Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	3	2	1	3	3	3	1	1
# contigs (>= 5000 bp)	1	2	1	3	3	3	1	1
# contigs (>= 10000 bp)	1	2	1	3	3	3	1	0
# contigs (>= 25000 bp)	0	2	1	3	3	3	1	0
# contigs (>= 50000 bp)	0	2	1	2	2	3	1	0
Total length (>= 1000 bp)	18870	390831	1690869	235761	820299	377329	235228	5548
Total length (>= 5000 bp)	11458	390831	1690869	235761	820299	377329	235228	5548
Total length (>= 10000 bp)	11458	390831	1690869	235761	820299	377329	235228	0
Total length (>= 25000 bp)	0	390831	1690869	235761	820299	377329	235228	0
Total length (>= 50000 bp)	0	390831	1690869	187636	790038	377329	235228	0
# contigs	3	2	1	3	3	3	1	1
Largest contig	11458	323982	1690869	134247	395019	250003	235228	5548
Total length	18870	390831	1690869	235761	820299	377329	235228	5548
Reference length	730	730	730	730	730	730	730	730
GC (%)	36.33	33.54	33.59	33.37	33.53	33.70	33.73	36.59
Reference GC (%)	49.73	49.73	49.73	49.73	49.73	49.73	49.73	49.73
N50	11458	323982	1690869	134247	395019	250003	235228	5548
NG50	11458	323982	1690869	134247	395019	250003	235228	5548
N75	3706	323982	1690869	53389	395019	63663	235228	5548
NG75	11458	323982	1690869	134247	395019	250003	235228	5548
L50	1	1	1	1	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	2	1	1	2	2	2	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	2	0	0
# unaligned contigs	0 + 3 part	0 + 2 part	0 + 1 part	0 + 3 part	0 + 3 part	0 + 3 part	0 + 1 part	0 + 1 part
Unaligned length	12771	389368	1690139	233571	818109	376077	234498	4818
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	8.355	2.004	1.000	3.000	3.000	1.715	1.000	1.000
# N's per 100 kbp	23672.50	0.77	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2465.75	0.00	0.00	0.00	0.00	0.00	136.99	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	730	730	730	730	730	730	730	730
Total aligned length	1632	1460	730	2190	2190	1252	730	730
NGA50	730	730	730	730	730	730	730	730
NGA75	730	730	730	730	730	730	730	730
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

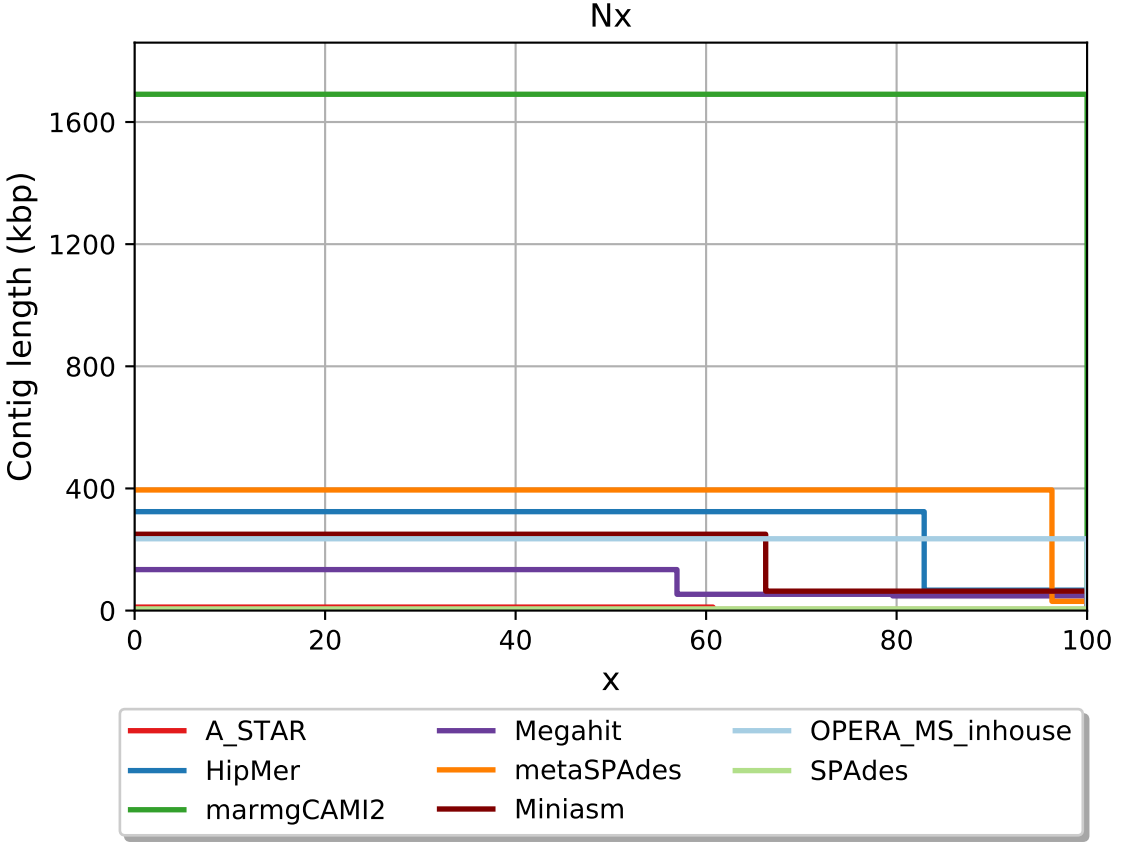
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	3	2	1	3	3	1	1	1
# possible misassemblies	3	4	2	6	6	2	2	2
# 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	2	0	0
# mismatches	18	0	0	0	0	0	1	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

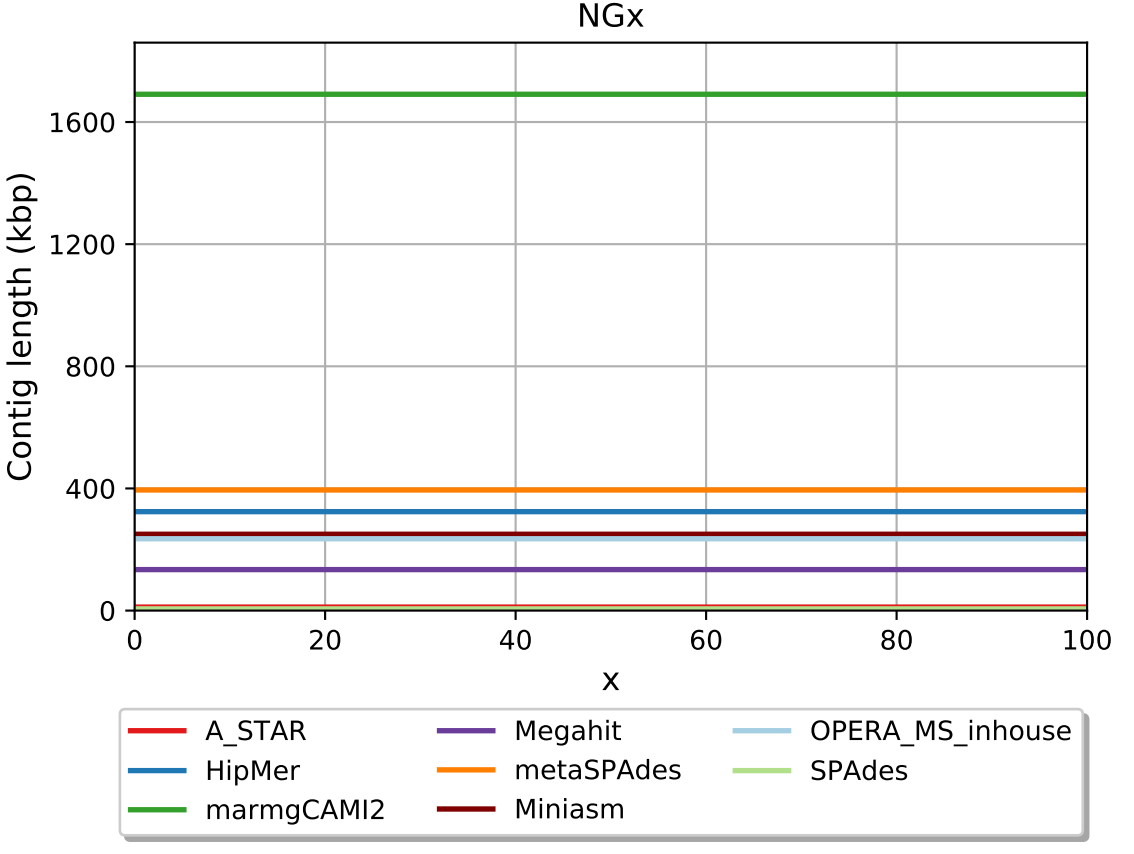
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

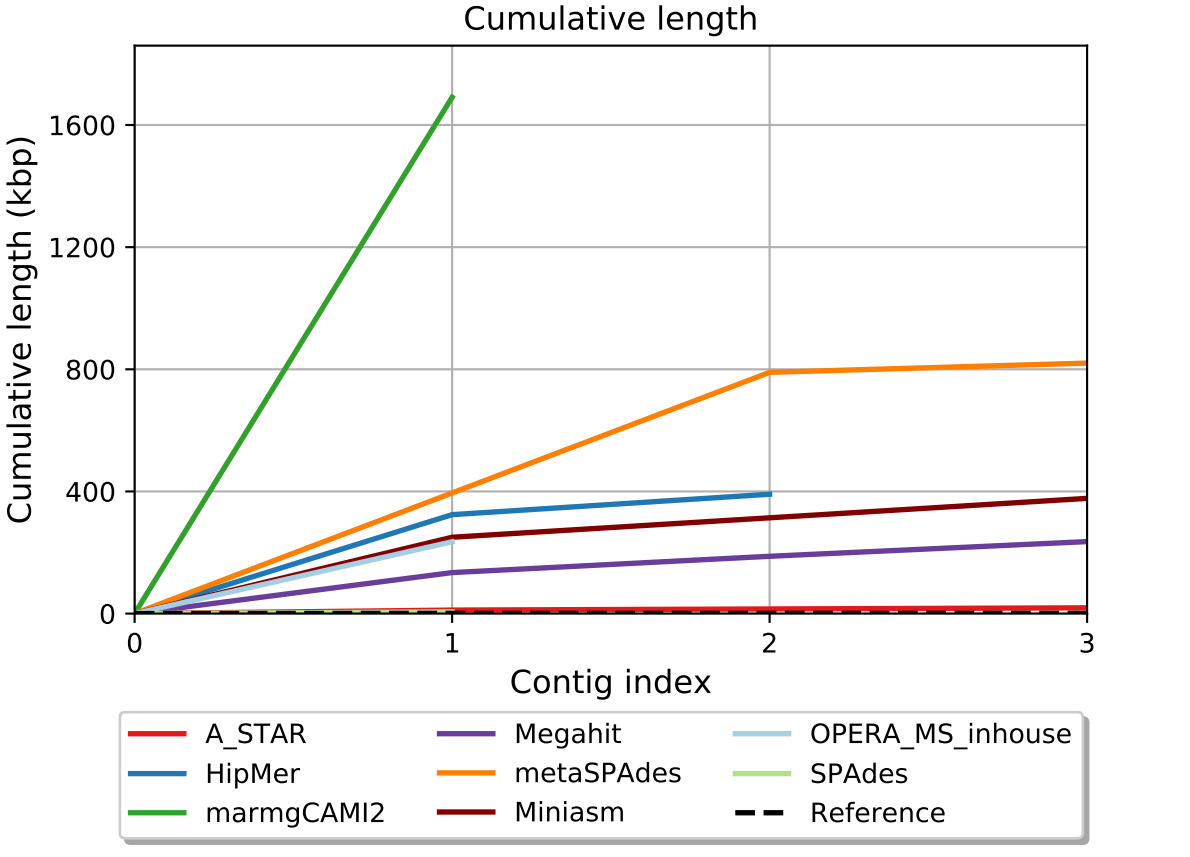
Unaligned report

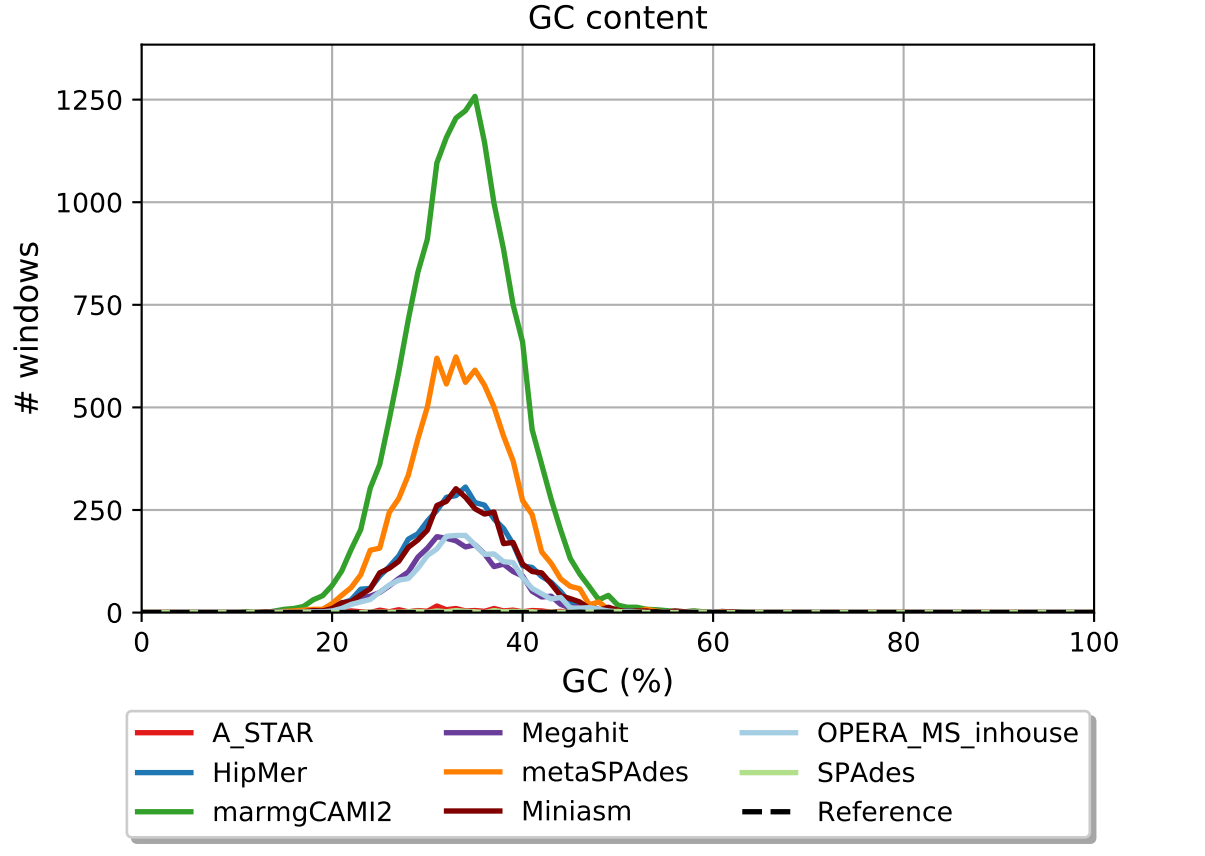
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	3	2	1	3	3	3	1	1
Partially unaligned length	12771	389368	1690139	233571	818109	376077	234498	4818
# N's	4467	3	0	0	0	0	0	0

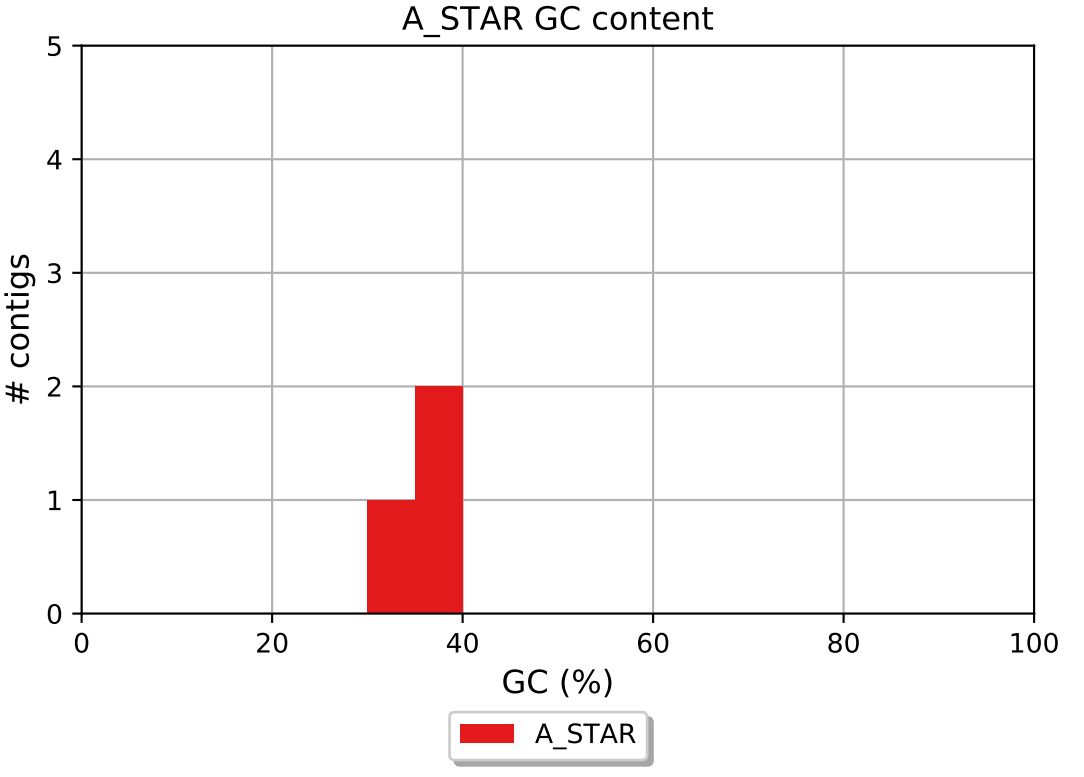
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

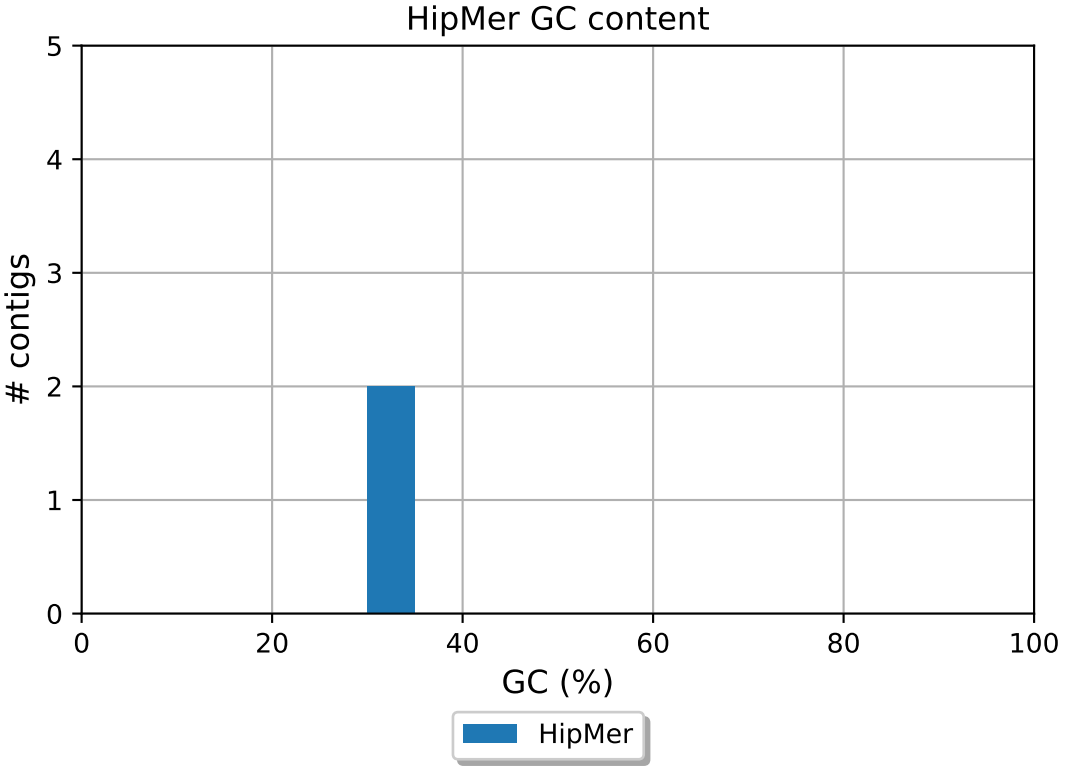

Nx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

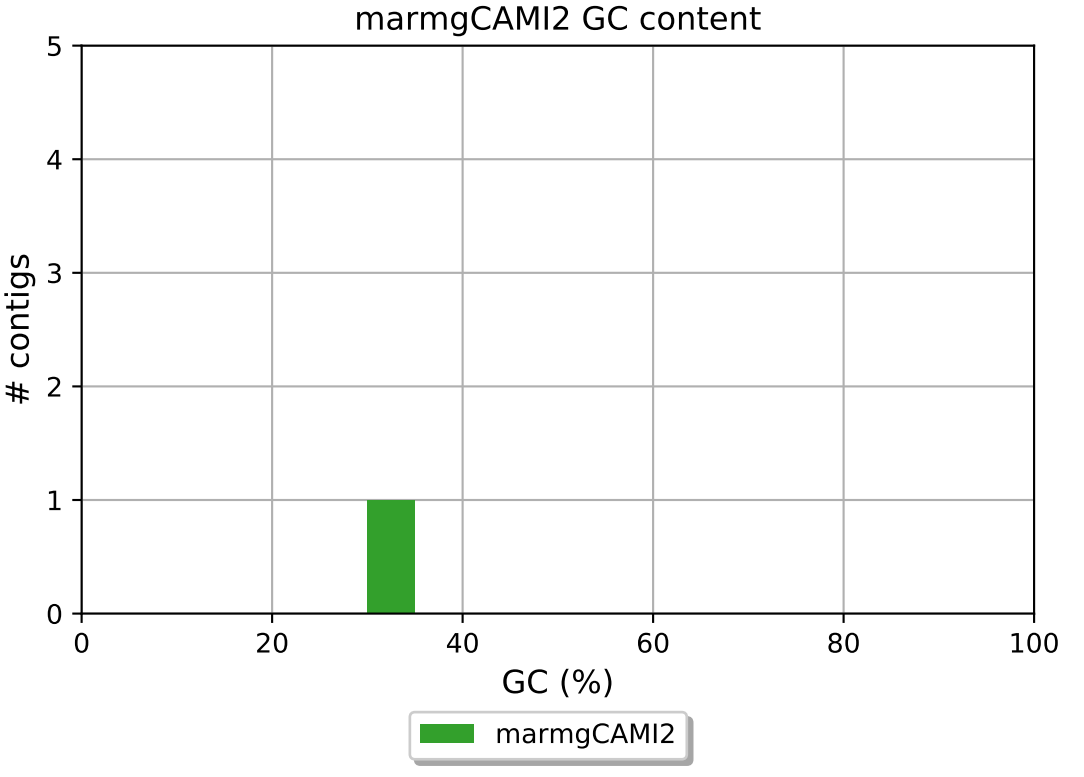

NGx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

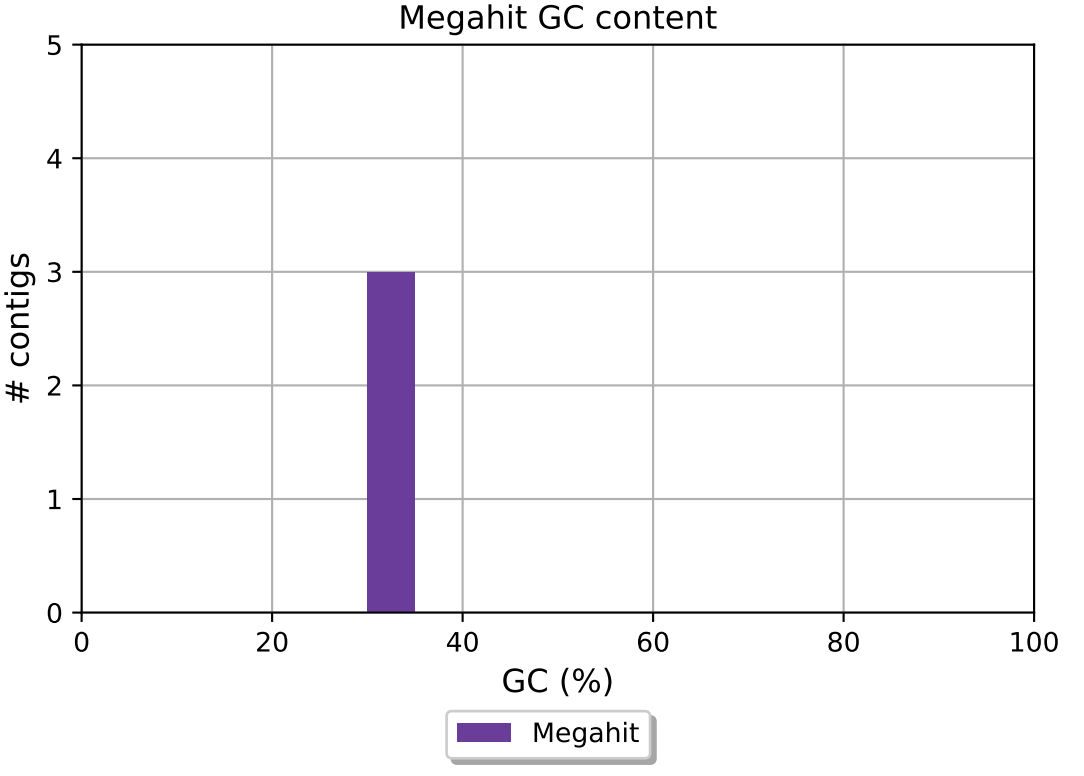

Cumulative length
Cumulative length (kbp)
1600
1200
800
400
0
0
1
2
3
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

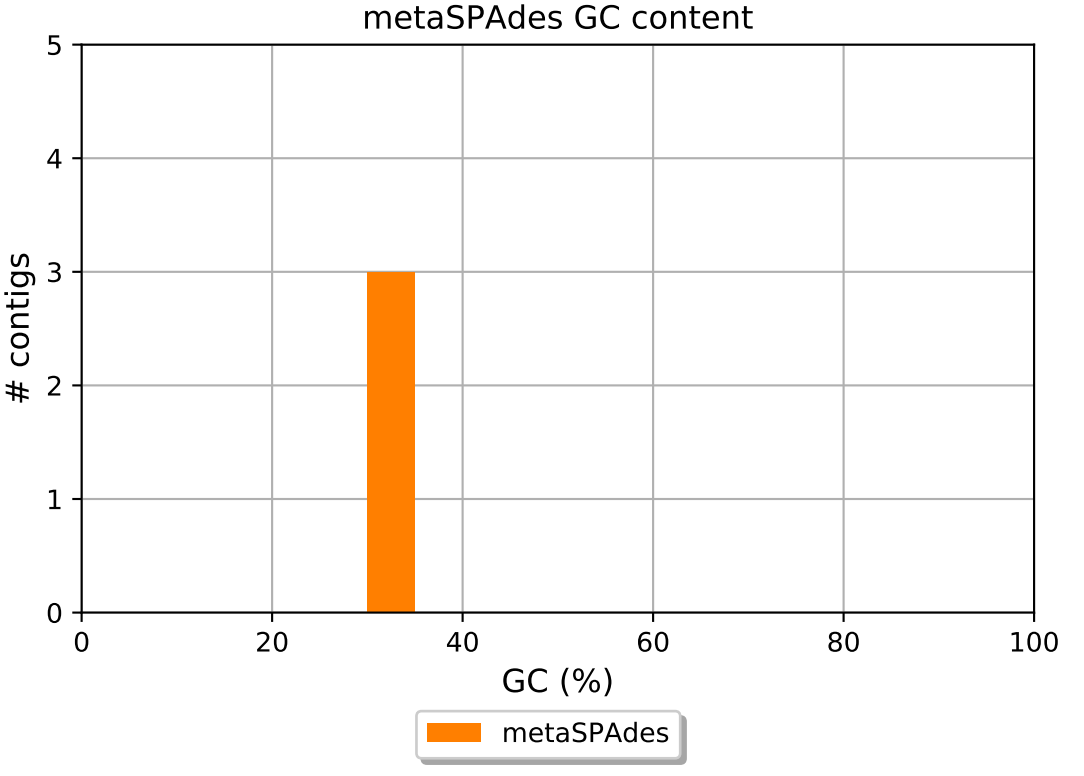

GC content
windows
GC (%)
0
250
500
750
1000
1250
0
20
40
60
80
100
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

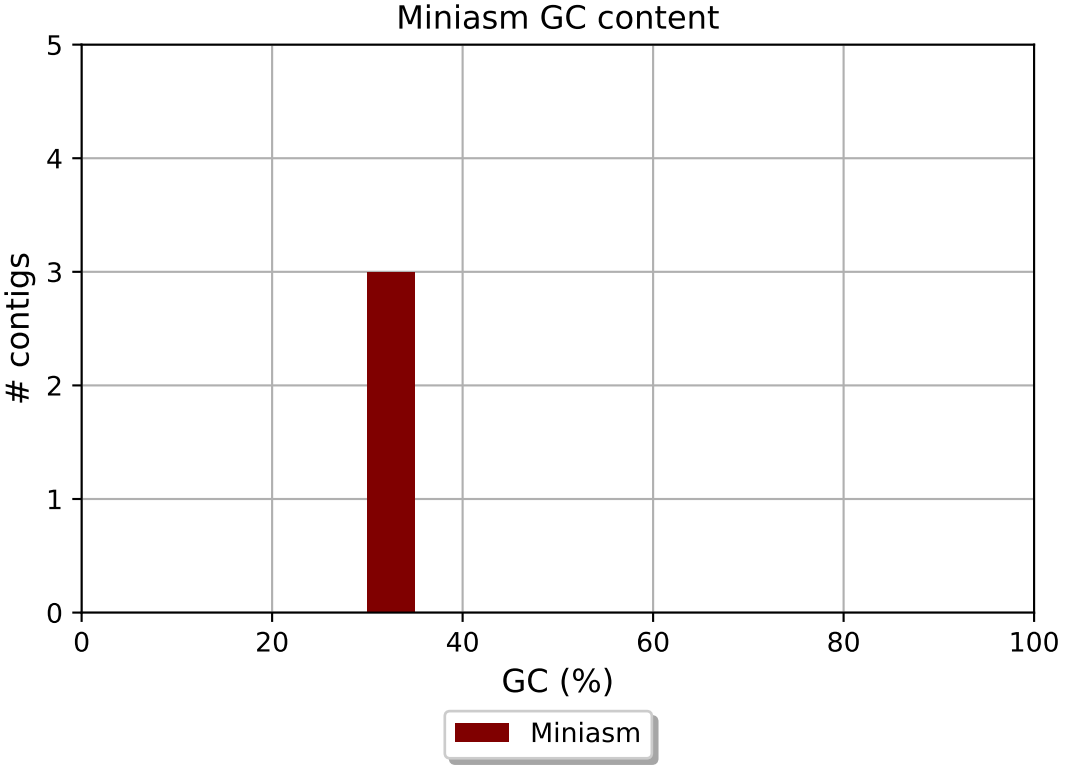

A_STAR GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
A_STAR

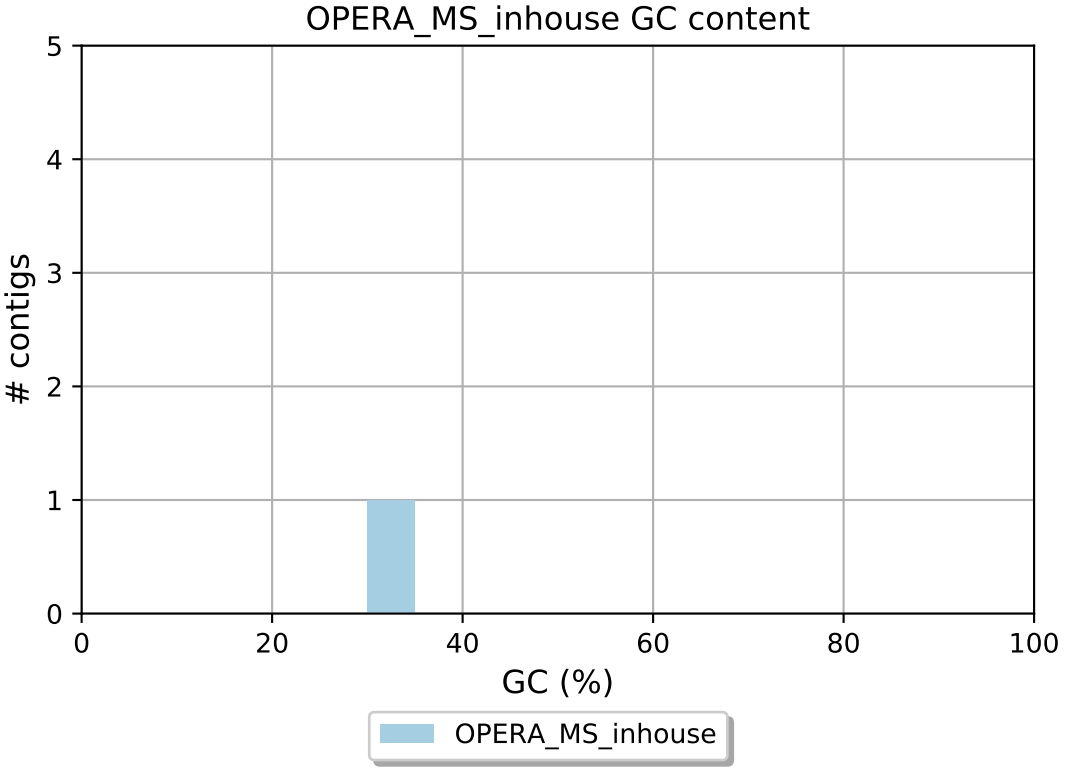

HipMer GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
HipMer

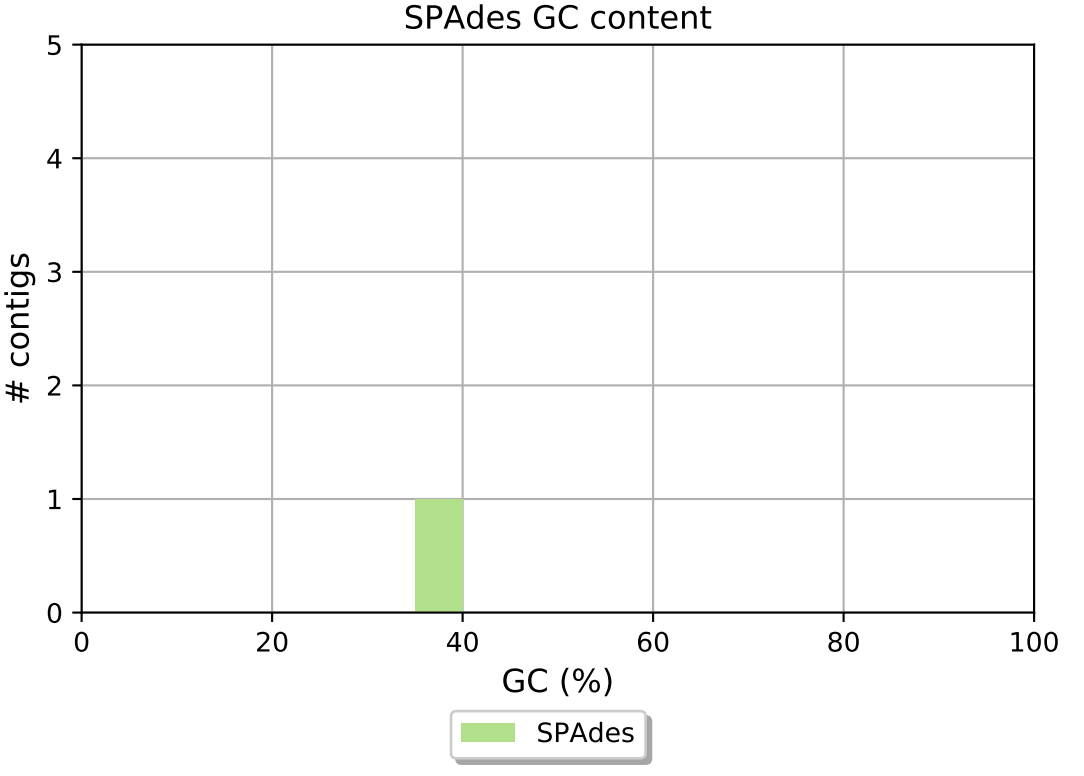

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

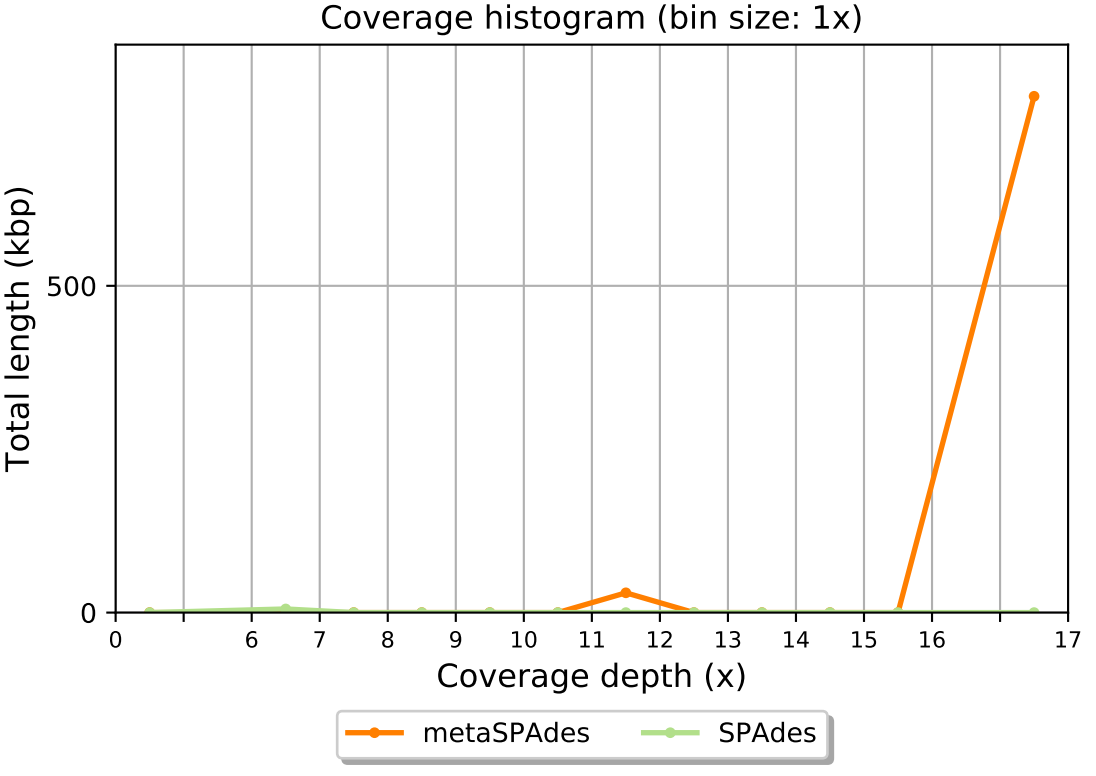

Megahit GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Megahit

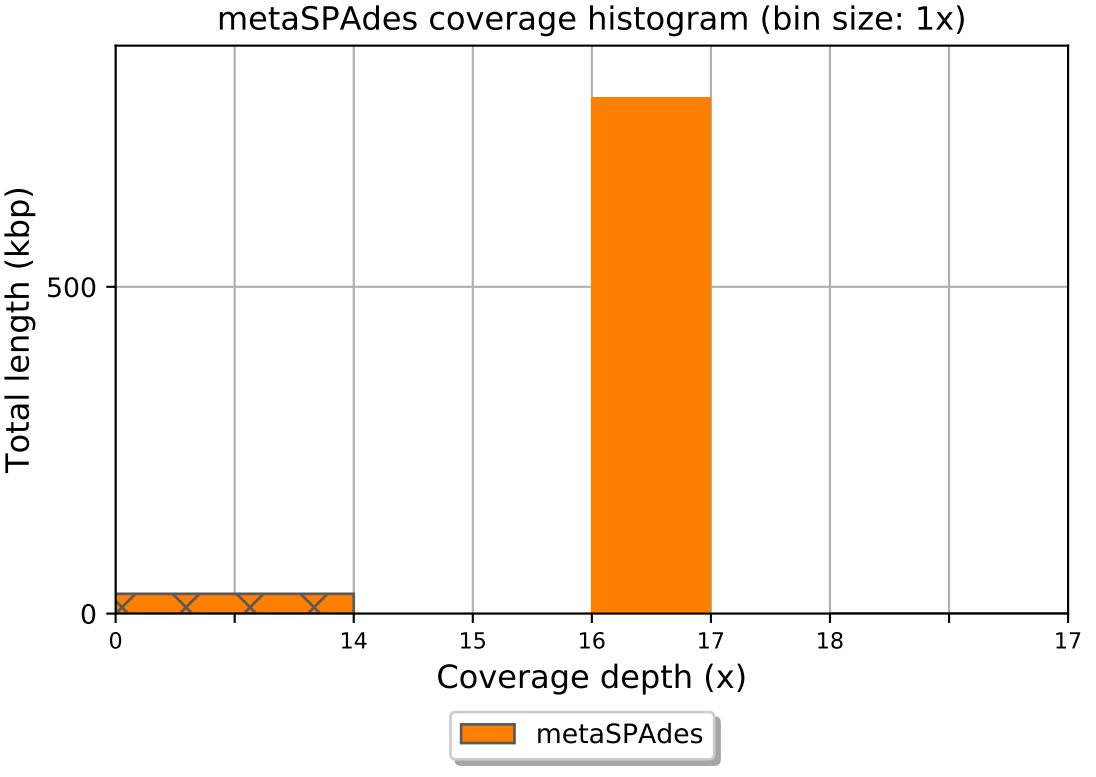

metaSPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
metaSPAdes

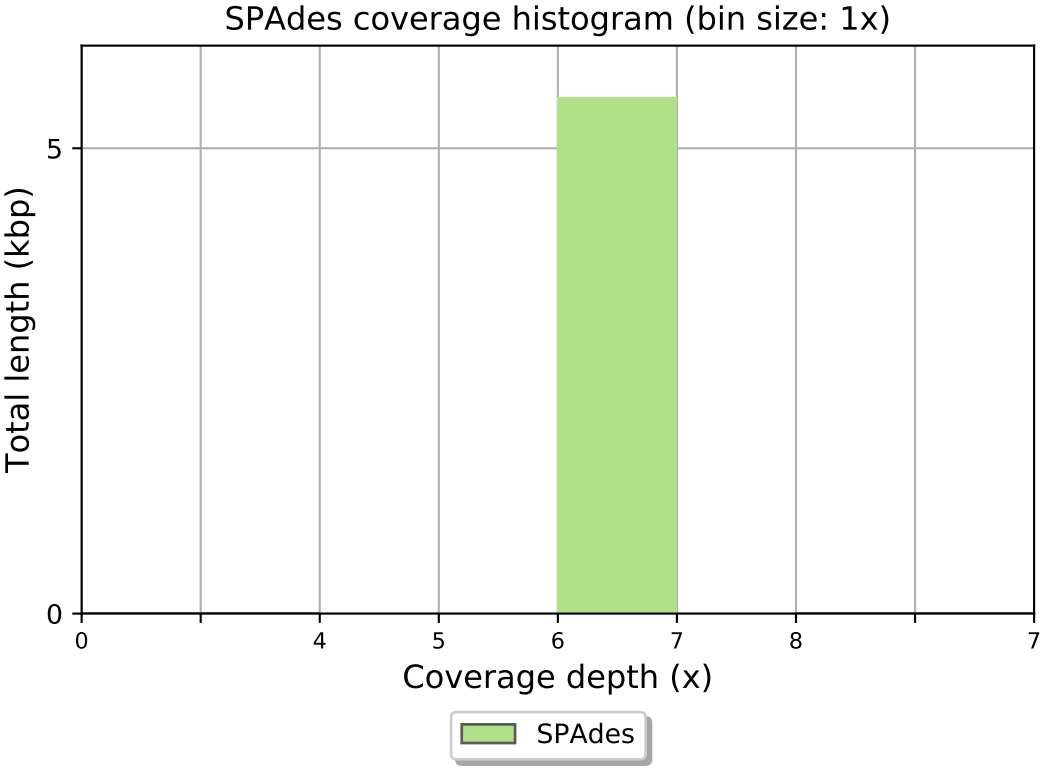

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

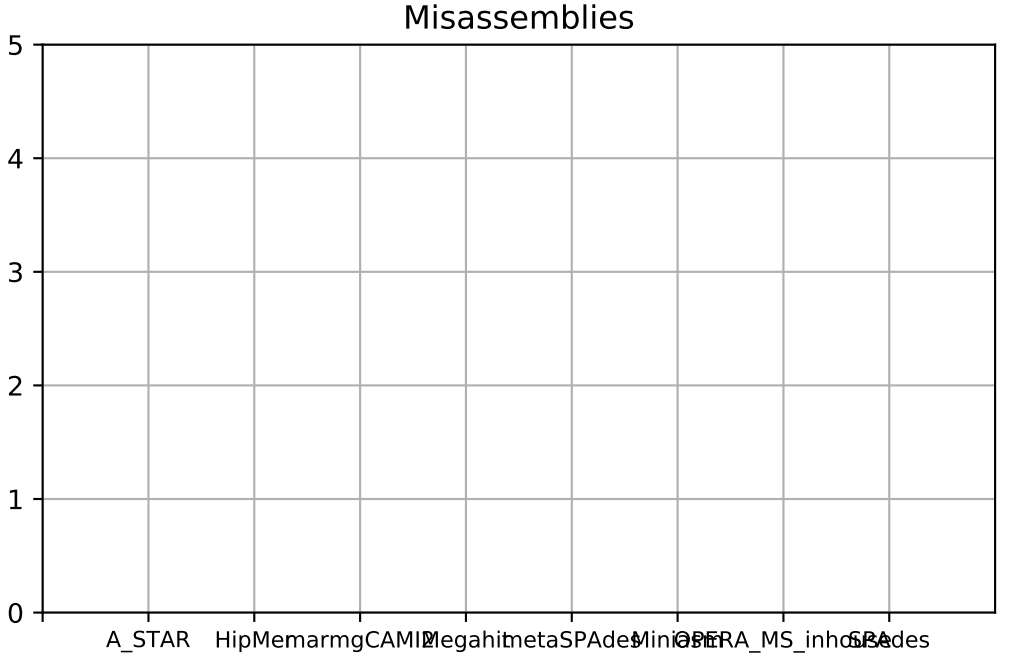

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

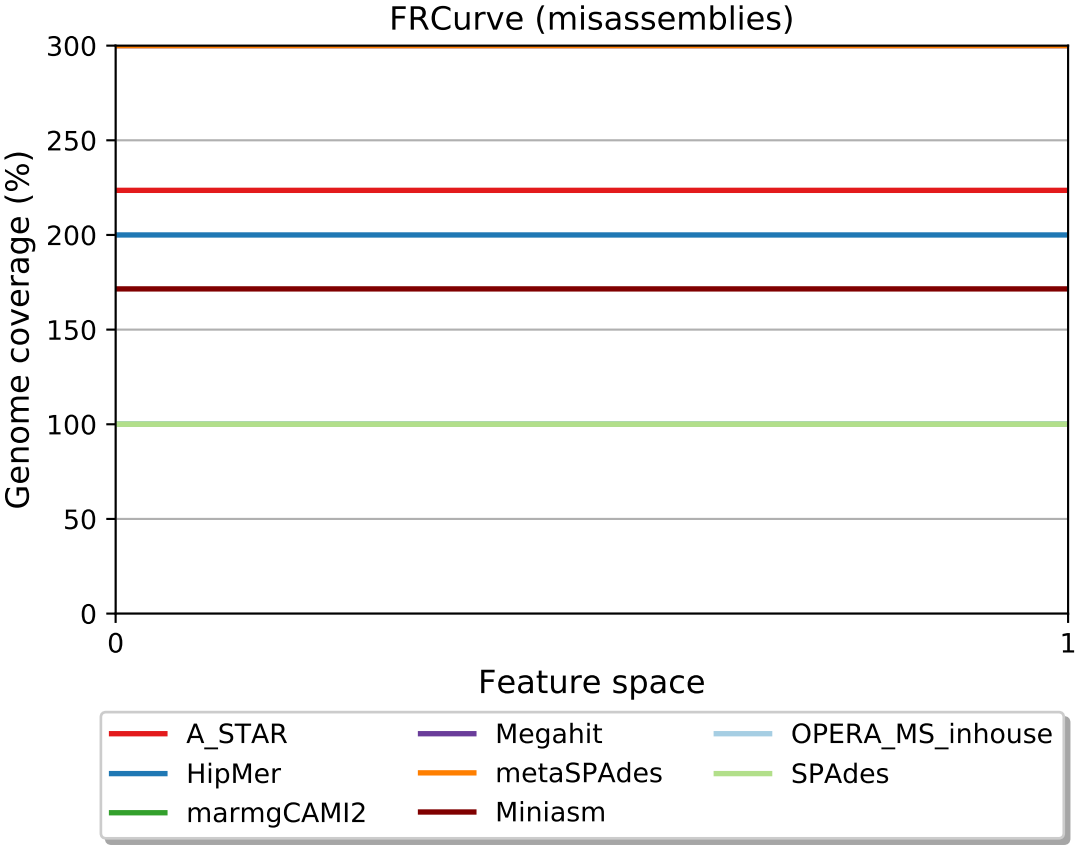

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

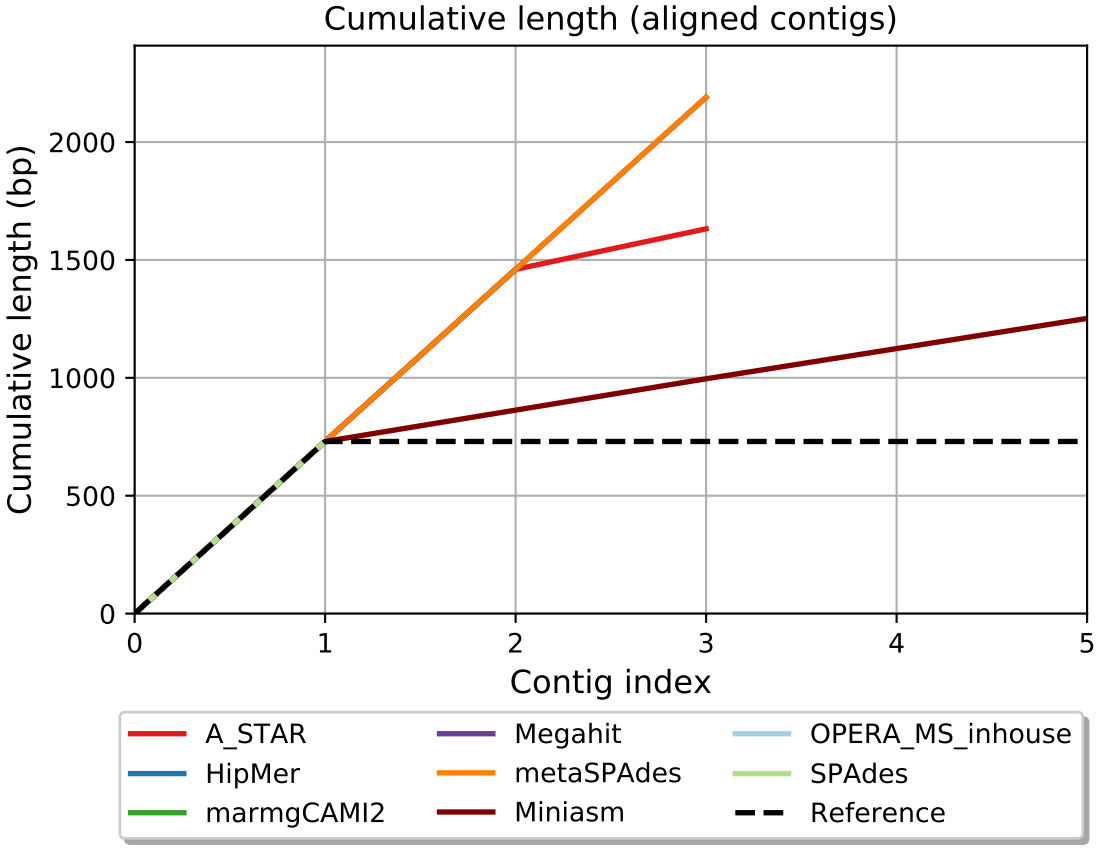

Coverage histogram (bin size: 1x)
Total length (kbp)
500
0
0
6
7
8
9
10
11
12
13
14
15
16
17
Coverage depth (x)
metaSPAdes
SPAdes

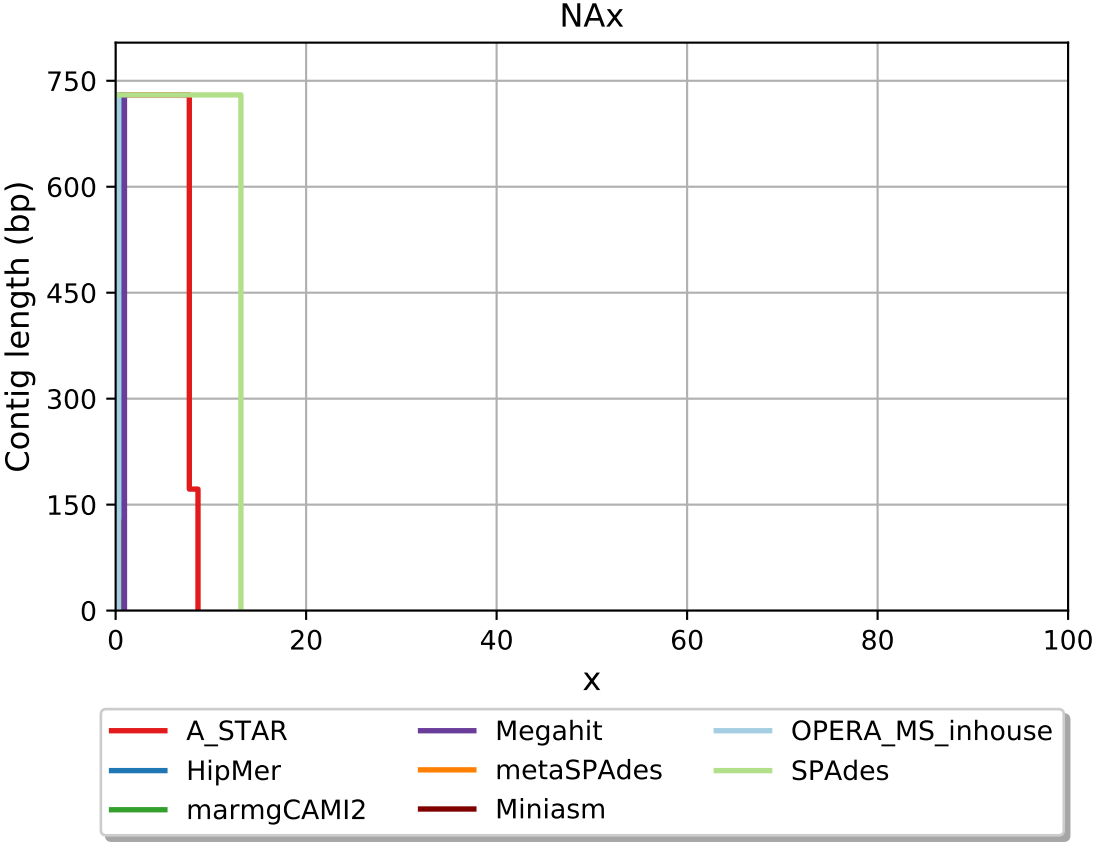

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
500
0
0
14
15
16
17
18
17
Coverage depth (x)
metaSPAdes

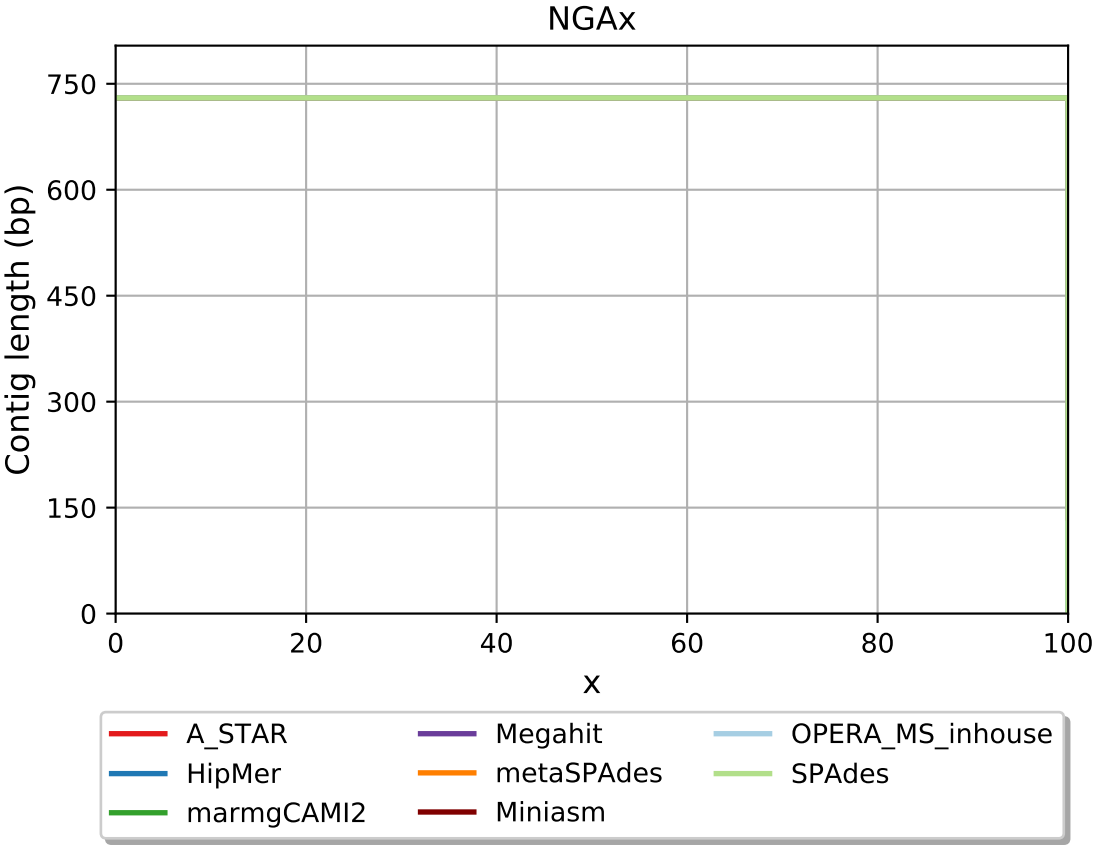

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
5
0
0
4
5
6
7
8
7
Coverage depth (x)
SPAdes

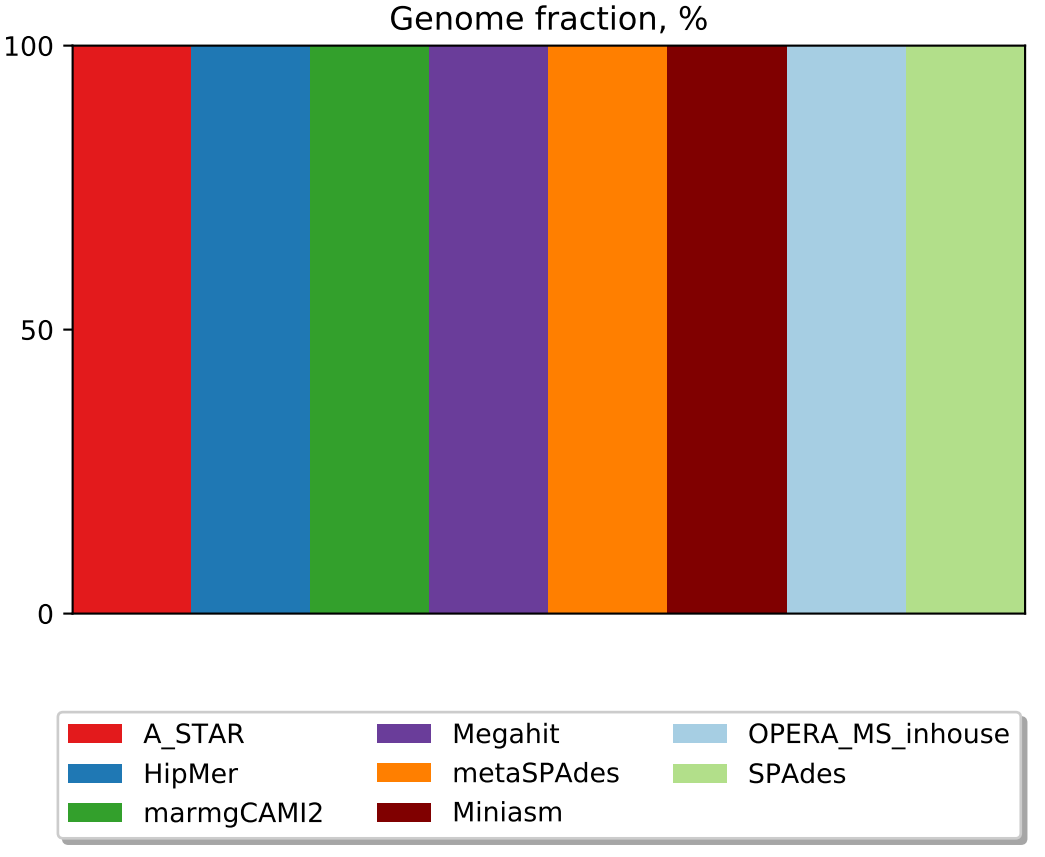

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL2
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes


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 (bp)
2000
1500
1000
500
0
0
1
2
3
4
5
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


NAx
Contig length (bp)
750
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)
750
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