Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	8	11	1	24	6	4	3	3
# contigs (>= 5000 bp)	4	9	1	13	6	4	2	3
# contigs (>= 10000 bp)	4	8	1	12	6	4	2	3
# contigs (>= 25000 bp)	4	8	1	12	6	4	2	1
# contigs (>= 50000 bp)	4	5	1	10	6	4	2	1
Total length (>= 1000 bp)	218466	1716304	3293431	1790085	1536717	802163	595037	95177
Total length (>= 5000 bp)	208818	1711864	3293431	1774415	1536717	802163	593948	95177
Total length (>= 10000 bp)	208818	1705711	3293431	1767618	1536717	802163	593948	95177
Total length (>= 25000 bp)	208818	1705711	3293431	1767618	1536717	802163	593948	50698
Total length (>= 50000 bp)	208818	1612829	3293431	1690220	1536717	802163	593948	50698
# contigs	8	11	1	27	6	4	3	3
Largest contig	52697	480126	3293431	477215	430579	505663	514901	50698
Total length	218466	1716304	3293431	1792111	1536717	802163	595037	95177
Reference length	17070	17070	17070	17070	17070	17070	17070	17070
GC (%)	45.32	43.87	45.04	43.88	43.80	44.01	43.60	44.38
Reference GC (%)	38.71	38.71	38.71	38.71	38.71	38.71	38.71	38.71
N50	51712	475759	3293431	468686	430579	505663	514901	50698
NG50	52697	480126	3293431	477215	430579	505663	514901	50698
N75	51712	377257	3293431	86290	162196	181620	514901	23155
NG75	52697	480126	3293431	477215	430579	505663	514901	50698
L50	3	2	1	2	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	4	3	1	5	4	2	1	2
LG75	1	1	1	1	1	1	1	1
# misassemblies	0	0	0	1	0	0	0	0
# misassembled contigs	0	0	0	1	0	0	0	0
Misassembled contigs length	0	0	0	2121	0	0	0	0
# local misassemblies	0	0	0	1	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	1	1	0	1	0	0
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 1 part	0 + 12 part	0 + 6 part	0 + 4 part	0 + 2 part	0 + 3 part
Unaligned length	213930	1682712	3276361	1752010	1485507	788029	577076	78187
Genome fraction (%)	13.257	99.625	100.000	100.000	100.000	79.022	100.000	99.227
Duplication ratio	2.004	1.975	1.000	2.349	3.000	1.048	1.052	1.003
# N's per 100 kbp	4.58	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	265.13	0.00	0.00	1646.16	35.15	51.89	486.23	82.65
# indels per 100 kbp	0.00	23.52	0.00	52.72	0.00	0.00	837.73	0.00
Largest alignment	894	7541	10622	6797	10622	6448	10599	9938
Total aligned length	4526	33592	17070	39422	51210	14134	17961	16990
NGA50	-	6290	10622	3378	10622	5335	10599	9938
NGA75	-	6290	6448	1894	10622	1706	6273	6316
LGA50	-	2	1	2	1	2	1	1
LGA75	-	2	2	4	2	3	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

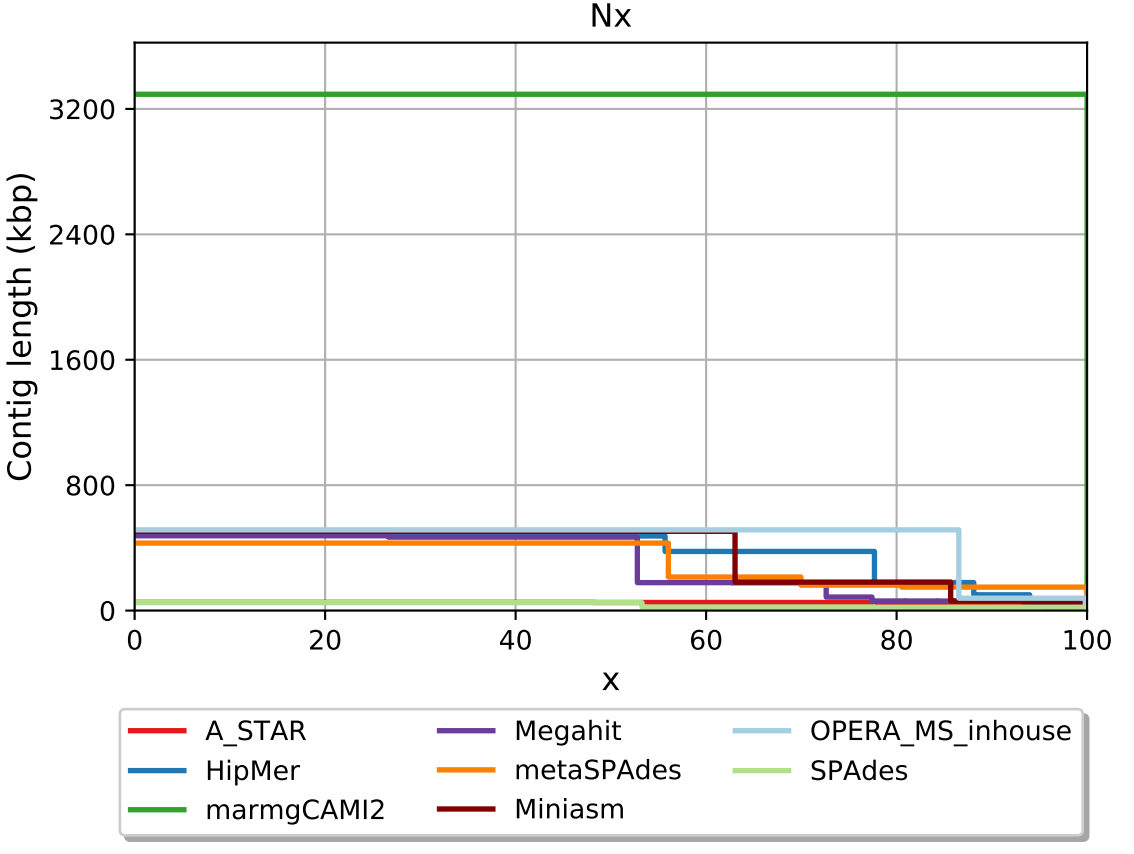
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	1	0	0	0	0
# contig misassemblies	0	0	0	1	0	0	0	0
# c. relocations	0	0	0	1	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	1	0	0	0	0
Misassembled contigs length	0	0	0	2121	0	0	0	0
# possibly misassembled contigs	8	7	0	11	6	3	1	3
# possible misassemblies	8	7	0	11	12	4	2	4
# local misassemblies	0	0	0	1	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	1	1	0	1	0	0
# mismatches	6	0	0	281	6	7	83	14
# indels	0	4	0	9	0	0	143	0
# indels (<= 5 bp)	0	0	0	4	0	0	138	0
# indels (> 5 bp)	0	4	0	5	0	0	5	0
Indels length	0	400	0	407	0	0	508	0

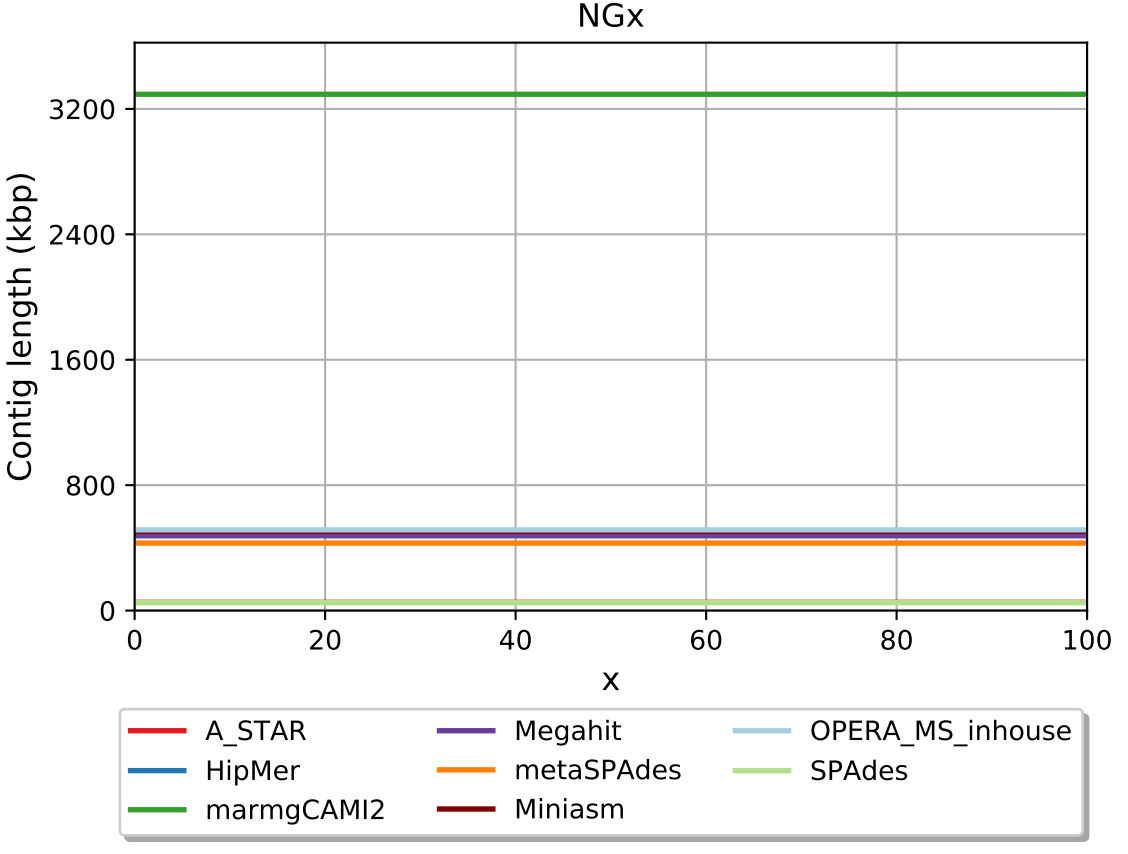
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

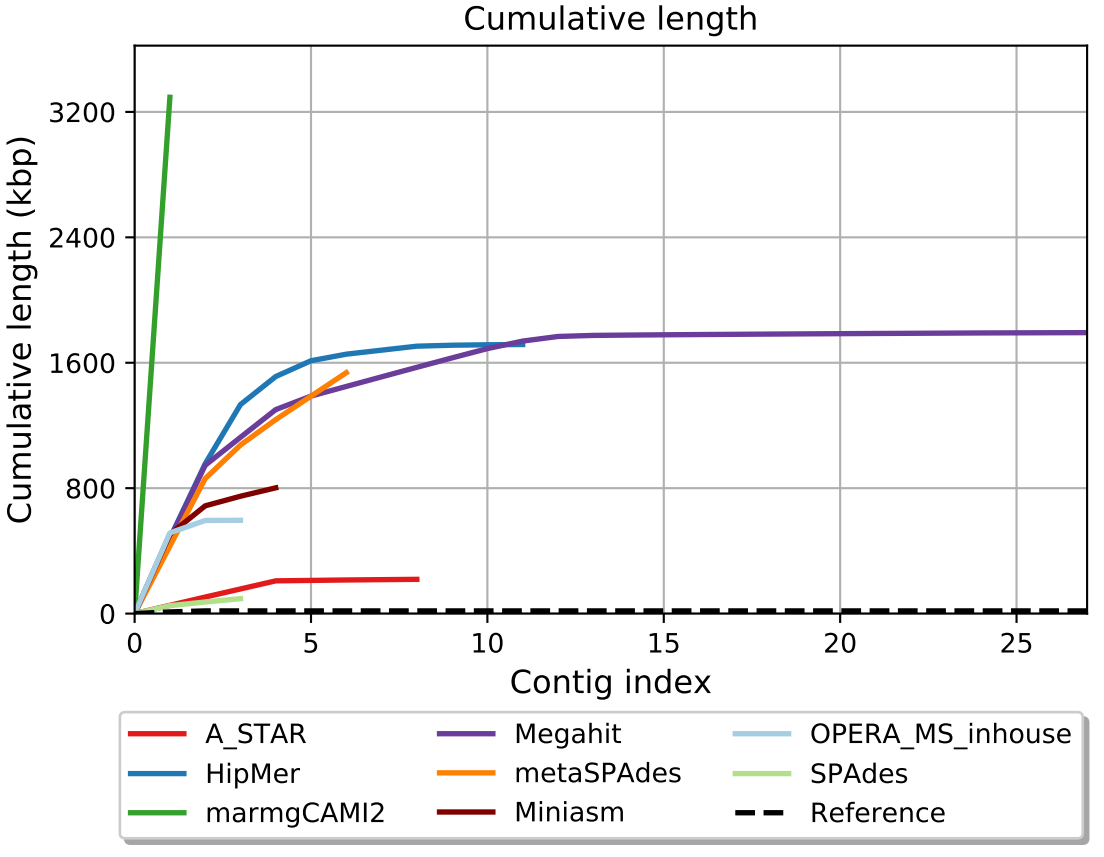
Unaligned report

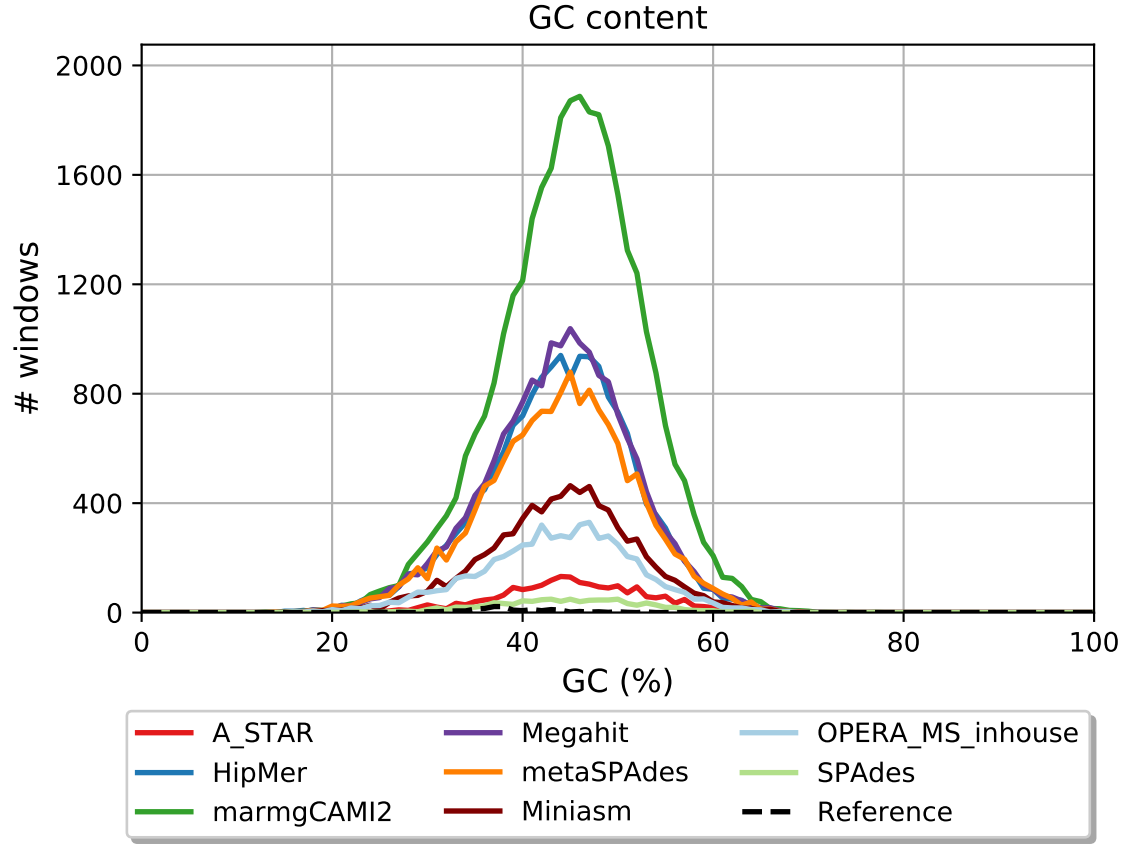
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	8	8	1	12	6	4	2	3
Partially unaligned length	213930	1682712	3276361	1752010	1485507	788029	577076	78187
# N's	10	0	0	0	0	0	0	0

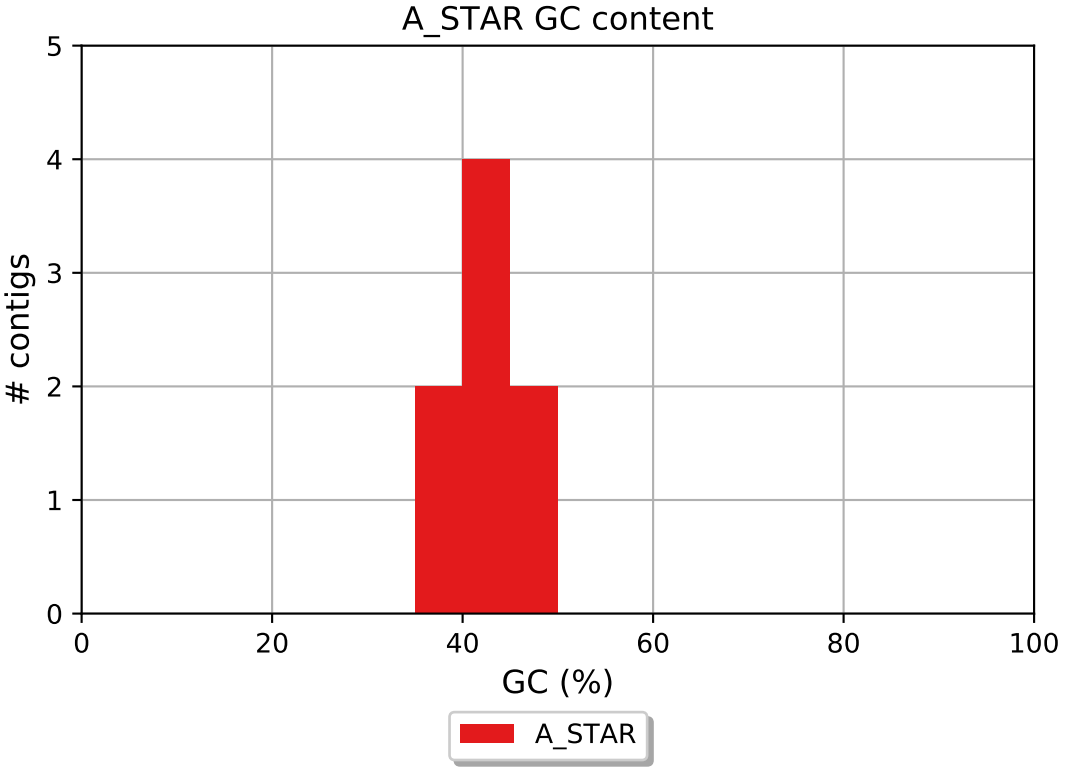
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

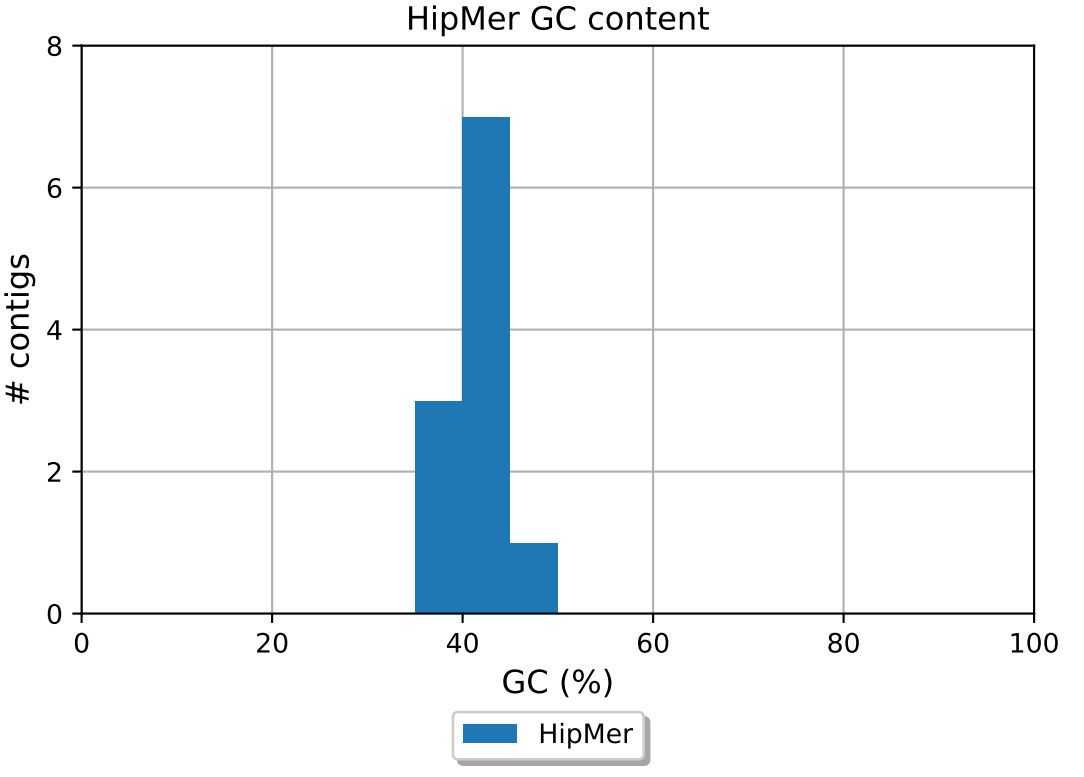

Nx
Contig length (kbp)
3200
2400
1600
800
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

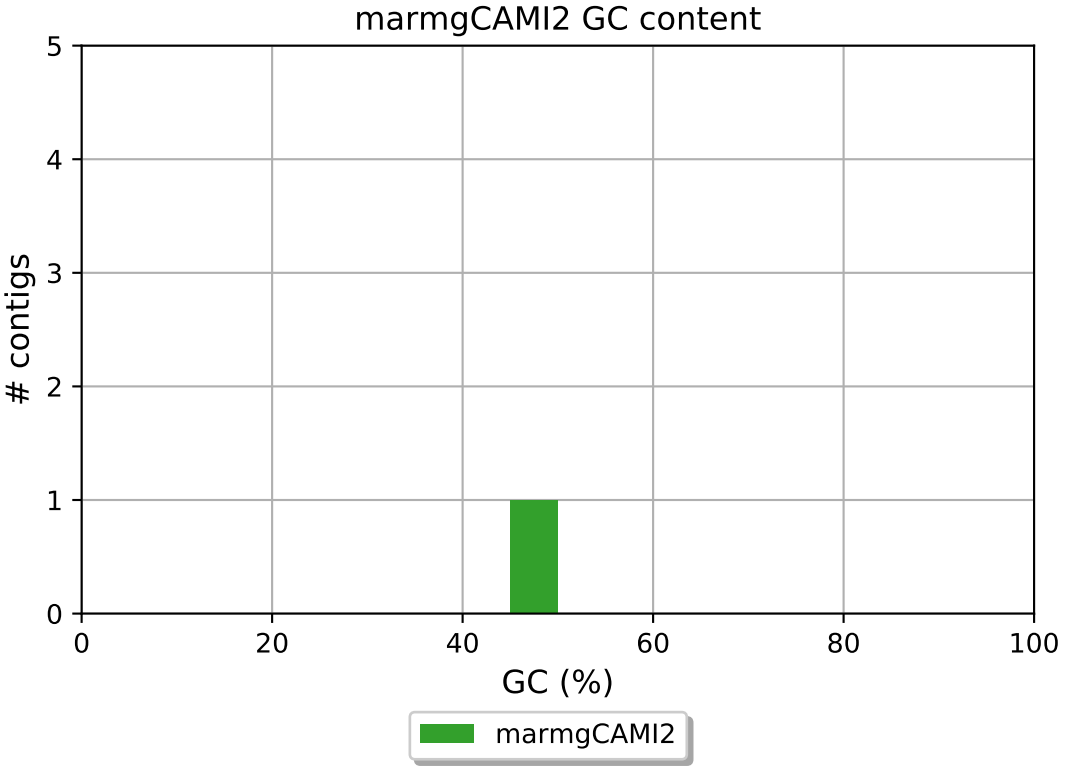

NGx
Contig length (kbp)
3200
2400
1600
800
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

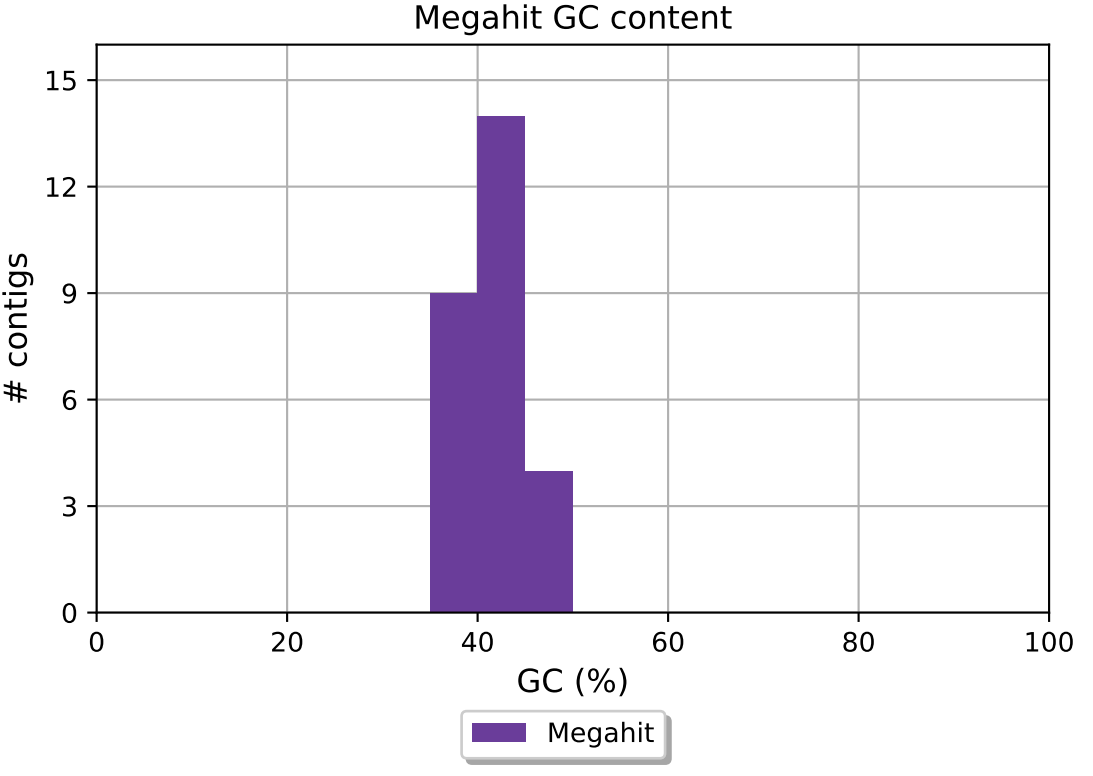

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
5
10
15
20
25
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

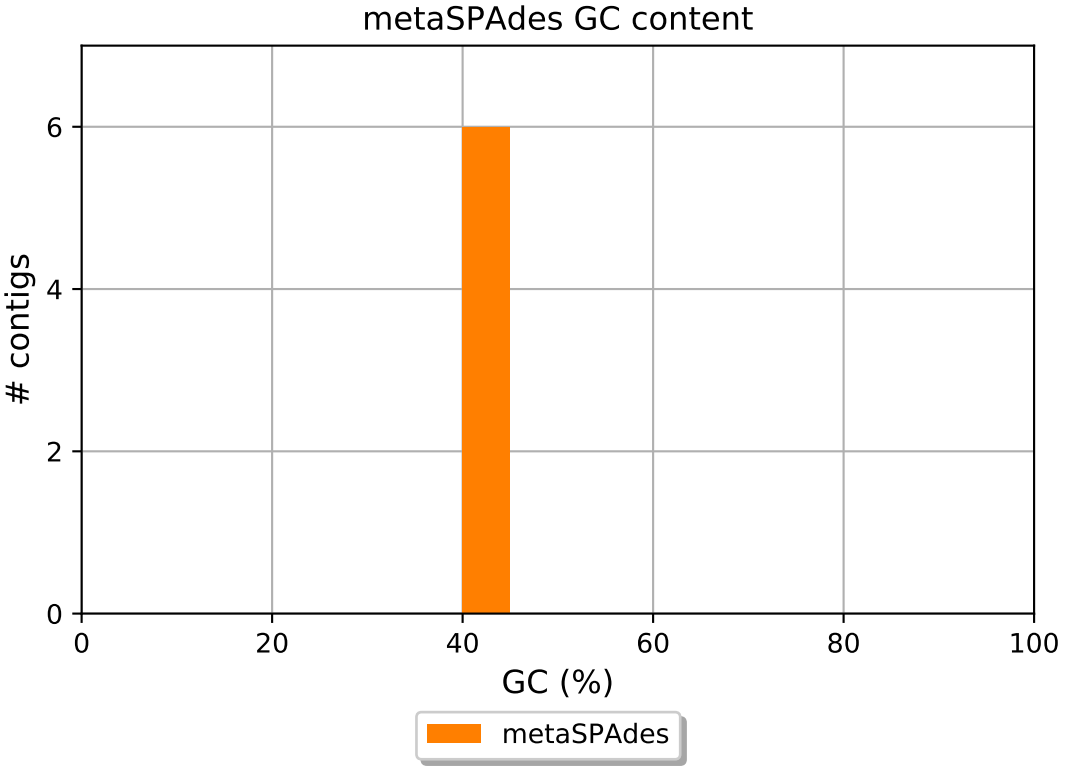

GC content
windows
GC (%)
0
400
800
1200
1600
2000
0
20
40
60
80
100
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

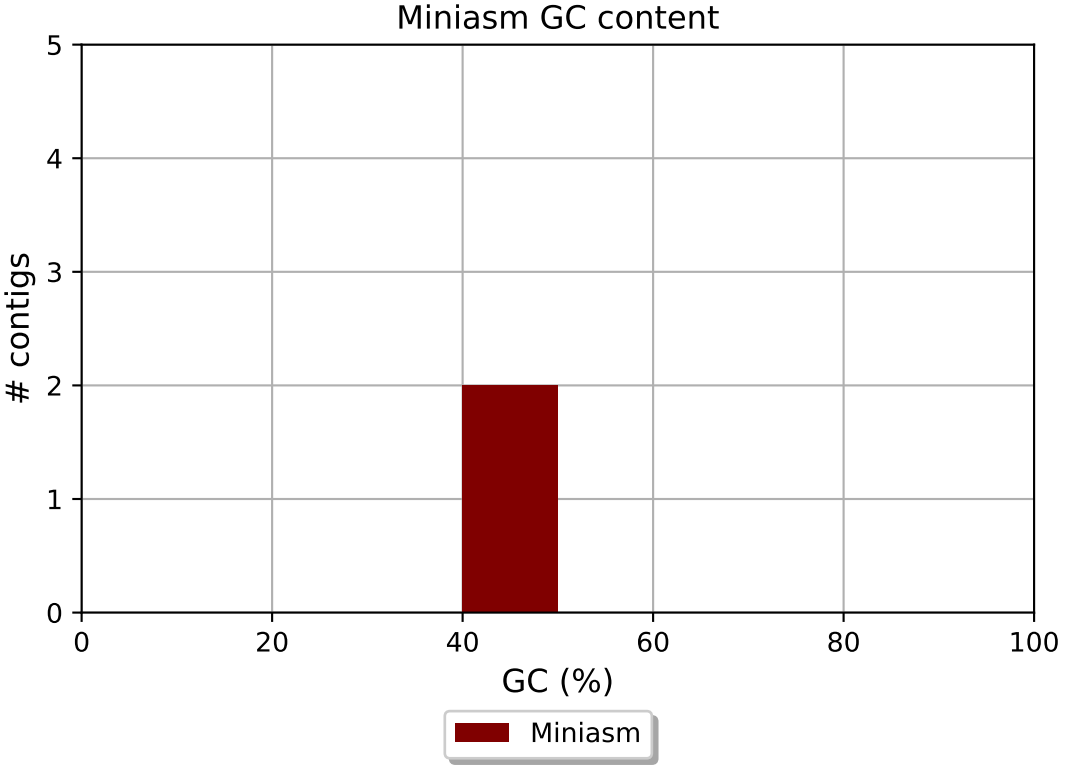

A_STAR GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
A_STAR

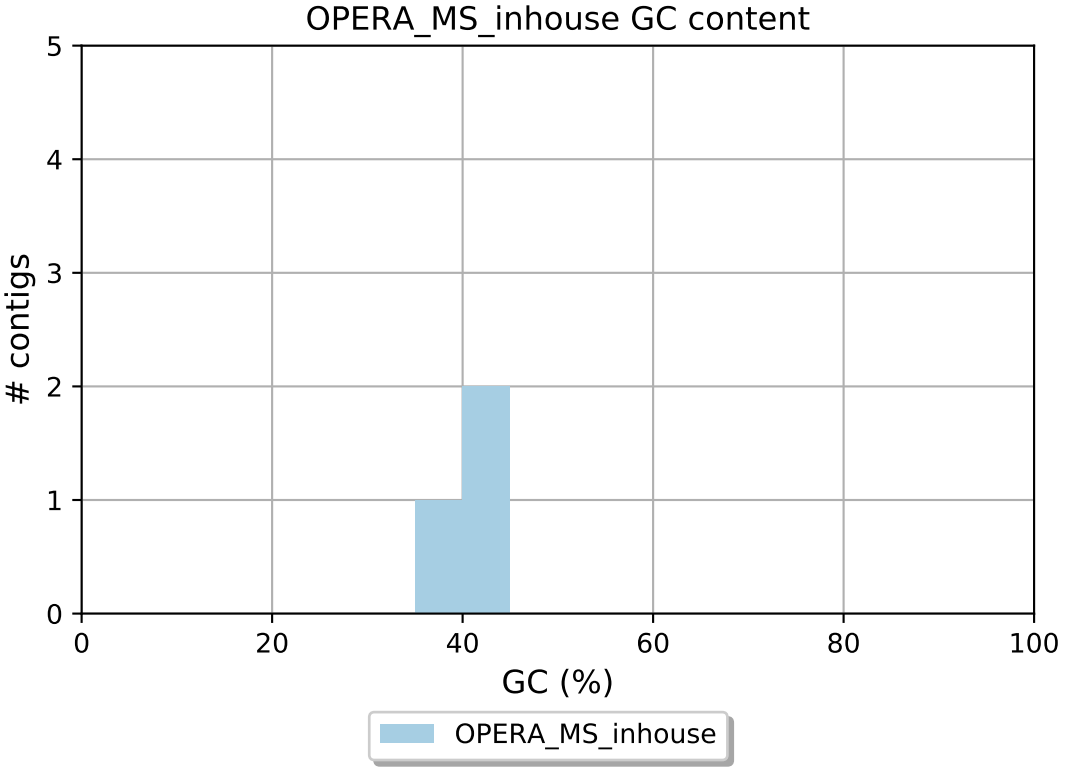

HipMer GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
HipMer

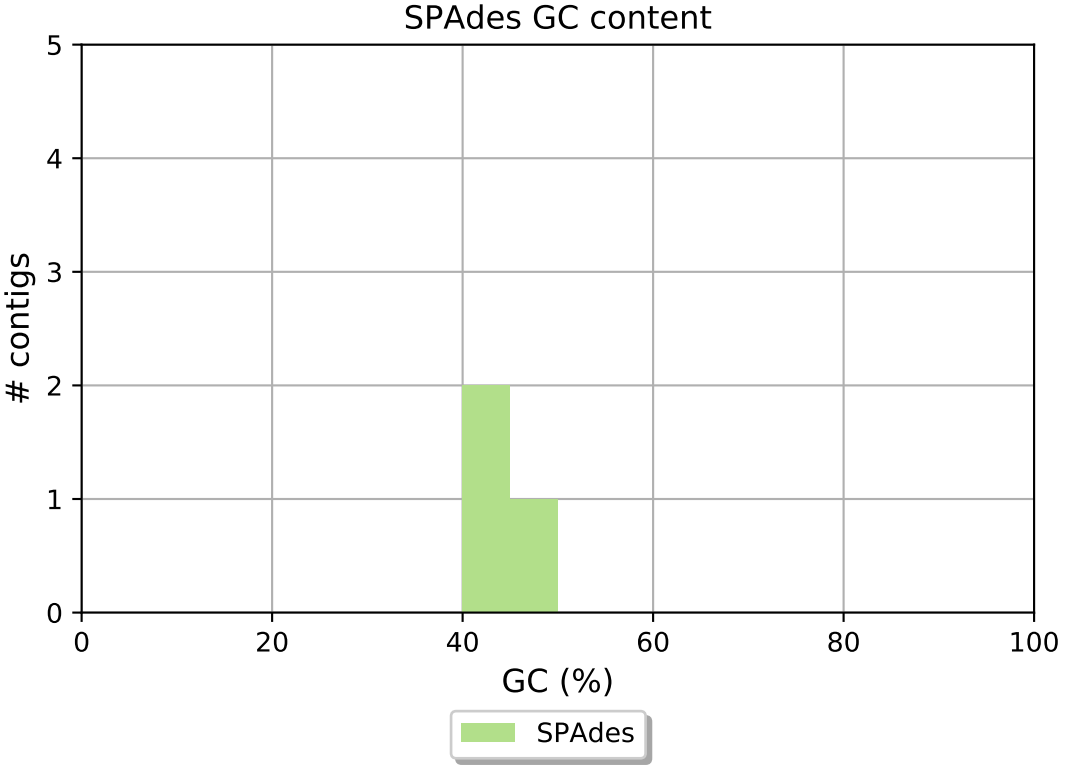

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

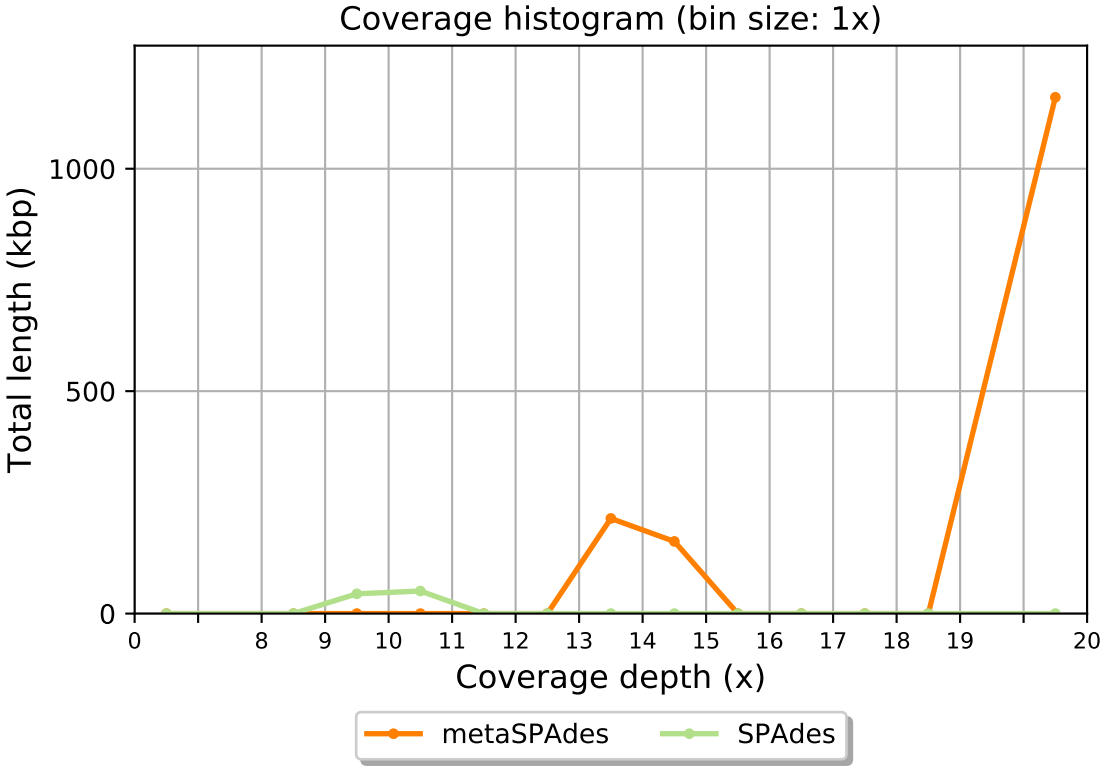

Megahit GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
Megahit

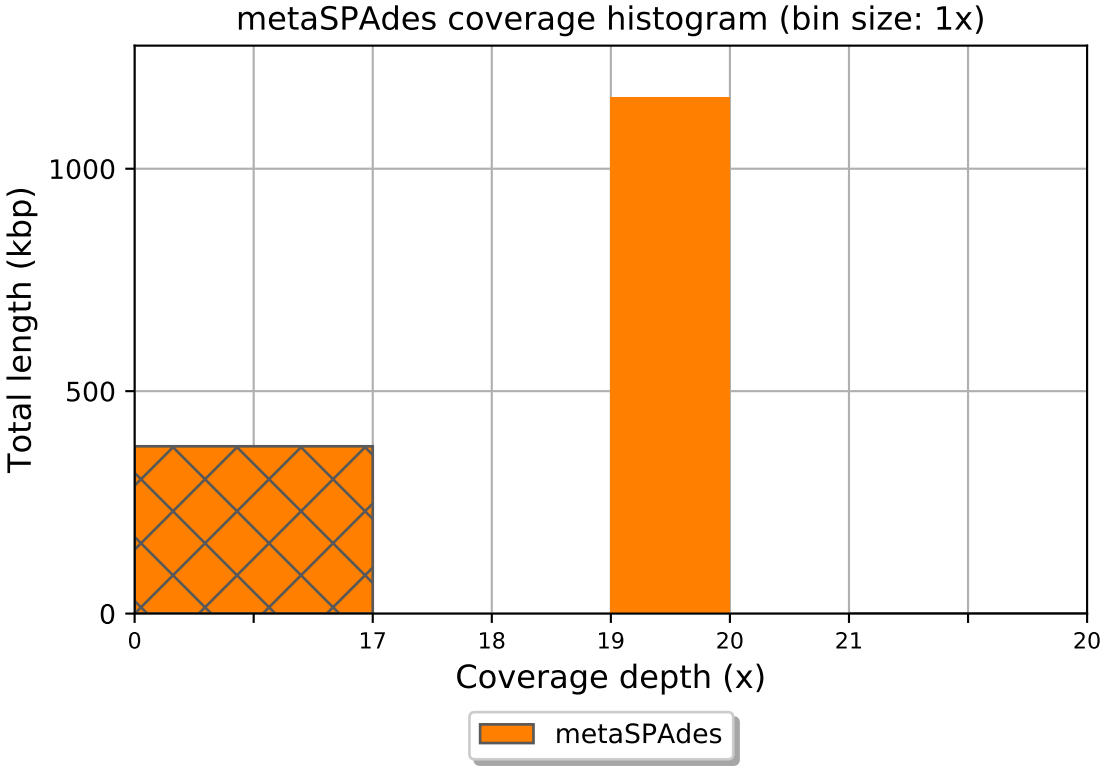

metaSPAdes GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
metaSPAdes

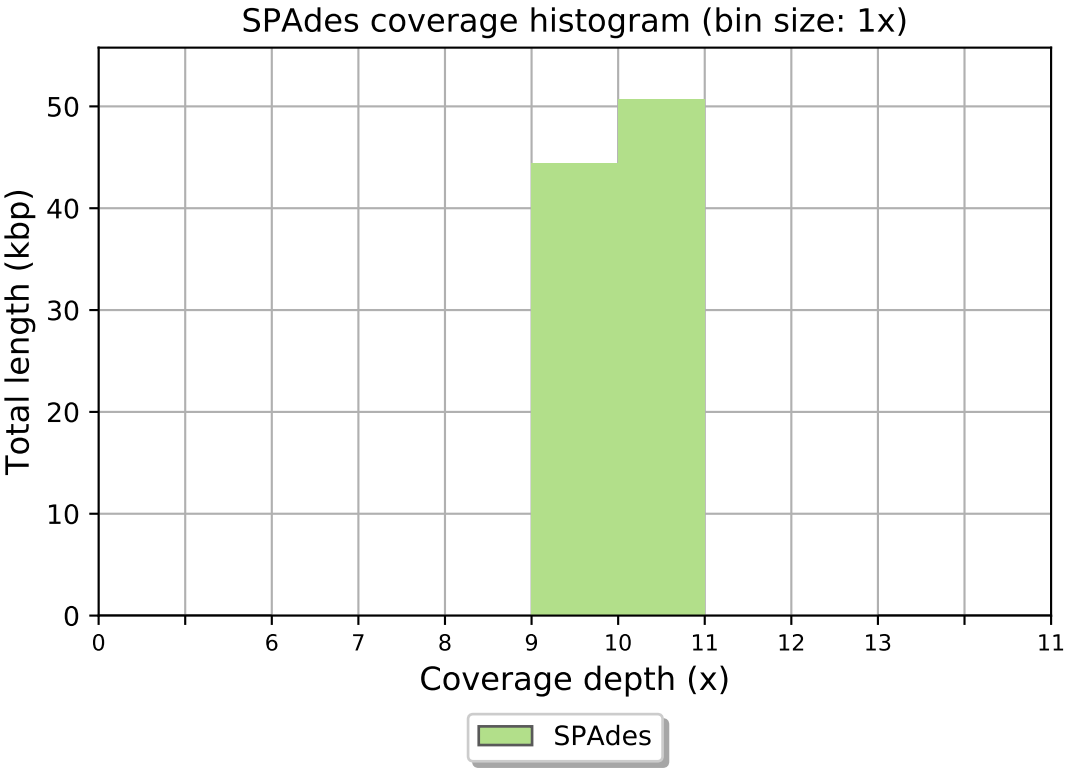

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

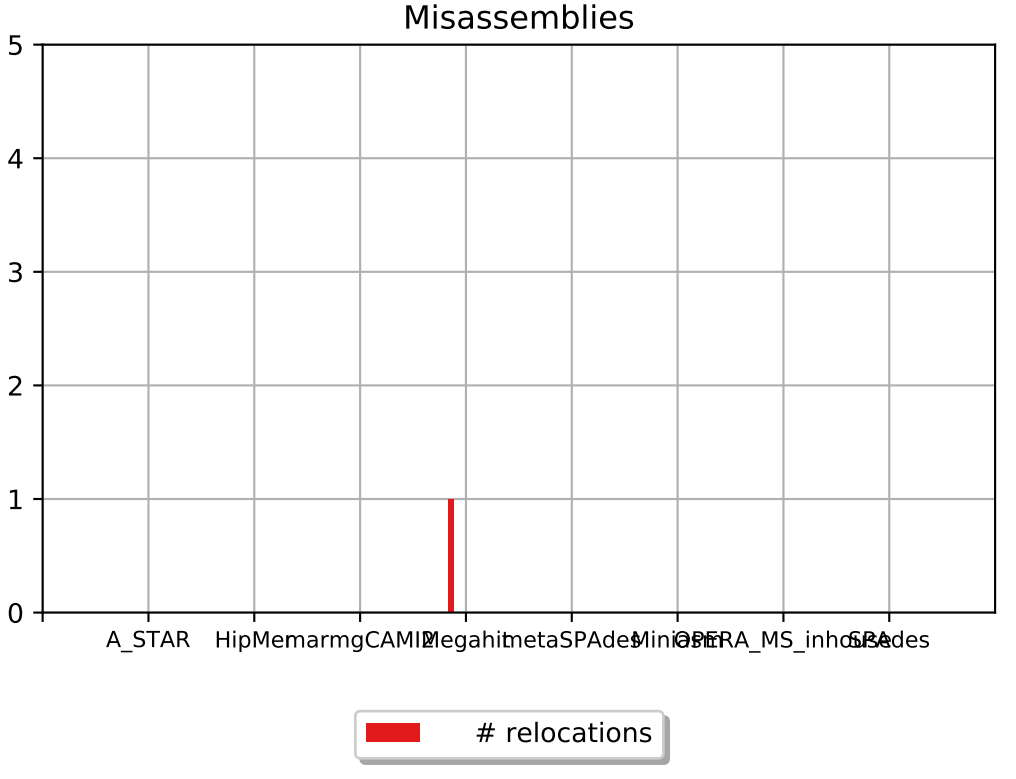

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

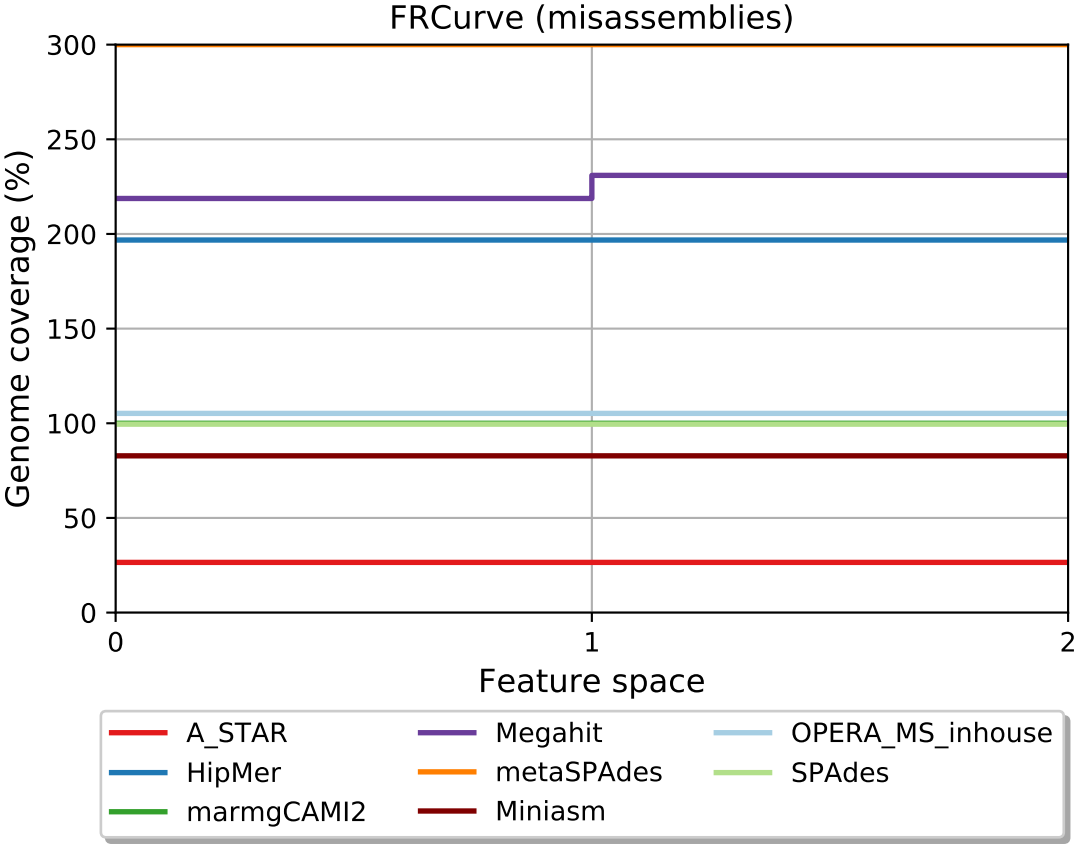

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

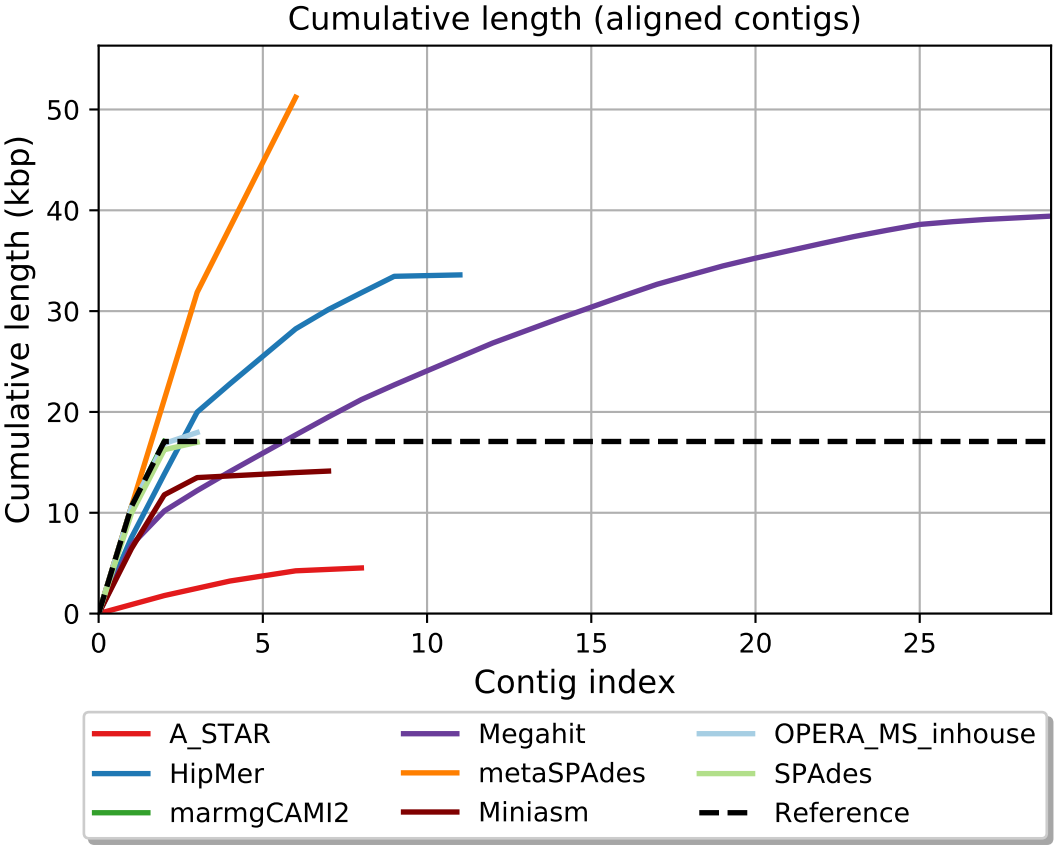

Coverage histogram (bin size: 1x)
Total length (kbp)
1000
500
0
0
8
9
10
11
12
13
14
15
16
17
18
19
20
Coverage depth (x)
metaSPAdes
SPAdes

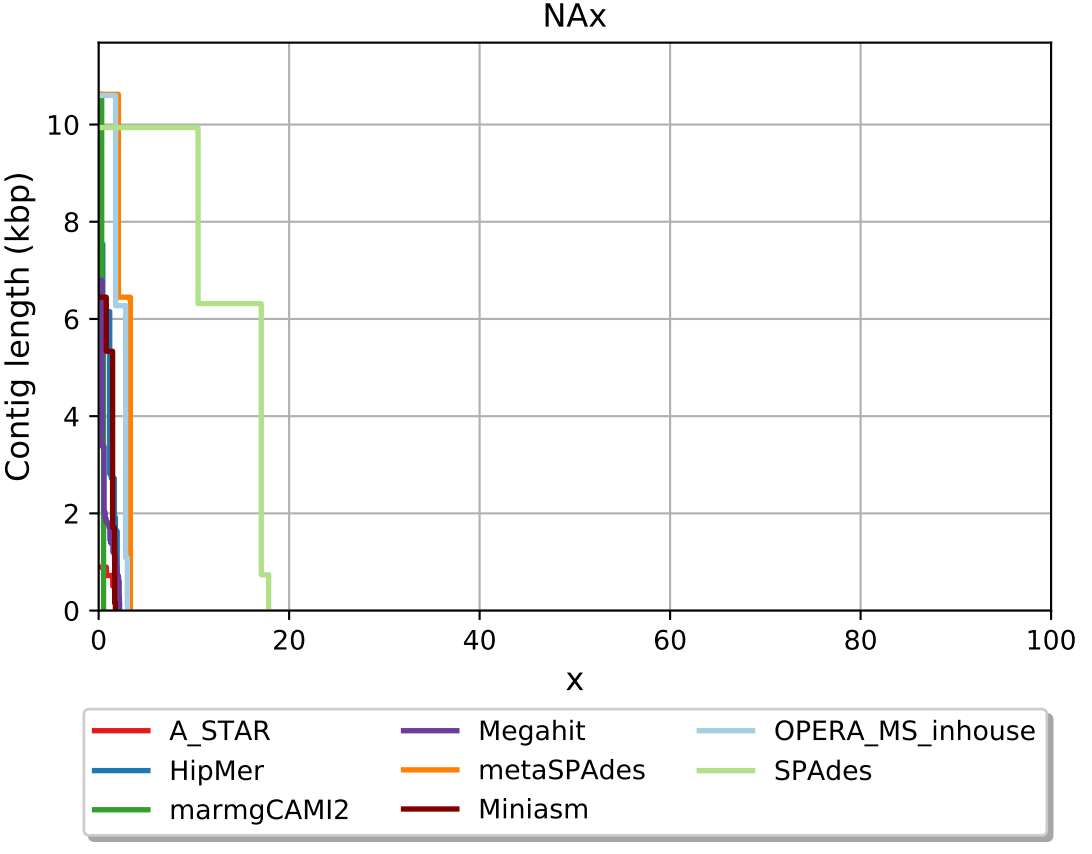

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
1000
500
0
0
17
18
19
20
21
20
Coverage depth (x)
metaSPAdes

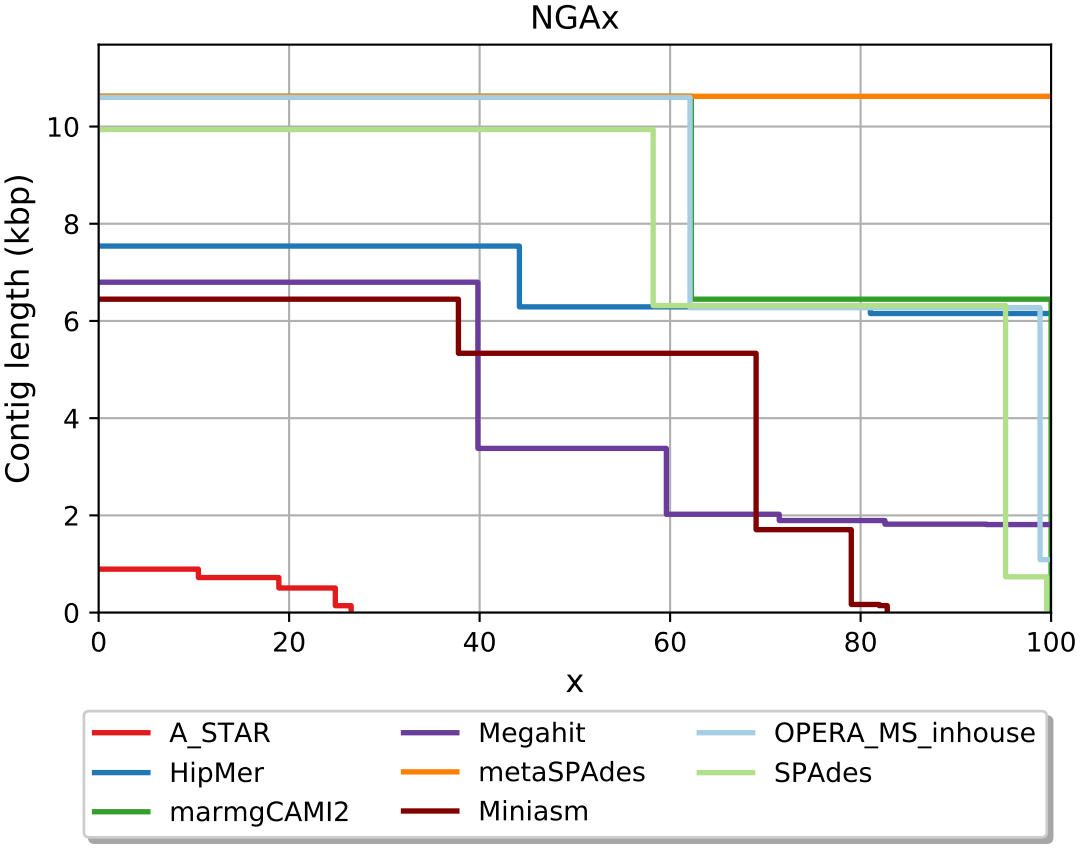

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
0
10
20
30
40
50
0
6
7
8
9
10
11
12
13
11
Coverage depth (x)
SPAdes

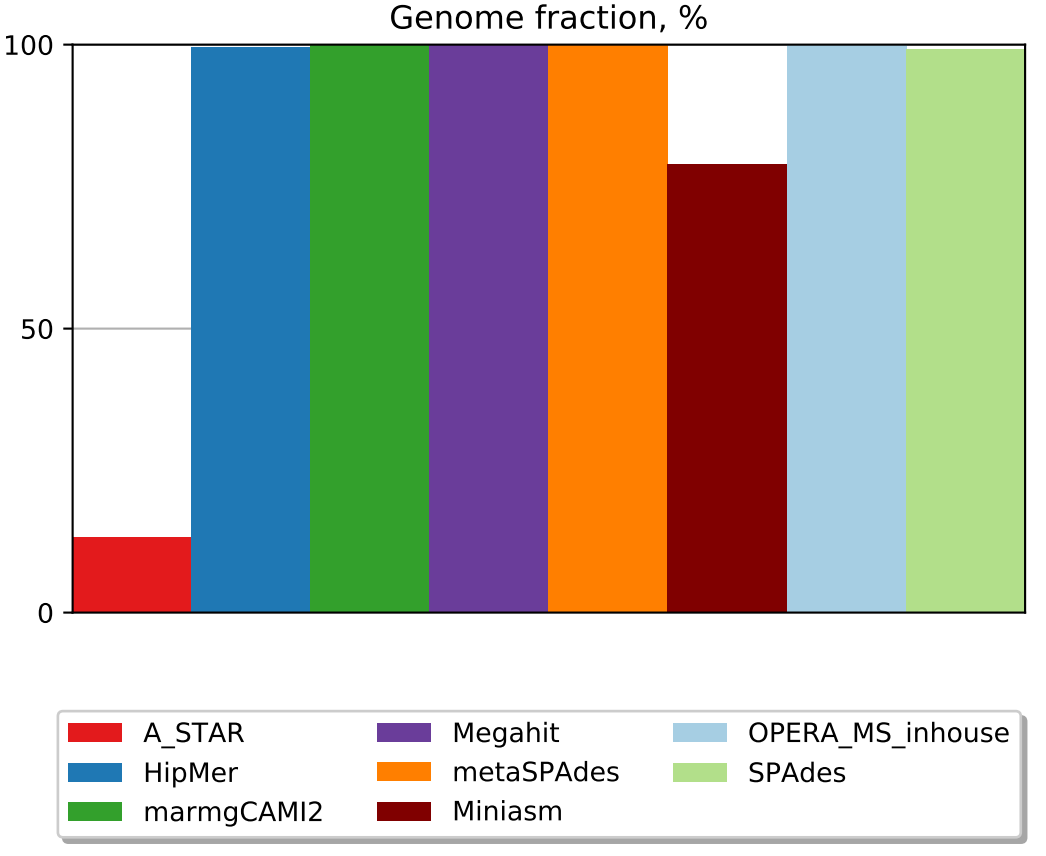

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes
relocations


FRCurve (misassemblies)
Genome coverage (%)
300
250
200
150
100
50
0
0
1
2
Feature space
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
10
20
30
40
50
0
5
10
15
20
25
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


NAx
Contig length (kbp)
0
2
4
6
8
10
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


NGAx
Contig length (kbp)
0
2
4
6
8
10
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