Report

	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	1	16	6	1	9	9	1	3	3
# contigs (>= 5000 bp)	0	12	6	1	9	9	1	3	3
# contigs (>= 10000 bp)	0	10	6	1	9	9	1	3	3
# contigs (>= 25000 bp)	0	10	6	1	9	9	1	3	3
# contigs (>= 50000 bp)	0	2	6	1	9	9	1	3	3
Total length (>= 1000 bp)	1751	467122	1733750	5197896	2541353	2220491	407302	911169	907922
Total length (>= 5000 bp)	0	458624	1733750	5197896	2541353	2220491	407302	911169	907922
Total length (>= 10000 bp)	0	444868	1733750	5197896	2541353	2220491	407302	911169	907922
Total length (>= 25000 bp)	0	444868	1733750	5197896	2541353	2220491	407302	911169	907922
Total length (>= 50000 bp)	0	121008	1733750	5197896	2541353	2220491	407302	911169	907922
# contigs	5	16	7	1	9	9	1	3	3
Largest contig	1751	60504	544740	5197896	543510	449204	407302	499331	544558
Total length	4488	467122	1734559	5197896	2541353	2220491	407302	911169	907922
Reference length	5418	5418	5418	5418	5418	5418	5418	5418	5418
GC (%)	37.04	41.58	41.46	41.45	41.50	41.54	42.37	41.38	41.31
Reference GC (%)	38.58	38.58	38.58	38.58	38.58	38.58	38.58	38.58	38.58
N50	868	46131	543682	5197896	543403	405883	407302	499331	544558
NG50	678	60504	544740	5197896	543510	449204	407302	499331	544558
N75	648	34607	170977	5197896	171079	169618	407302	288702	306195
NG75	543	60504	544740	5197896	543510	449204	407302	499331	544558
L50	2	5	2	1	3	3	1	1	1
LG50	3	1	1	1	1	1	1	1	1
L75	4	8	4	1	5	6	1	2	2
LG75	5	1	1	1	1	1	1	1	1
# misassemblies	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	1	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 16 part	0 + 6 part	0 + 1 part	0 + 9 part	0 + 9 part	0 + 1 part	0 + 3 part	0 + 3 part
Unaligned length	0	456908	1723422	5192478	2529069	2204237	405422	905797	902404
Genome fraction (%)	65.282	63.529	100.000	100.000	100.000	100.000	34.072	100.000	100.000
Duplication ratio	1.269	2.967	2.056	1.000	2.267	3.000	1.018	0.992	1.018
# N's per 100 kbp	311.94	0.86	5.59	0.00	0.00	0.00	0.00	0.00	11.01
# mismatches per 100 kbp	0.00	871.59	0.00	0.00	295.31	0.00	595.88	369.14	0.00
# indels per 100 kbp	28.27	174.32	0.00	0.00	36.91	0.00	2925.24	221.48	0.00
Largest alignment	1751	2051	4504	4504	4370	4504	1880	4458	4504
Total aligned length	3647	10212	10759	5418	12284	16254	1880	5372	5418
NA50	678	-	-	-	-	-	-	-	-
NGA50	543	2051	4504	4504	4370	4504	-	4458	4504
NA75	471	-	-	-	-	-	-	-	-
NGA75	-	2051	4504	4504	4370	4504	-	4458	4504
LA50	2	-	-	-	-	-	-	-	-
LGA50	3	2	1	1	1	1	-	1	1
LA75	4	-	-	-	-	-	-	-	-
LGA75	-	2	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

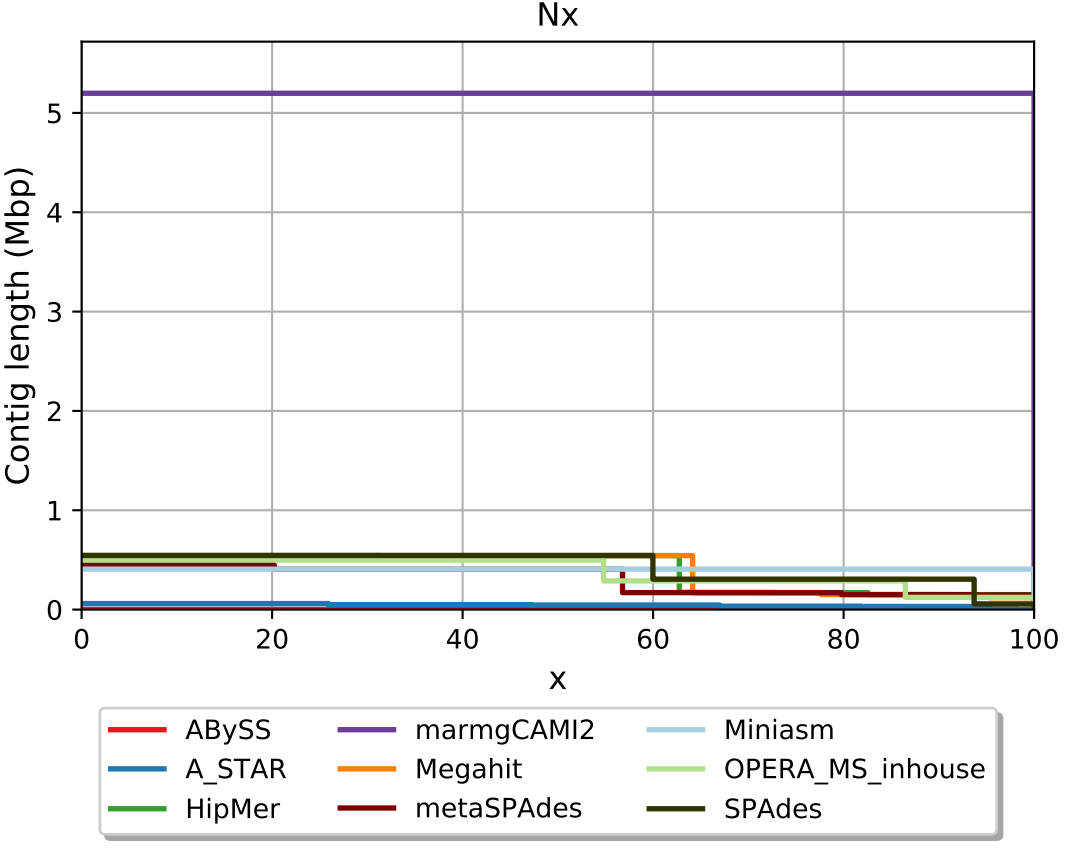
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0
# possibly misassembled contigs	0	16	6	0	9	9	1	3	3
# possible misassemblies	0	20	9	0	12	12	2	4	4
# local misassemblies	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	1	0	0	0	0	0
# mismatches	0	30	0	0	16	0	11	20	0
# indels	1	6	0	0	2	0	54	12	0
# indels (<= 5 bp)	0	2	0	0	0	0	54	11	0
# indels (> 5 bp)	1	4	0	0	2	0	0	1	0
Indels length	7	150	0	0	332	0	66	74	0

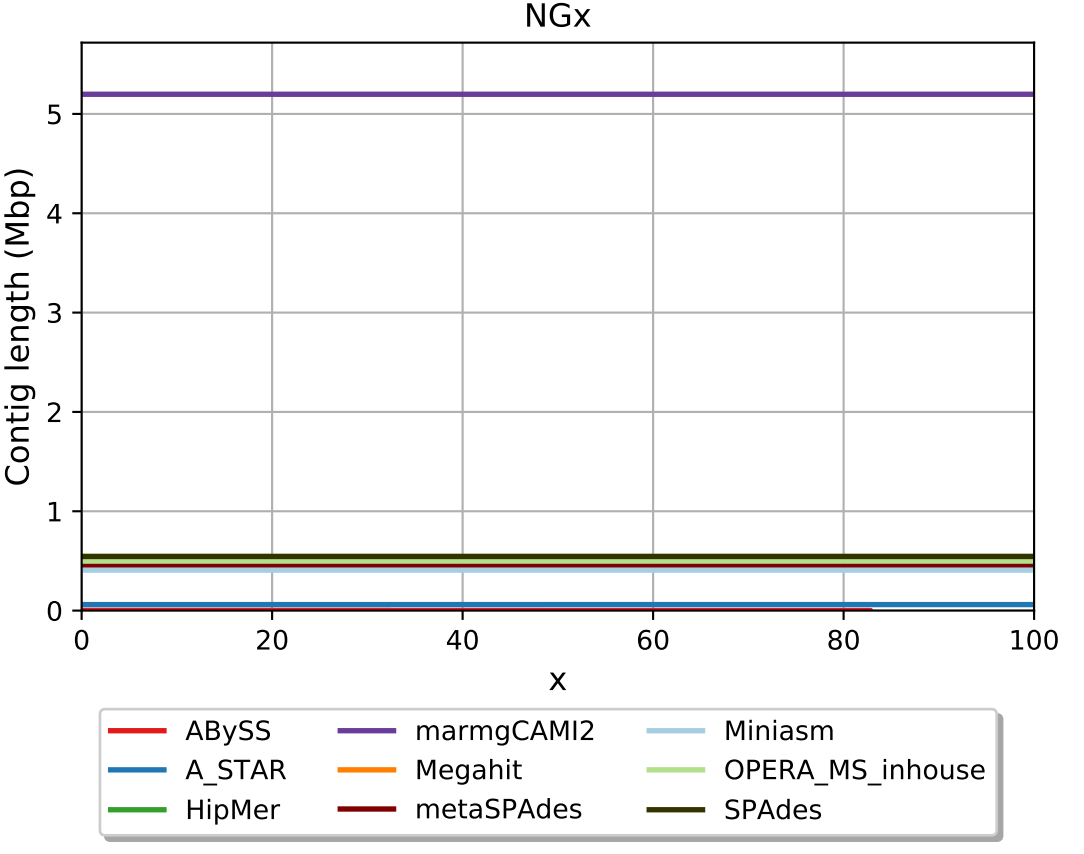
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

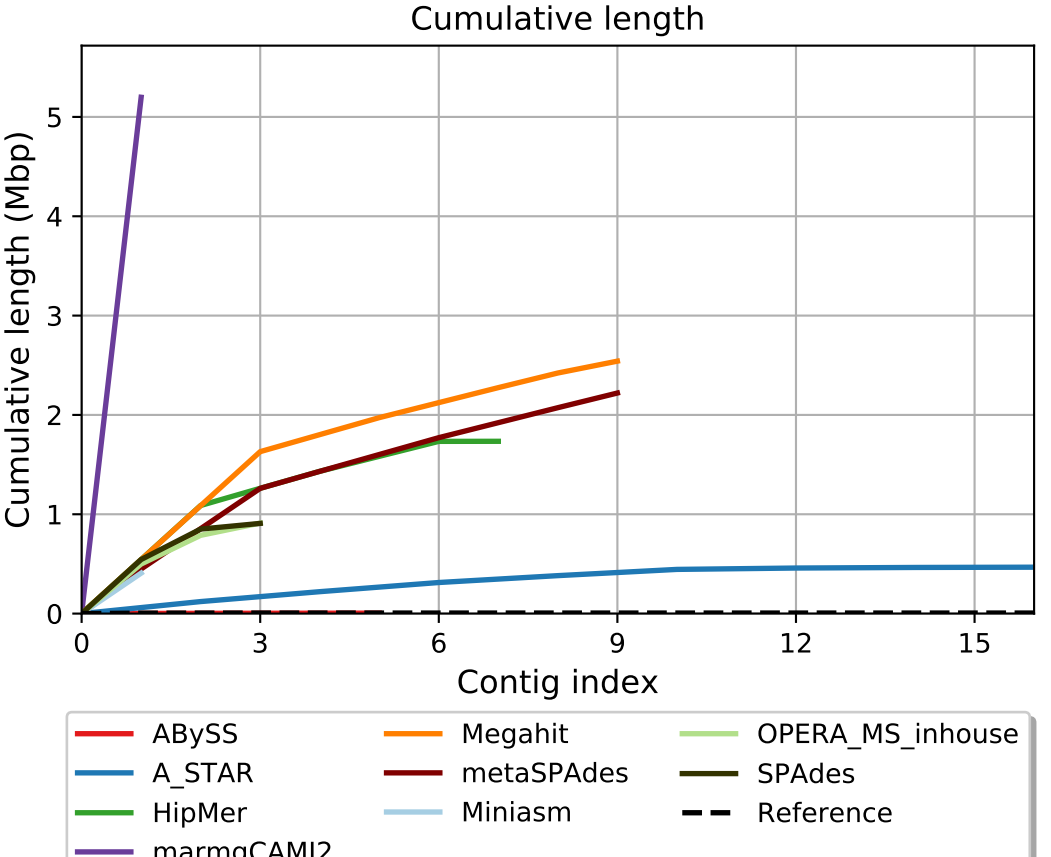
Unaligned report

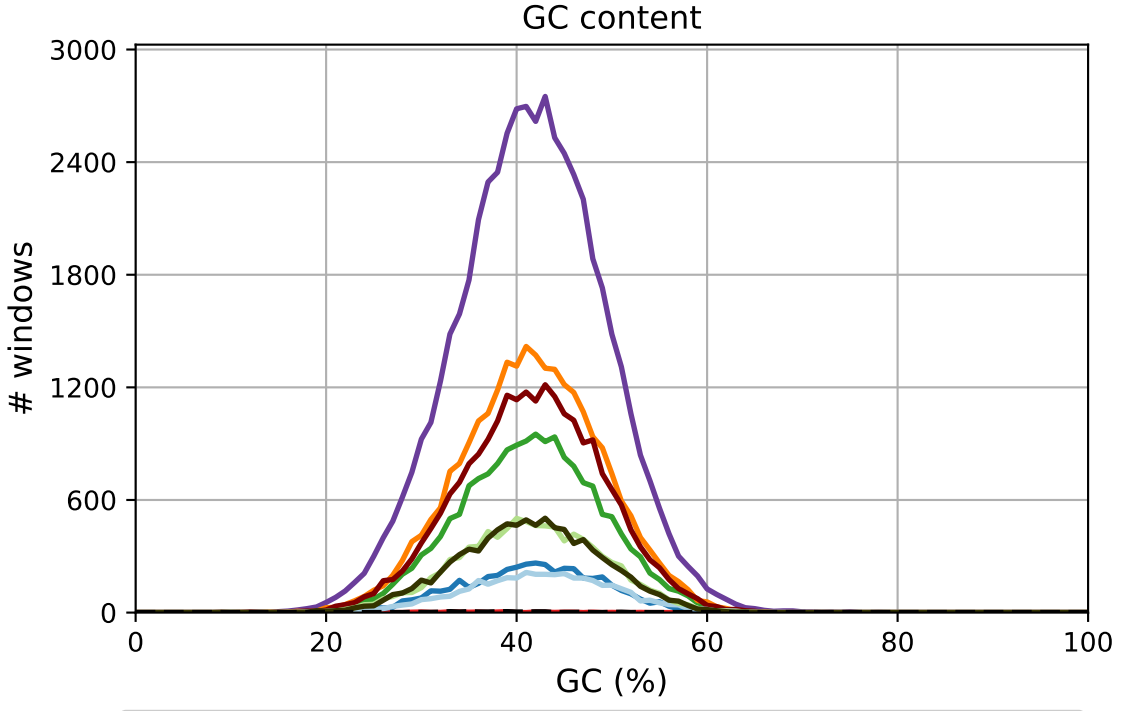
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	0	16	6	1	9	9	1	3	3
Partially unaligned length	0	456908	1723422	5192478	2529069	2204237	405422	905797	902404
# N's	14	4	97	0	0	0	0	0	100

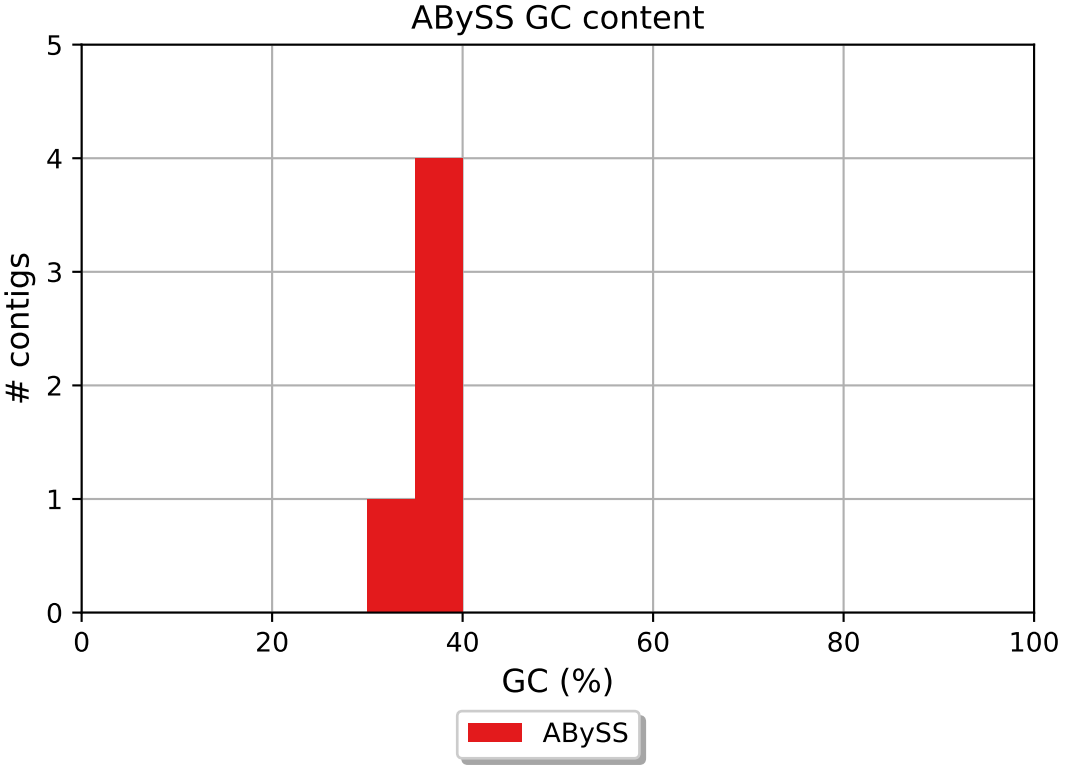
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

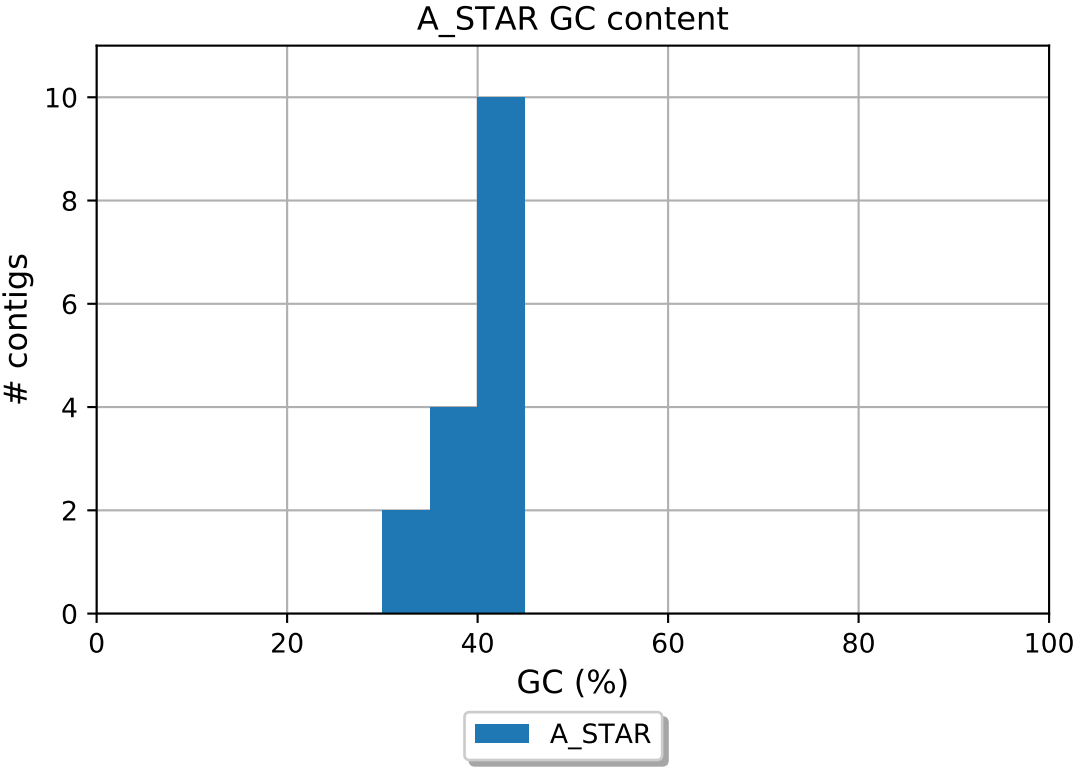

Nx
Contig length (Mbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

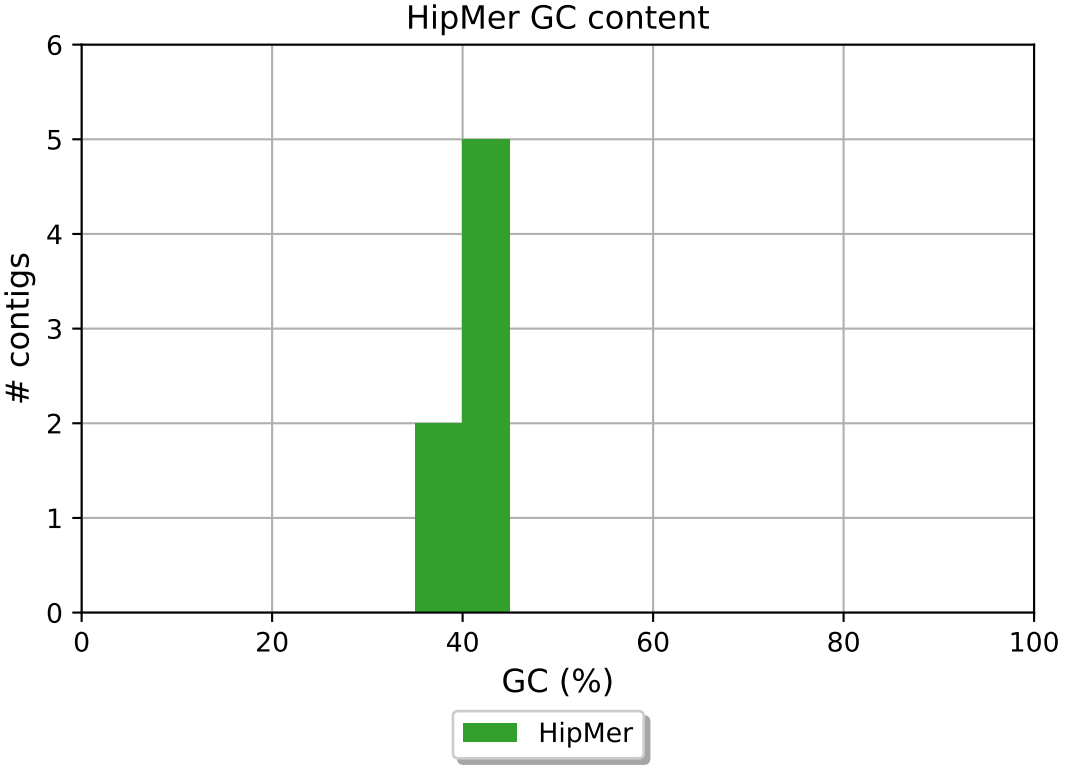

NGx
Contig length (Mbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

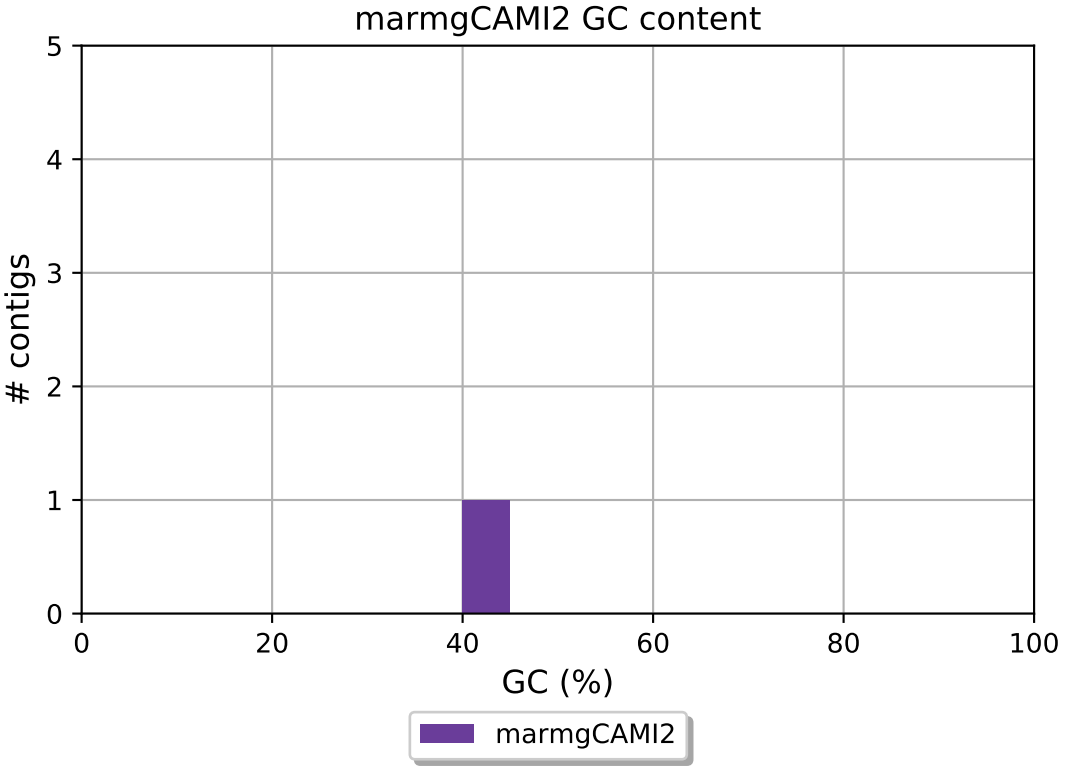

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
3
6
9
12
15
Contig index
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

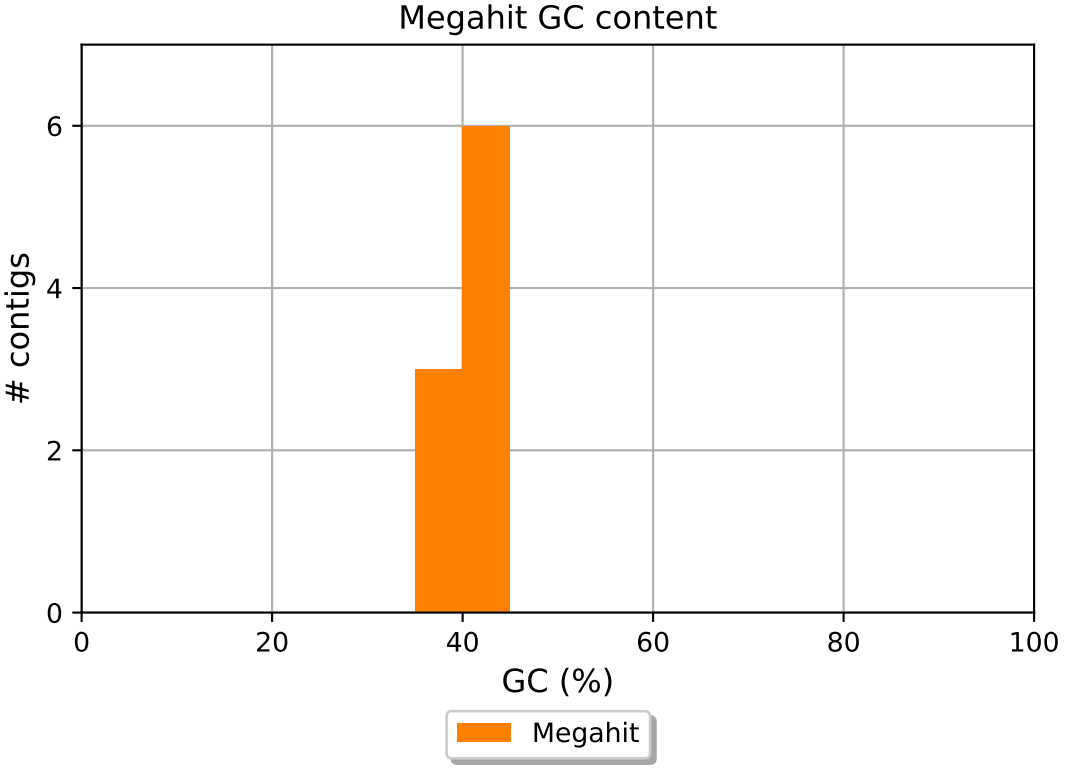

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

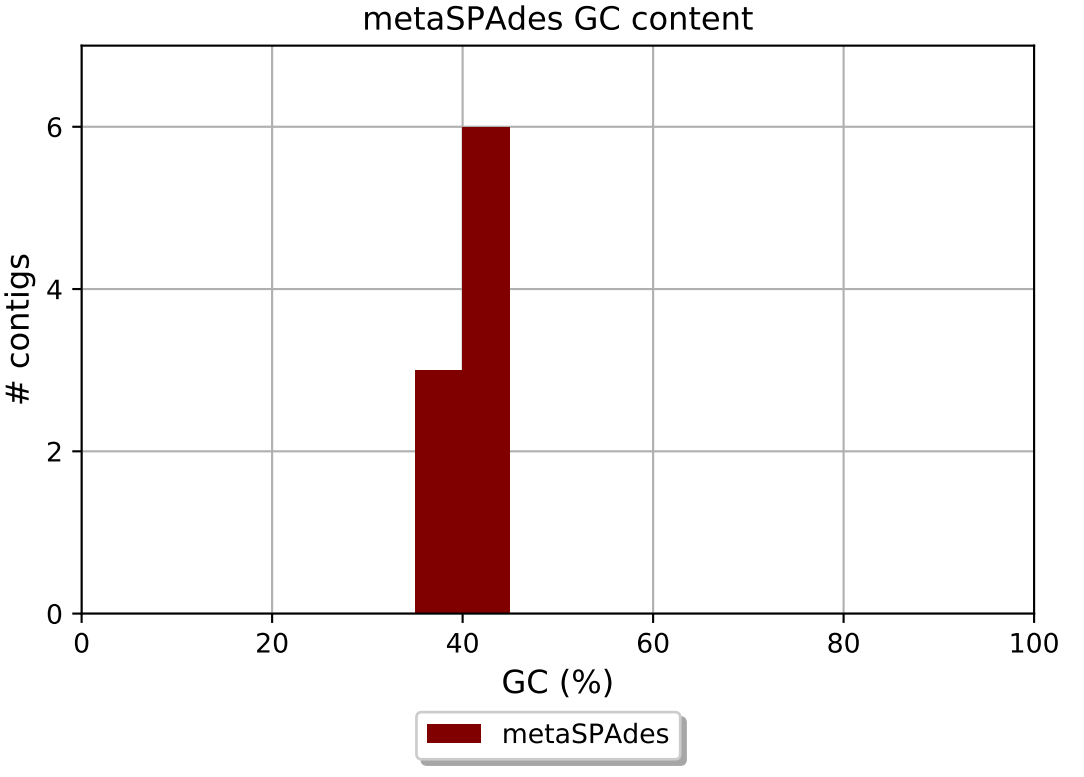

ABySS GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
ABySS

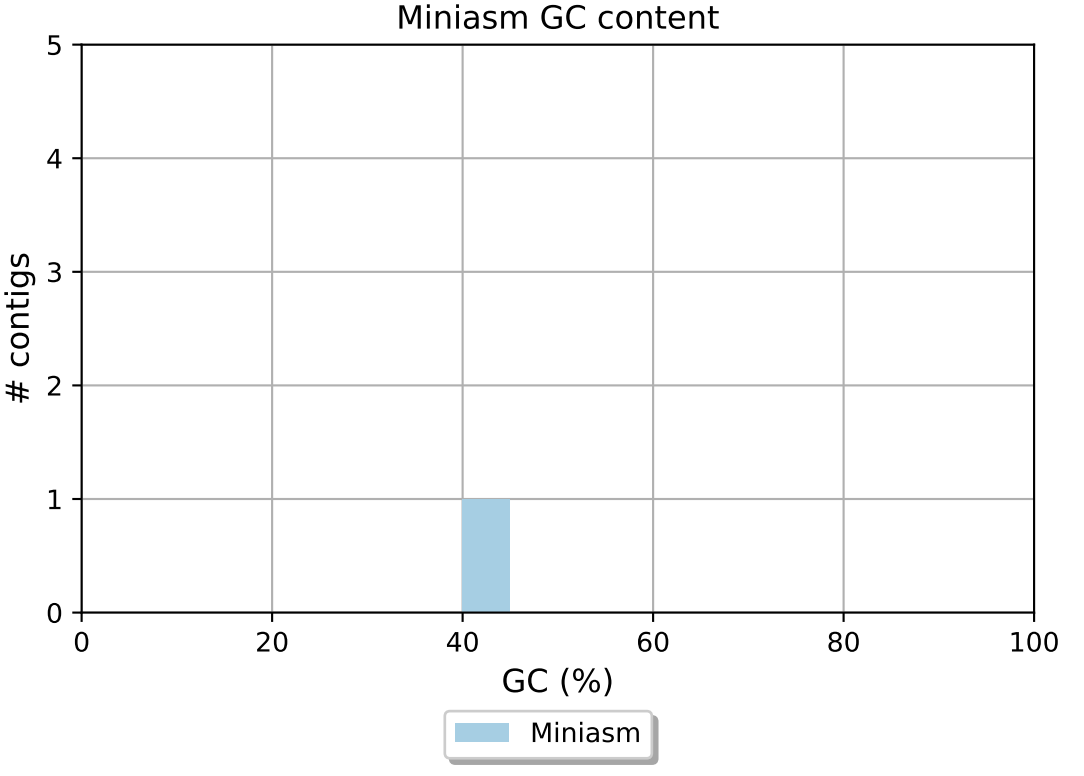

A_STAR GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
A_STAR

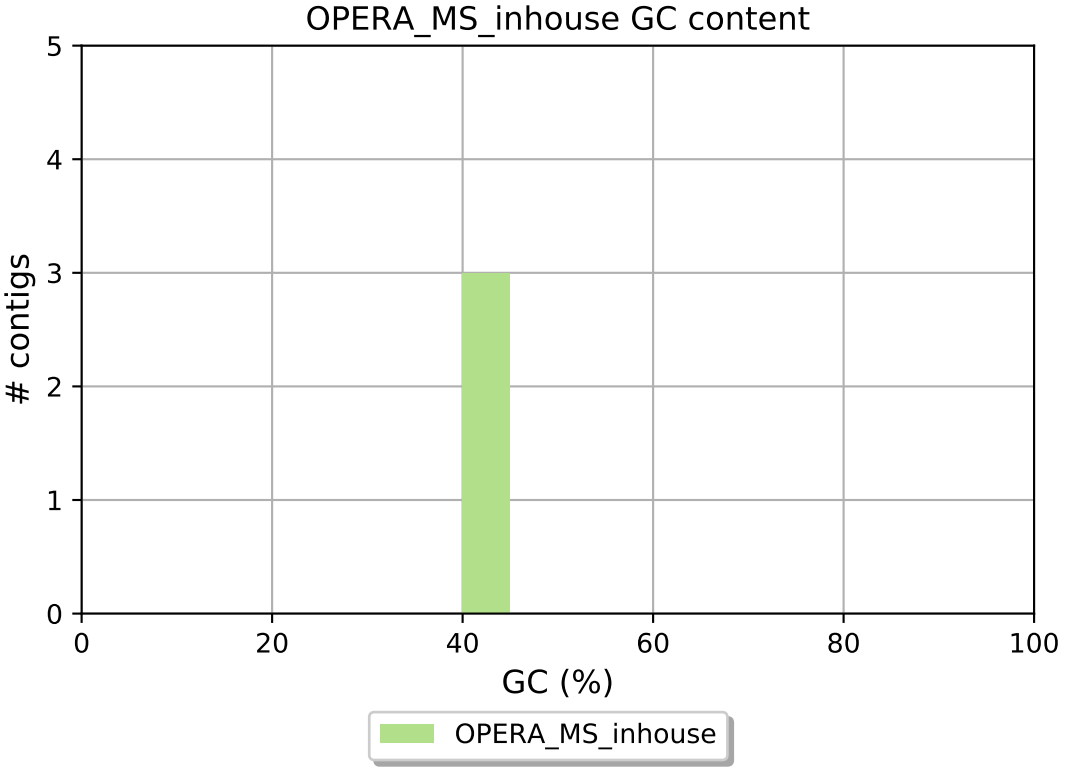

HipMer GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
HipMer

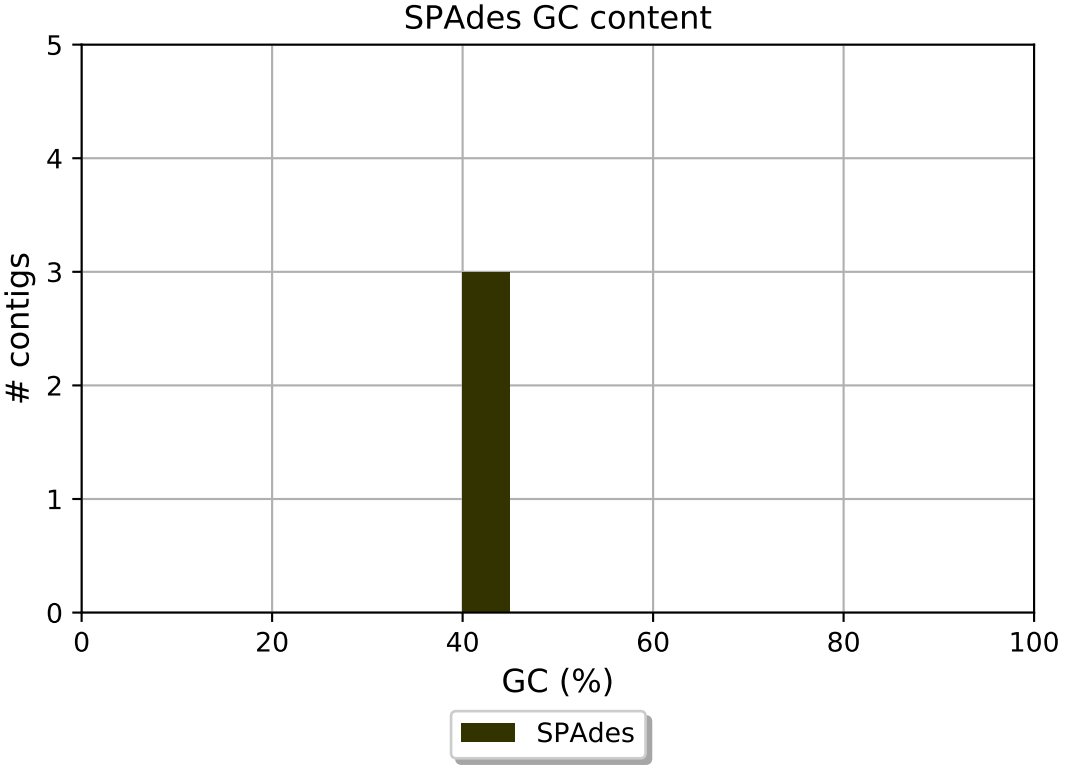

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

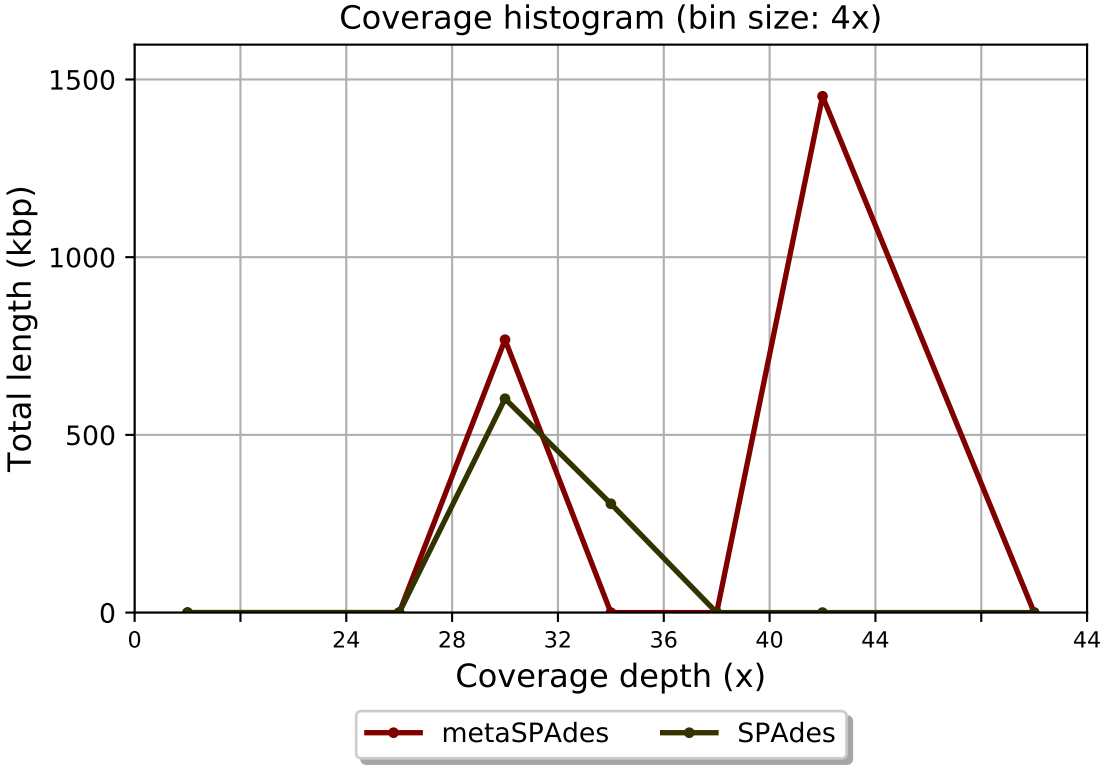

Megahit GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
Megahit

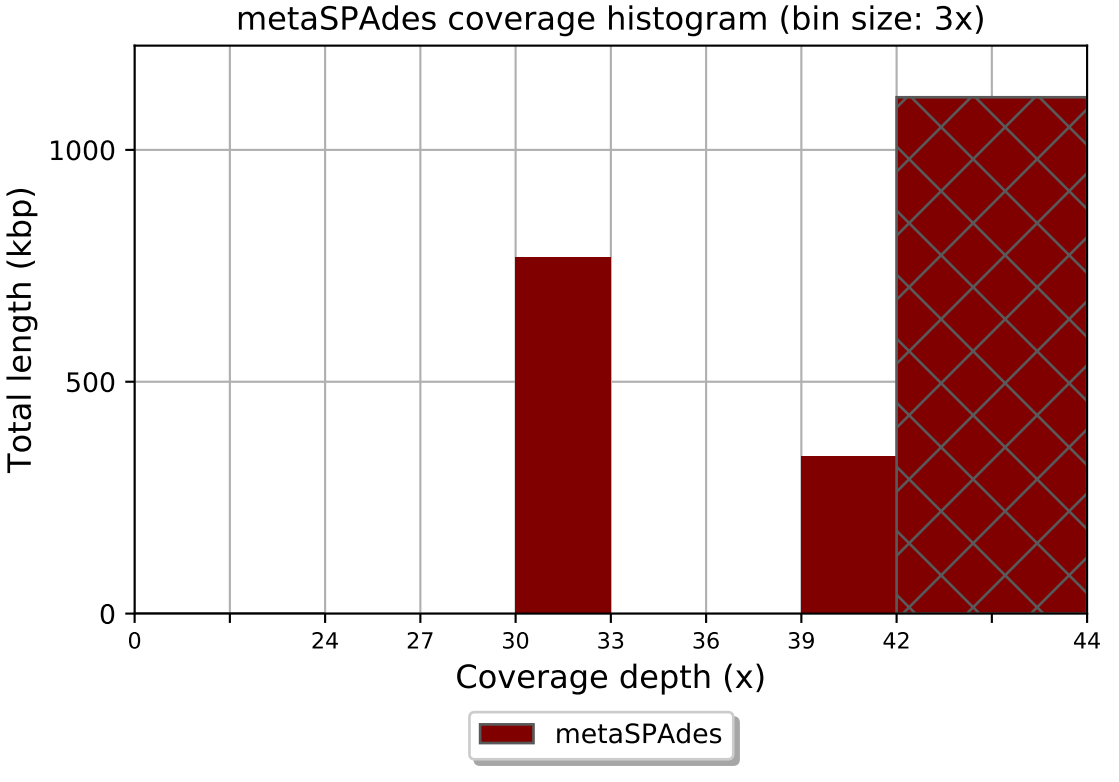

metaSPAdes GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
metaSPAdes

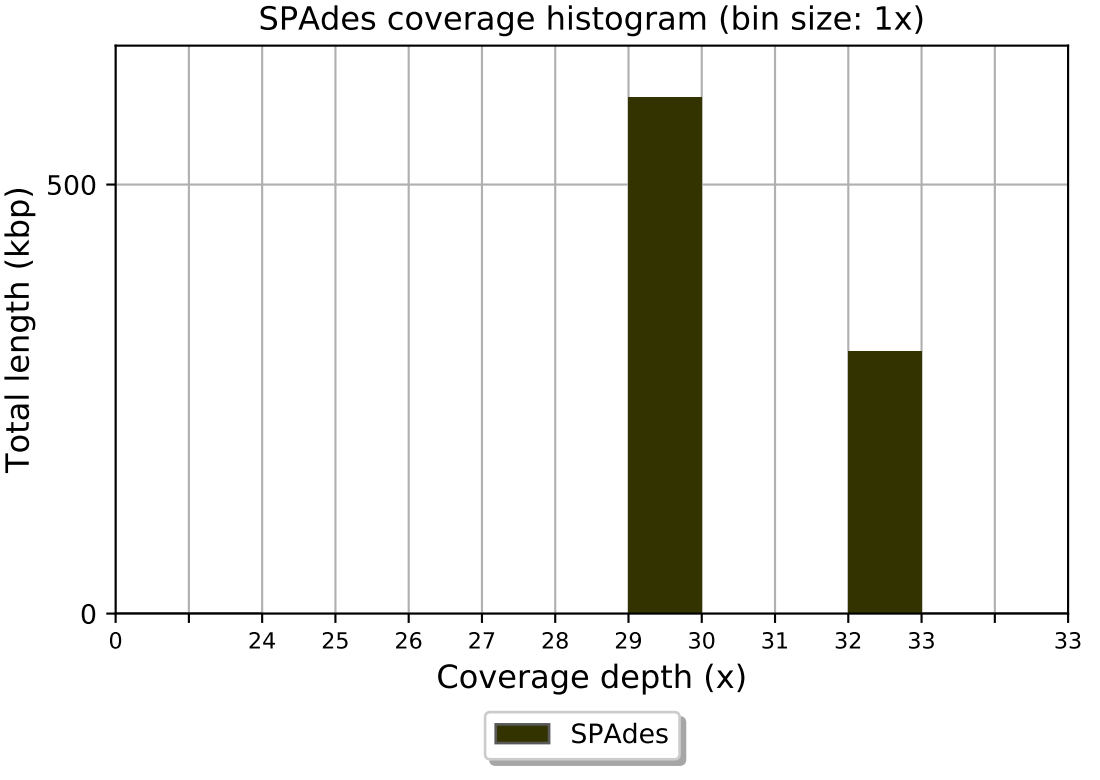

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

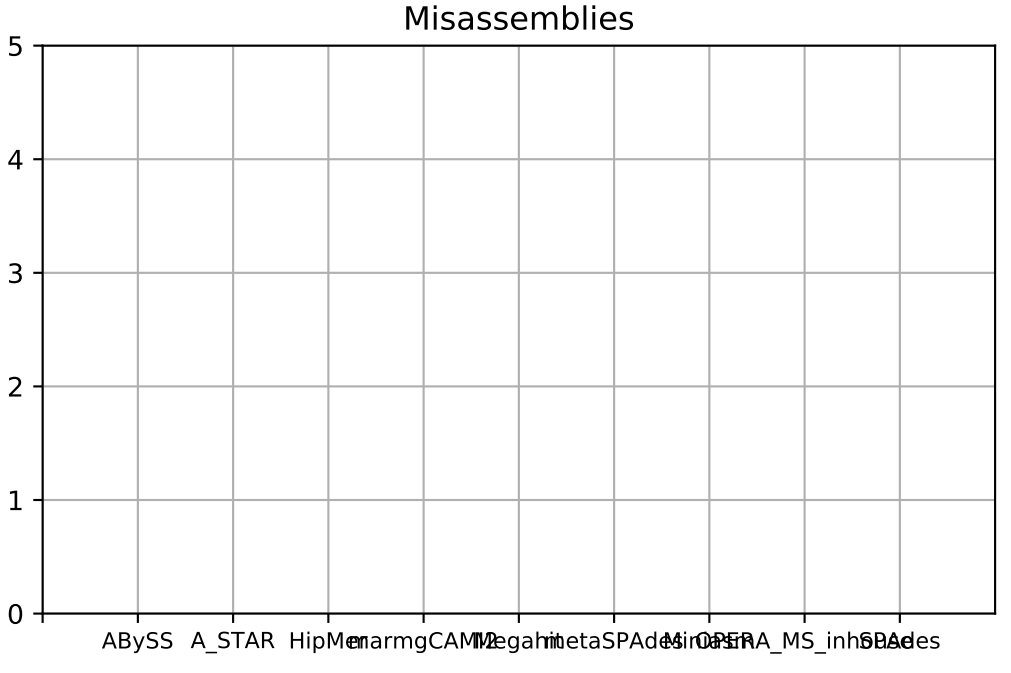

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

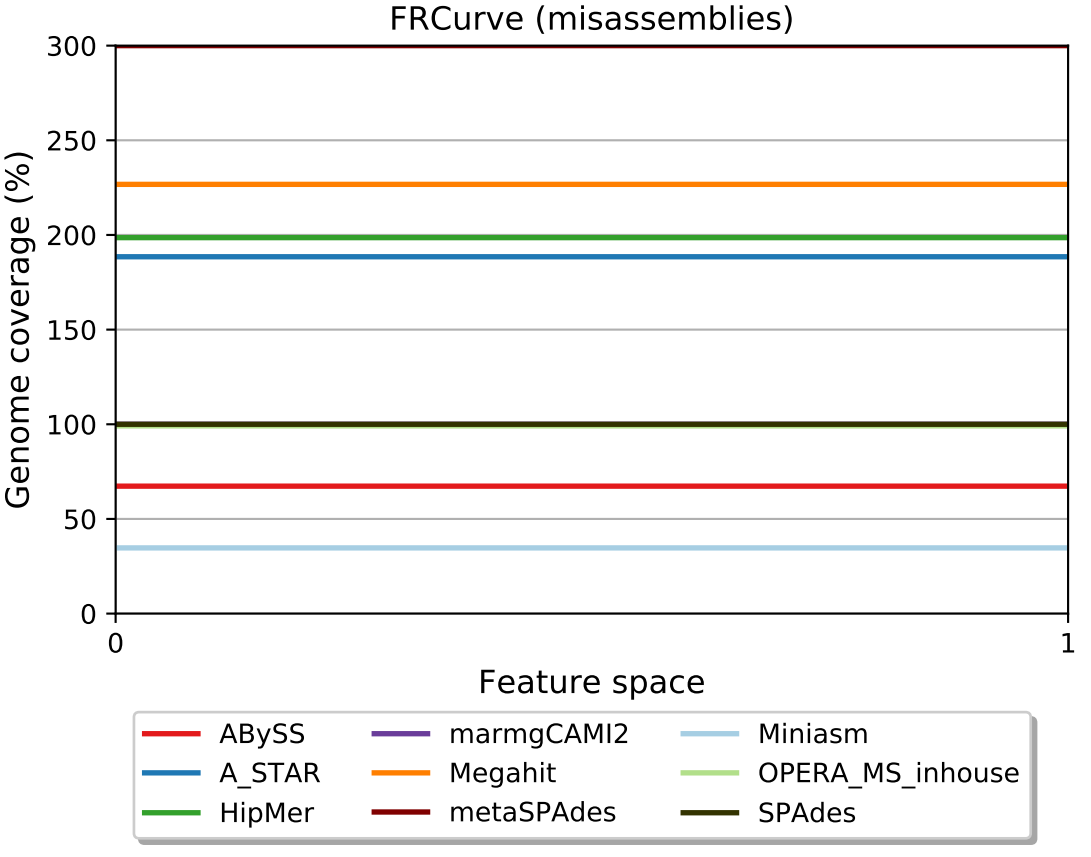

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

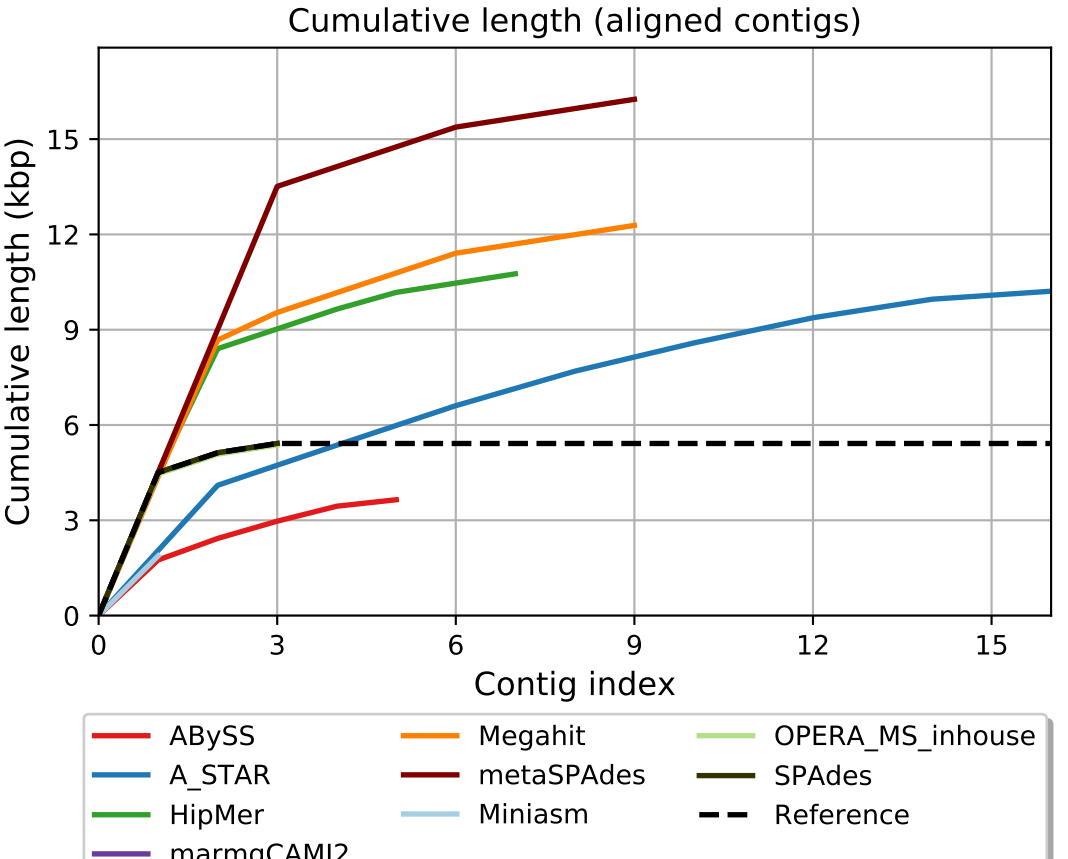

Coverage histogram (bin size: 4x)
Total length (kbp)
1500
1000
500
0
0
24
28
32
36
40
44
44
Coverage depth (x)
metaSPAdes
SPAdes

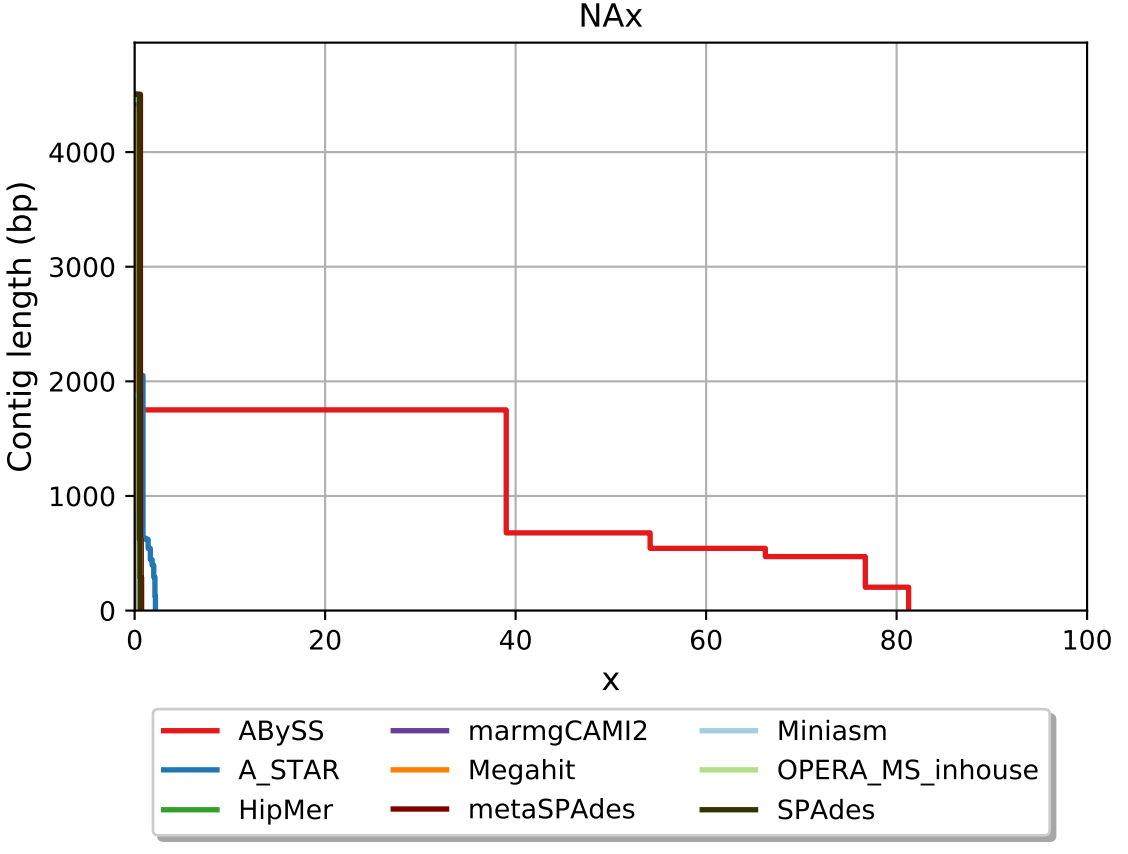

metaSPAdes coverage histogram (bin size: 3x)
Total length (kbp)
1000
500
0
0
24
27
30
33
36
39
42
44
Coverage depth (x)
metaSPAdes

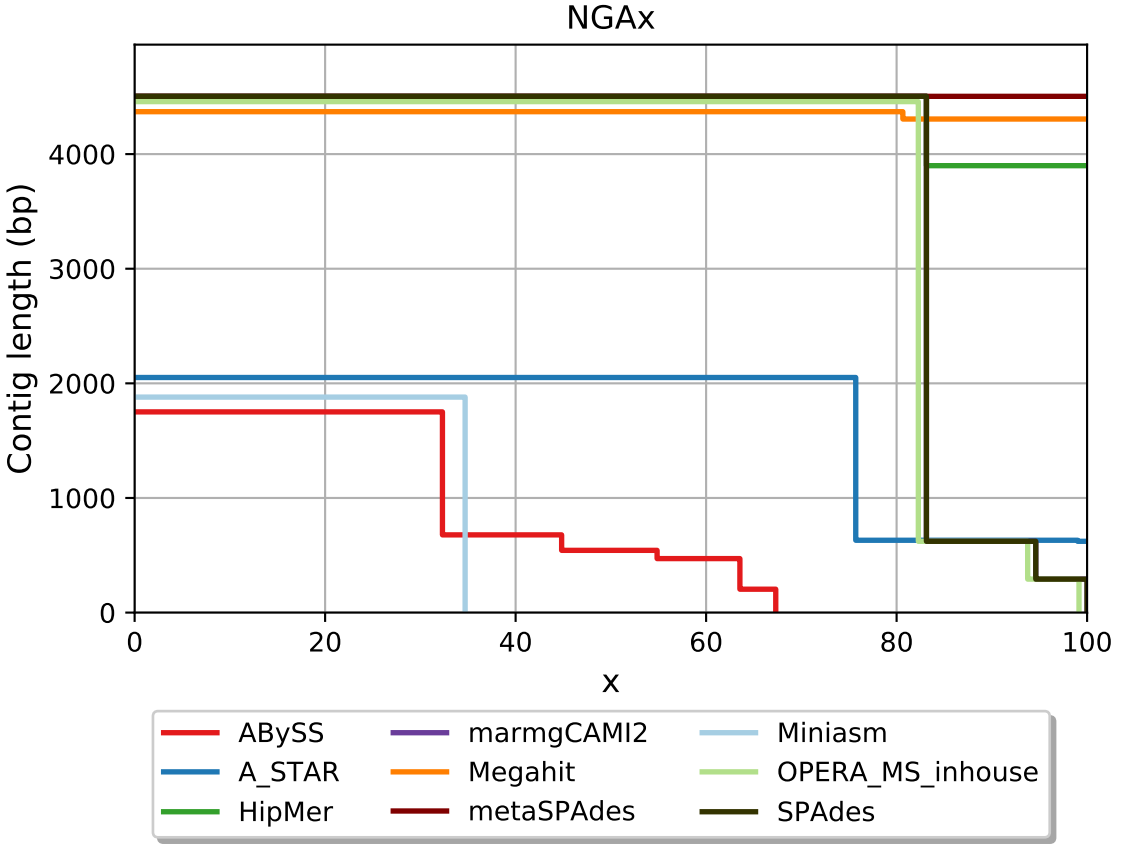

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
500
0
0
24
25
26
27
28
29
30
31
32
33
33
Coverage depth (x)
SPAdes

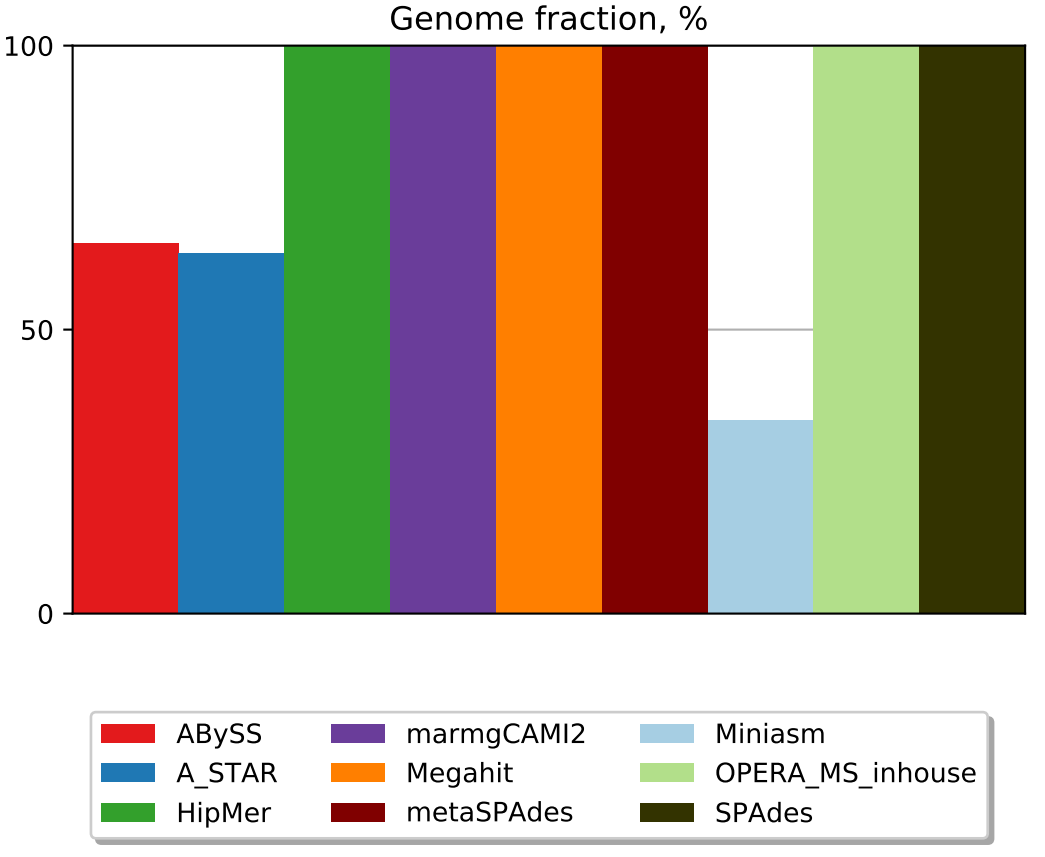

Misassemblies
5
4
3
2
1
0
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
MinoPER
A_MS_inhouse
SPAdes


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
3
6
9
12
15
Contig index
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


NAx
Contig length (bp)
0
1000
2000
3000
4000
0
20
40
60
80
100
x
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


NGAx
Contig length (bp)
0
1000
2000
3000
4000
0
20
40
60
80
100
x
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Genome fraction, %
100
50
0
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes