Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	2	1	3	3	1	1	2
# contigs (>= 5000 bp)	2	2	1	3	3	1	1	1
# contigs (>= 10000 bp)	2	2	1	3	3	1	1	0
# contigs (>= 25000 bp)	1	2	1	2	2	1	1	0
# contigs (>= 50000 bp)	0	1	1	1	2	1	1	0
Total length (>= 1000 bp)	58217	96870	3914609	232110	213430	323167	72798	10039
Total length (>= 5000 bp)	58217	96870	3914609	232110	213430	323167	72798	6444
Total length (>= 10000 bp)	58217	96870	3914609	232110	213430	323167	72798	0
Total length (>= 25000 bp)	42211	96870	3914609	221656	188442	323167	72798	0
Total length (>= 50000 bp)	0	65860	3914609	191383	188442	323167	72798	0
# contigs	2	2	1	3	3	1	1	2
Largest contig	42211	65860	3914609	191383	94221	323167	72798	6444
Total length	58217	96870	3914609	232110	213430	323167	72798	10039
Reference length	1160	1160	1160	1160	1160	1160	1160	1160
GC (%)	35.82	35.60	35.32	35.67	35.74	35.74	35.87	35.26
Reference GC (%)	32.33	32.33	32.33	32.33	32.33	32.33	32.33	32.33
N50	42211	65860	3914609	191383	94221	323167	72798	6444
NG50	42211	65860	3914609	191383	94221	323167	72798	6444
N75	16006	31010	3914609	191383	94221	323167	72798	3595
NG75	42211	65860	3914609	191383	94221	323167	72798	6444
L50	1	1	1	1	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	2	1	1	2	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	2	1	3	3	1	1	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 + 2 part
Unaligned length	55669	94550	3913449	228630	207630	322007	71638	8879
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	2.197	2.000	1.000	3.000	5.000	1.000	1.000	1.000
# N's per 100 kbp	391.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	172.41	689.66	0.00	172.41	431.03
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	610	610	610	610	610	610	610	610
Total aligned length	2320	2320	1160	3480	5800	1160	1160	1160
NGA50	610	610	610	610	610	610	610	610
NGA75	610	610	550	610	610	550	550	550
LGA50	1	1	1	1	1	1	1	1
LGA75	2	2	2	2	2	2	2	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

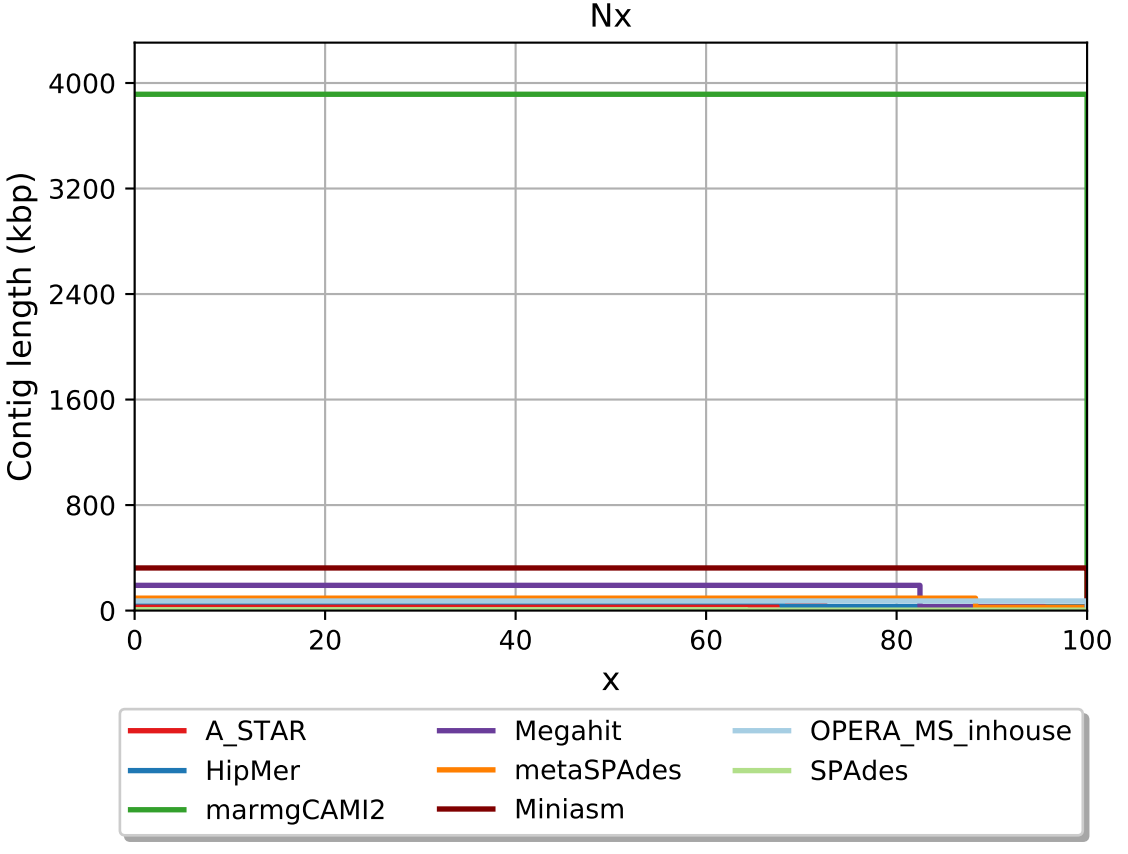
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	0	0	0	0	0	0	2
# possible misassemblies	0	0	0	0	0	0	0	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	2	1	3	3	1	1	0
# mismatches	0	0	0	2	8	0	2	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

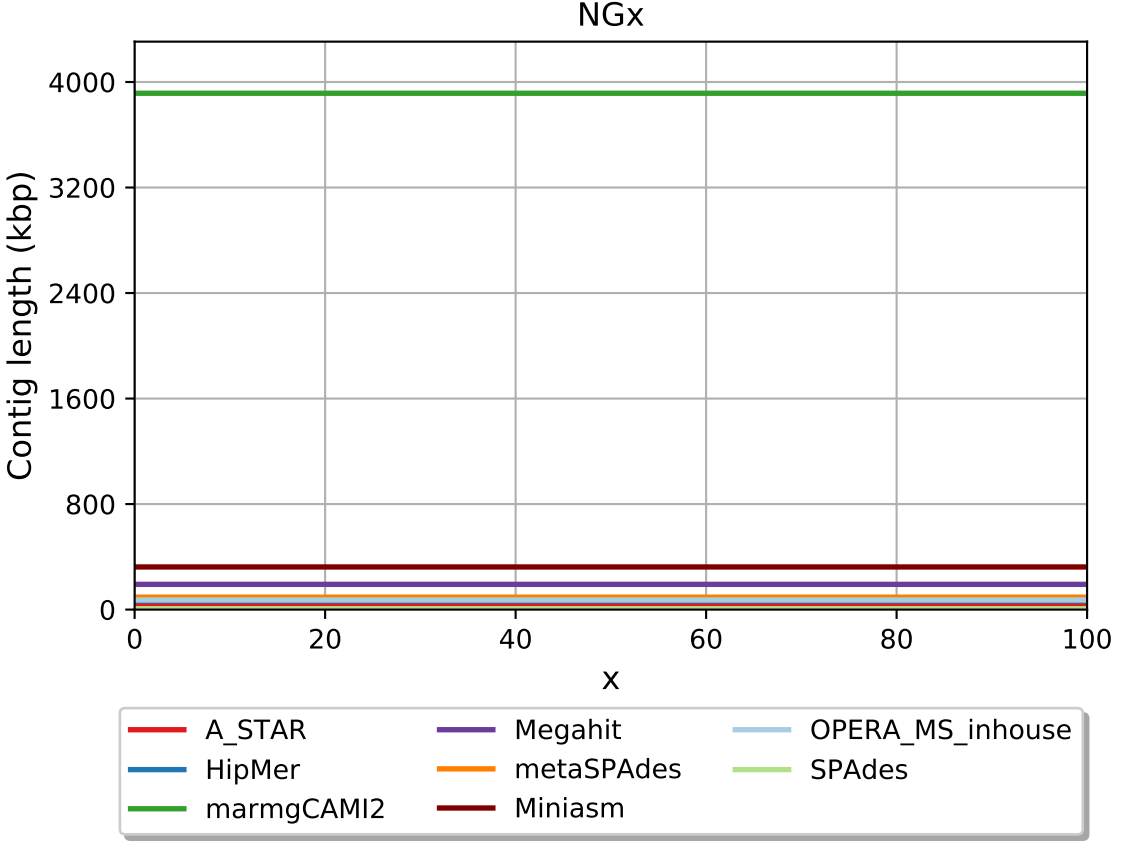
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

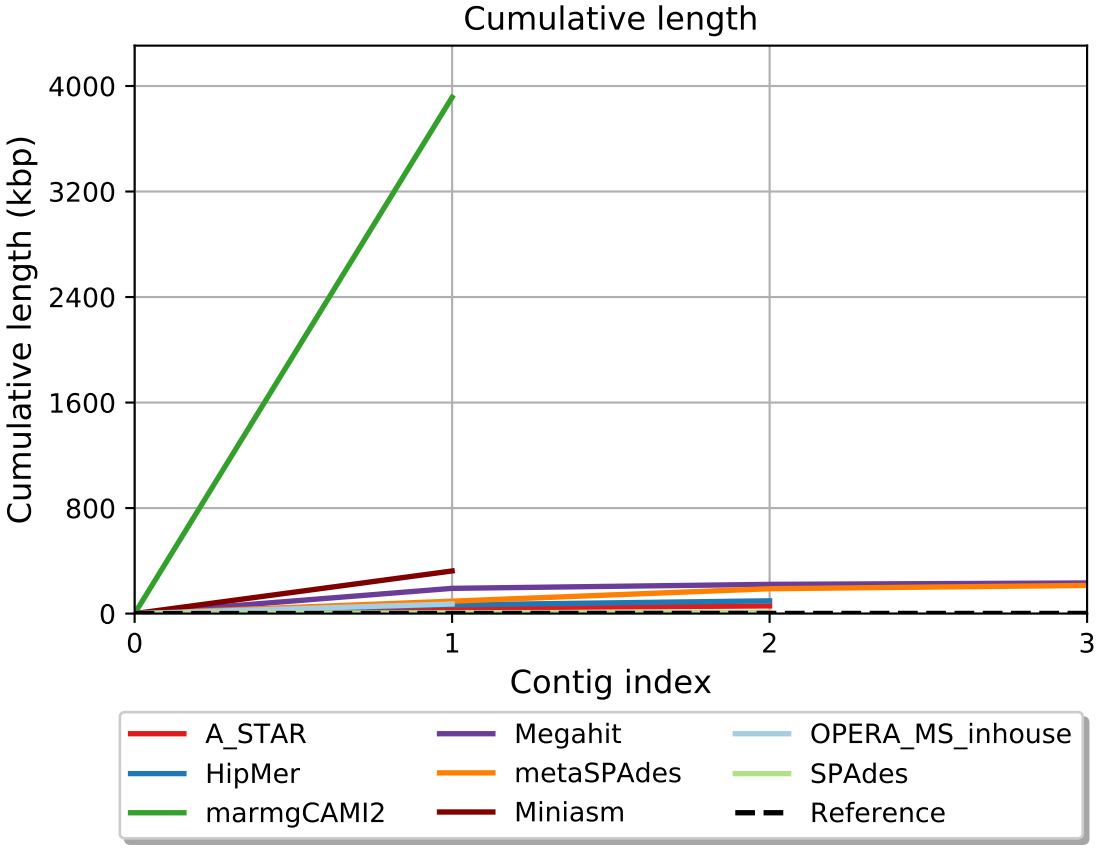
Unaligned report

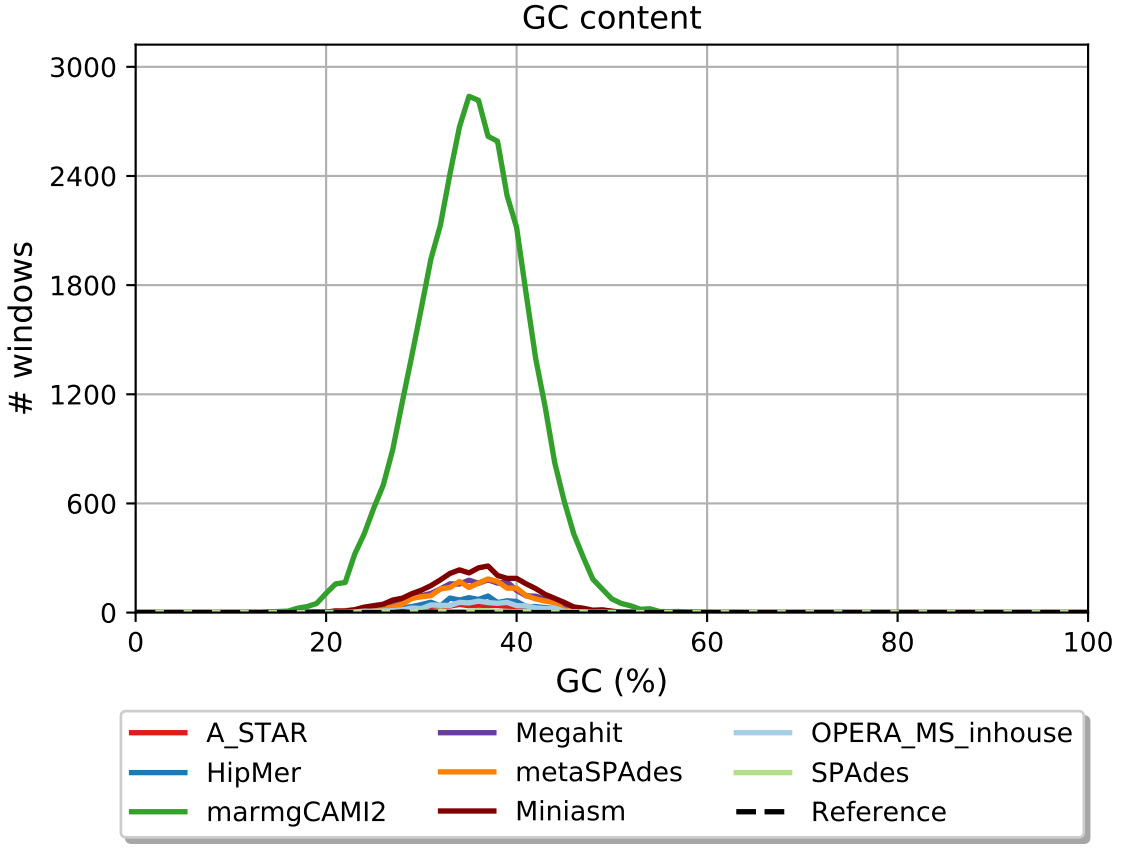
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	2	2	1	3	3	1	1	2
Partially unaligned length	55669	94550	3913449	228630	207630	322007	71638	8879
# N's	228	0	0	0	0	0	0	0

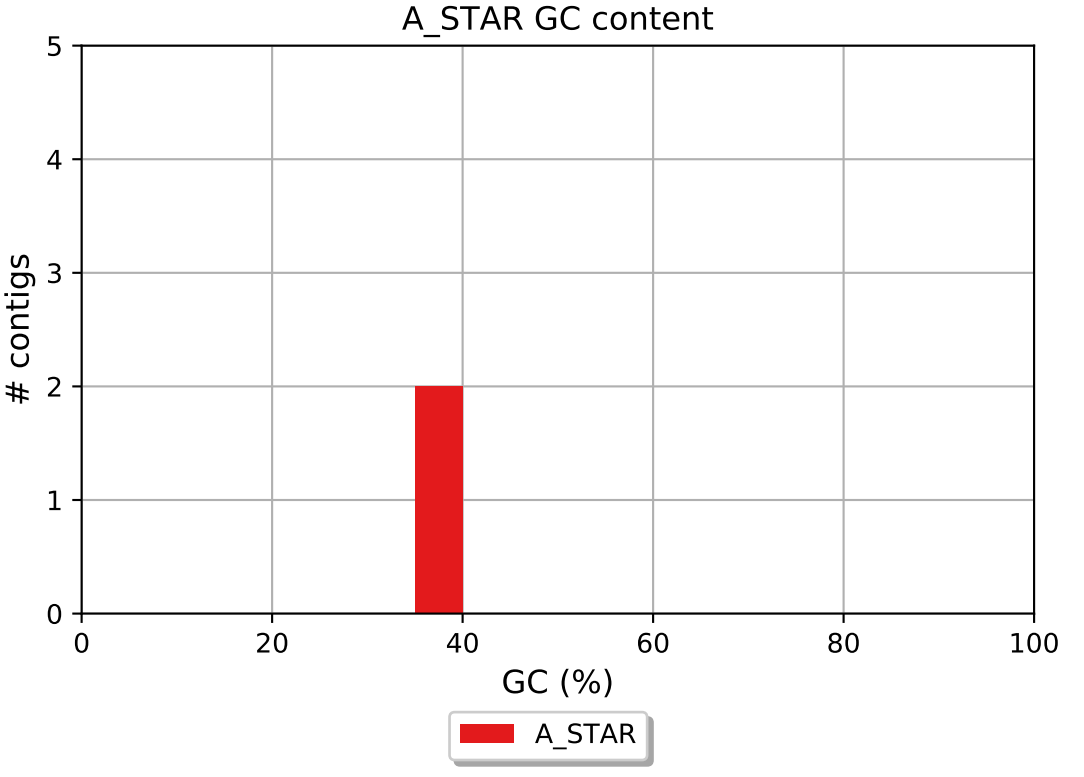
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

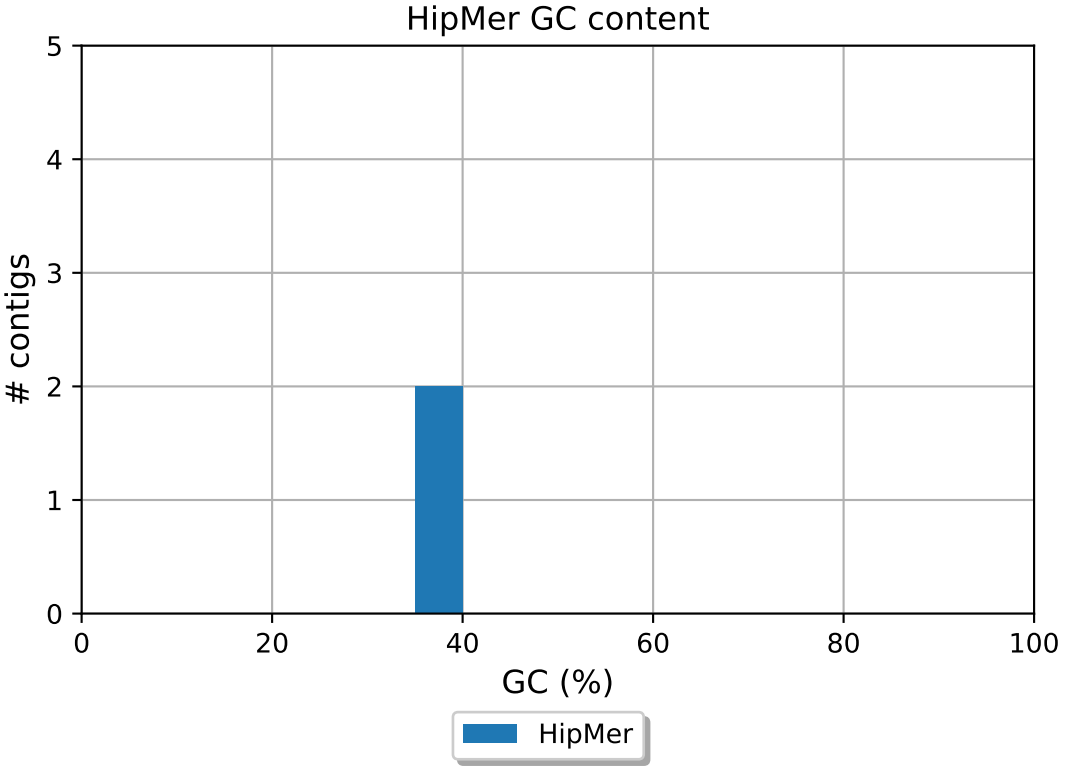

Nx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

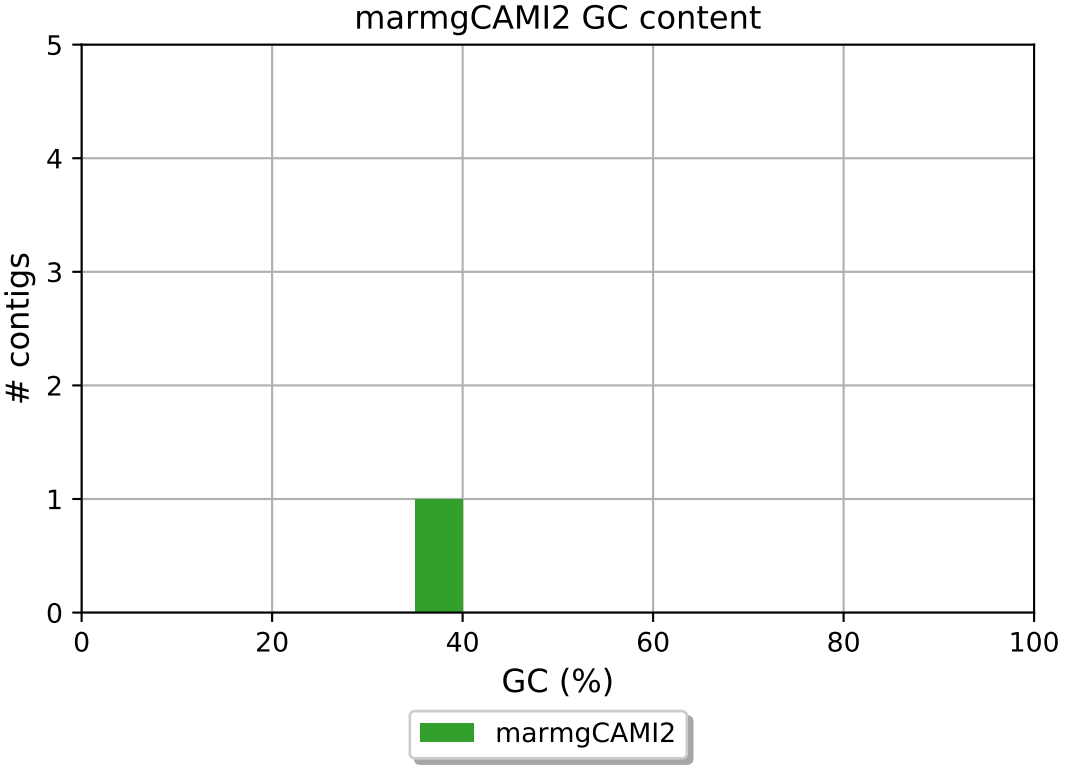

NGx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

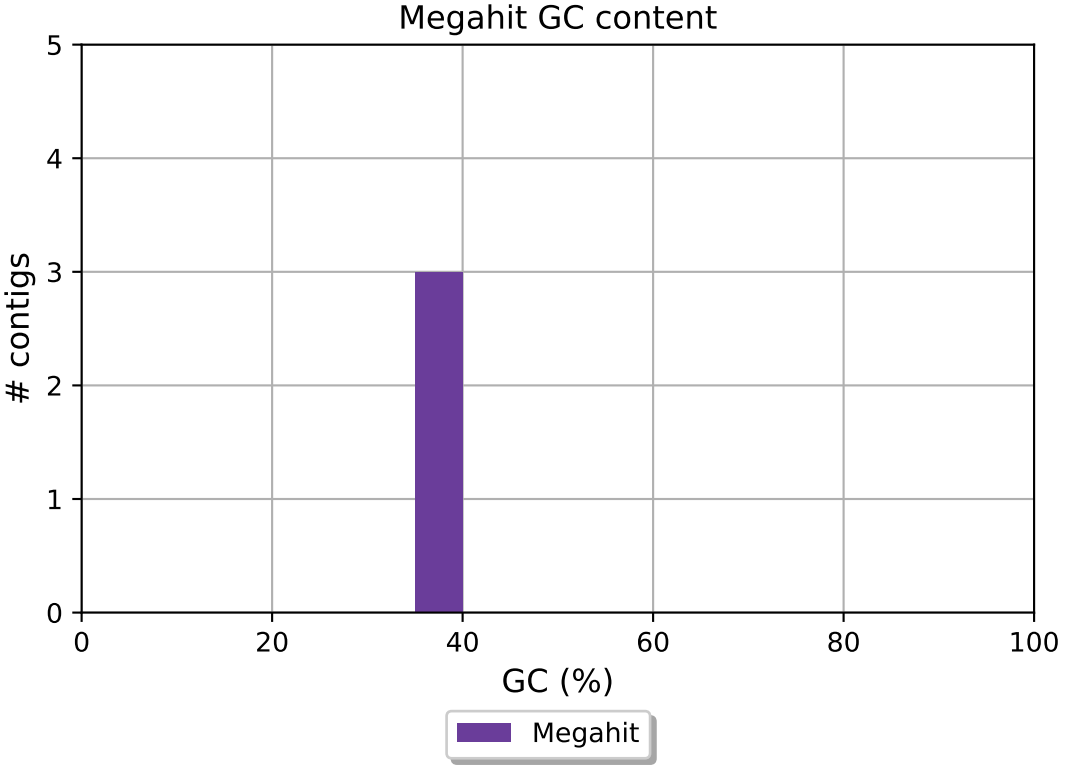

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
1
2
3
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

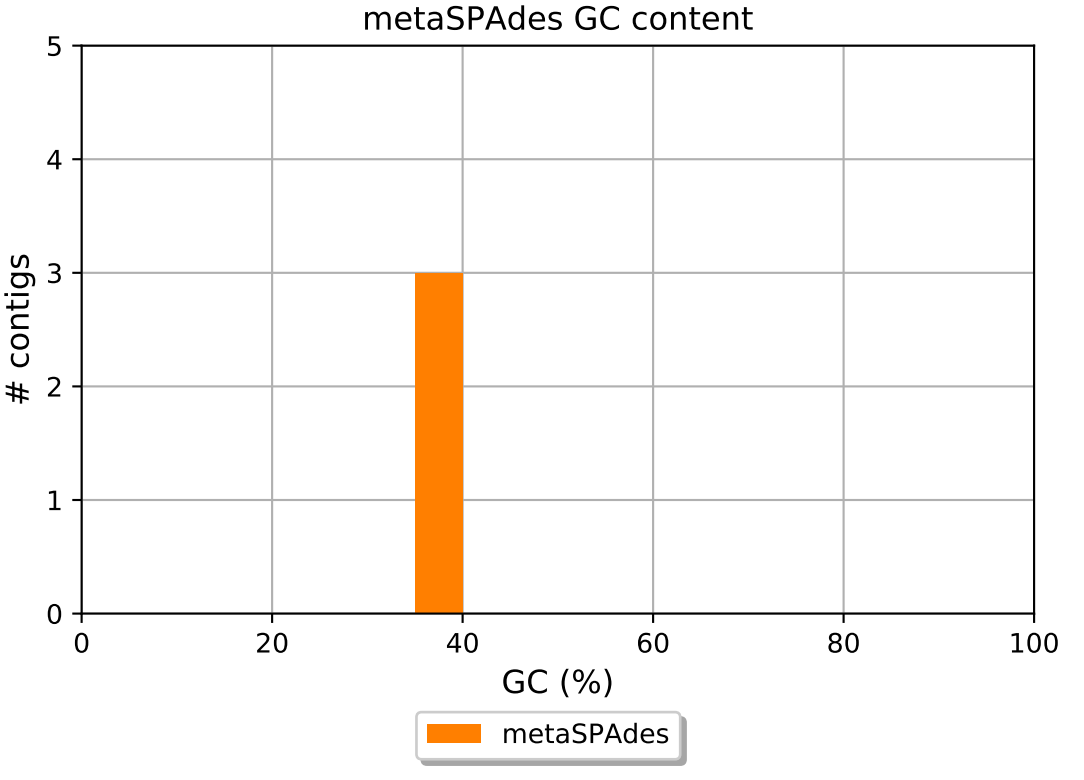

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

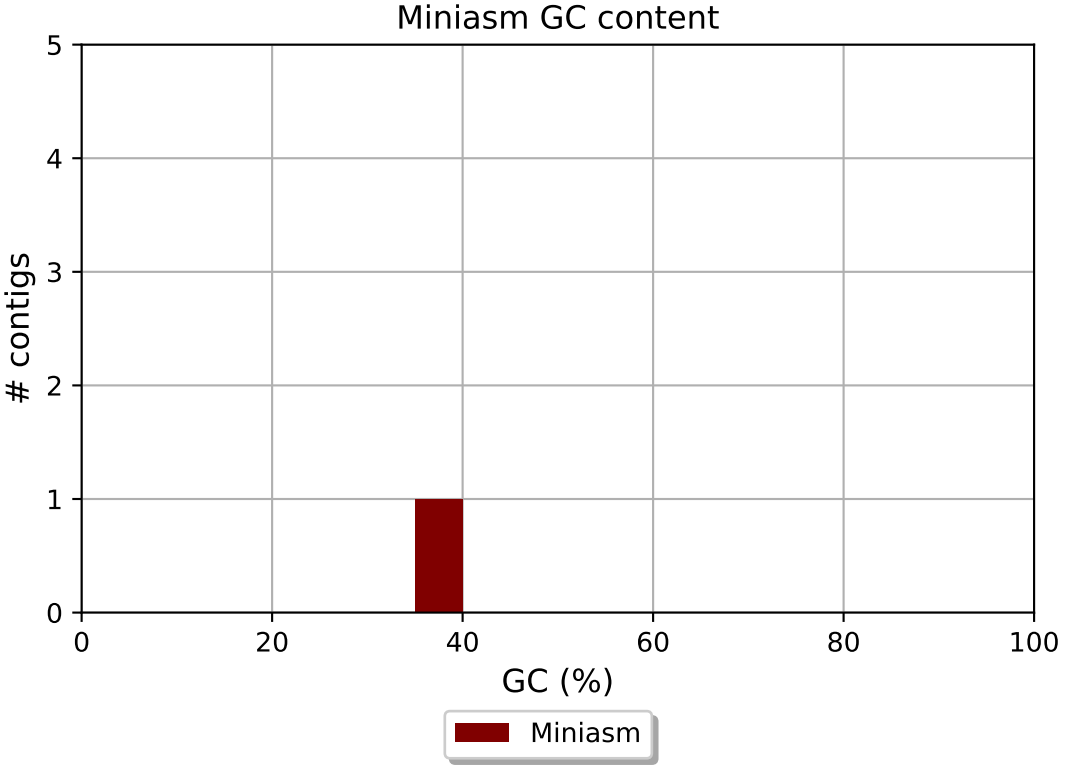

A_STAR GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
A_STAR

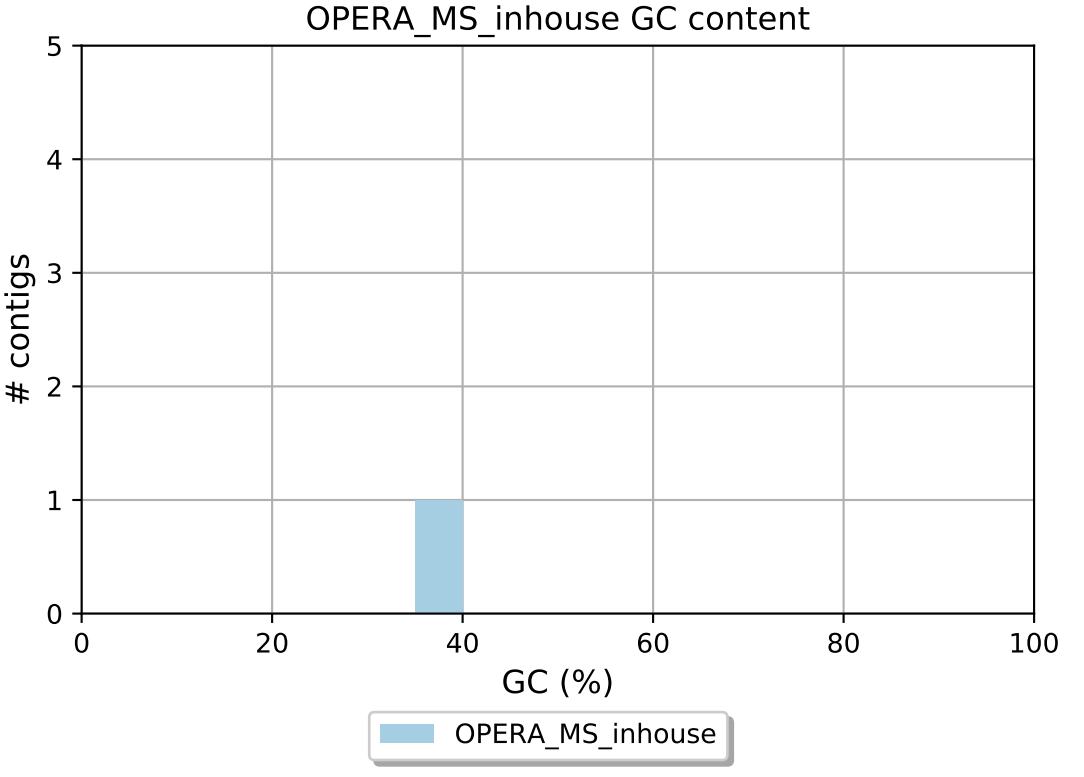

HipMer GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
HipMer

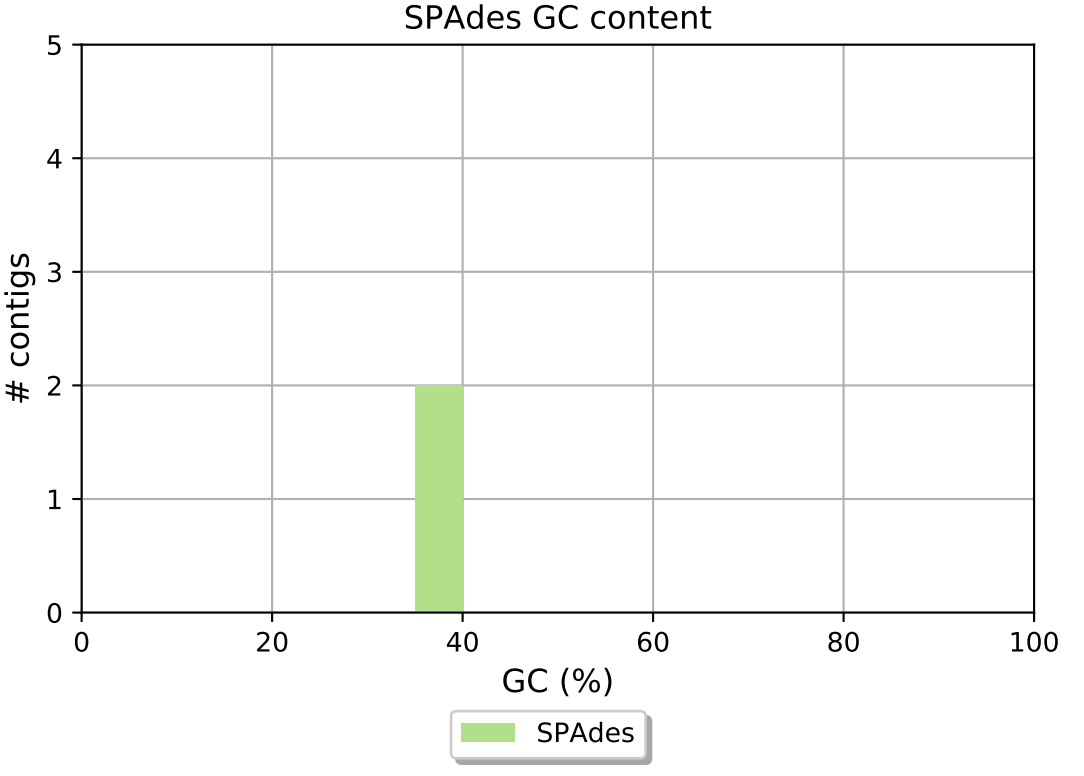

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

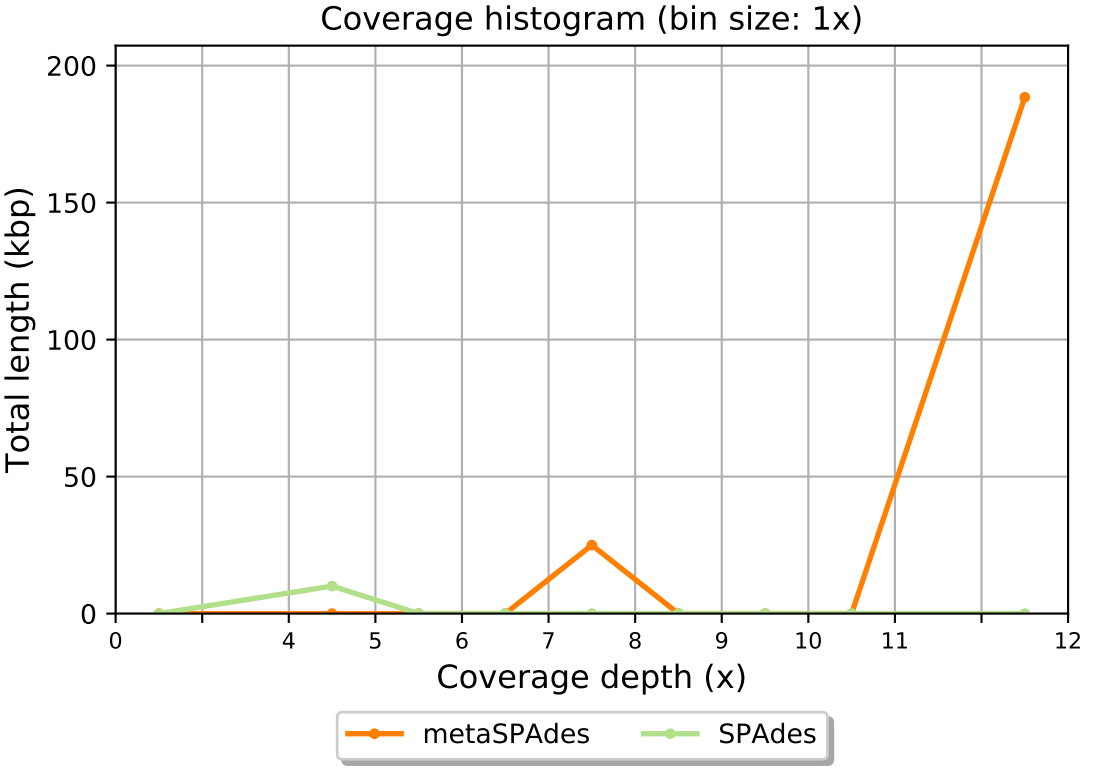

Megahit GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Megahit

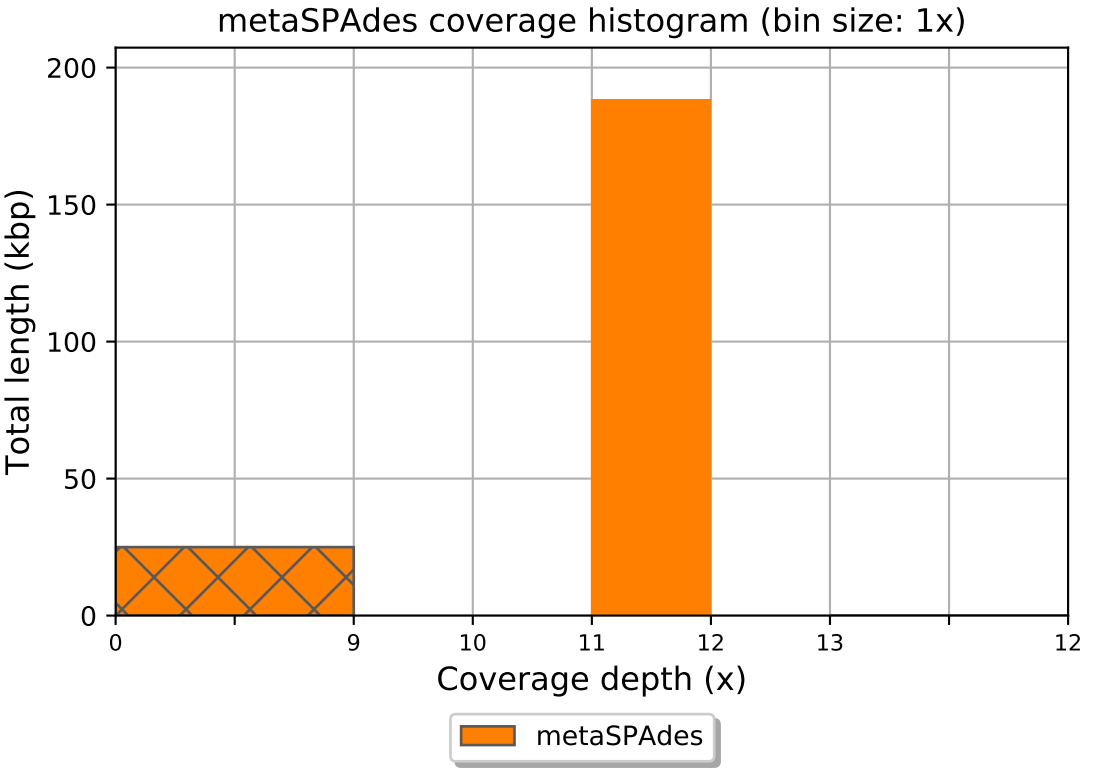

metaSPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
metaSPAdes

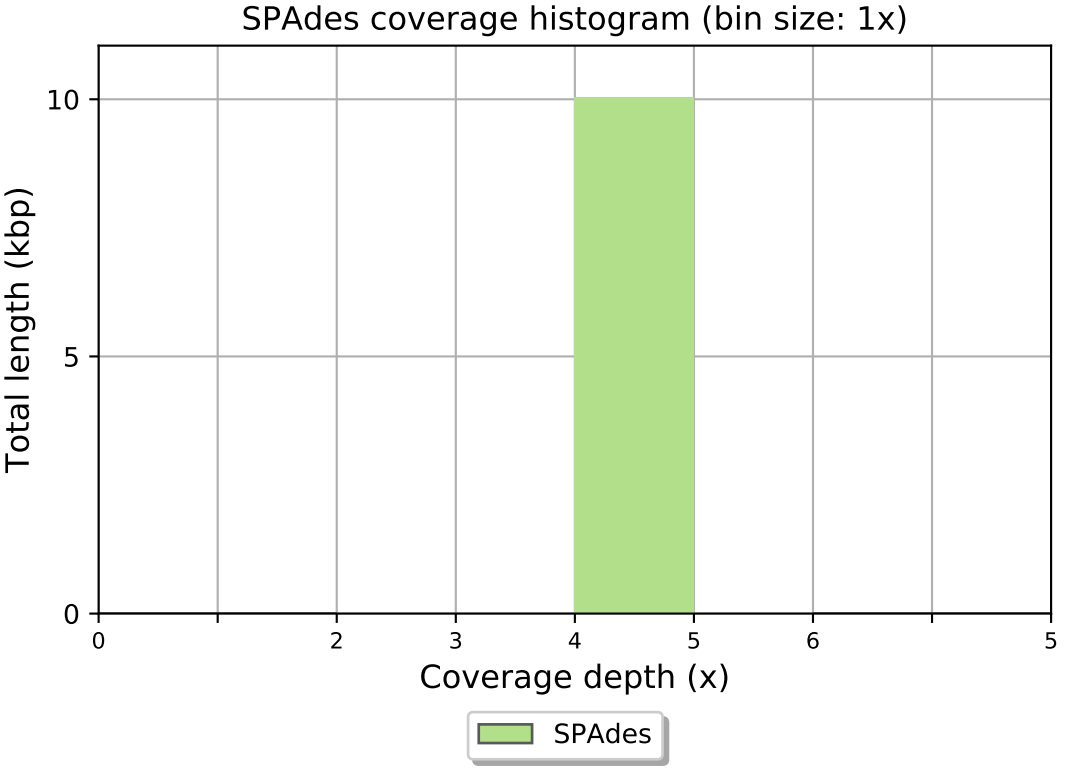

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

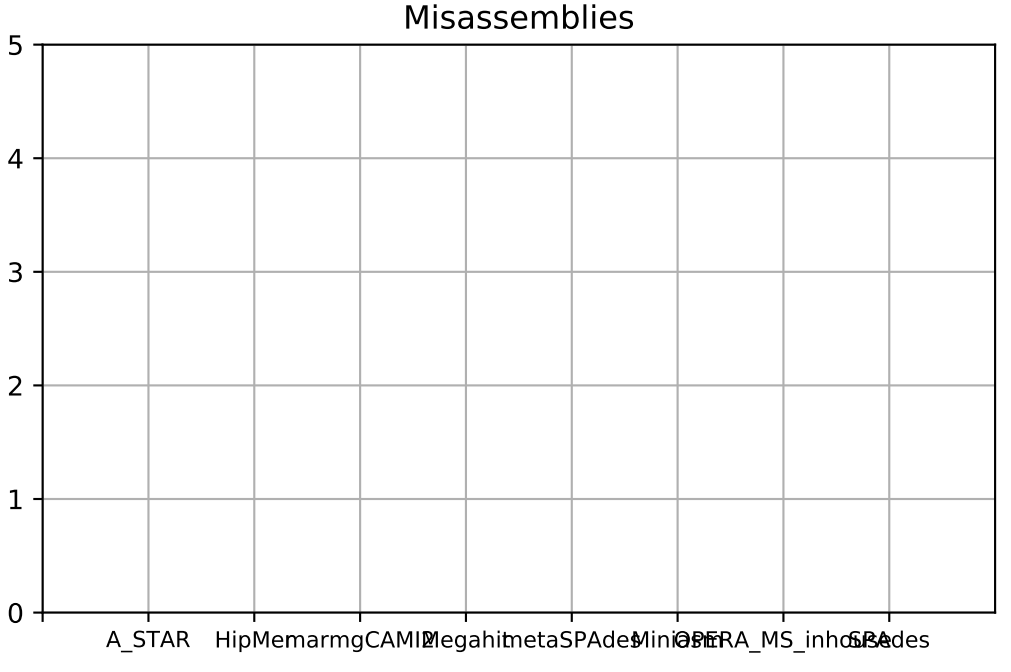

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

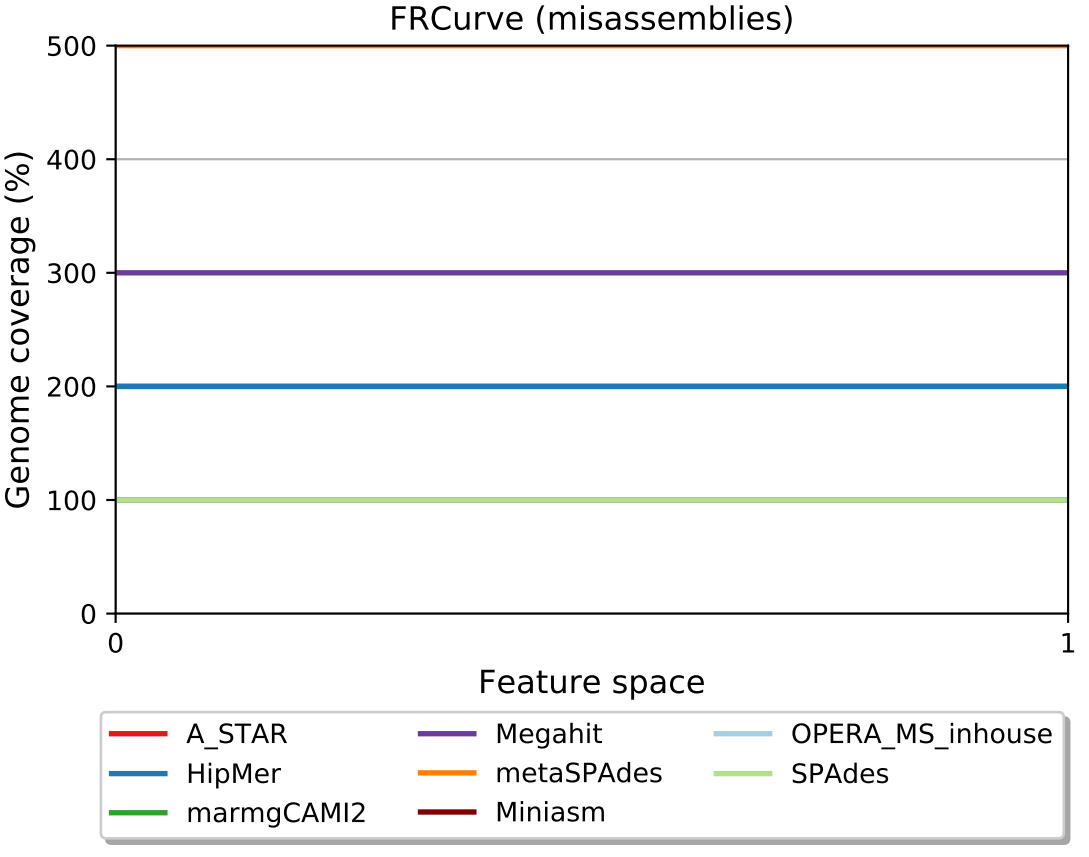

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

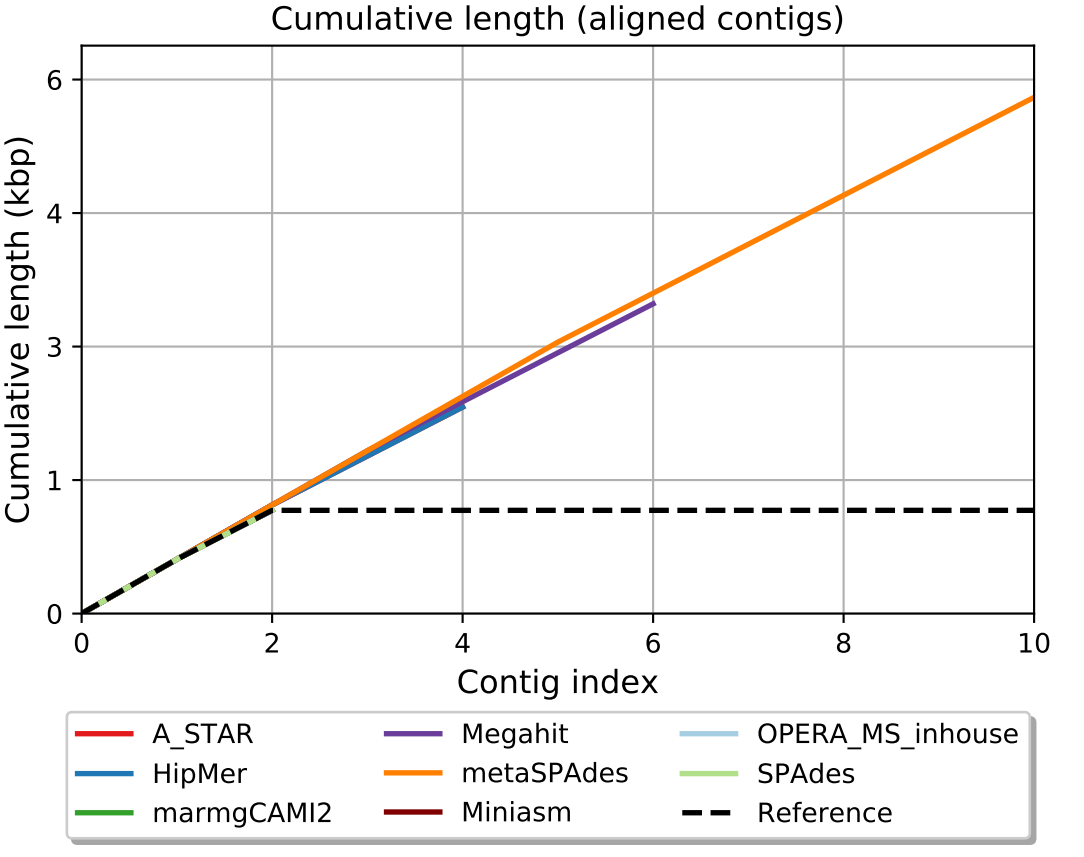

Coverage histogram (bin size: 1x)
Total length (kbp)
200
150
100
50
0
0
4
5
6
7
8
9
10
11
12
Coverage depth (x)
metaSPAdes
SPAdes

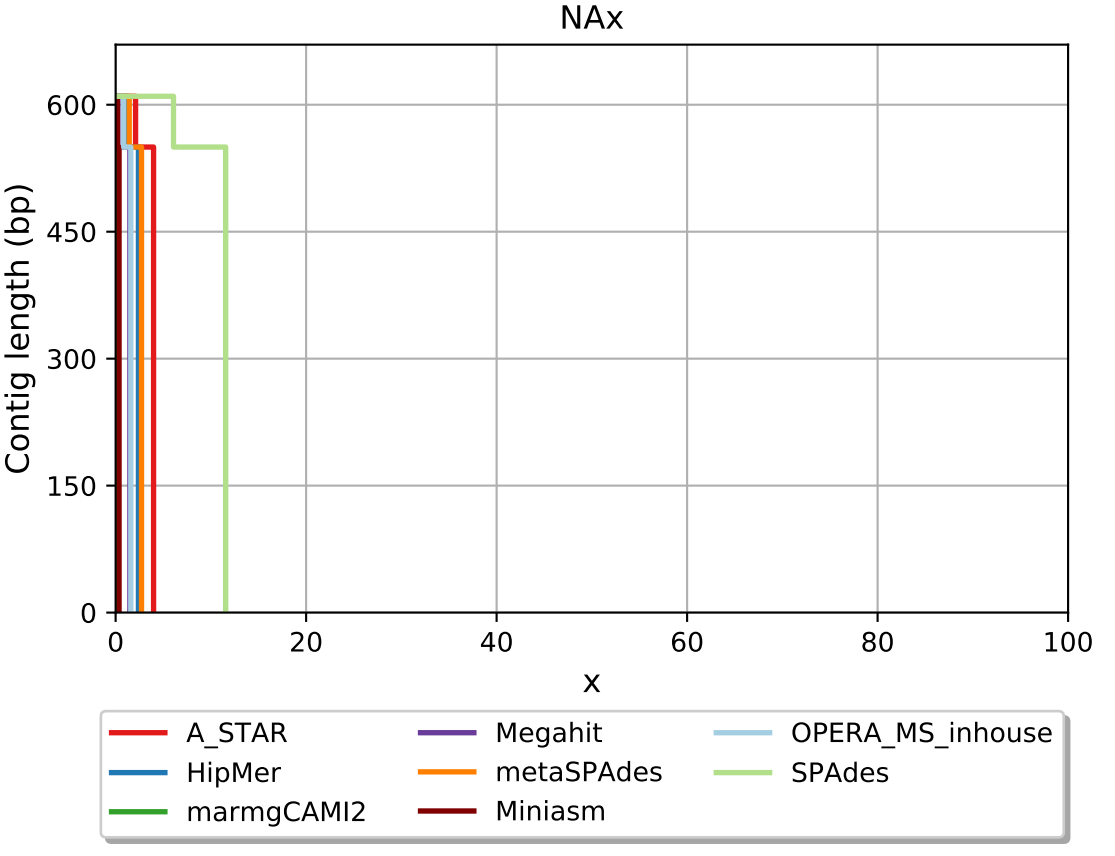

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
200
150
100
50
0
0
9
10
11
12
13
12
Coverage depth (x)
metaSPAdes

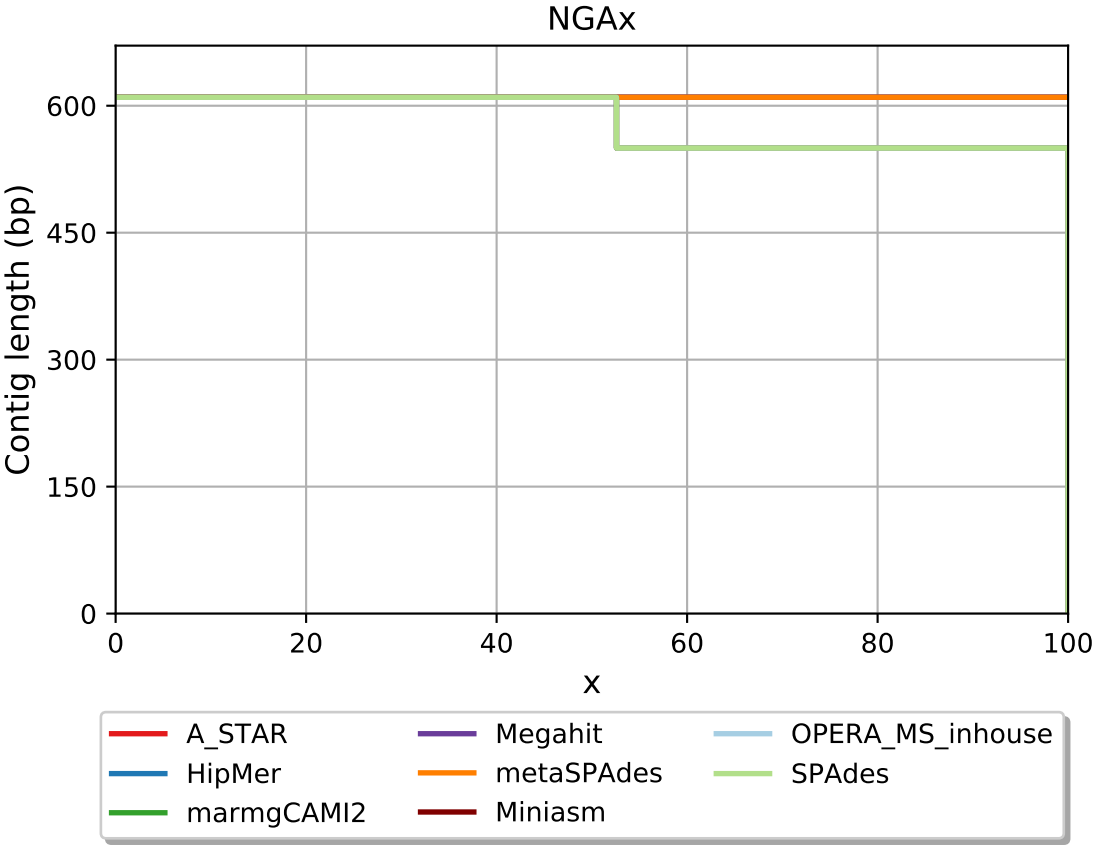

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
10
5
0
0
2
3
4
5
6
5
Coverage depth (x)
SPAdes

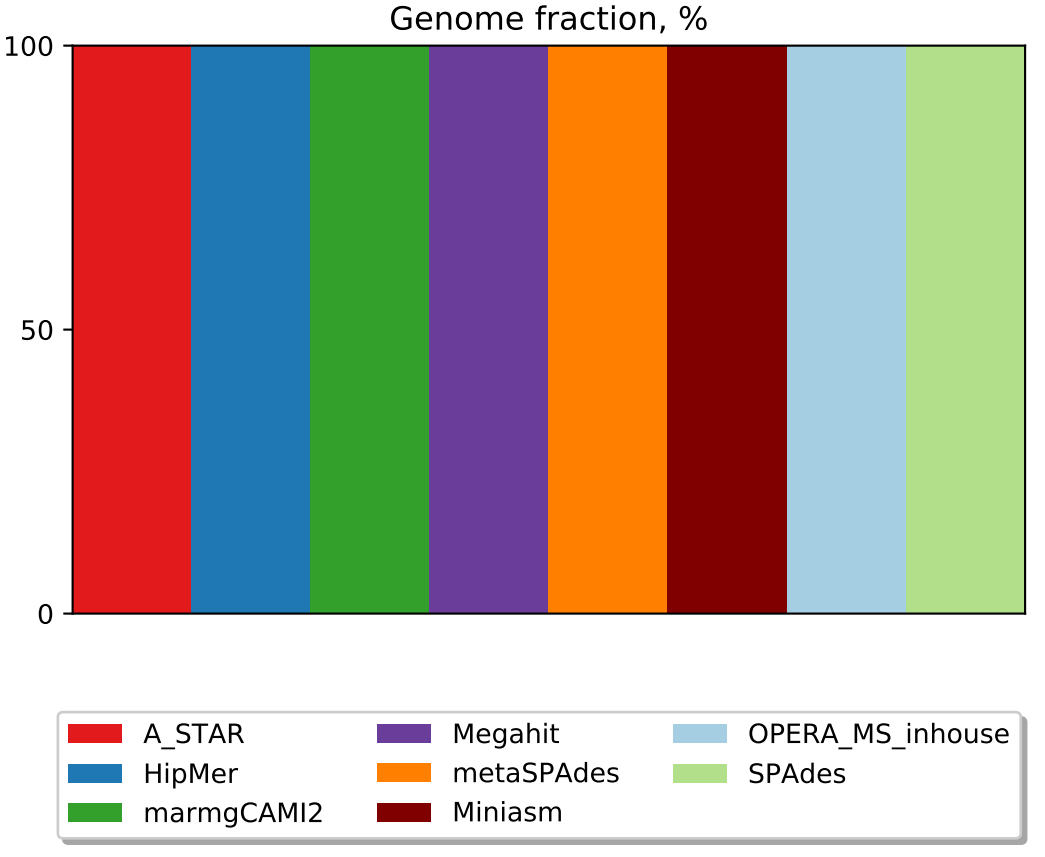

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL2
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes


FRCurve (misassemblies)
Genome coverage (%)
500
400
300
200
100
0
0
1
Feature space
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
1
3
4
6
0
2
4
6
8
10
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


NAx
Contig length (bp)
600
450
300
150
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


NGAx
Contig length (bp)
600
450
300
150
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