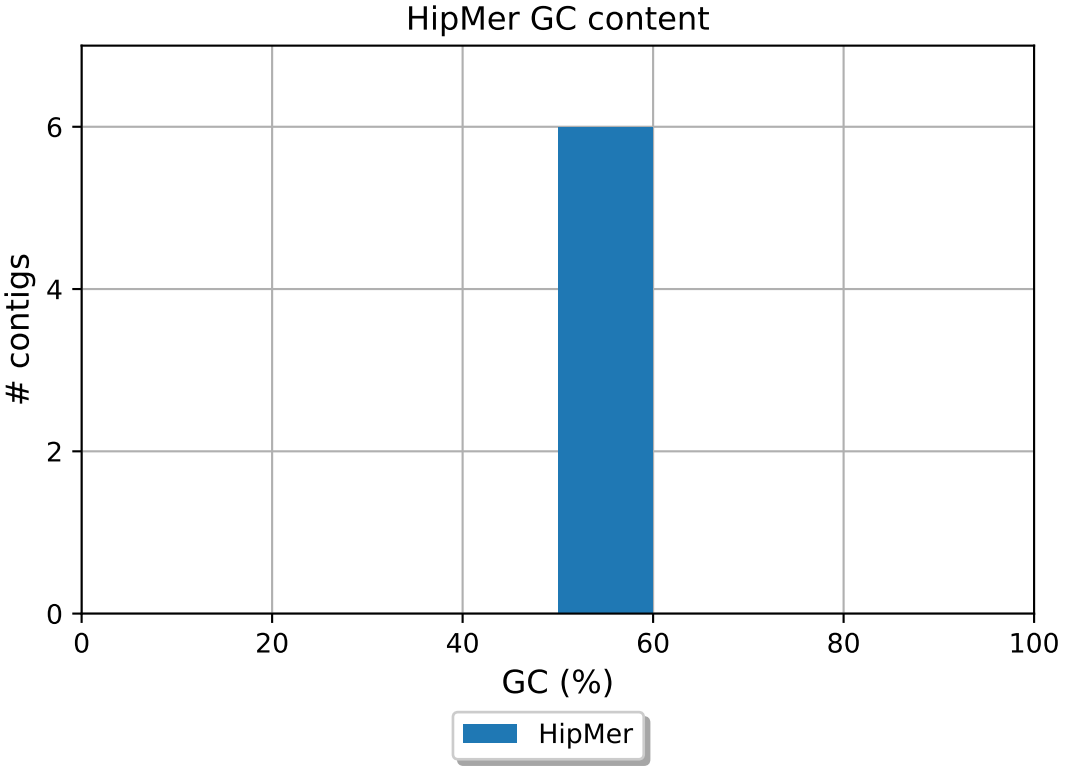

Nx
Contig length (Mbp)
7
6
4
3
1
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

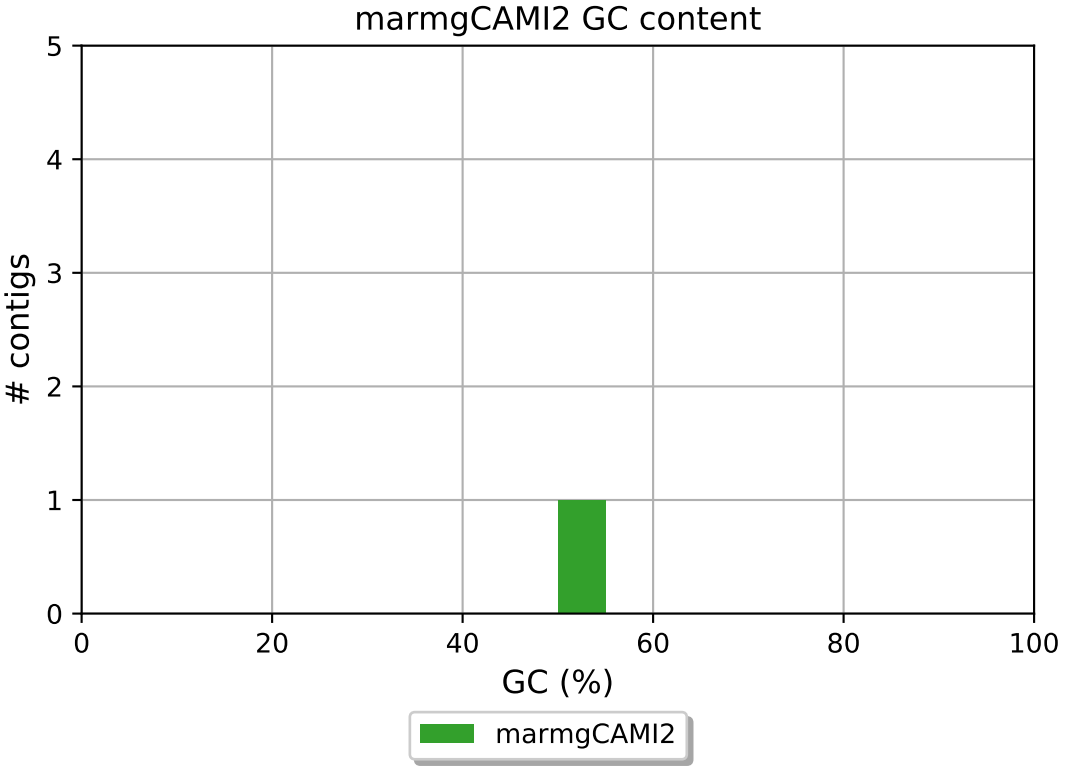

NGx
Contig length (Mbp)
7
6
4
3
1
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

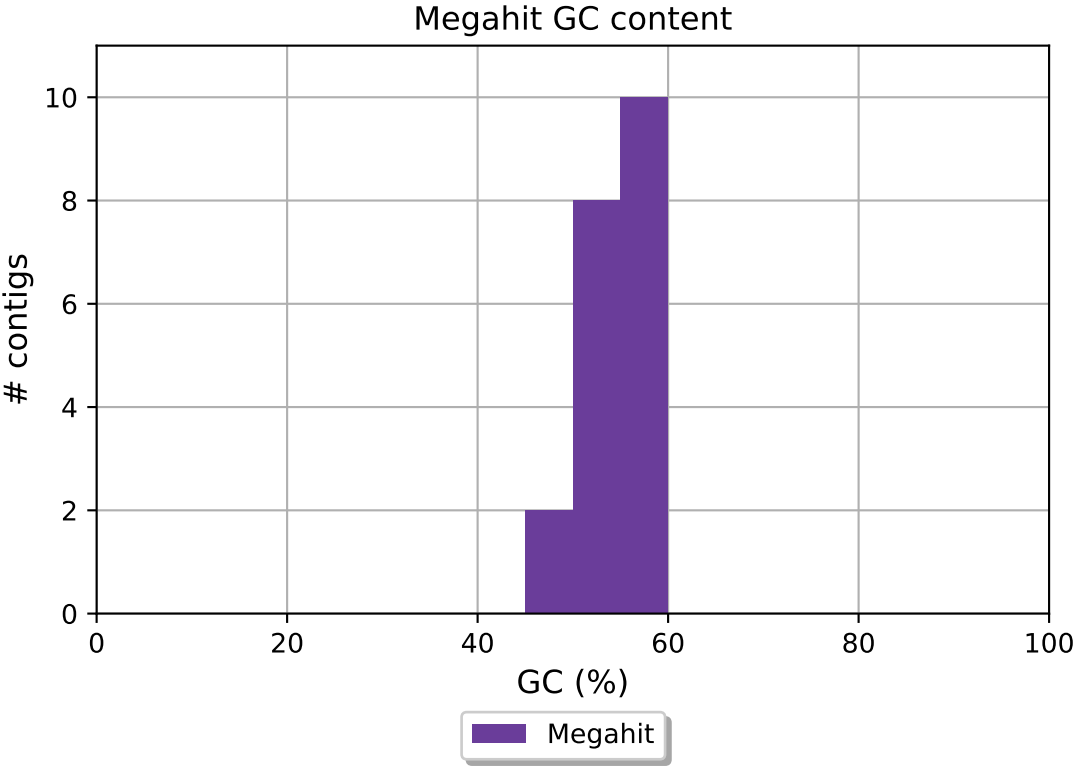

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
7
0
4
8
12
16
20
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

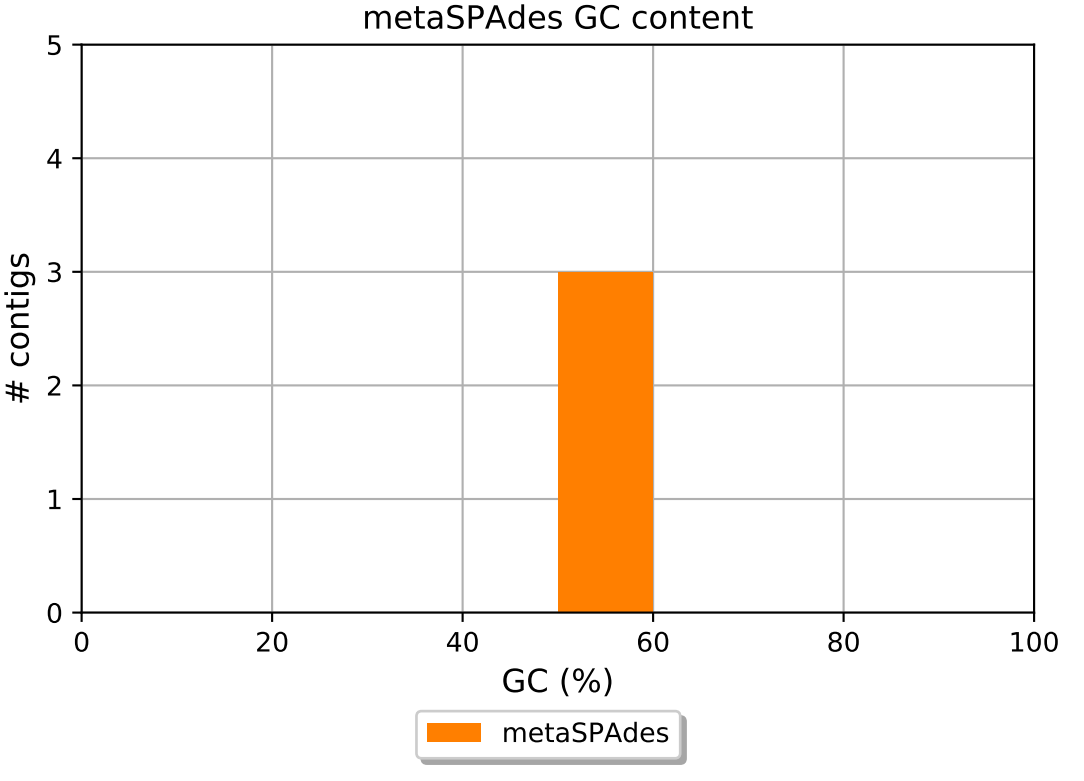

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

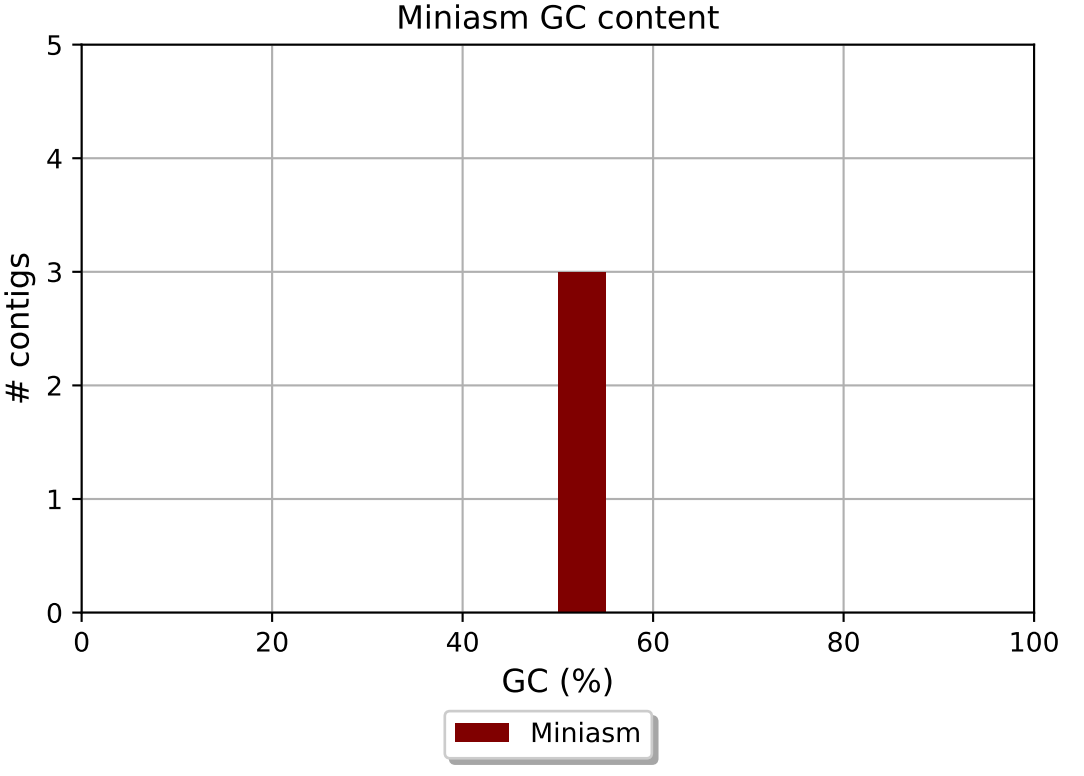

A_STAR GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
A_STAR

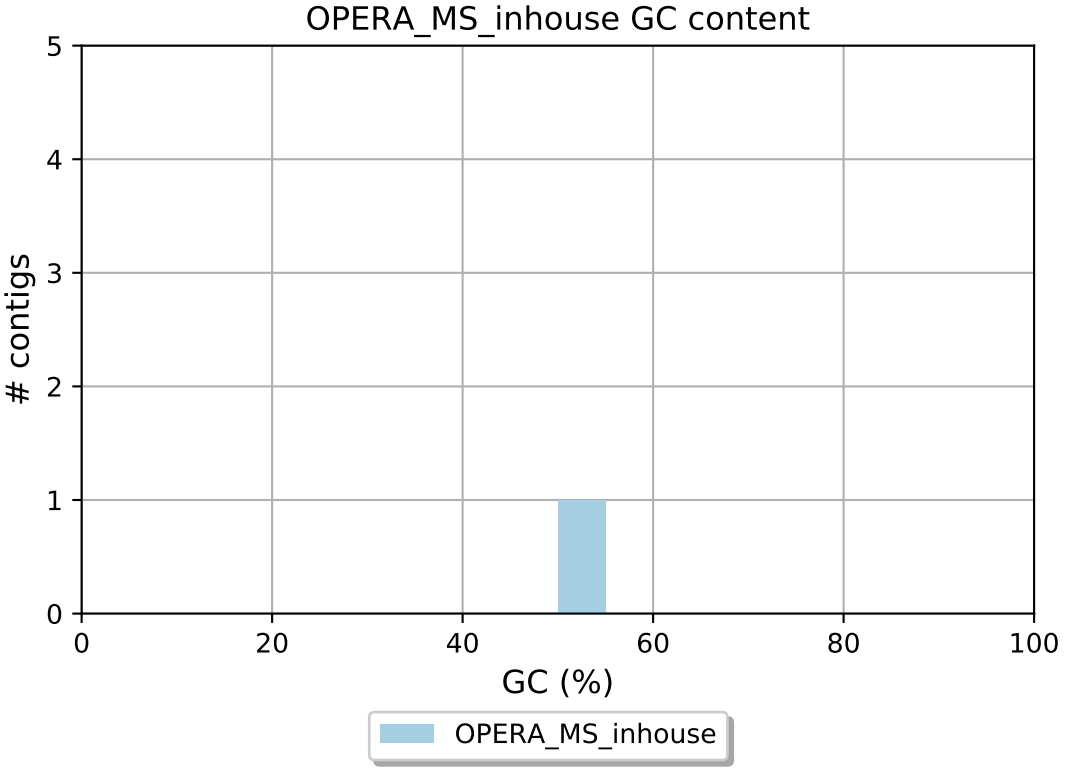

HipMer GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
HipMer

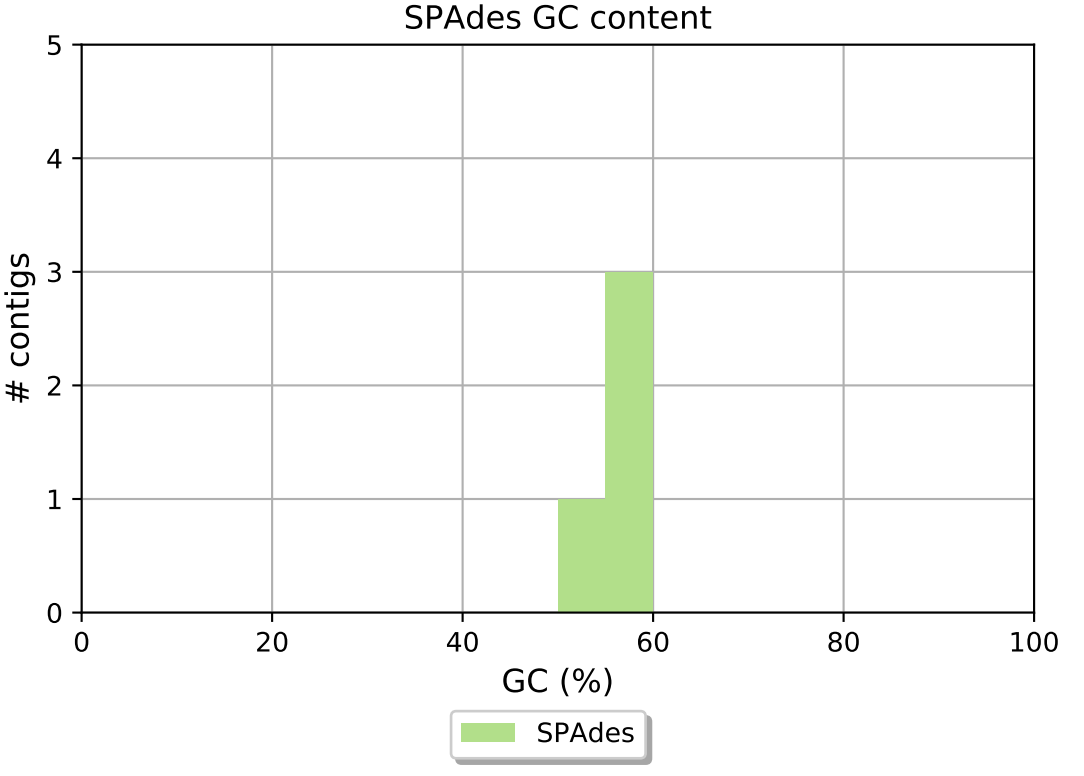

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

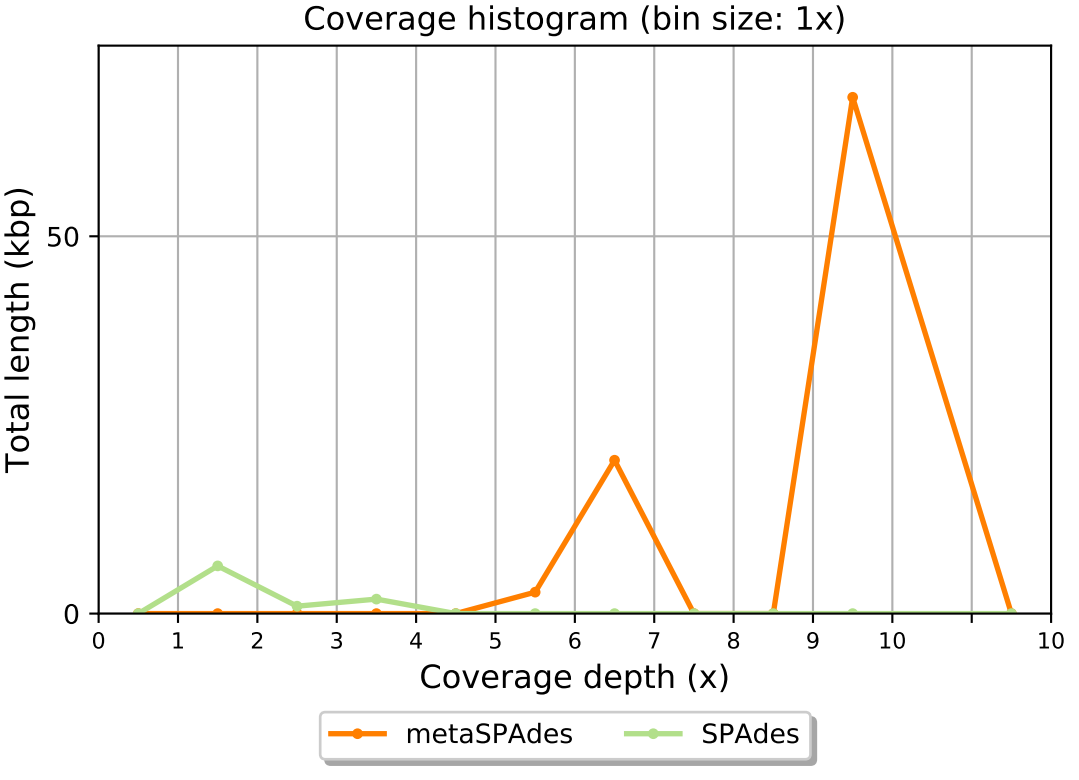

Megahit GC content
contigs
0
2
4
6
8
10
0
20
40
60
80
100
GC (%)
Megahit

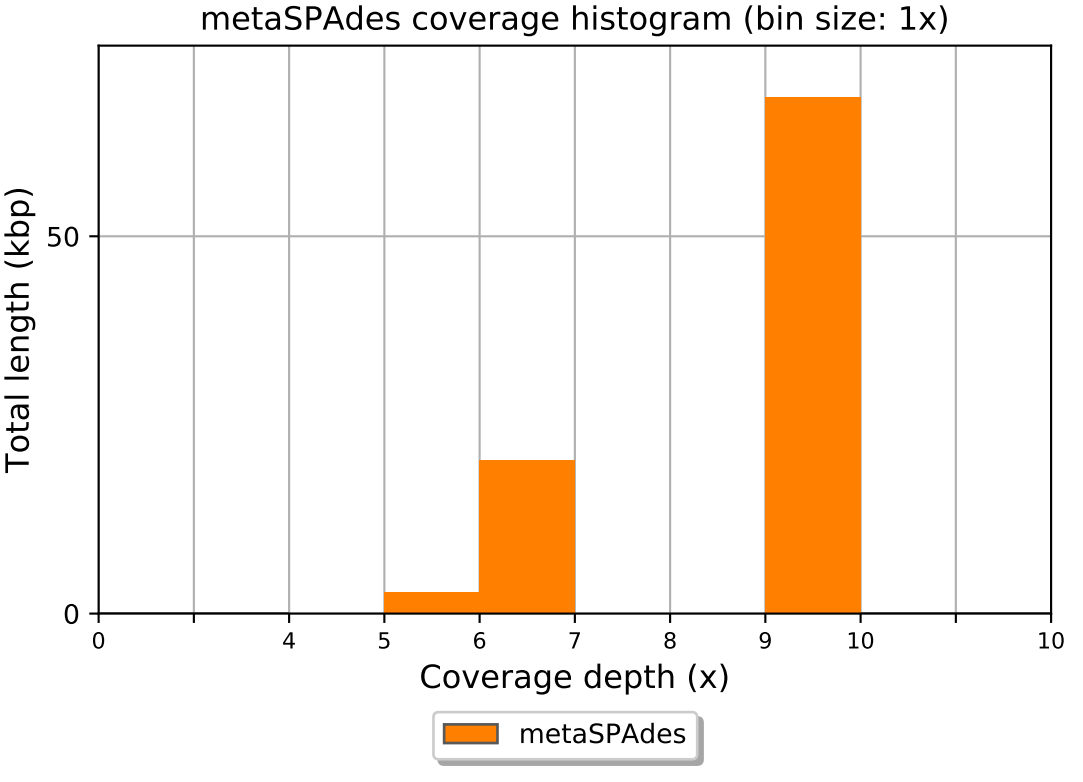

metaSPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
metaSPAdes

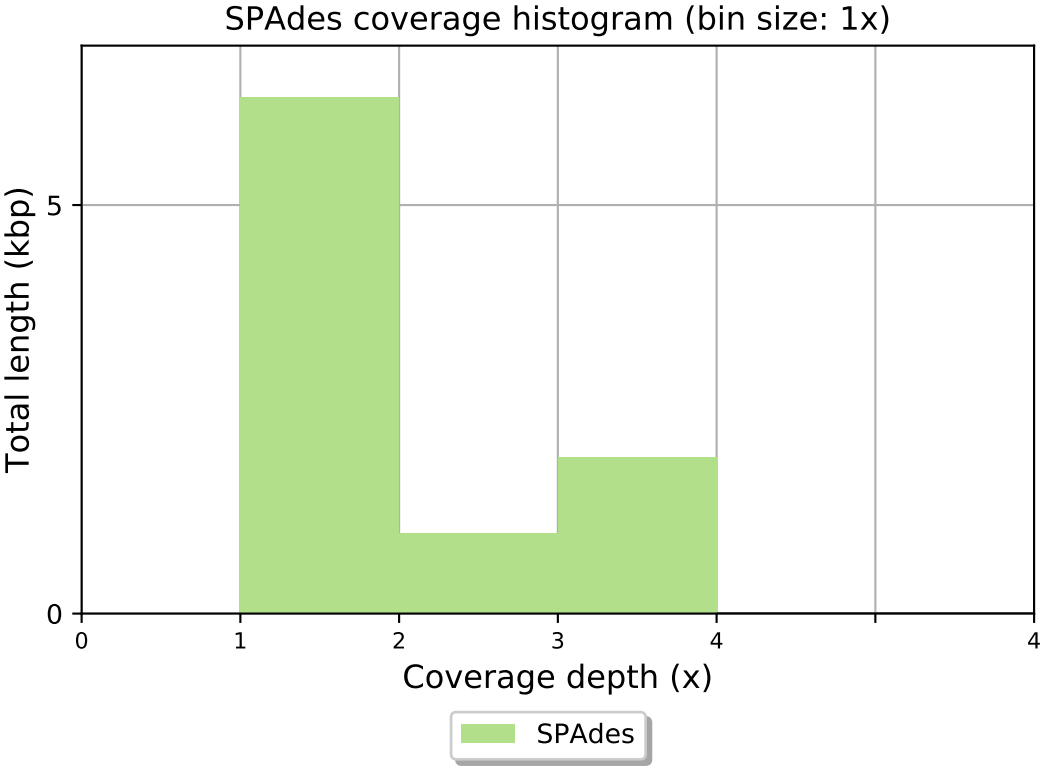

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

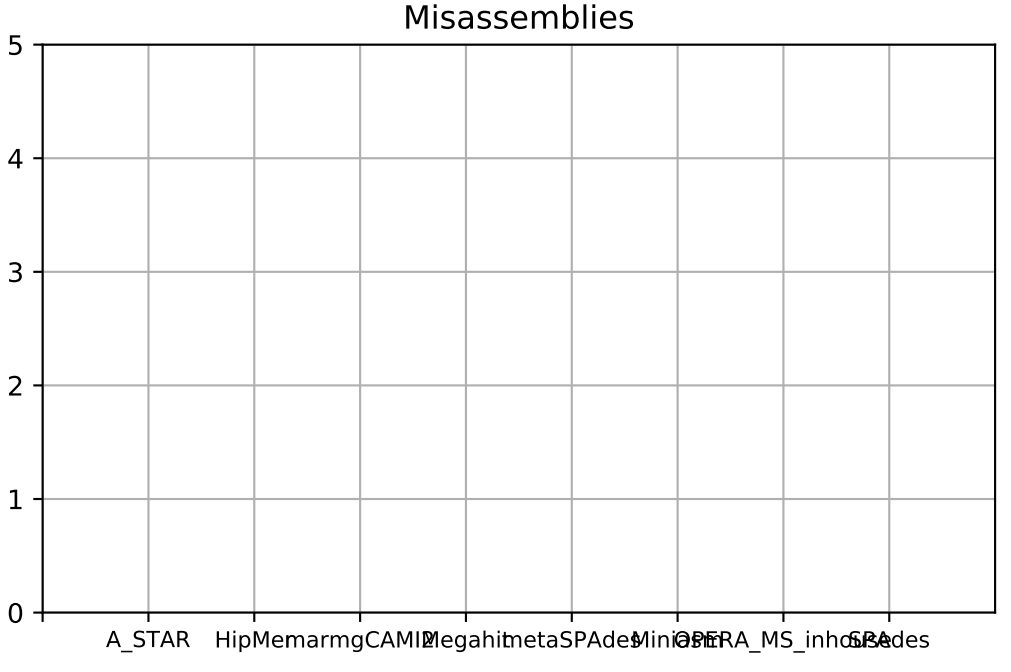

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

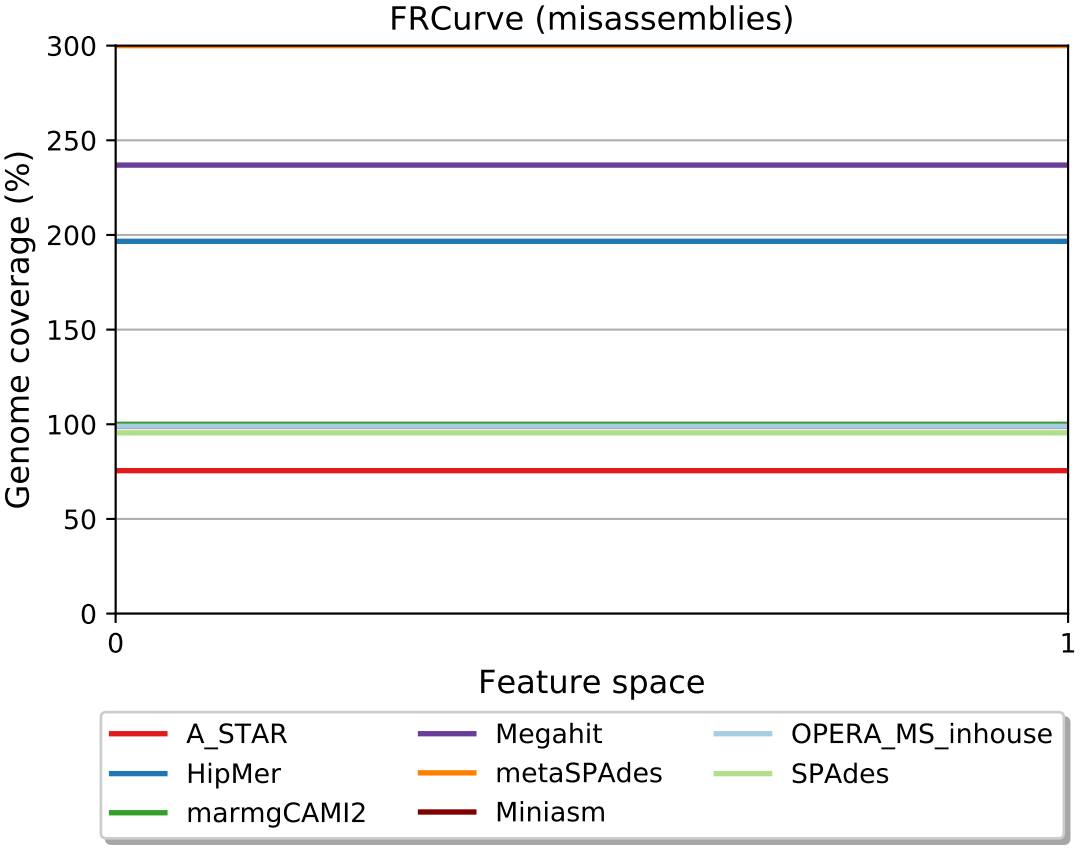

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

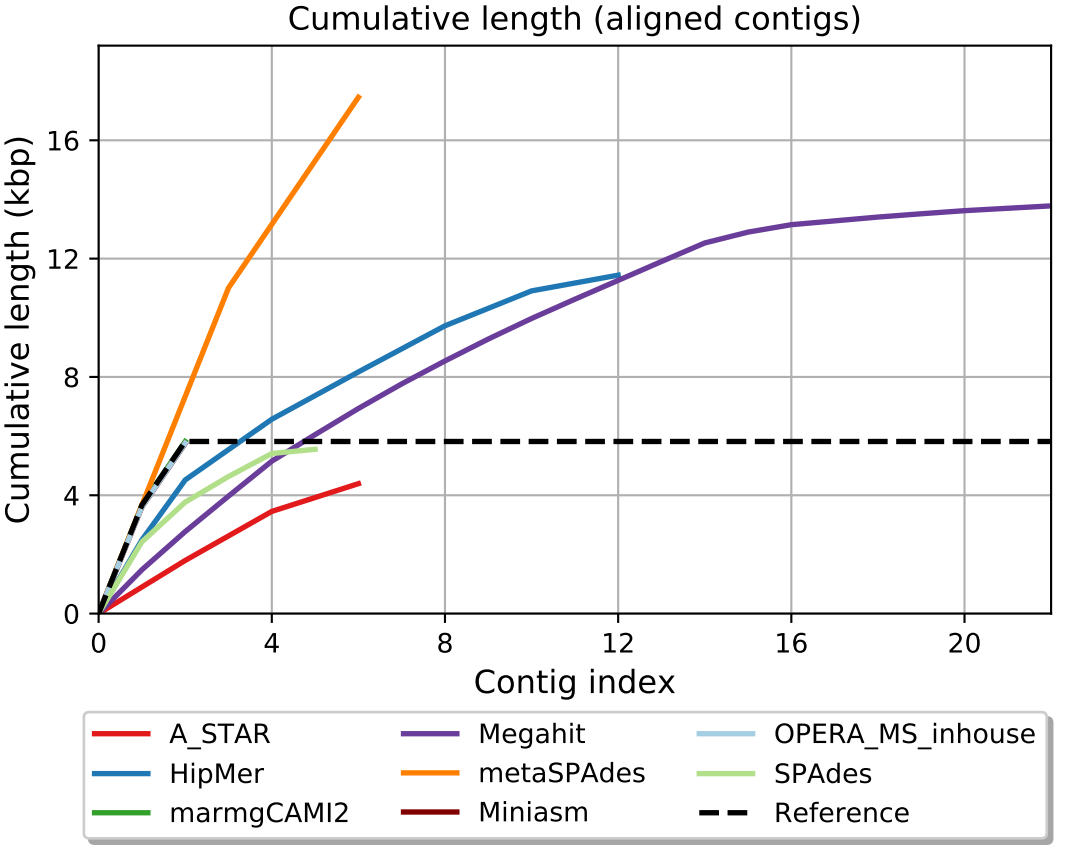

Coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
1
2
3
4
5
6
7
8
9
10
10
Coverage depth (x)
metaSPAdes
SPAdes

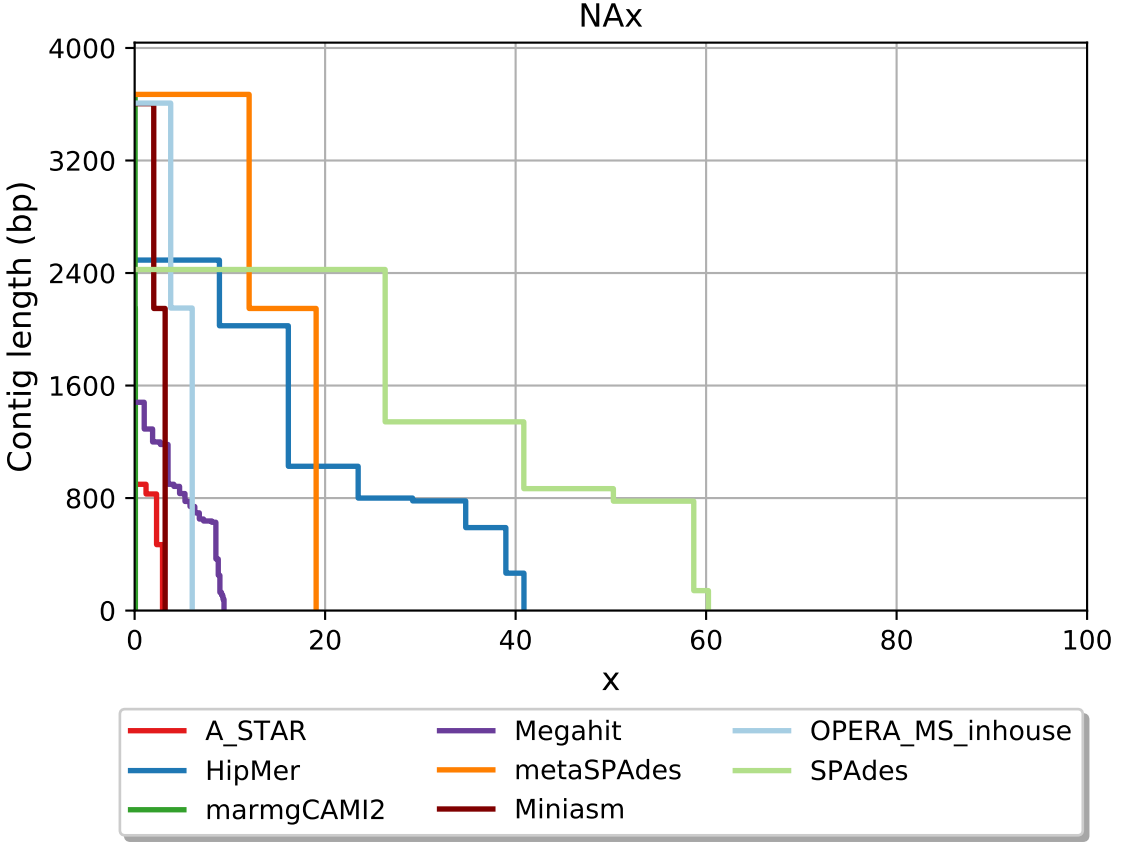

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
4
5
6
7
8
9
10
10
Coverage depth (x)
metaSPAdes

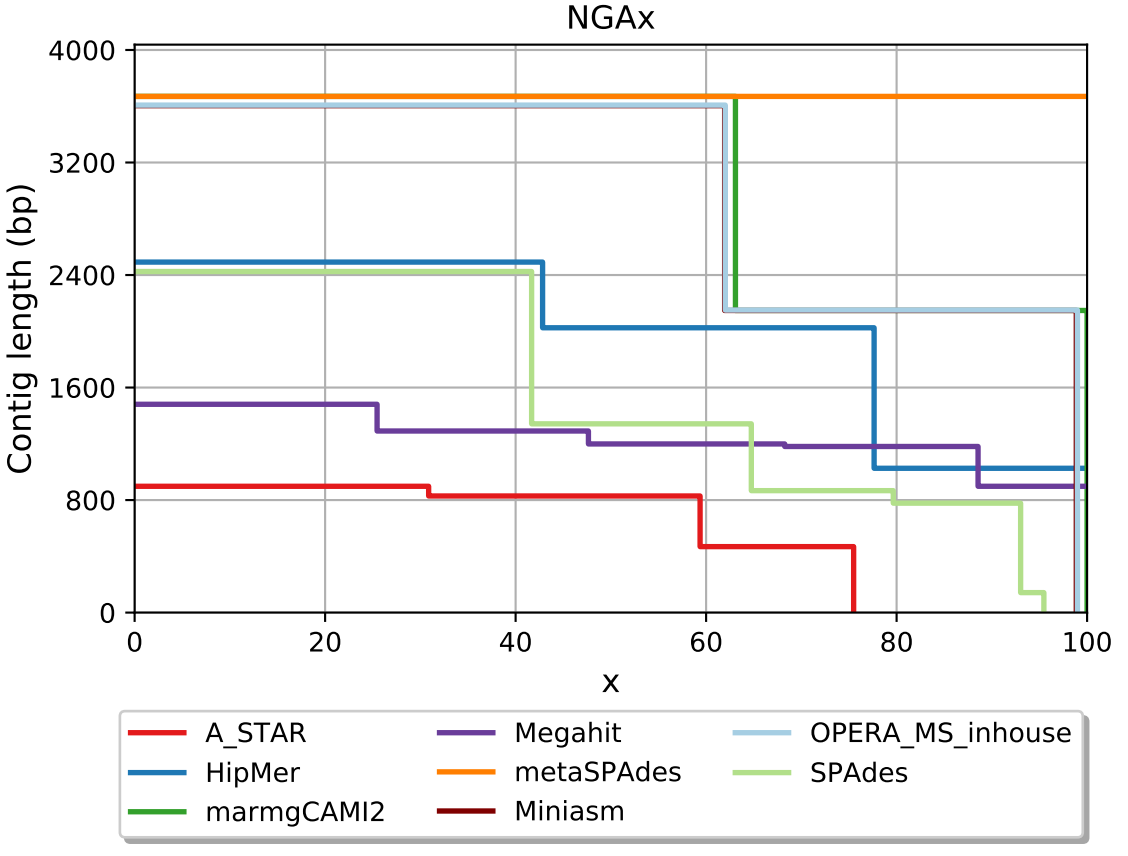

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
5
0
0
1
2
3
4
4
Coverage depth (x)
SPAdes

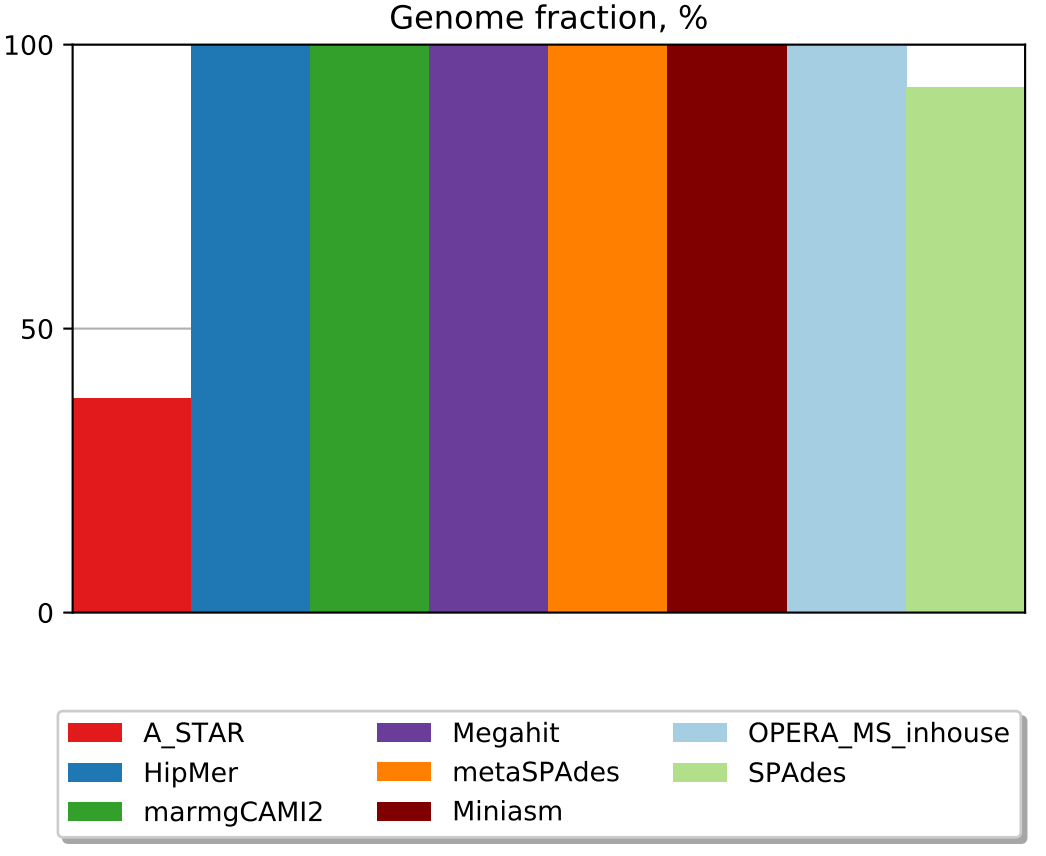

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL2
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes


FRCurve (misassemblies)
Genome coverage (%)
300
250
200
150
100
50
0
0
1
Feature space
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
4
8
12
16
0
4
8
12
16
20
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Genome fraction, %
100
50
0
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes