Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	10	9	1	14	11	3	4	4
# contigs (>= 5000 bp)	10	8	1	14	11	3	4	4
# contigs (>= 10000 bp)	6	8	1	13	11	3	4	4
# contigs (>= 25000 bp)	4	7	1	8	11	3	4	0
# contigs (>= 50000 bp)	4	5	1	6	7	3	4	0
Total length (>= 1000 bp)	315960	807750	4684311	1021397	894208	396596	371708	83540
Total length (>= 5000 bp)	315960	806333	4684311	1021397	894208	396596	371708	83540
Total length (>= 10000 bp)	292442	806333	4684311	1013935	894208	396596	371708	83540
Total length (>= 25000 bp)	271428	782639	4684311	926879	894208	396596	371708	0
Total length (>= 50000 bp)	271428	715096	4684311	834489	743381	396596	371708	0
# contigs	10	10	1	15	11	3	4	5
Largest contig	74413	333744	4684311	231064	132475	229334	201639	24754
Total length	315960	808566	4684311	1022080	894208	396596	371708	84053
Reference length	10146	10146	10146	10146	10146	10146	10146	10146
GC (%)	44.63	44.21	44.13	44.09	44.32	44.03	43.66	45.10
Reference GC (%)	49.62	49.62	49.62	49.62	49.62	49.62	49.62	49.62
N50	61301	139945	4684311	122131	124560	229334	201639	23209
NG50	74413	333744	4684311	231064	132475	229334	201639	24754
N75	61301	67441	4684311	76024	78851	111769	52360	19019
NG75	74413	333744	4684311	231064	132475	229334	201639	24754
L50	3	2	1	3	4	1	1	2
LG50	1	1	1	1	1	1	1	1
L75	4	4	1	5	6	2	3	3
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	2	3	1	1	0
# unaligned contigs	0 + 10 part	0 + 8 part	0 + 1 part	0 + 14 part	0 + 11 part	0 + 3 part	0 + 4 part	0 + 4 part
Unaligned length	306978	788696	4674165	996138	863775	392044	361753	73392
Genome fraction (%)	43.249	99.704	100.000	100.000	100.000	42.480	94.372	100.000
Duplication ratio	2.047	1.964	1.000	2.557	3.000	1.056	1.040	1.051
# N's per 100 kbp	65.20	6.18	0.00	0.00	11.18	0.00	0.00	0.00
# mismatches per 100 kbp	227.89	0.00	0.00	995.47	19.71	23.20	229.77	59.14
# indels per 100 kbp	0.00	9.89	0.00	108.42	29.57	0.00	0.00	19.71
Largest alignment	929	3088	4153	3614	4153	3148	3148	4155
Total aligned length	8776	19827	10146	25942	30433	4552	9957	10523
NGA50	739	2247	3148	3148	4152	-	2247	3148
NGA75	598	2168	2247	3148	4152	-	1086	2247
LGA50	6	2	2	2	2	-	2	2
LGA75	10	4	3	3	2	-	4	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

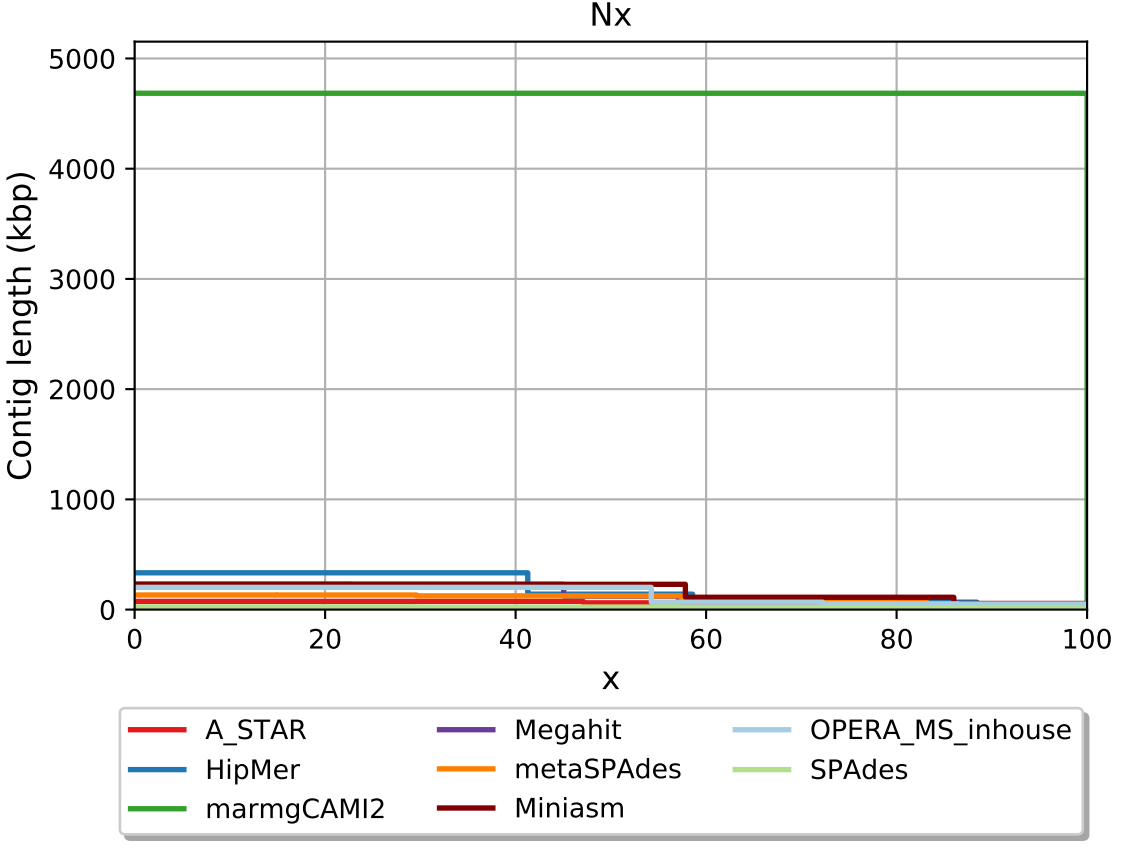
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	8	6	0	12	8	2	3	4
# possible misassemblies	10	9	0	16	12	4	5	8
# 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	2	3	1	1	0
# mismatches	10	0	0	101	2	1	22	6
# indels	0	1	0	11	3	0	0	2
# indels (<= 5 bp)	0	0	0	9	1	0	0	2
# indels (> 5 bp)	0	1	0	2	2	0	0	0
Indels length	0	60	0	159	245	0	0	2

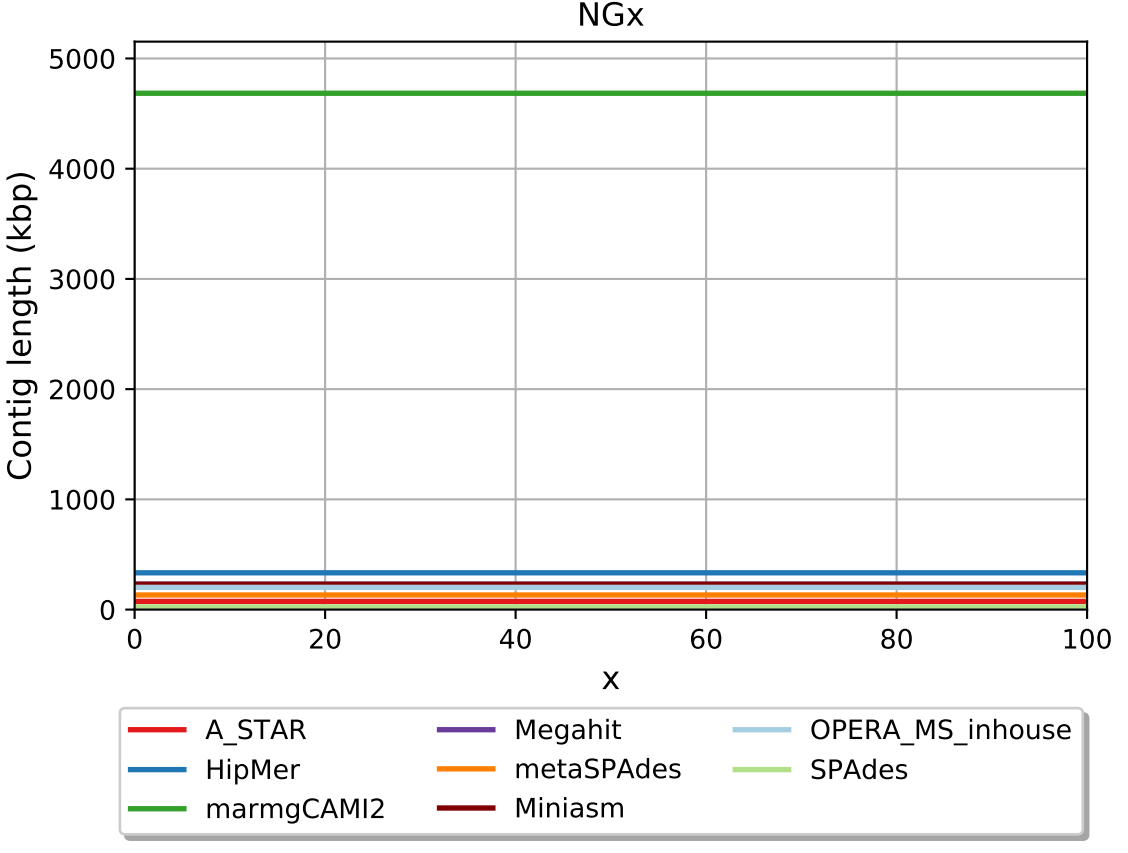
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

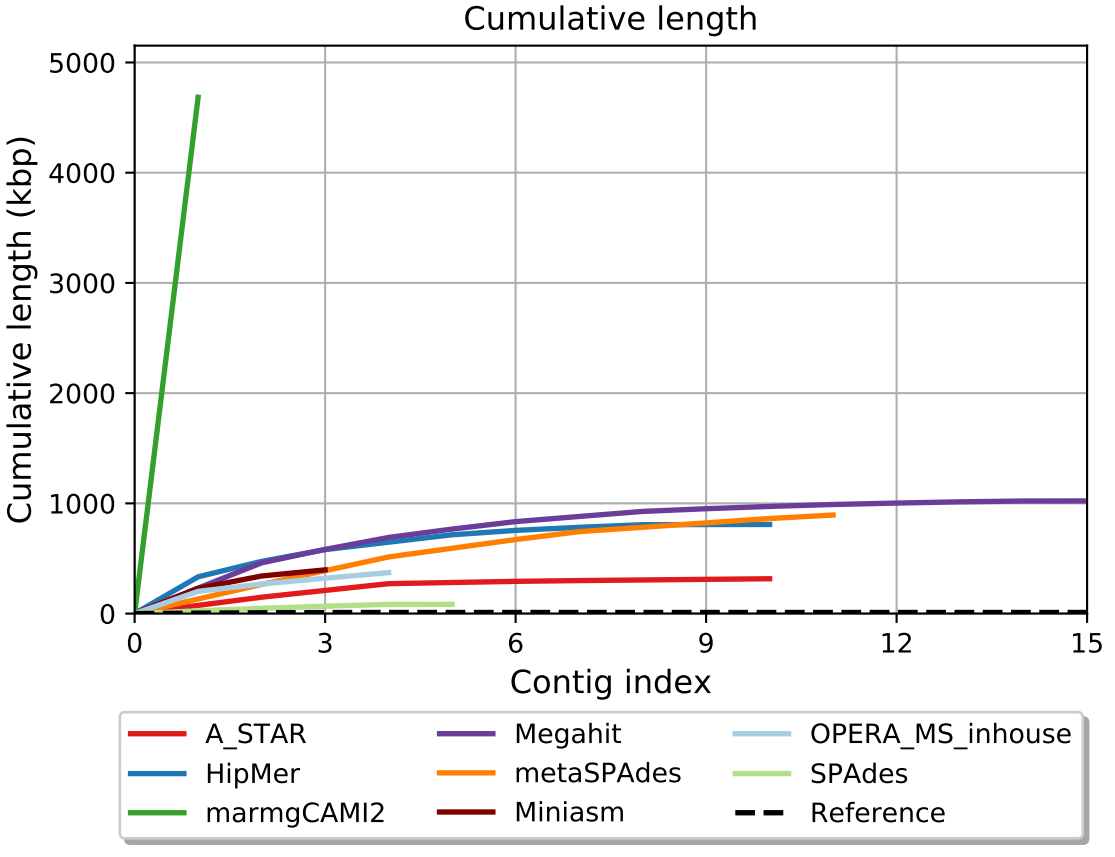
Unaligned report

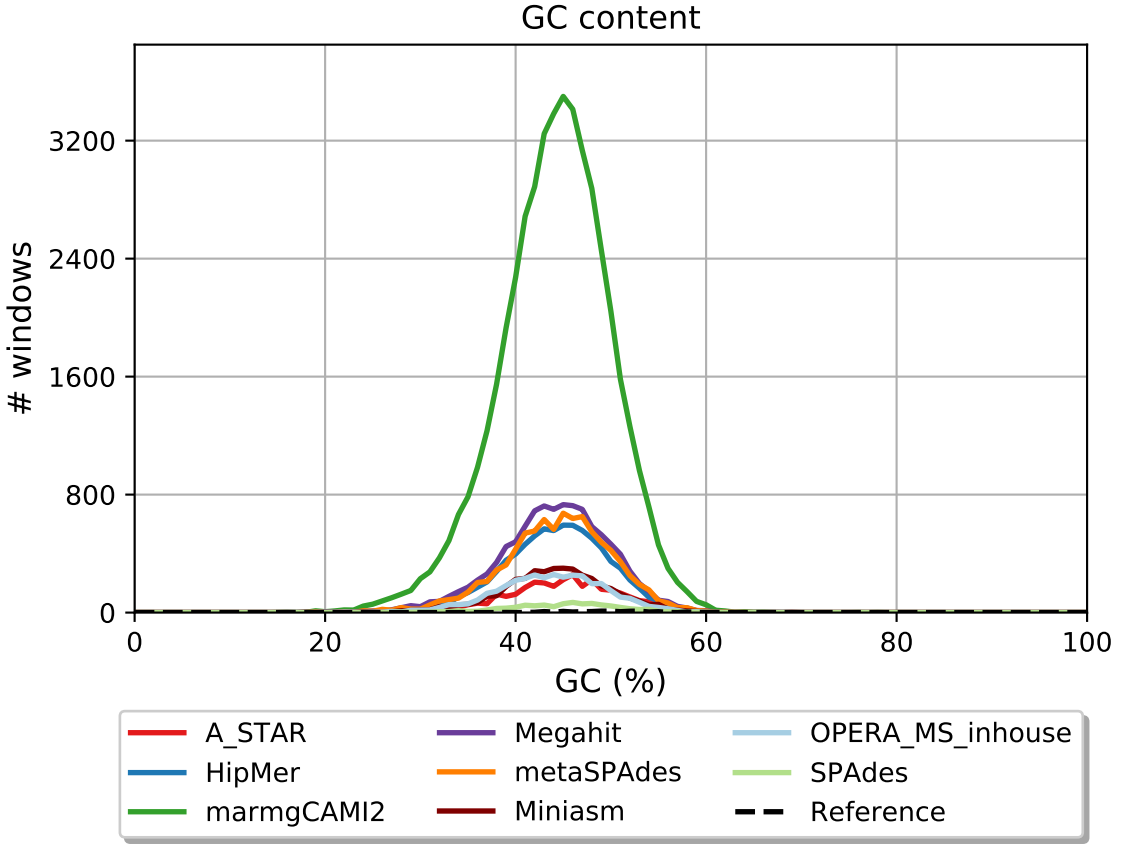
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	10	8	1	14	11	3	4	4
Partially unaligned length	306978	788696	4674165	996138	863775	392044	361753	73392
# N's	206	50	0	0	100	0	0	0

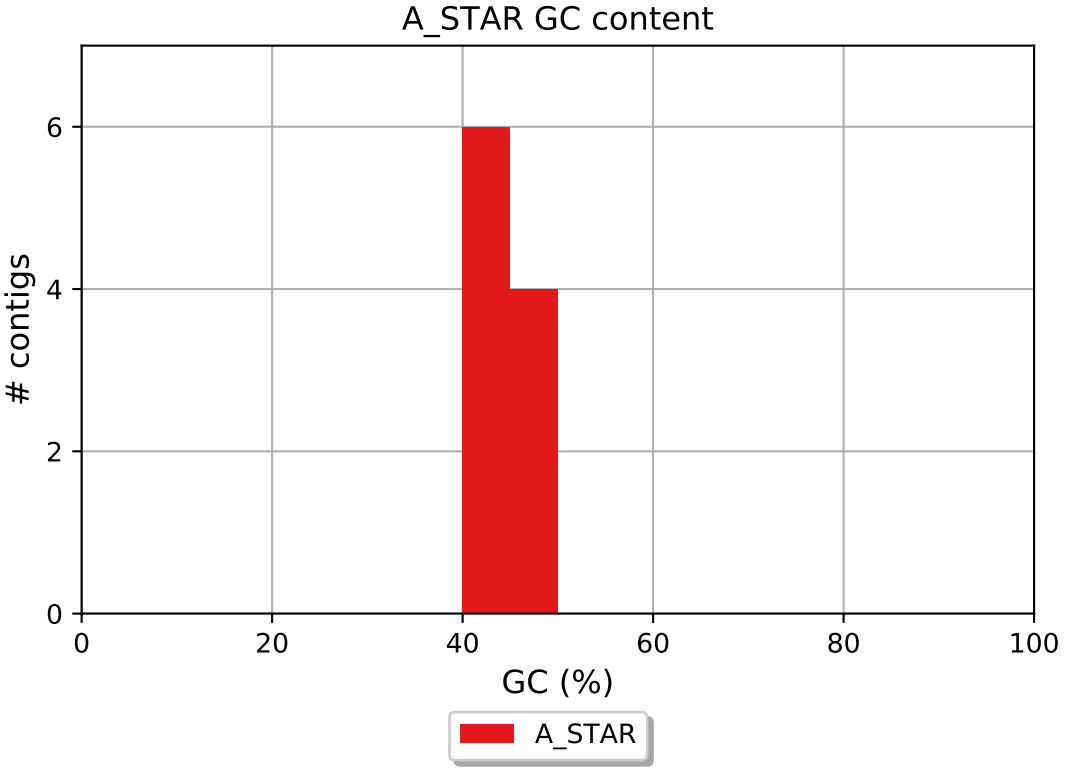
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

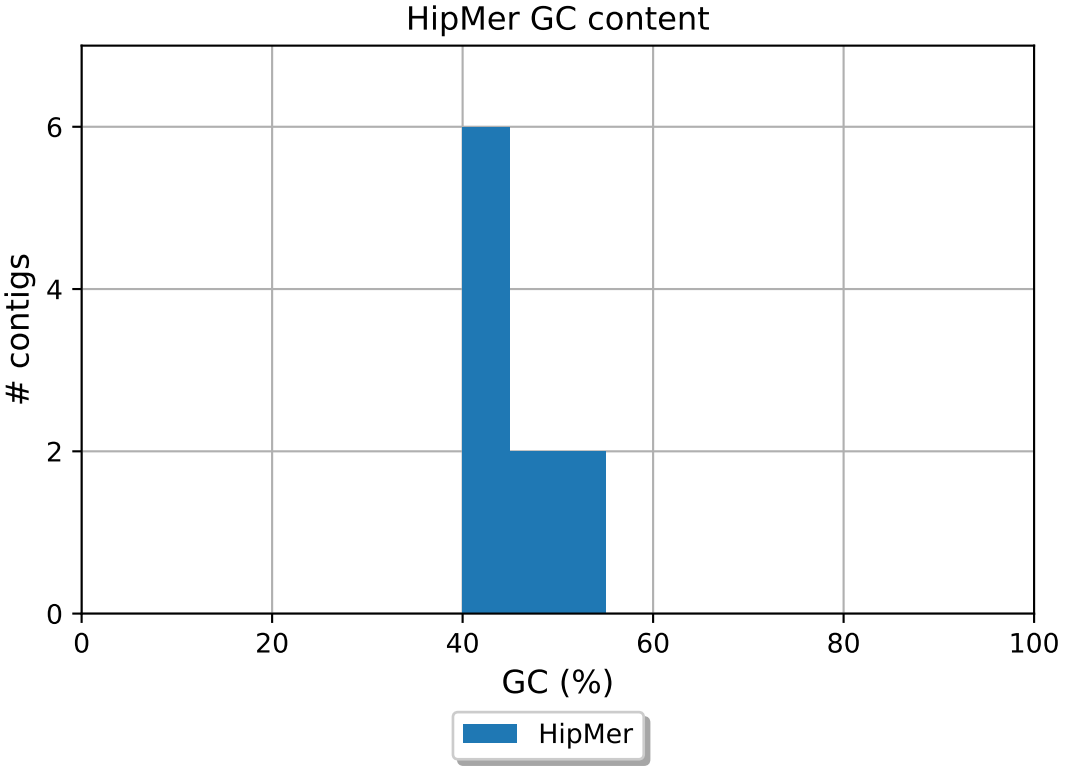

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

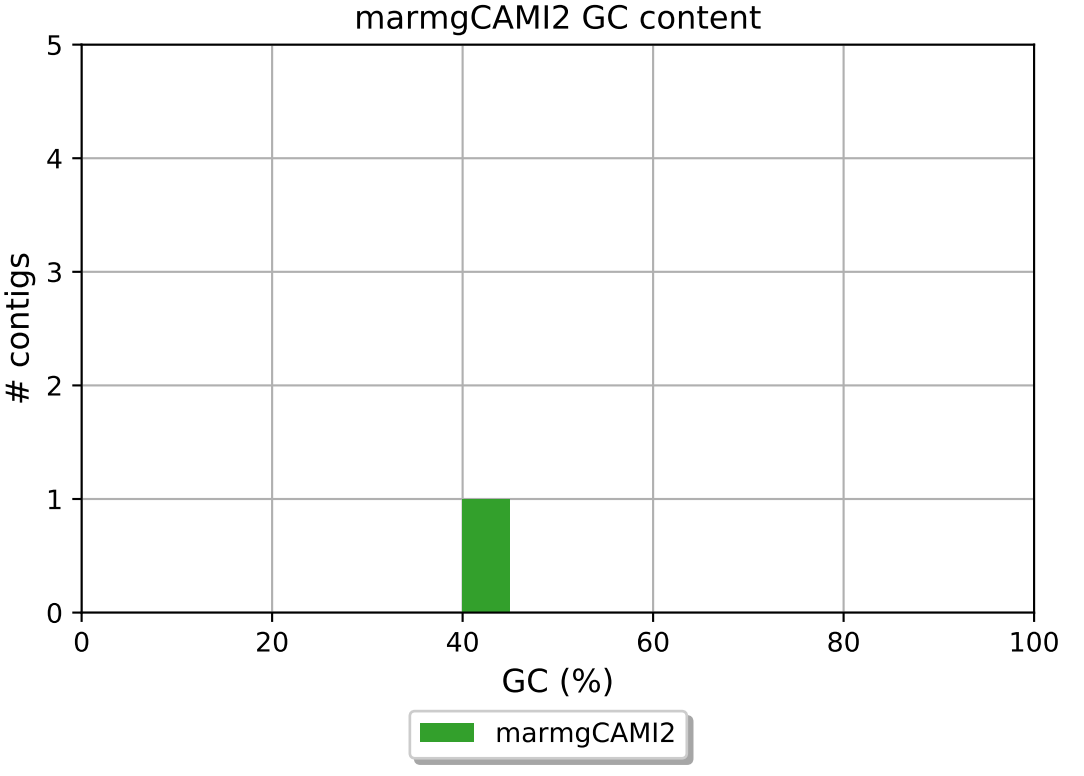

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

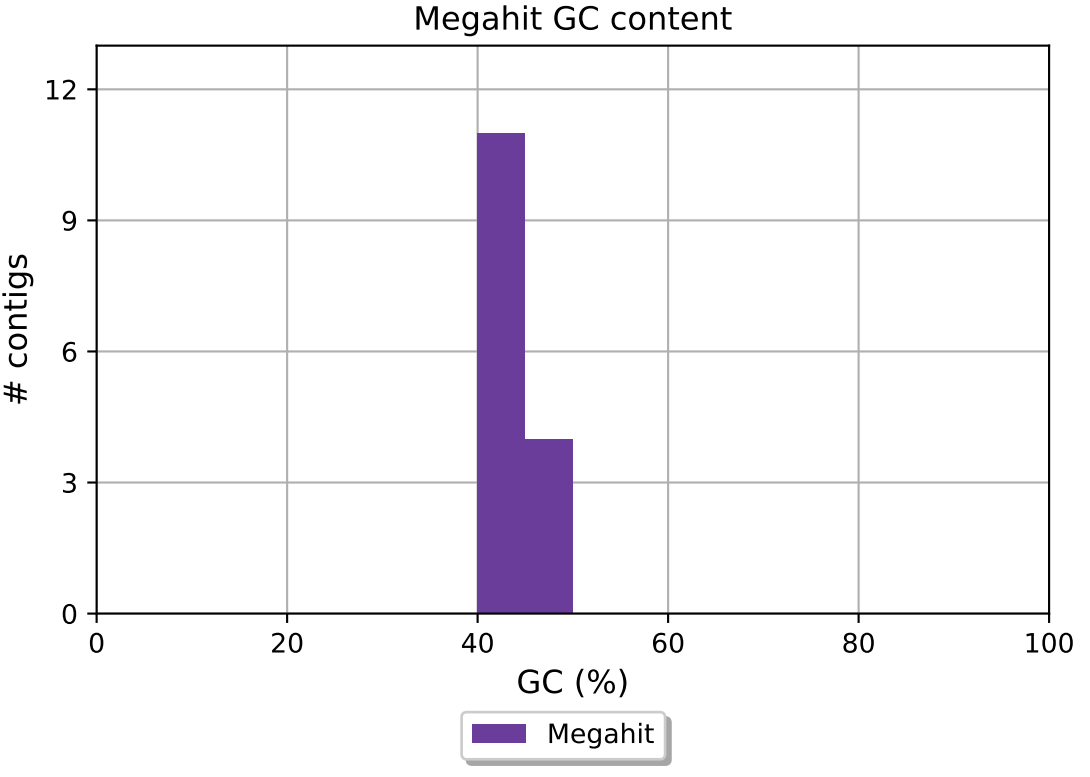

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

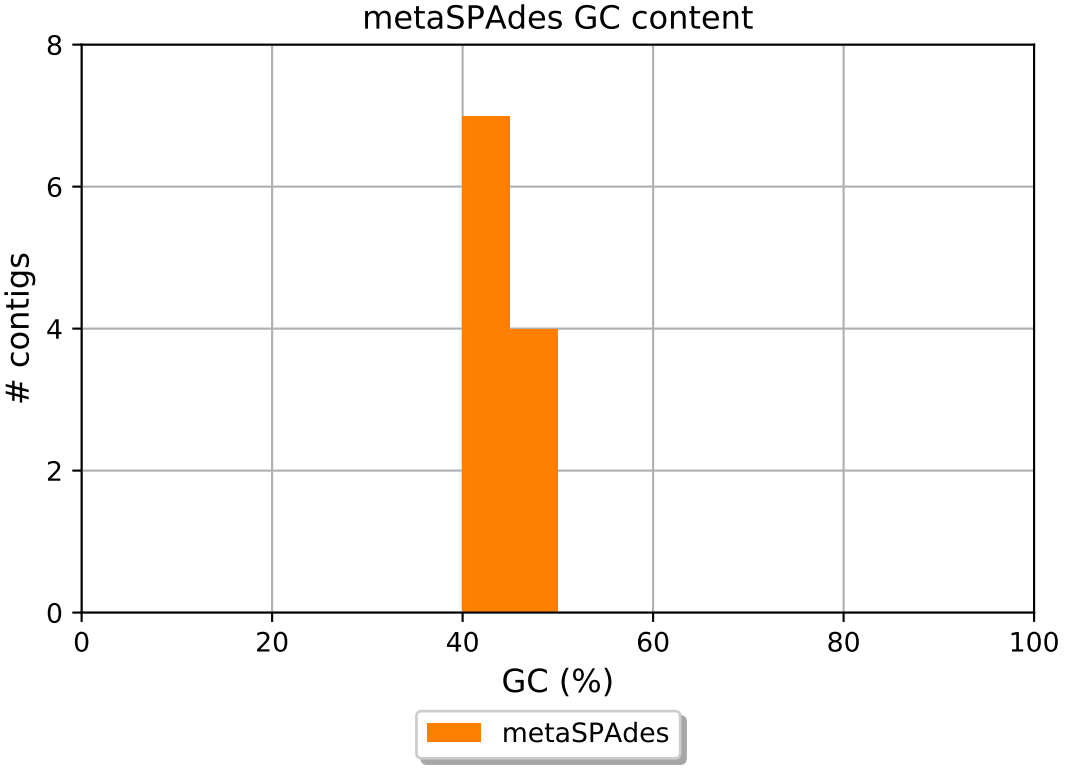

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

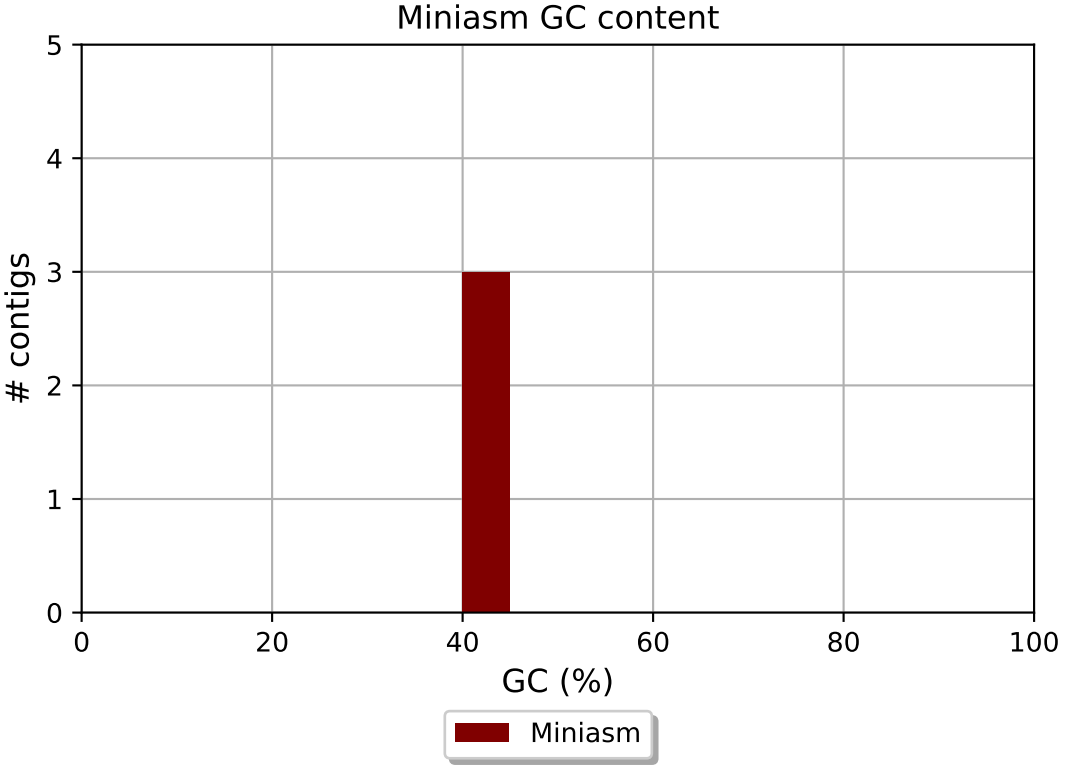

A_STAR GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
A_STAR

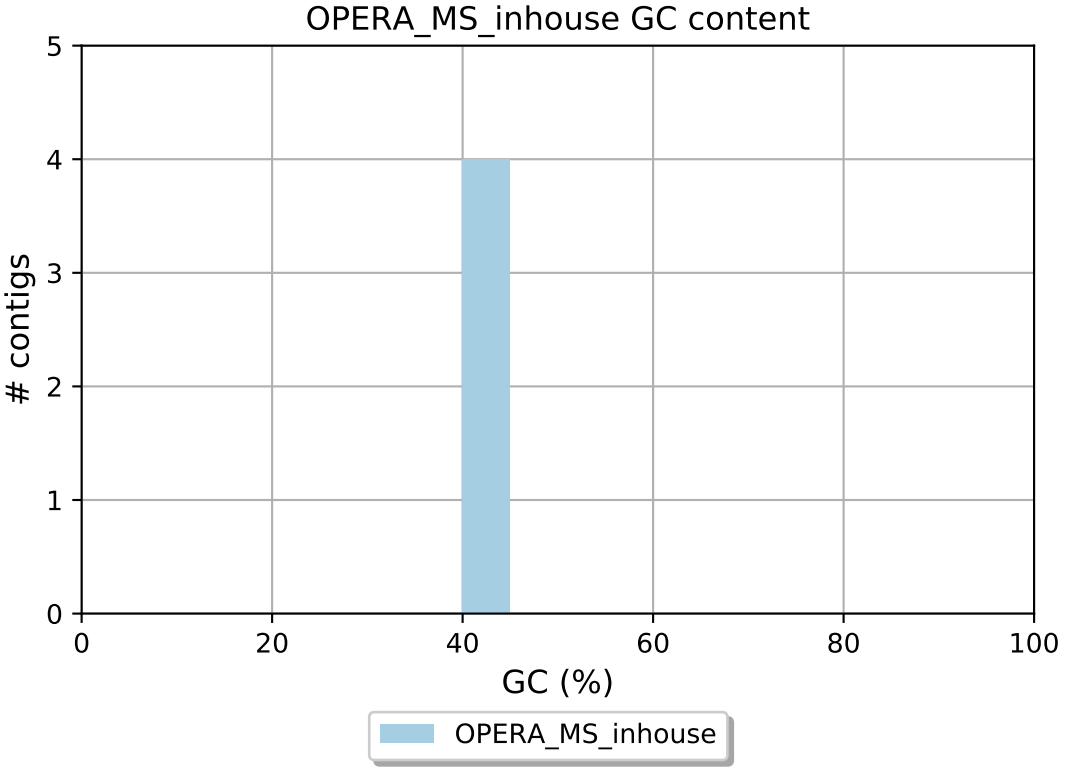

HipMer GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
HipMer

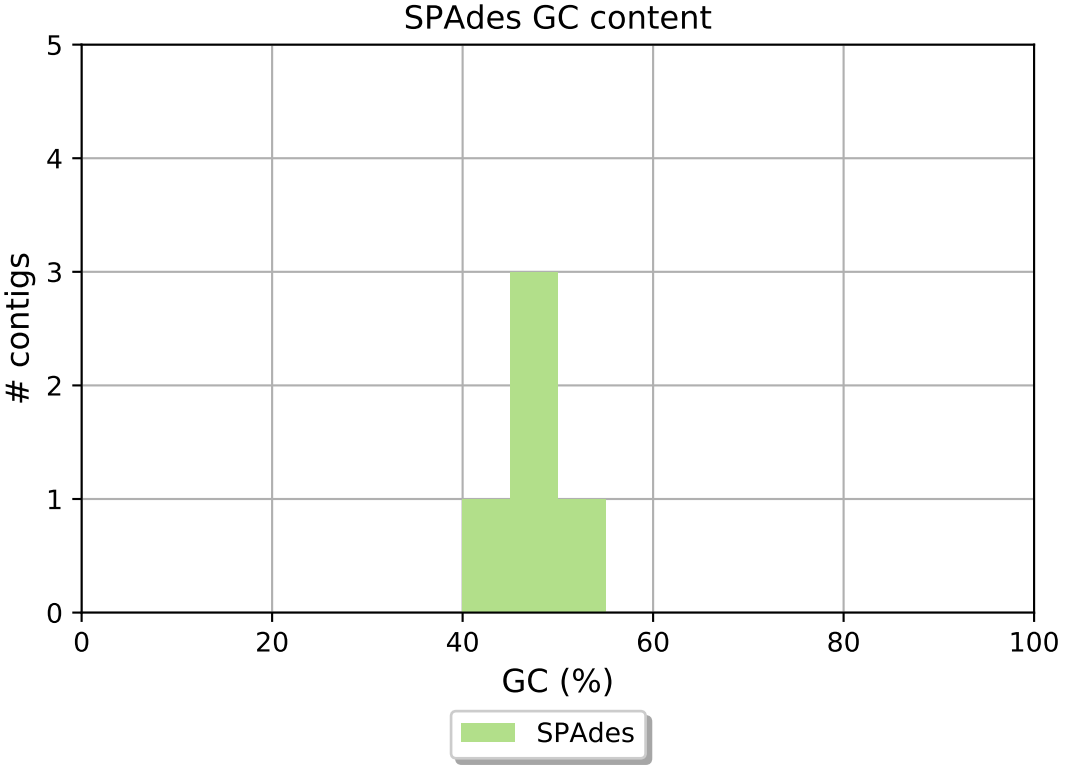

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

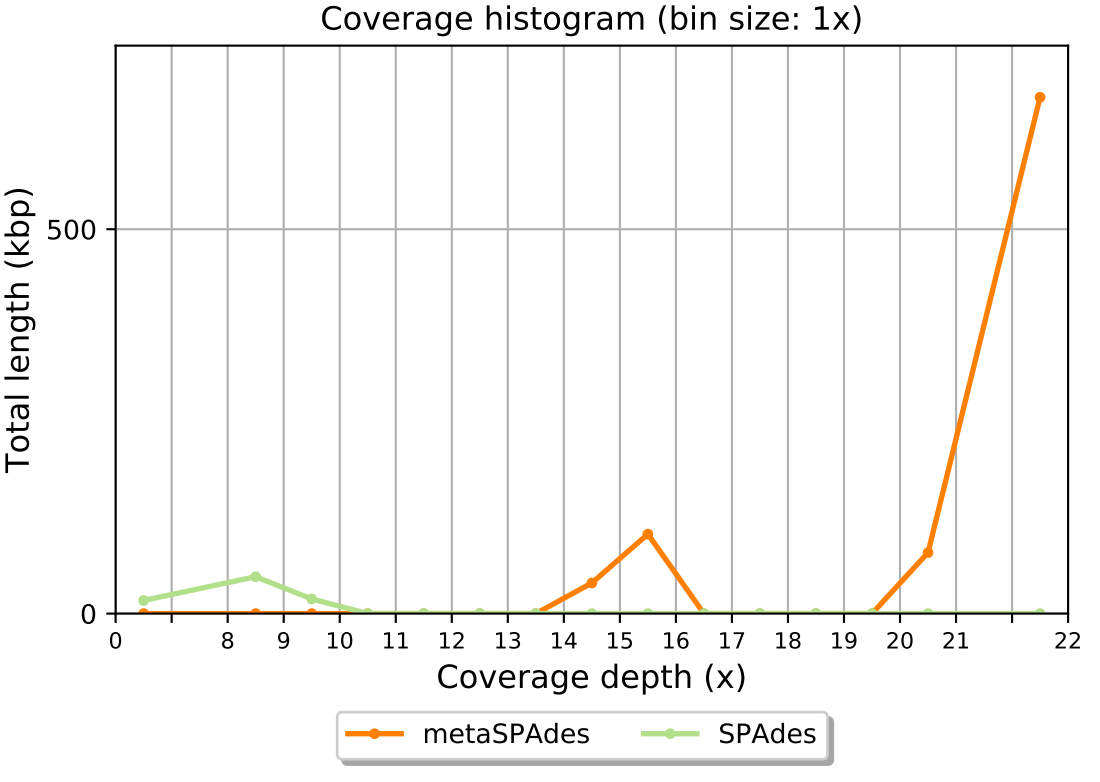

Megahit GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
Megahit

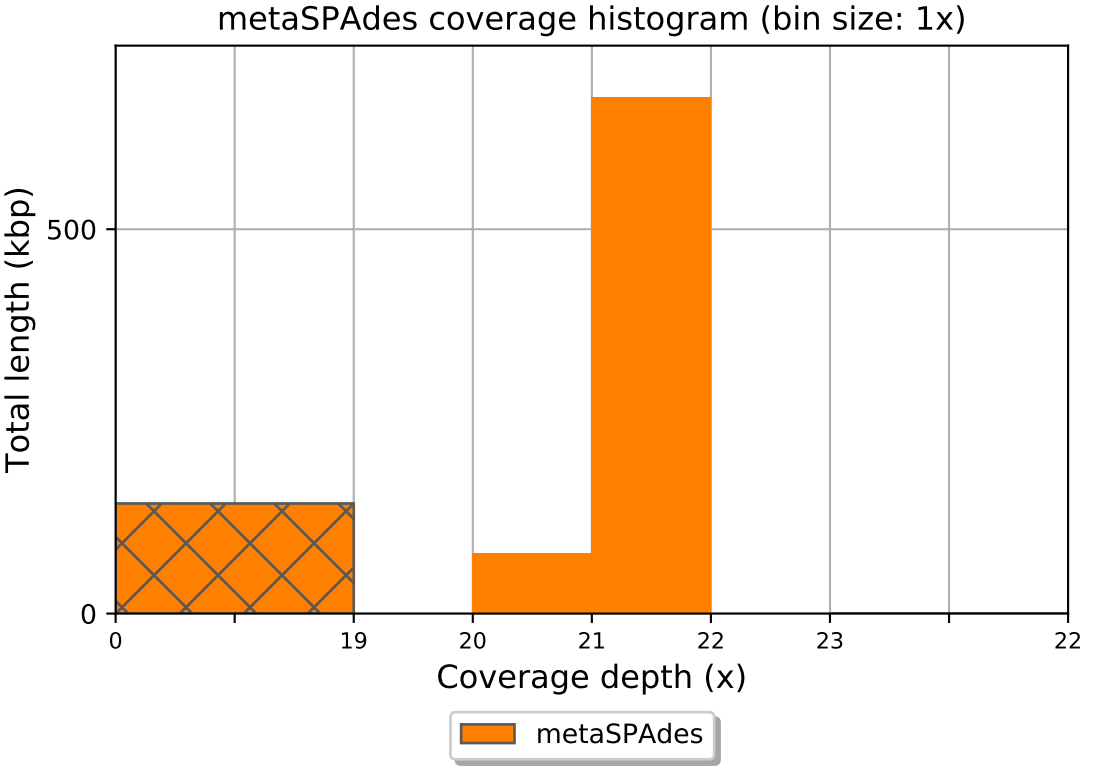

metaSPAdes GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
metaSPAdes

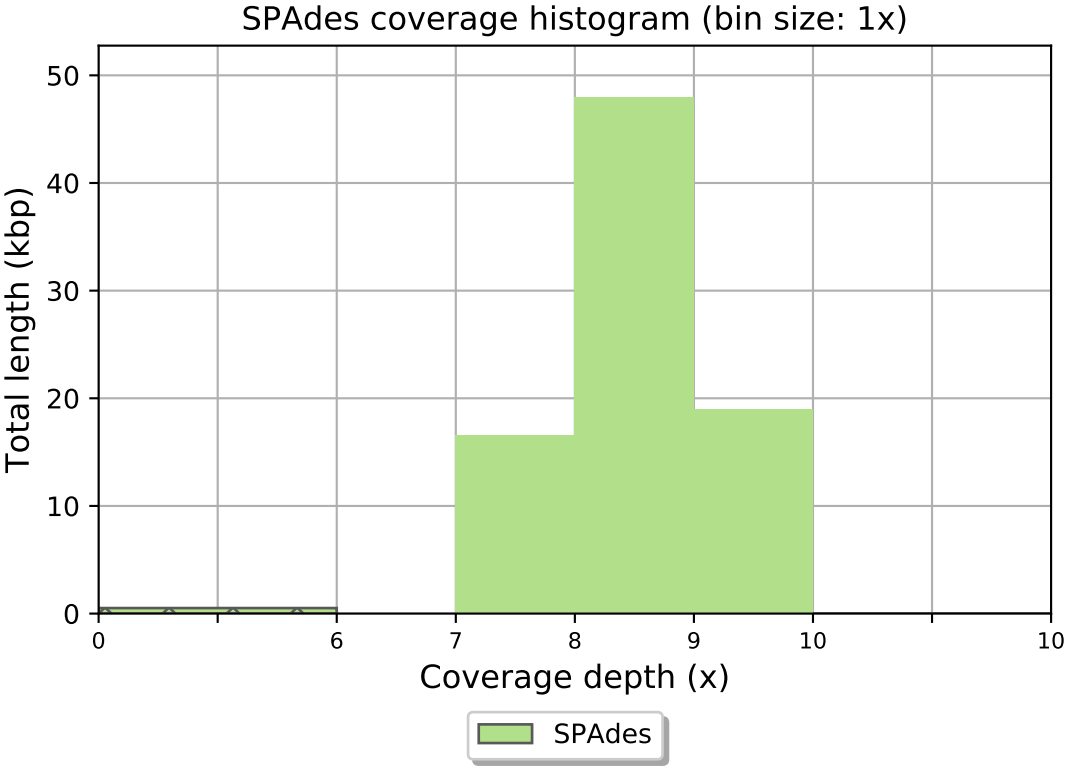

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

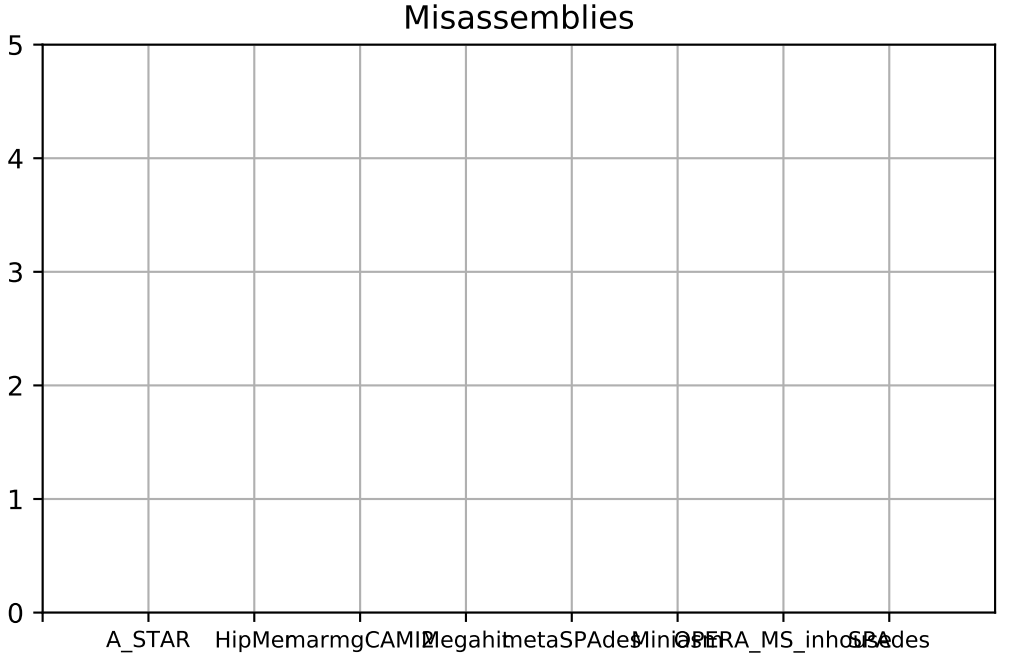

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

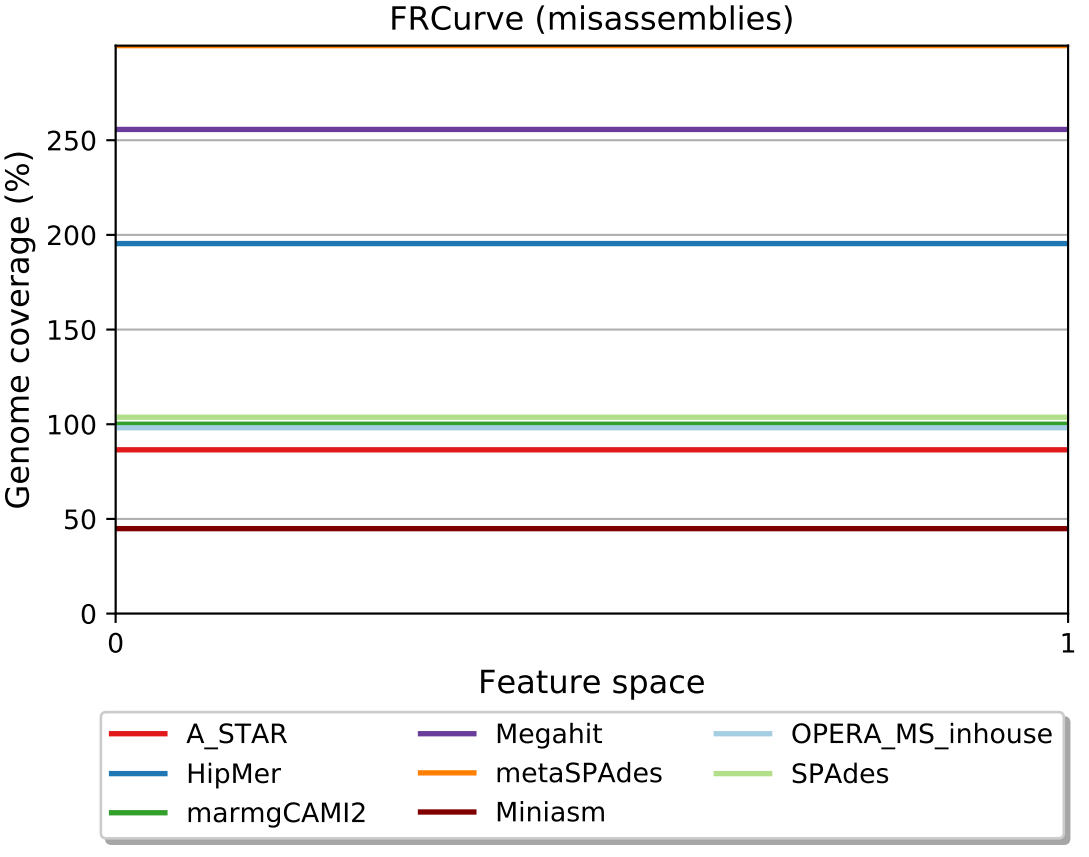

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

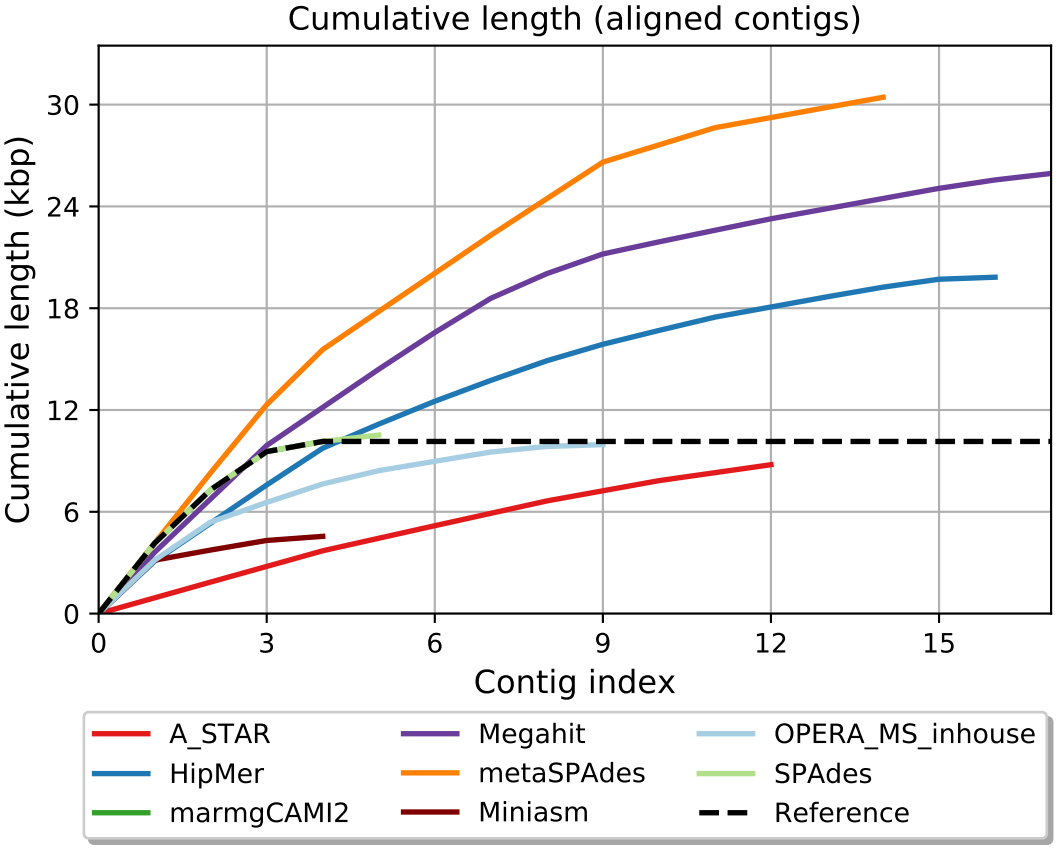

Coverage histogram (bin size: 1x)
Total length (kbp)
500
0
0
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
Coverage depth (x)
metaSPAdes
SPAdes

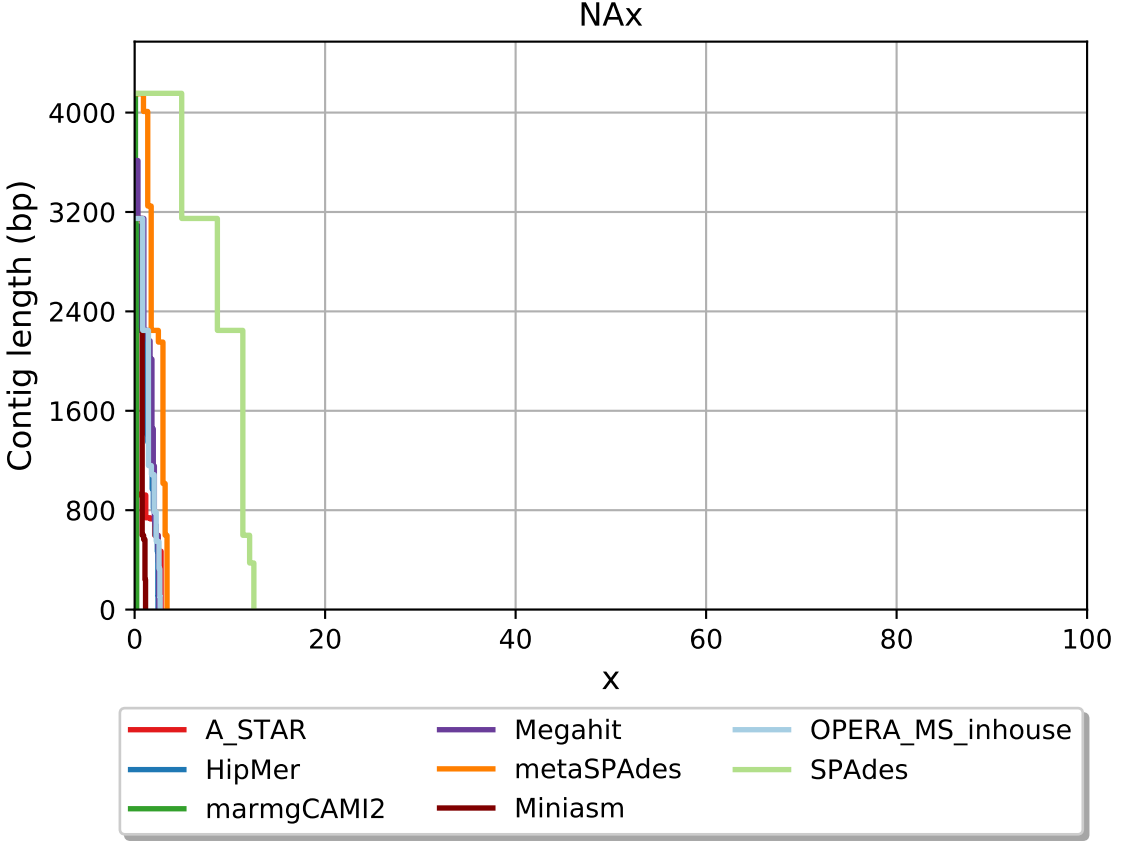

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
500
0
0
19
20
21
22
23
22
Coverage depth (x)
metaSPAdes

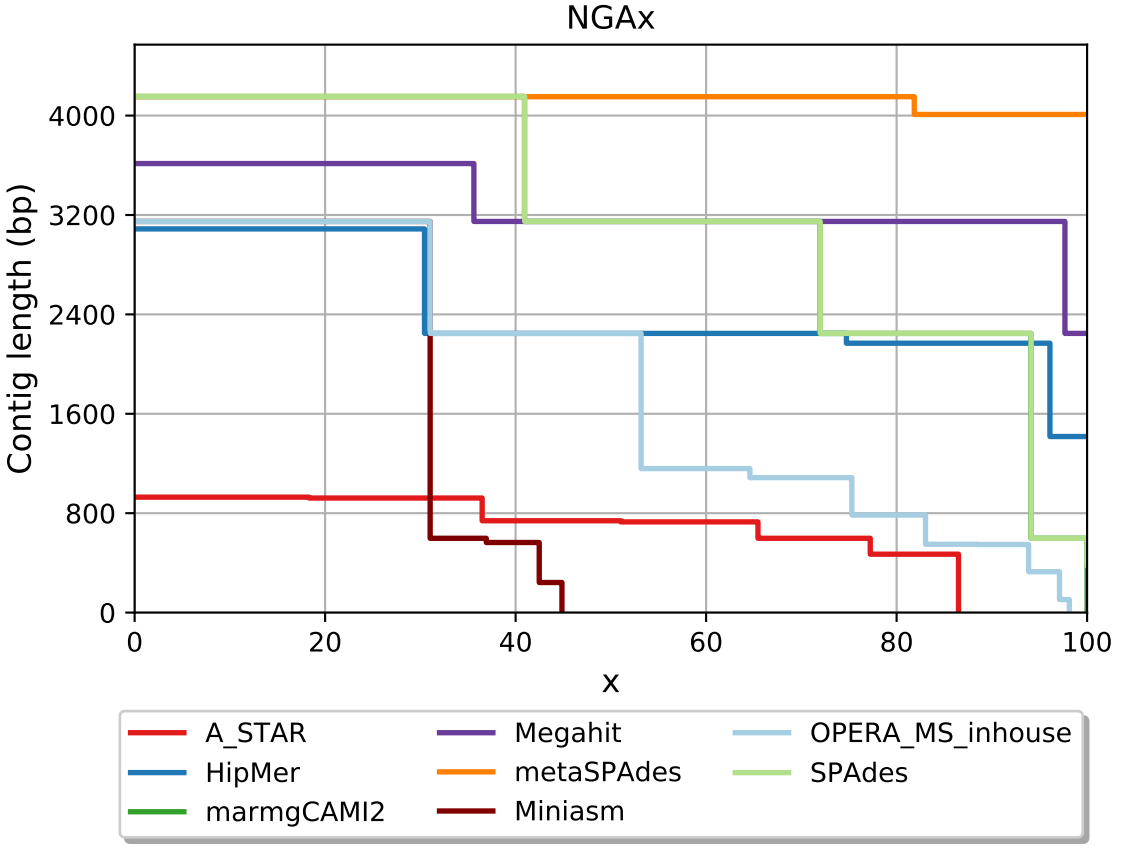

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
0
10
20
30
40
50
0
6
7
8
9
10
10
Coverage depth (x)
SPAdes

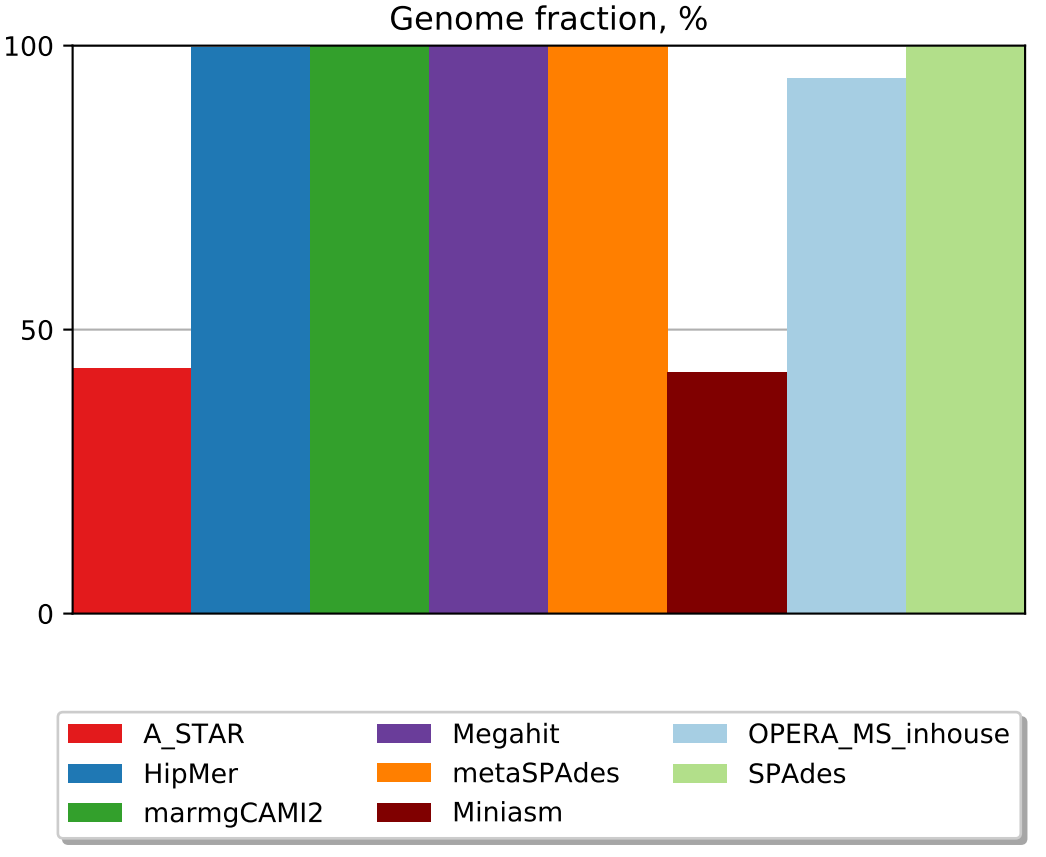

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes


FRCurve (misassemblies)
Genome coverage (%)
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
6
12
18
24
30
0
3
6
9
12
15
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