Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	3	3	1	6	6	1	2	1
# contigs (>= 5000 bp)	1	3	1	6	6	1	2	1
# contigs (>= 10000 bp)	1	3	1	6	5	1	2	1
# contigs (>= 25000 bp)	1	3	1	3	5	1	1	0
# contigs (>= 50000 bp)	0	2	1	0	3	0	0	0
Total length (>= 1000 bp)	57529	161758	5226895	144448	396476	27129	45435	10441
Total length (>= 5000 bp)	48997	161758	5226895	144448	396476	27129	45435	10441
Total length (>= 10000 bp)	48997	161758	5226895	144448	390830	27129	45435	10441
Total length (>= 25000 bp)	48997	161758	5226895	95561	390830	27129	31673	0
Total length (>= 50000 bp)	0	129546	5226895	0	299374	0	0	0
# contigs	4	3	1	7	8	1	3	2
Largest contig	48997	72944	5226895	32409	116288	27129	31673	10441
Total length	58433	161758	5226895	145229	397798	27129	45979	11307
Reference length	700	700	700	700	700	700	700	700
GC (%)	44.83	43.14	44.59	42.75	43.32	38.73	41.15	43.33
Reference GC (%)	49.43	49.43	49.43	49.43	49.43	49.43	49.43	49.43
N50	48997	56602	5226895	31155	115726	27129	31673	10441
NG50	48997	72944	5226895	32409	116288	27129	31673	10441
N75	48997	56602	5226895	19191	67360	27129	13762	10441
NG75	48997	72944	5226895	32409	116288	27129	31673	10441
L50	1	2	1	3	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	1	2	1	4	3	1	2	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	1	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	1	2	1	2	1	1	0	1
# unaligned contigs	0 + 3 part	0 + 3 part	0 + 1 part	1 + 5 part	0 + 6 part	0 + 1 part	0 + 2 part	0 + 2 part
Unaligned length	55432	159981	5226009	142503	395098	26904	45227	10592
Genome fraction (%)	96.143	100.000	100.000	100.000	96.143	24.714	85.429	74.286
Duplication ratio	4.459	2.539	1.266	3.894	4.012	1.301	1.258	1.375
# N's per 100 kbp	1841.43	40.80	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	1485.88	1714.29	1000.00	5428.57	4754.83	5202.31	1003.34	2884.62
# indels per 100 kbp	297.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	642	700	700	700	645	128	496	376
Total aligned length	1664	1711	886	2570	2449	225	704	774
NGA50	642	700	700	700	645	-	496	376
NGA75	642	700	700	700	645	-	106	176
LGA50	1	1	1	1	1	-	1	1
LGA75	1	1	1	1	1	-	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

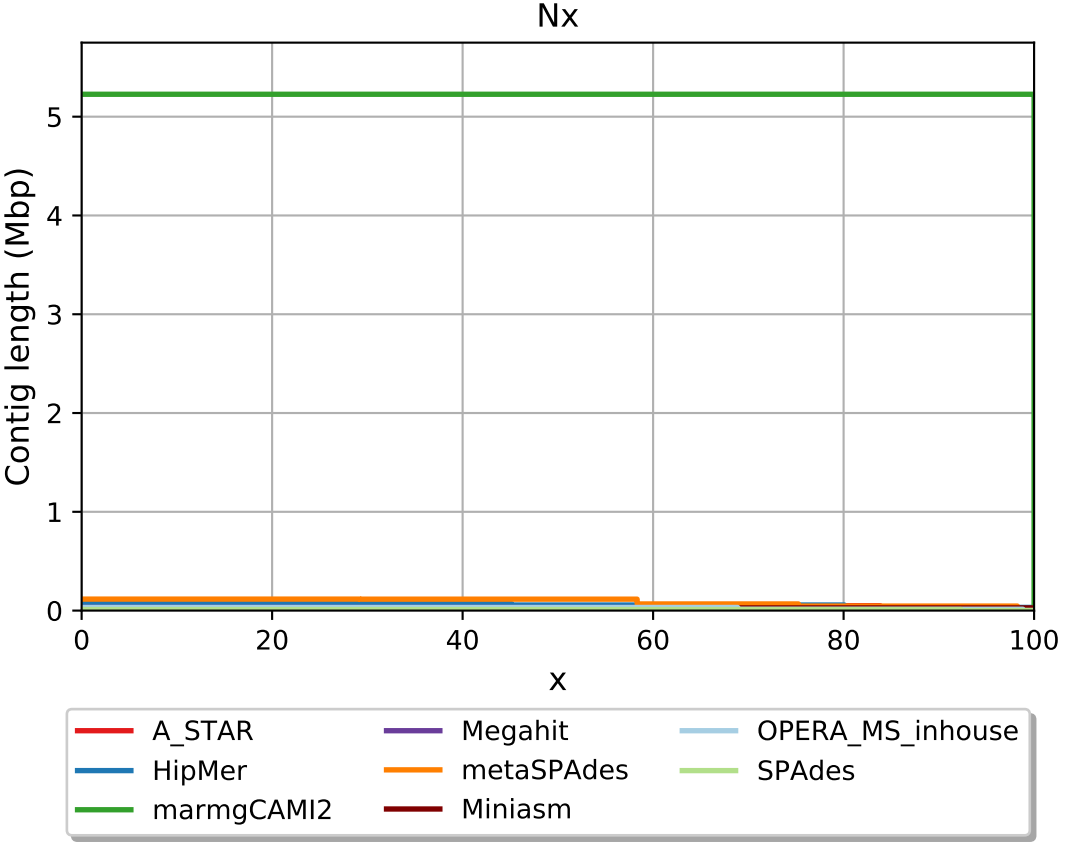
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	1	1	0	3	5	0	2	1
# possible misassemblies	1	1	0	3	7	0	3	1
# local misassemblies	0	0	0	0	1	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	1	2	1	2	1	1	0	1
# mismatches	10	12	7	38	32	9	6	15
# indels	2	0	0	0	0	0	0	0
# indels (<= 5 bp)	0	0	0	0	0	0	0	0
# indels (> 5 bp)	2	0	0	0	0	0	0	0
Indels length	60	0	0	0	0	0	0	0

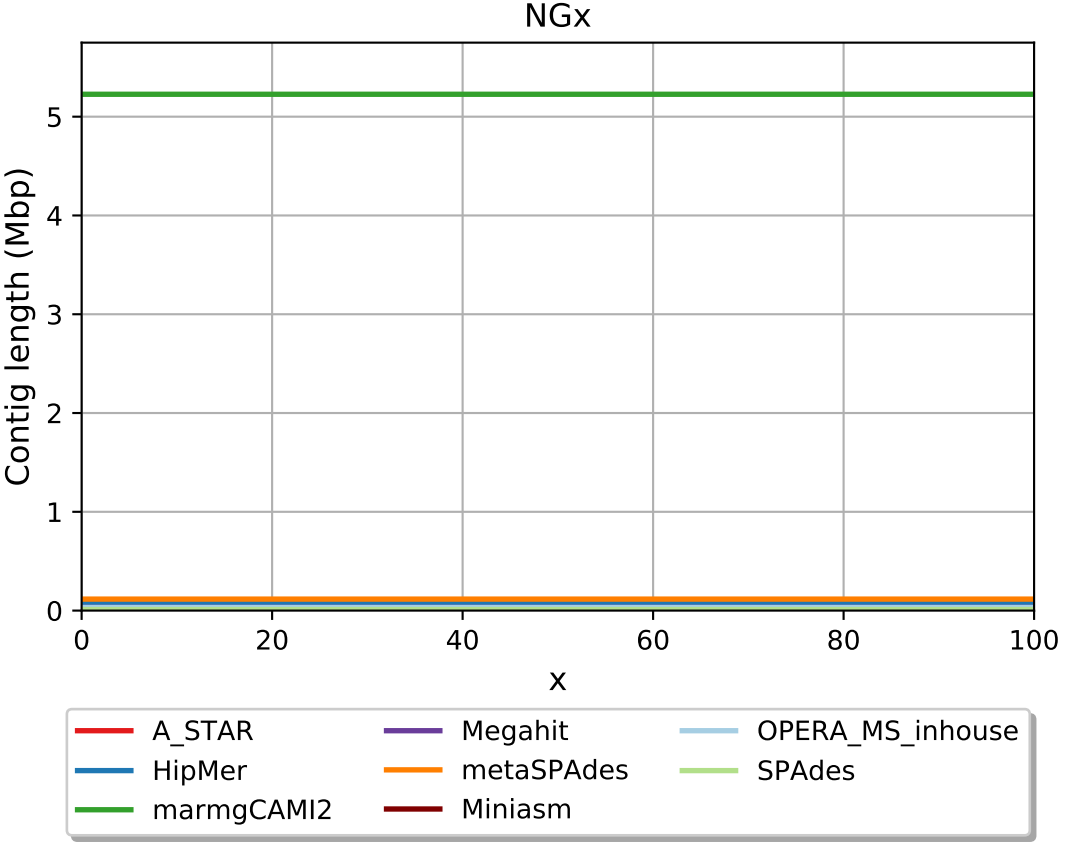
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

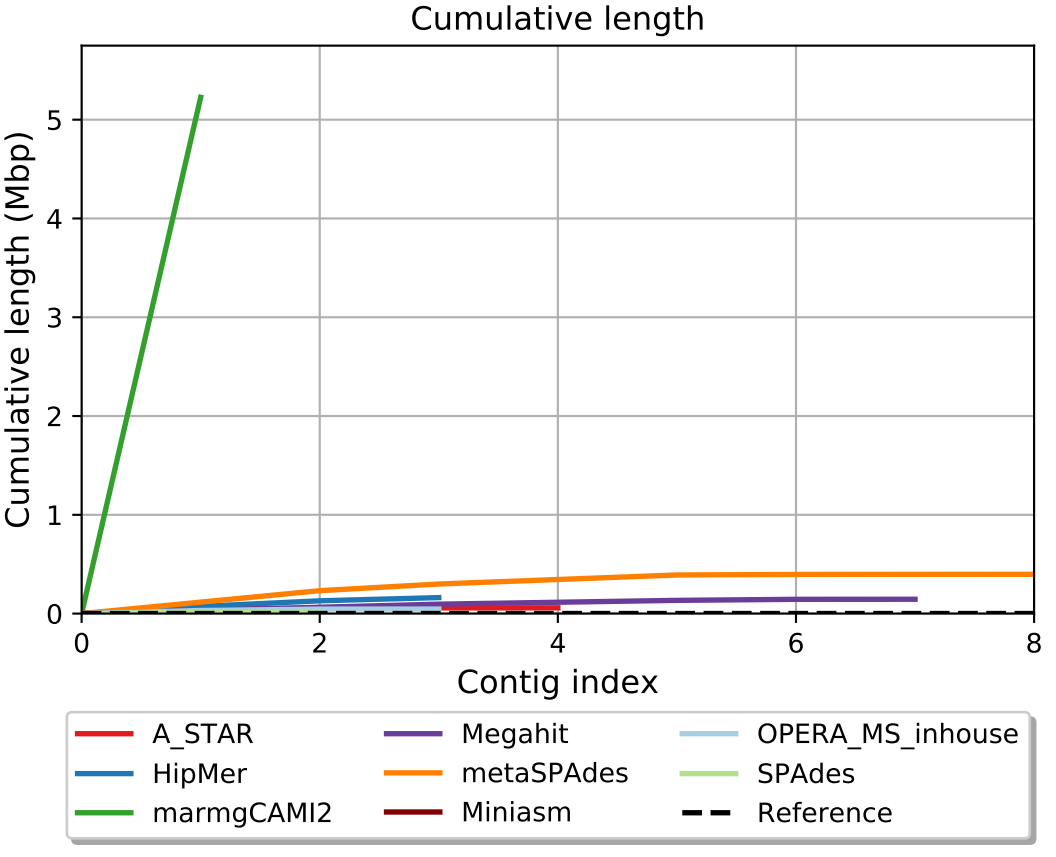
Unaligned report

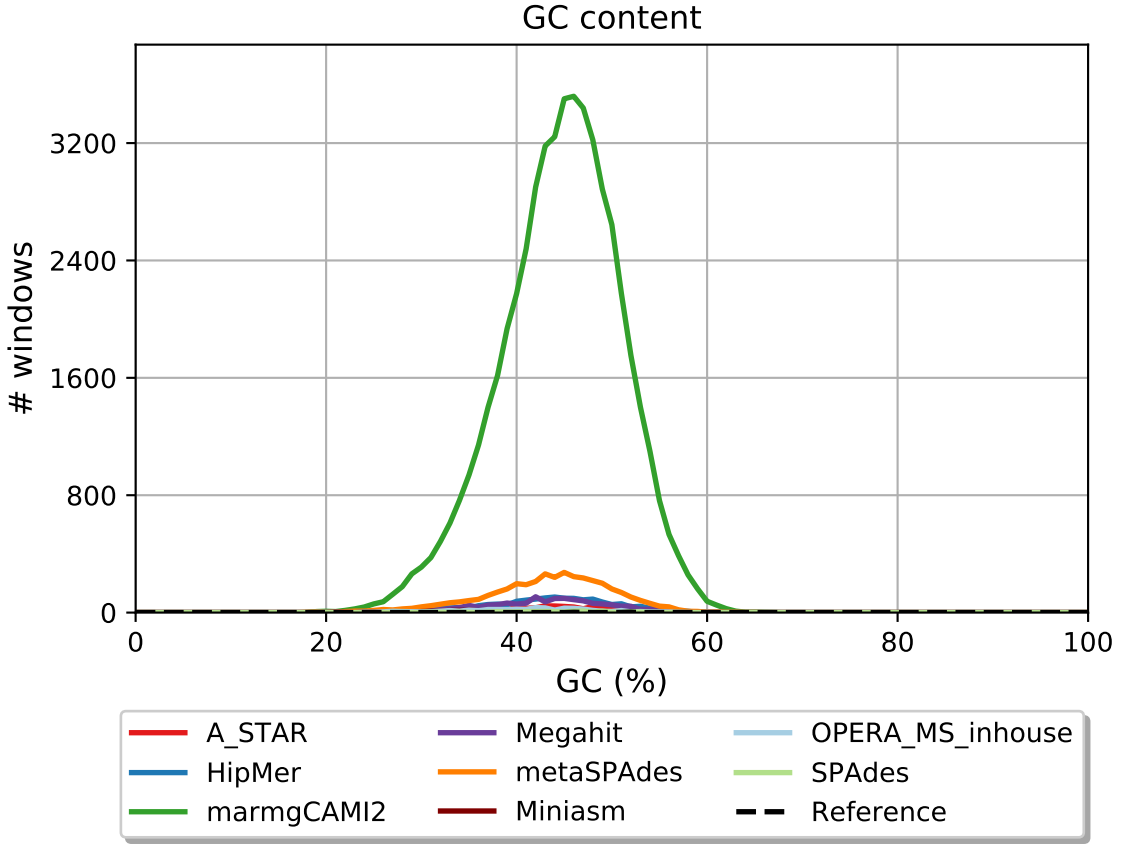
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	1	0	0	0	0
Fully unaligned length	0	0	0	31997	0	0	0	0
# partially unaligned contigs	3	3	1	5	6	1	2	2
Partially unaligned length	55432	159981	5226009	110506	395098	26904	45227	10592
# N's	1076	66	0	0	0	0	0	0

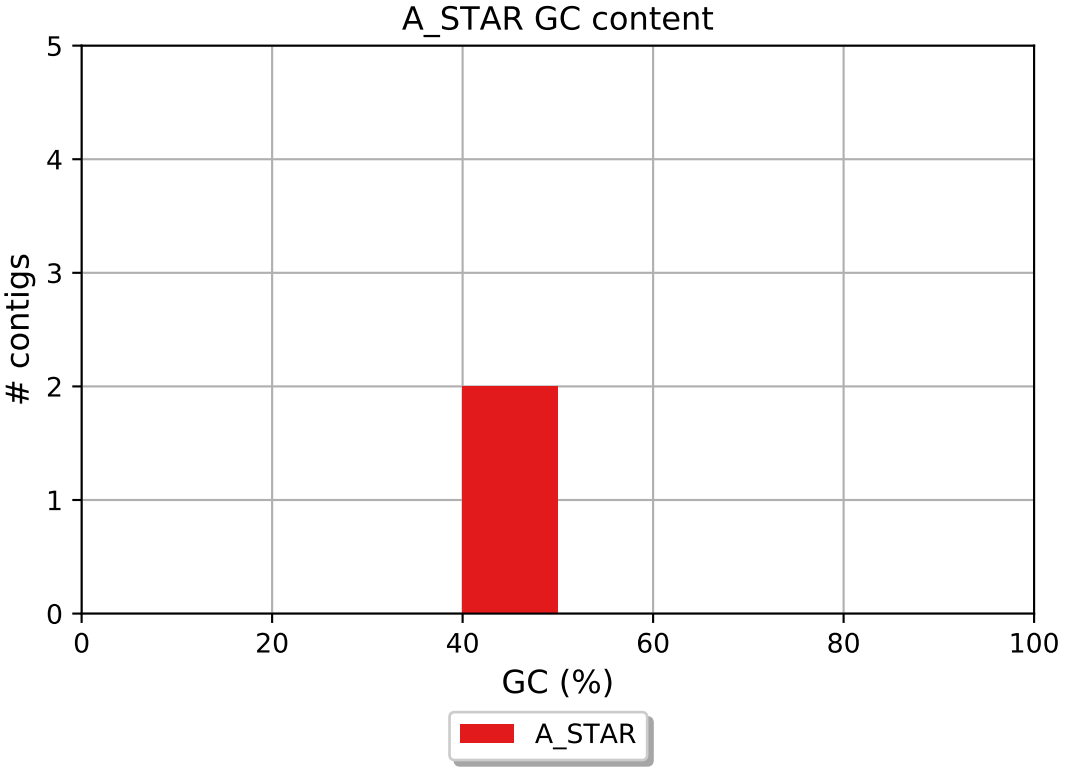
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

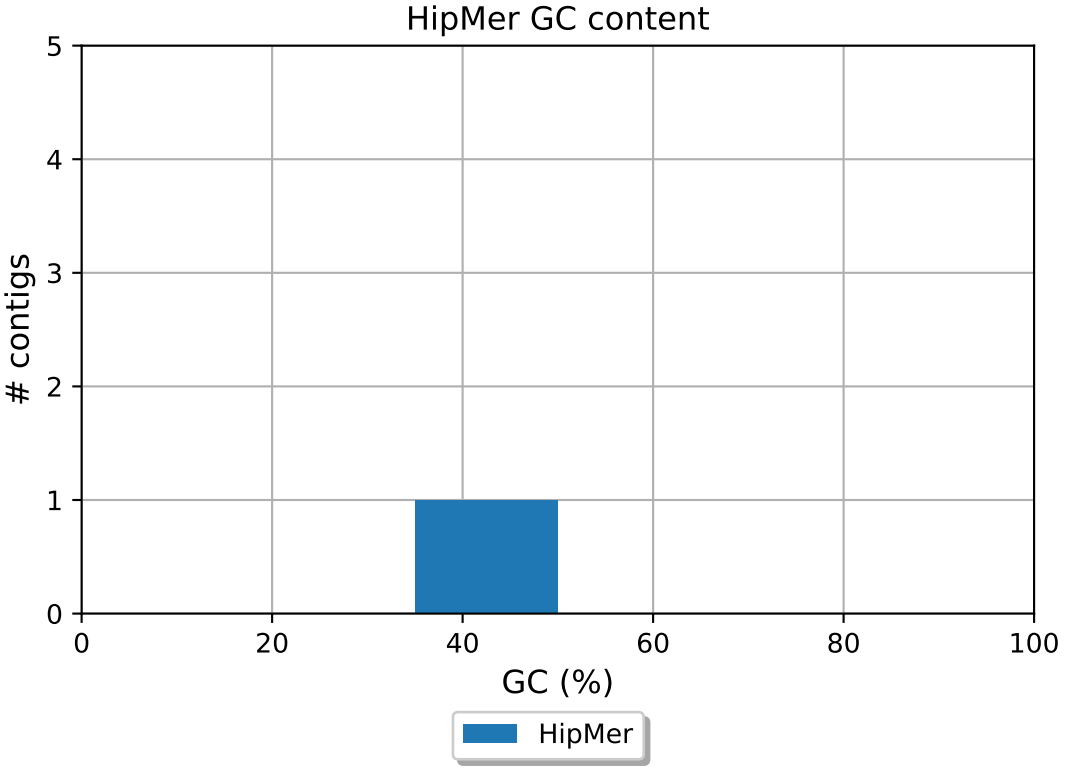

Nx
Contig length (Mbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

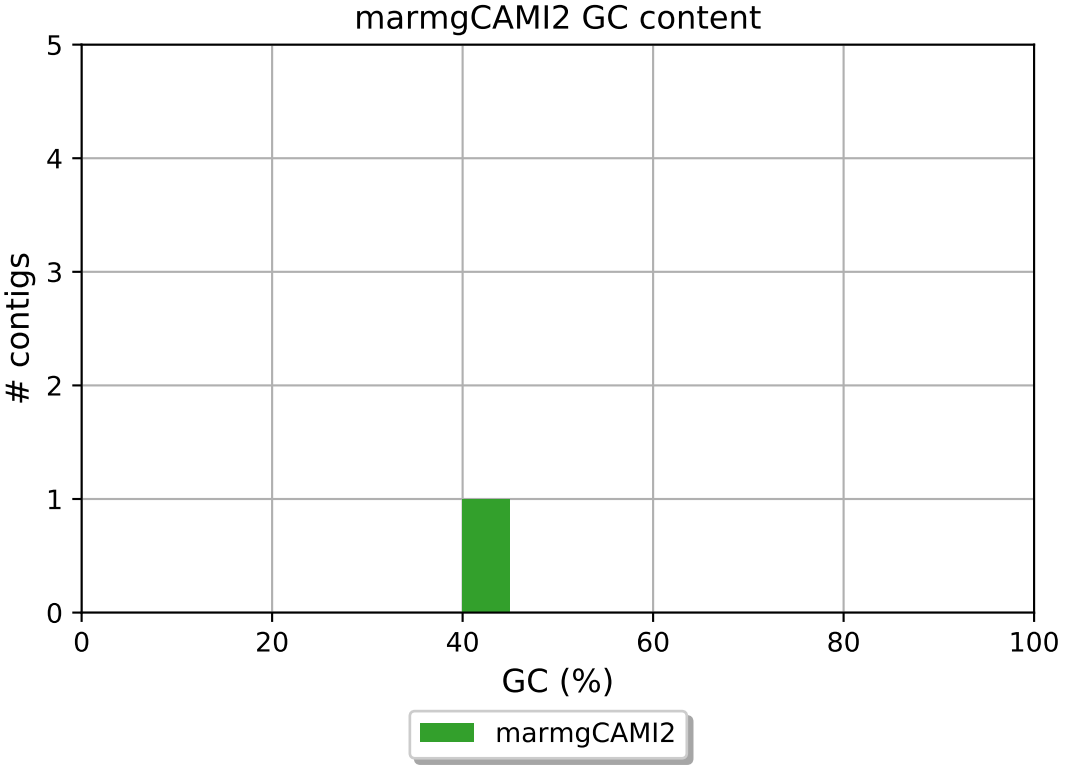

NGx
Contig length (Mbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

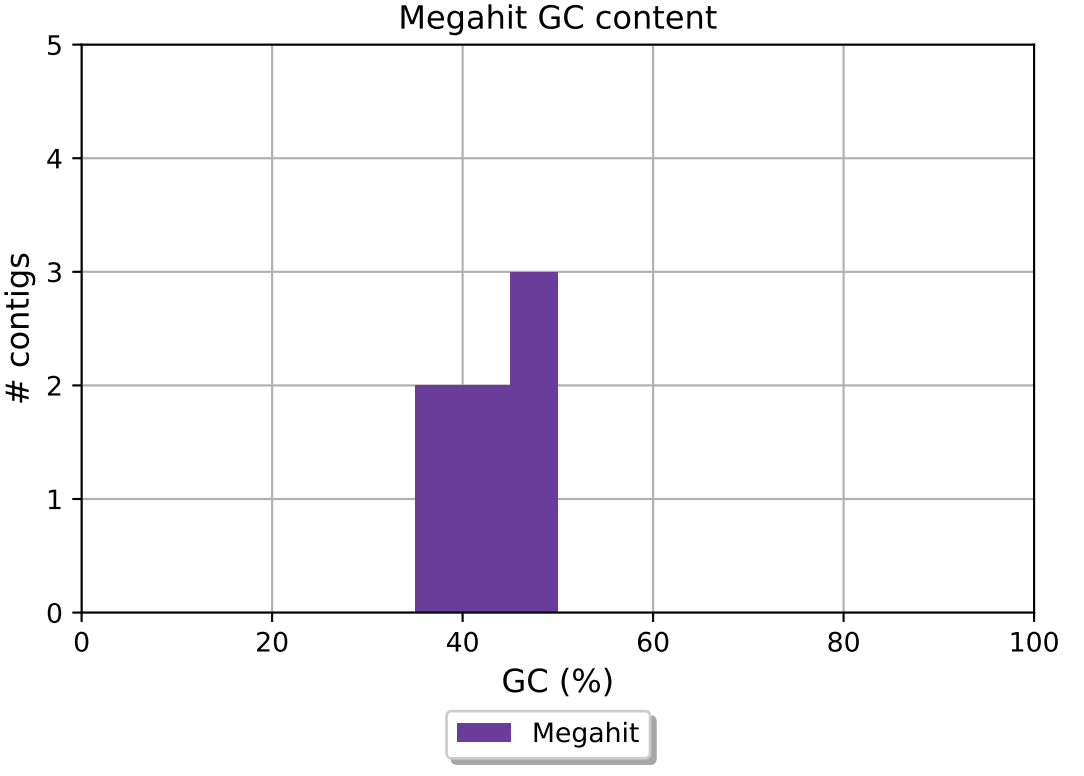

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
2
4
6
8
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

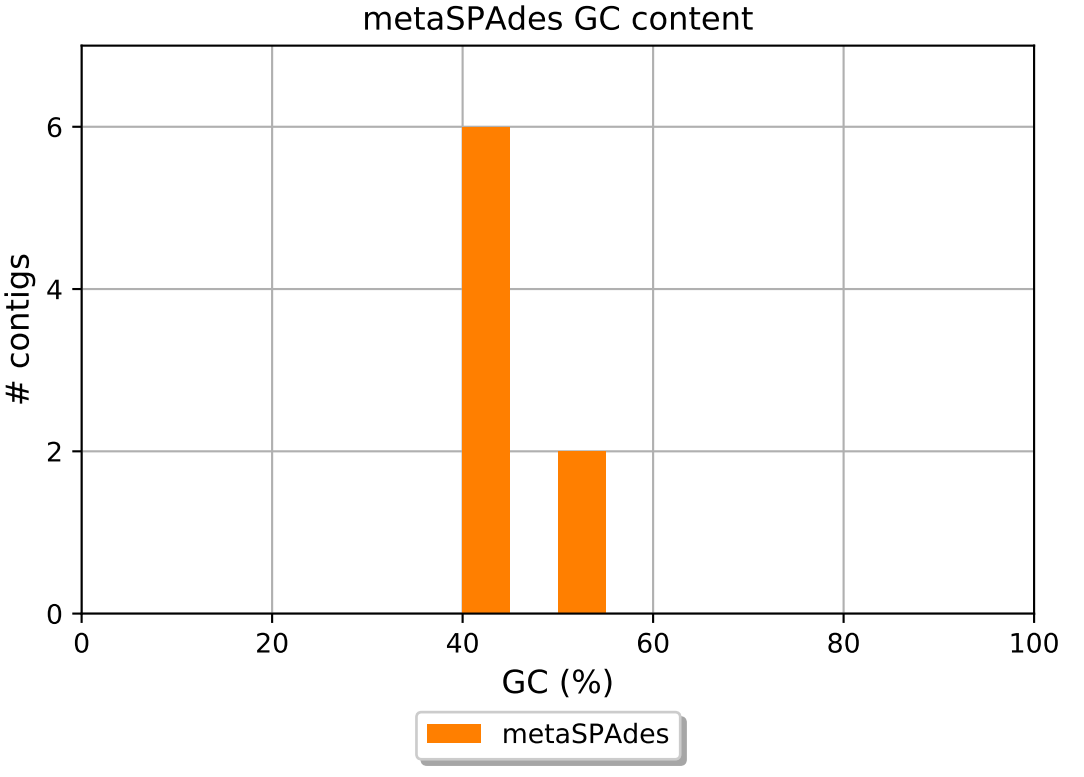

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

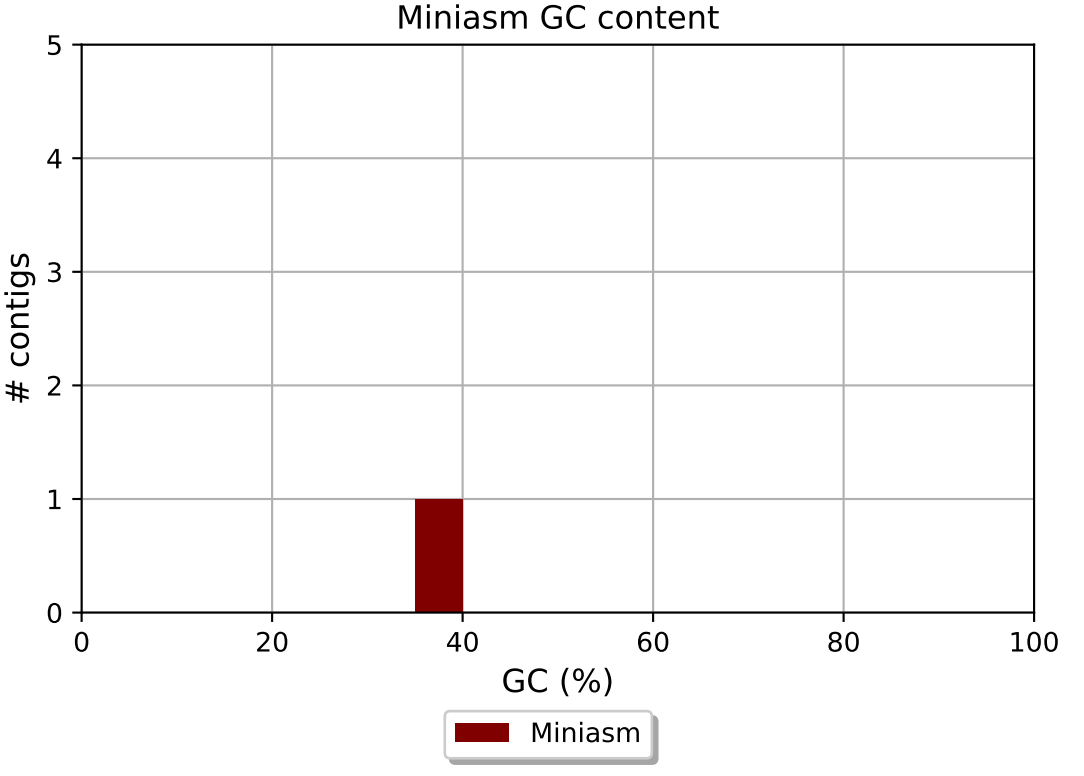

A_STAR GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
A_STAR

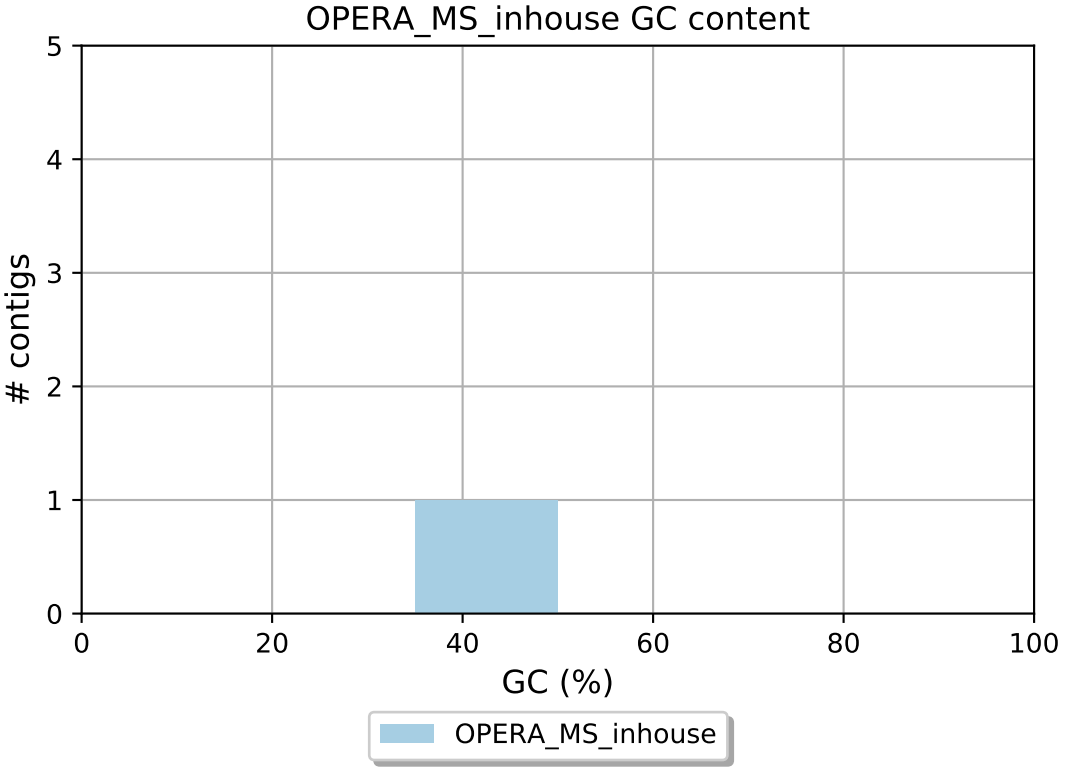

HipMer GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
HipMer

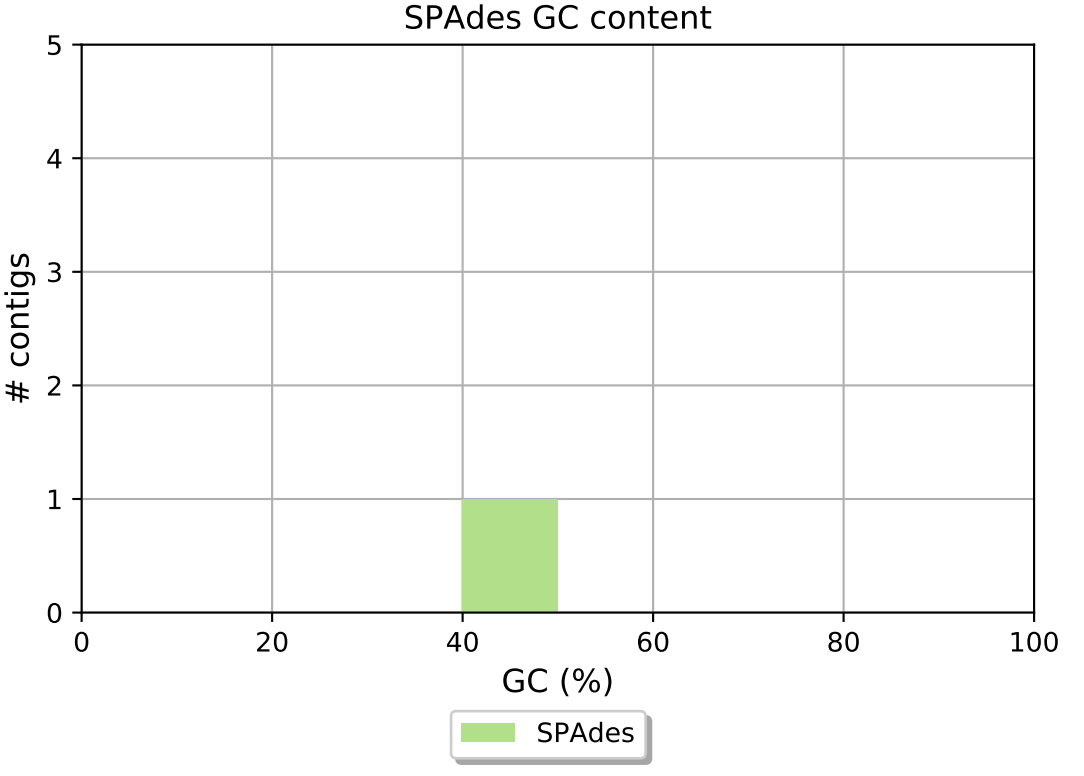

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

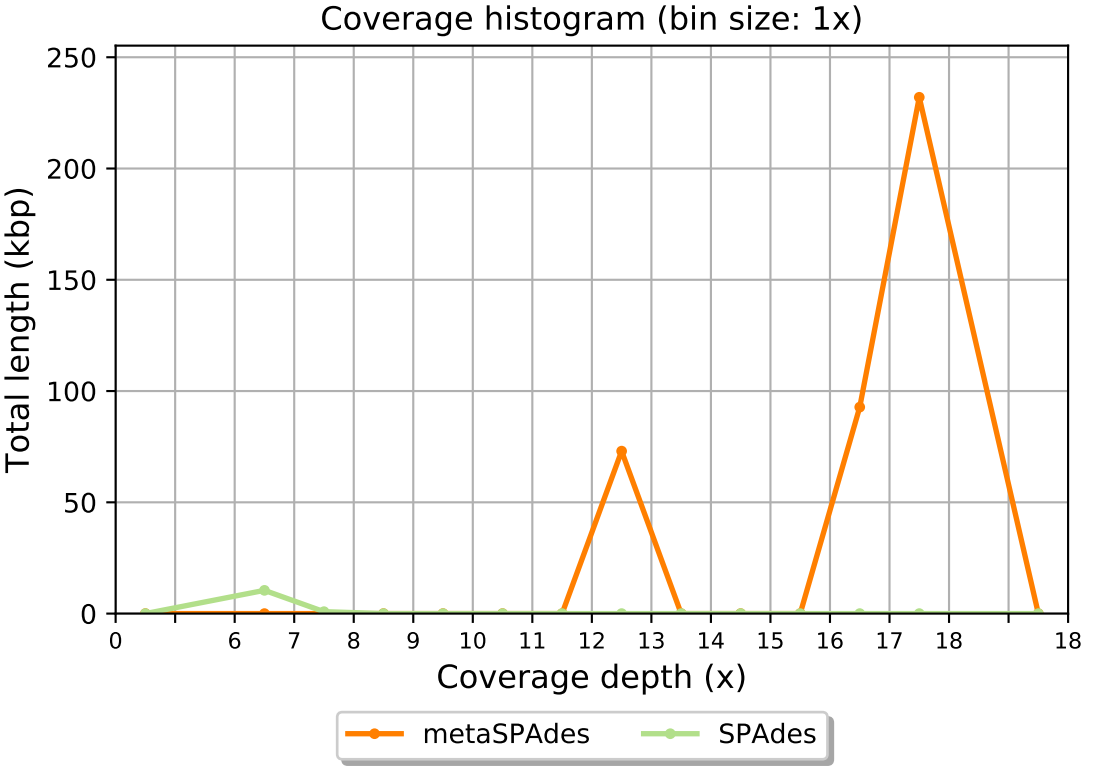

Megahit GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Megahit

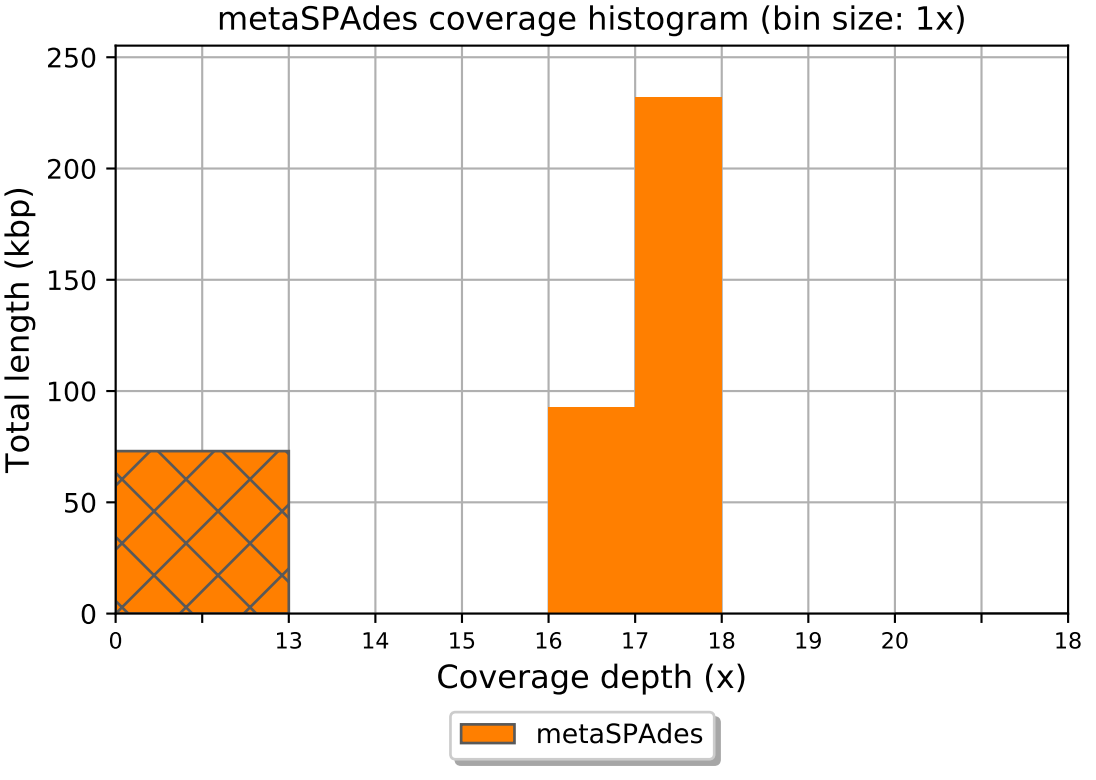

metaSPAdes GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
metaSPAdes

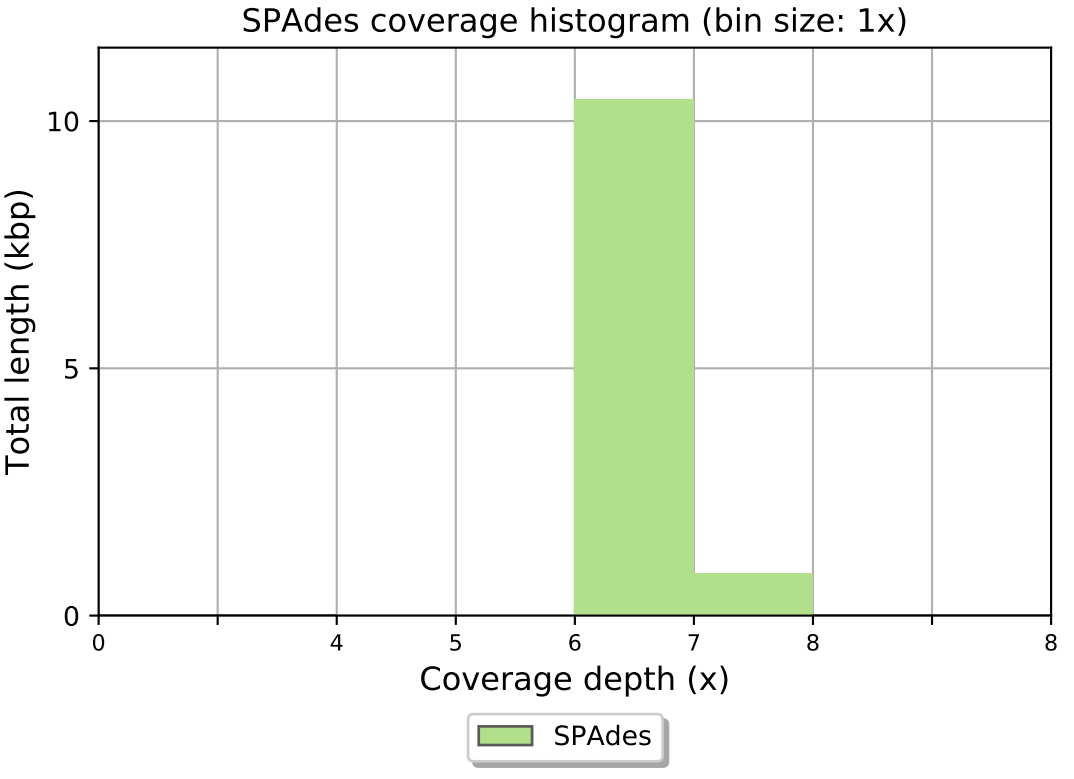

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

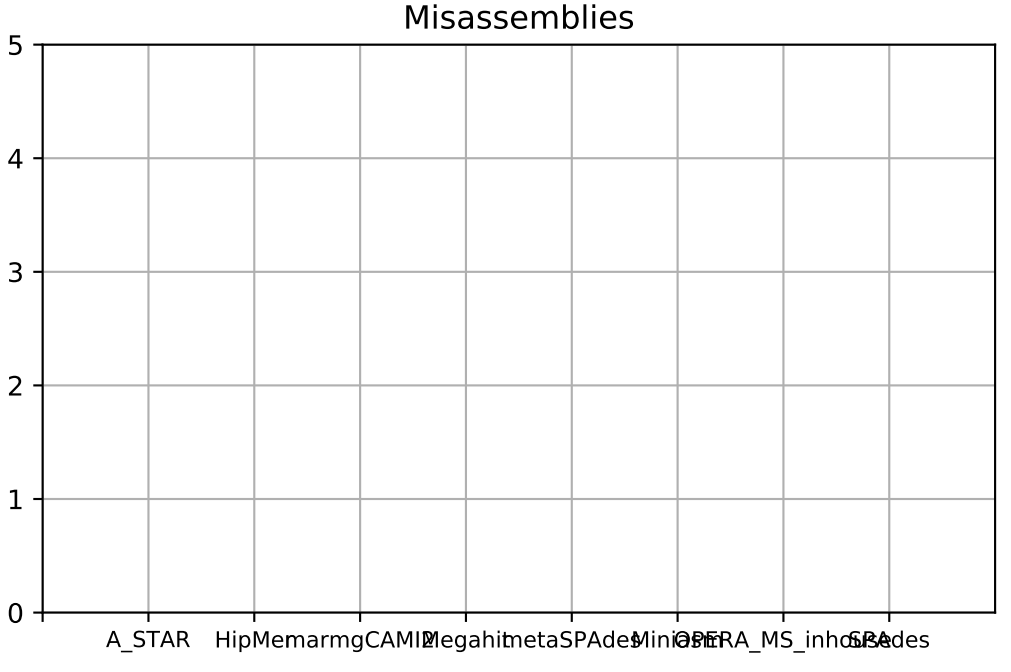

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

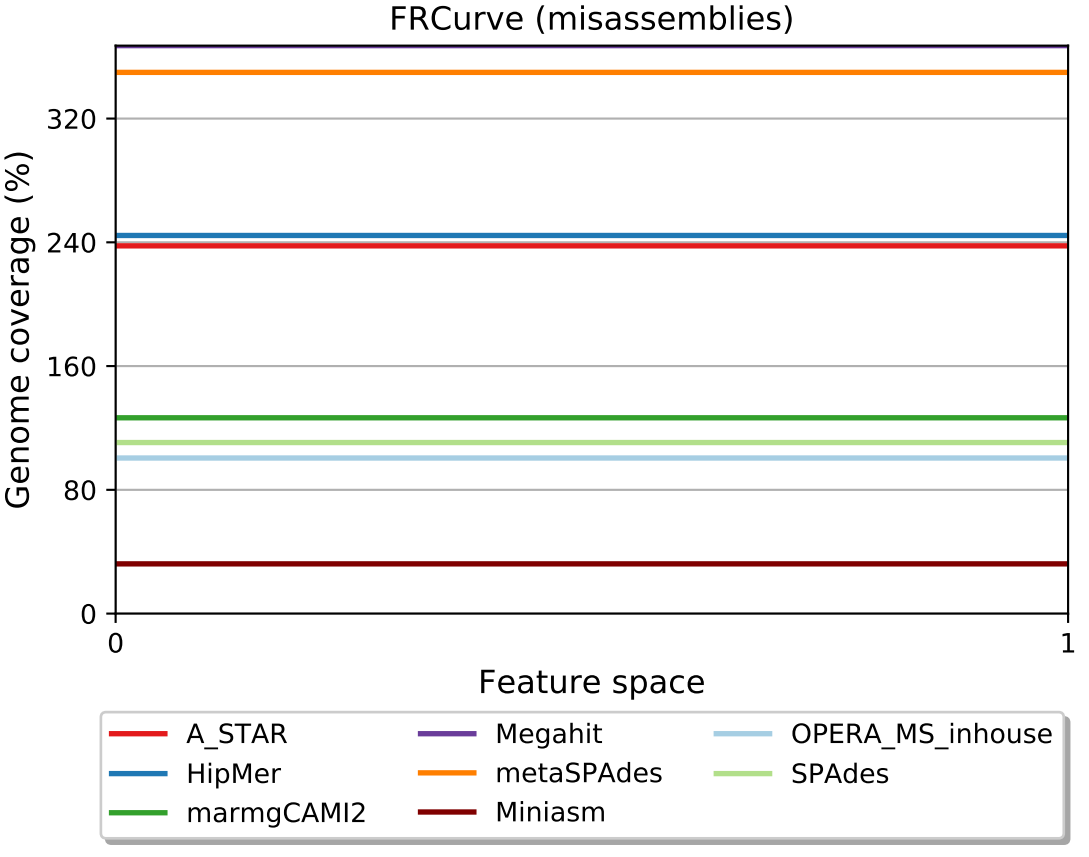

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

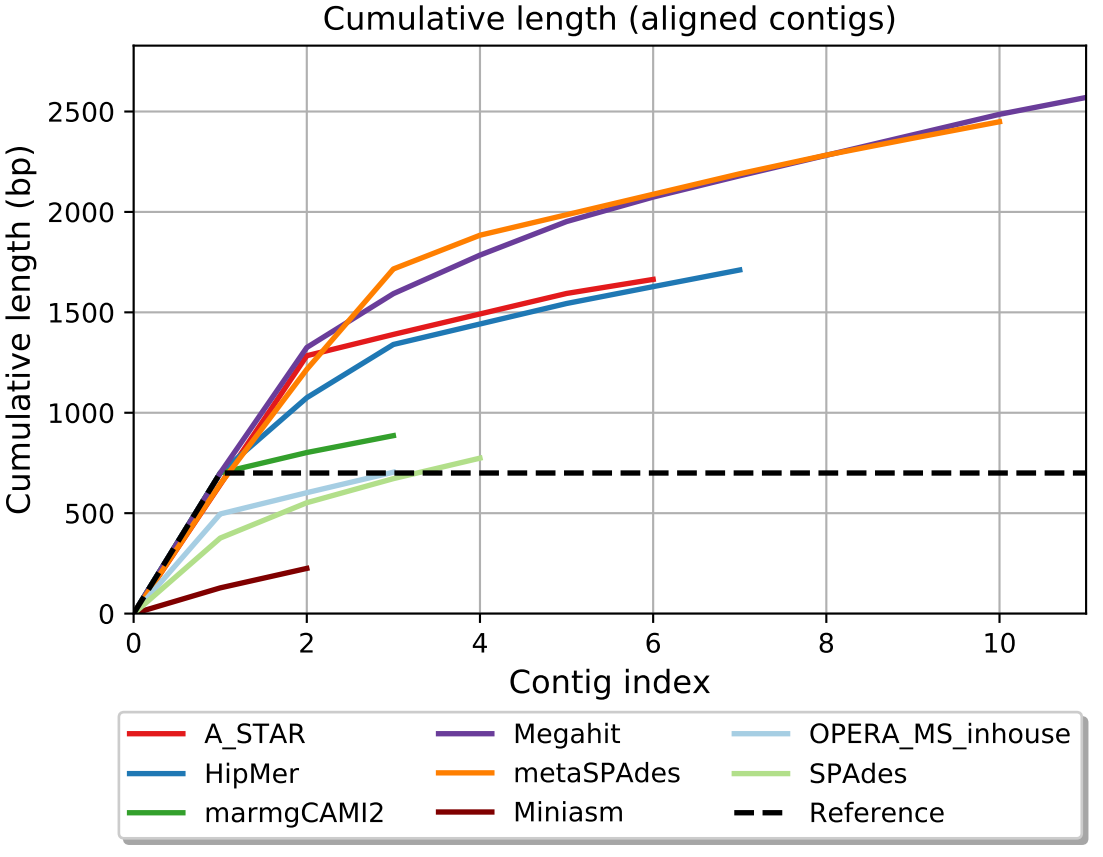

Coverage histogram (bin size: 1x)
Total length (kbp)
250
200
150
100
50
0
0
6
7
8
9
10
11
12
13
14
15
16
17
18
18
Coverage depth (x)
metaSPAdes
SPAdes

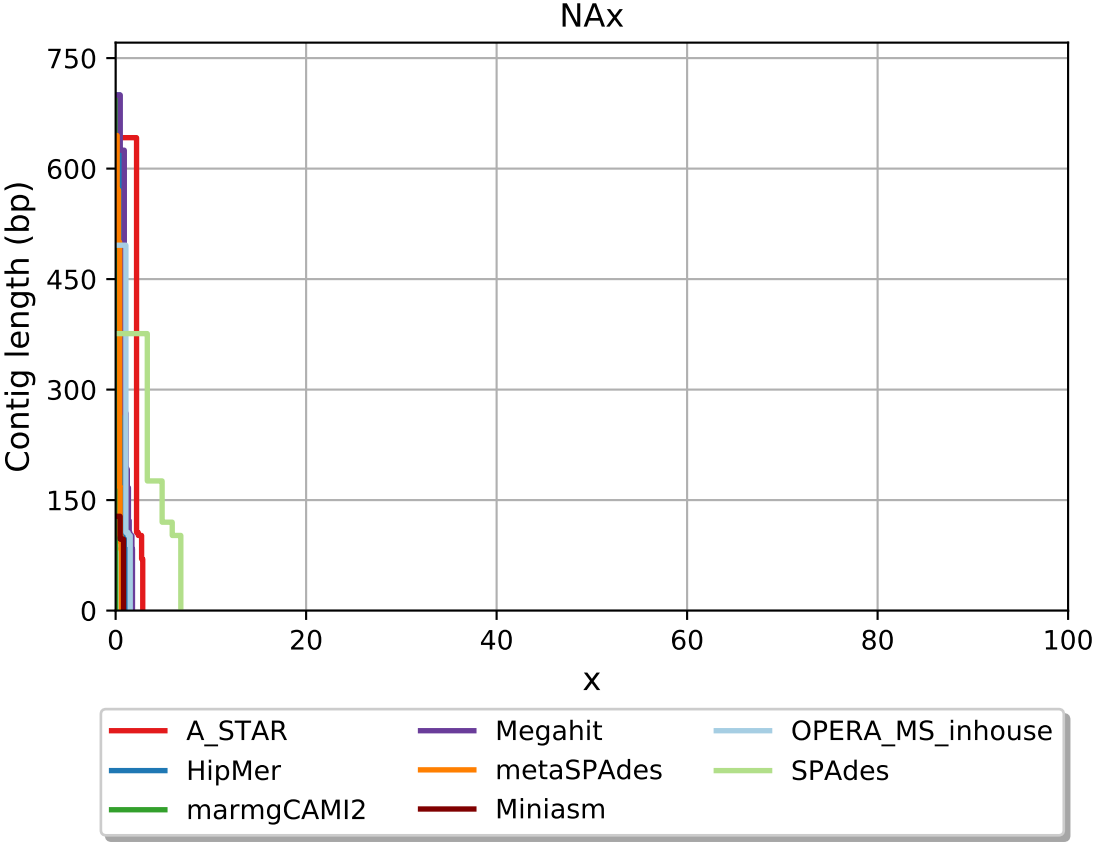

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
250
200
150
100
50
0
0
13
14
15
16
17
18
19
20
18
Coverage depth (x)
metaSPAdes

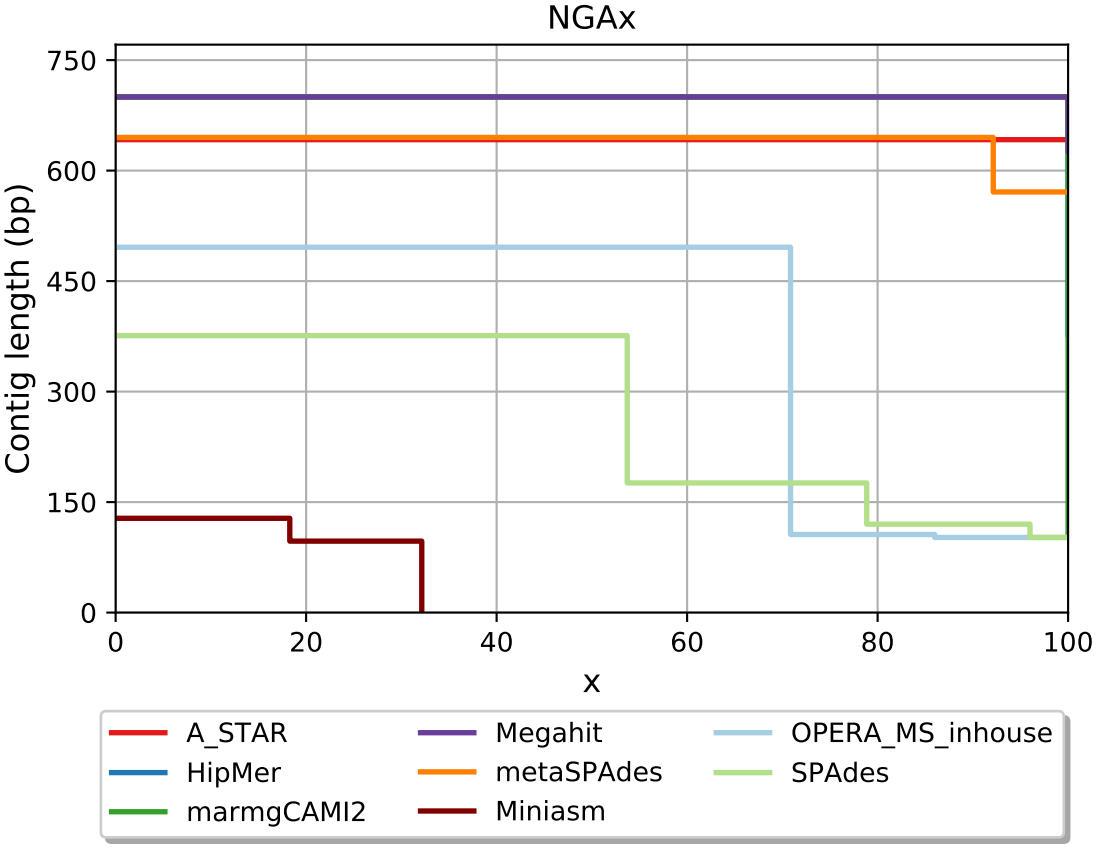

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
10
5
0
0
4
5
6
7
8
8
Coverage depth (x)
SPAdes

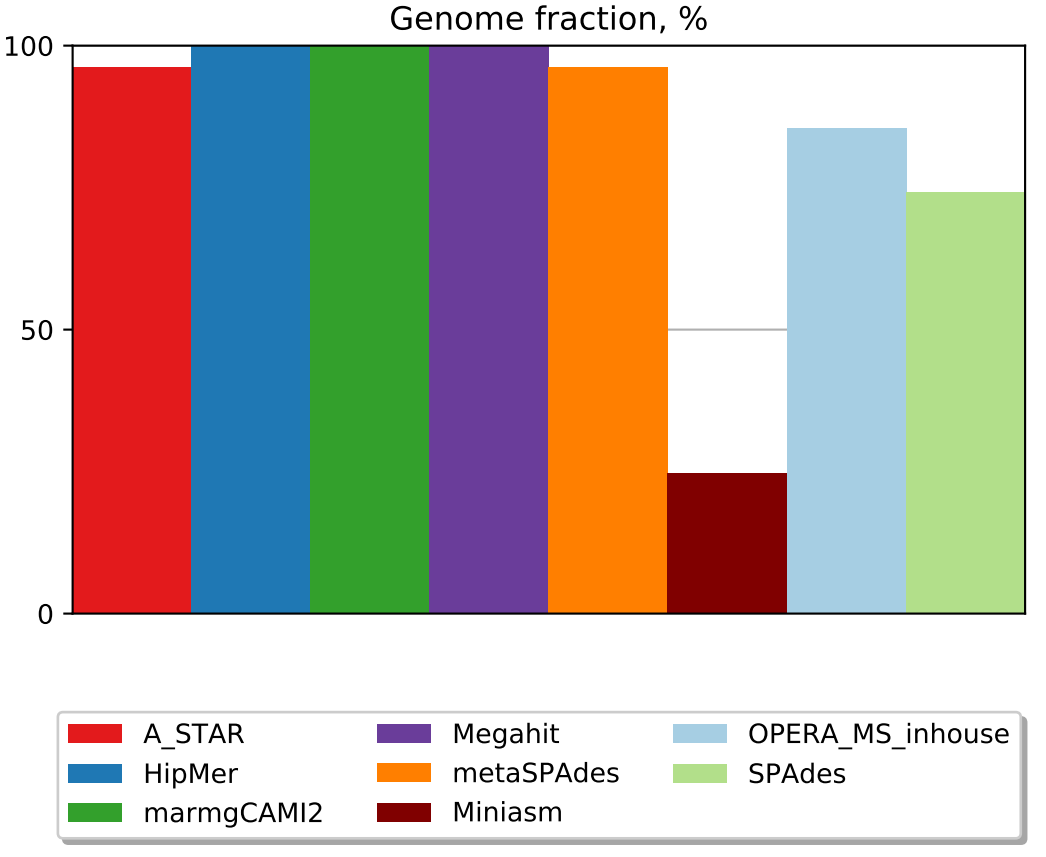

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL2
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes


FRCurve (misassemblies)
Genome coverage (%)
320
240
160
80
0
0
1
Feature space
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Cumulative length (aligned contigs)
Cumulative length (bp)
2500
2000
1500
1000
500
0
0
2
4
6
8
10
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