Report

	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	6	18	5	1	11	9	4	2	2
# contigs (>= 5000 bp)	6	13	5	1	11	9	4	2	2
# contigs (>= 10000 bp)	6	13	5	1	11	9	4	2	2
# contigs (>= 25000 bp)	6	9	4	1	10	9	4	2	2
# contigs (>= 50000 bp)	4	6	4	1	8	9	4	2	2
Total length (>= 1000 bp)	500944	2178583	2731938	1859369	1991448	4558984	8381890	1513471	1854709
Total length (>= 5000 bp)	500944	2164197	2731938	1859369	1991448	4558984	8381890	1513471	1854709
Total length (>= 10000 bp)	500944	2164197	2731938	1859369	1991448	4558984	8381890	1513471	1854709
Total length (>= 25000 bp)	500944	2115033	2707560	1859369	1966961	4558984	8381890	1513471	1854709
Total length (>= 50000 bp)	424122	2022878	2707560	1859369	1912003	4558984	8381890	1513471	1854709
# contigs	6	18	5	1	12	9	4	2	2
Largest contig	148370	421667	1524395	1859369	541757	762996	2428999	763998	1091680
Total length	500944	2178583	2731938	1859369	1992135	4558984	8381890	1513471	1854709
Reference length	7308	7308	7308	7308	7308	7308	7308	7308	7308
GC (%)	43.32	42.70	43.04	43.04	42.67	42.95	49.45	42.97	42.99
Reference GC (%)	36.21	36.21	36.21	36.21	36.21	36.21	36.21	36.21	36.21
N50	148370	327935	1524395	1859369	541642	762974	2428999	763998	1091680
NG50	148370	421667	1524395	1859369	541757	762996	2428999	763998	1091680
N75	63691	261837	642266	1859369	194498	504133	2428999	749473	763029
NG75	148370	421667	1524395	1859369	541757	762996	2428999	763998	1091680
L50	2	3	1	1	2	3	2	1	1
LG50	1	1	1	1	1	1	1	1	1
L75	4	5	2	1	5	6	3	2	2
LG75	1	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	1	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	2	1	1	0	0	4	1	1
# unaligned contigs	0 + 6 part	0 + 18 part	0 + 5 part	0 + 1 part	0 + 11 part	0 + 9 part	0 + 4 part	0 + 2 part	0 + 2 part
Unaligned length	486120	2151938	2716626	1852061	1971784	4537060	8369894	1506634	1847368
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	89.997	95.265	100.000
Duplication ratio	2.028	3.646	2.095	1.000	2.785	3.000	1.824	0.982	1.005
# N's per 100 kbp	41.52	122.88	32.10	0.00	0.00	0.00	0.00	0.00	5.39
# mismatches per 100 kbp	0.00	574.71	0.00	0.00	766.28	0.00	471.34	215.46	0.00
# indels per 100 kbp	0.00	82.10	54.73	0.00	41.05	0.00	805.84	114.91	13.68
Largest alignment	3437	3303	3370	3437	3504	3437	2105	3303	3470
Total aligned length	14616	23968	14512	7308	20296	21924	11996	6837	7341
NGA50	3437	3303	2617	2095	3303	3437	1933	2104	2095
NGA75	3437	3303	2617	2095	3303	3437	1933	667	2095
LGA50	2	2	2	2	2	2	2	2	2
LGA75	2	2	2	2	2	2	3	3	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

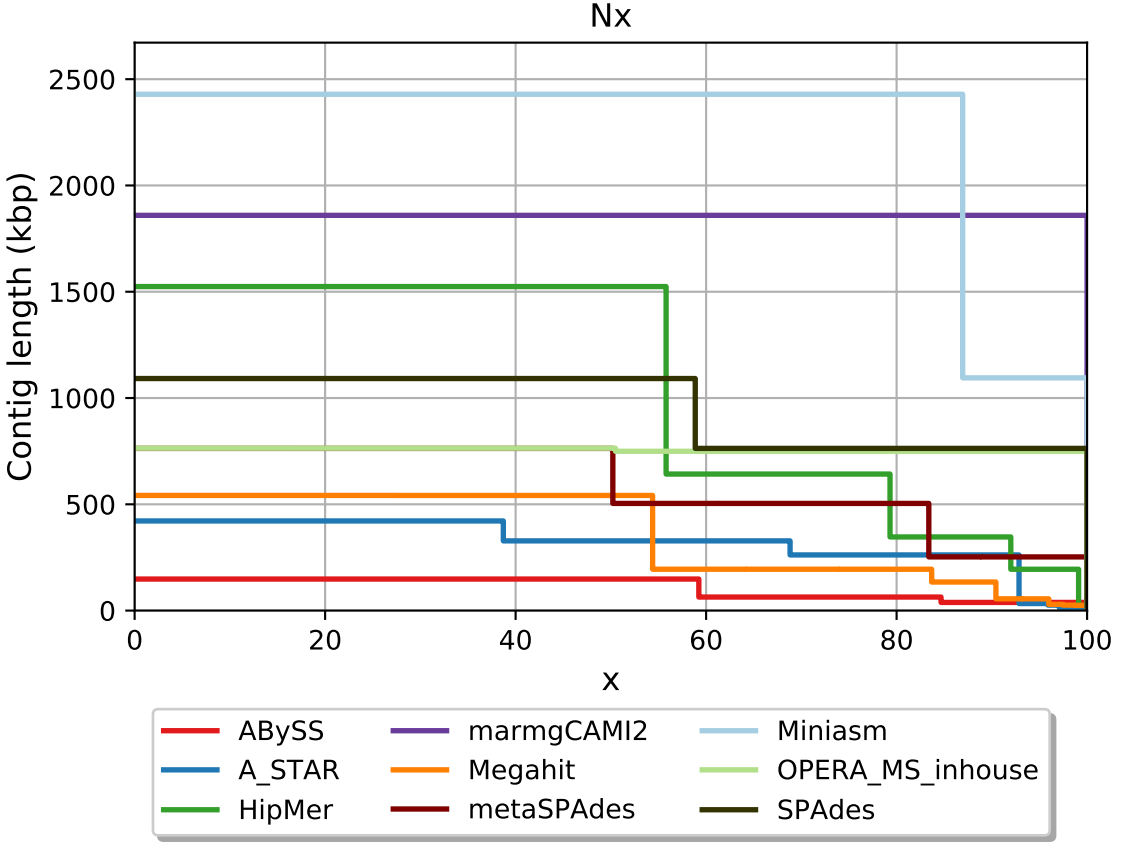
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	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	6	14	4	0	11	9	0	1	1
# possible misassemblies	12	21	6	0	18	18	0	2	2
# local misassemblies	0	0	0	0	1	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	2	1	1	0	0	4	1	1
# mismatches	0	42	0	0	56	0	31	15	0
# indels	0	6	4	0	3	0	53	8	1
# indels (<= 5 bp)	0	2	0	0	0	0	52	7	0
# indels (> 5 bp)	0	4	4	0	3	0	1	1	1
Indels length	0	406	138	0	268	0	71	145	33

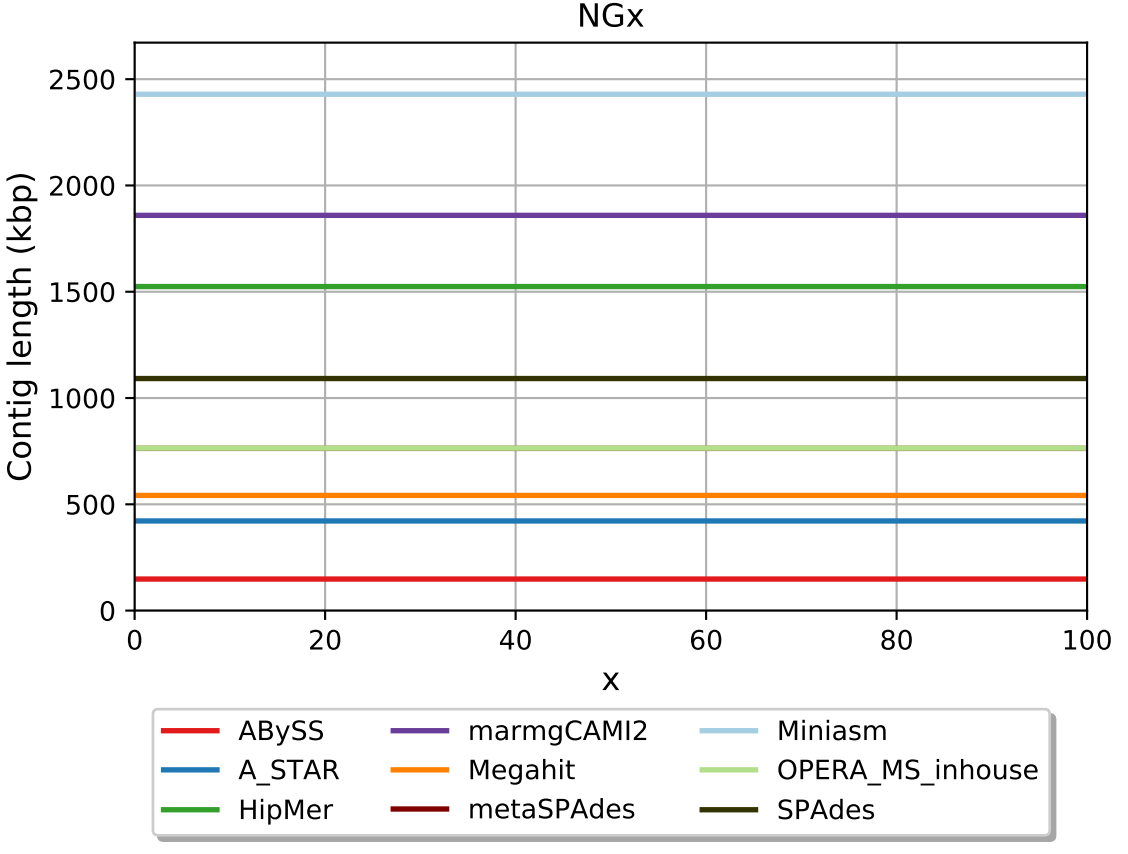
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

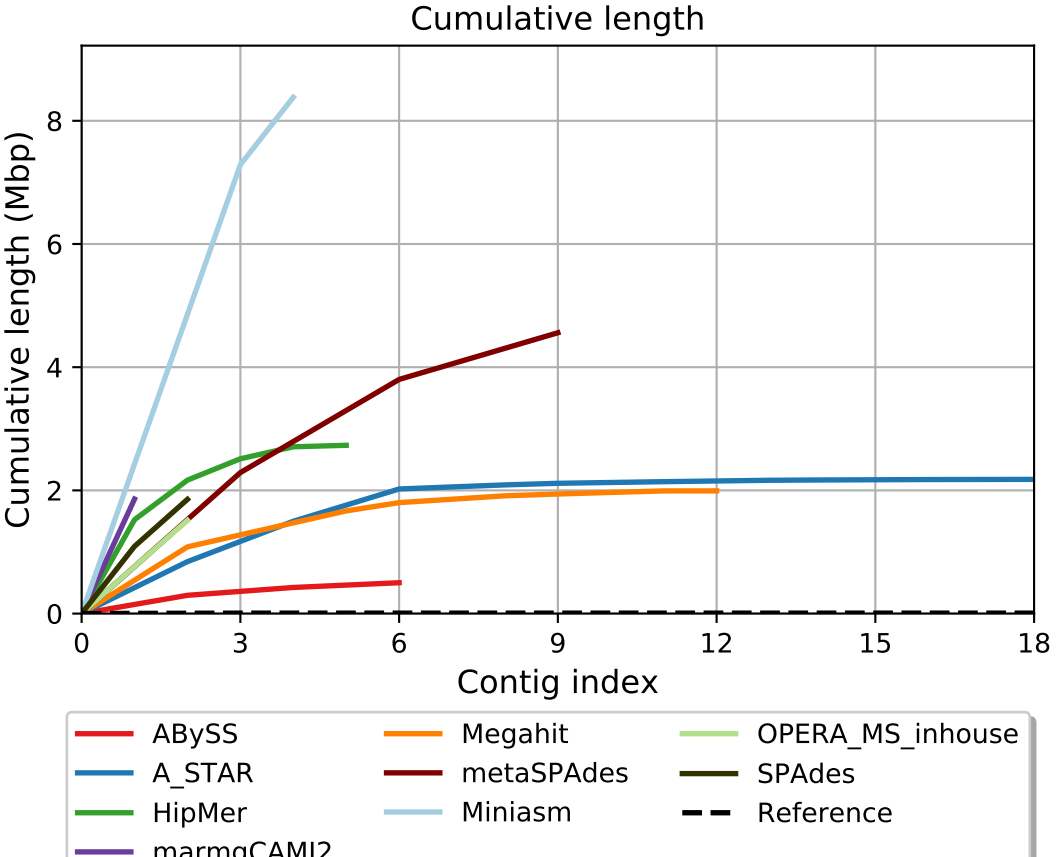
Unaligned report

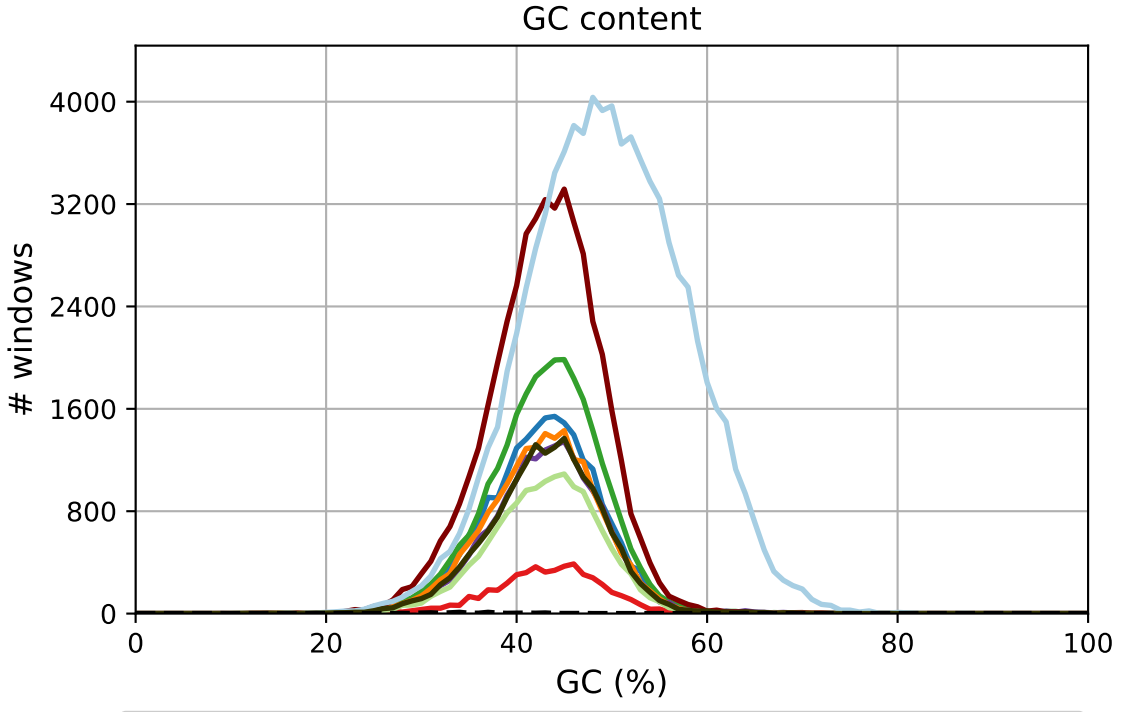
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	6	18	5	1	11	9	4	2	2
Partially unaligned length	486120	2151938	2716626	1852061	1971784	4537060	8369894	1506634	1847368
# N's	208	2677	877	0	0	0	0	0	100

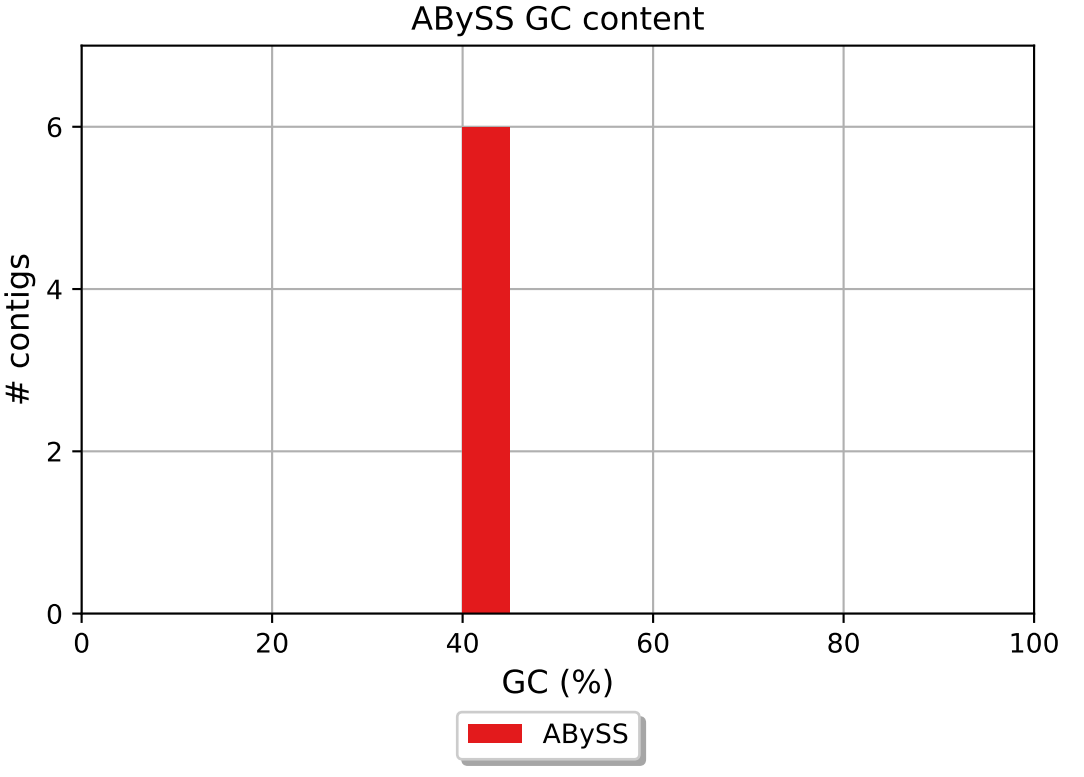
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

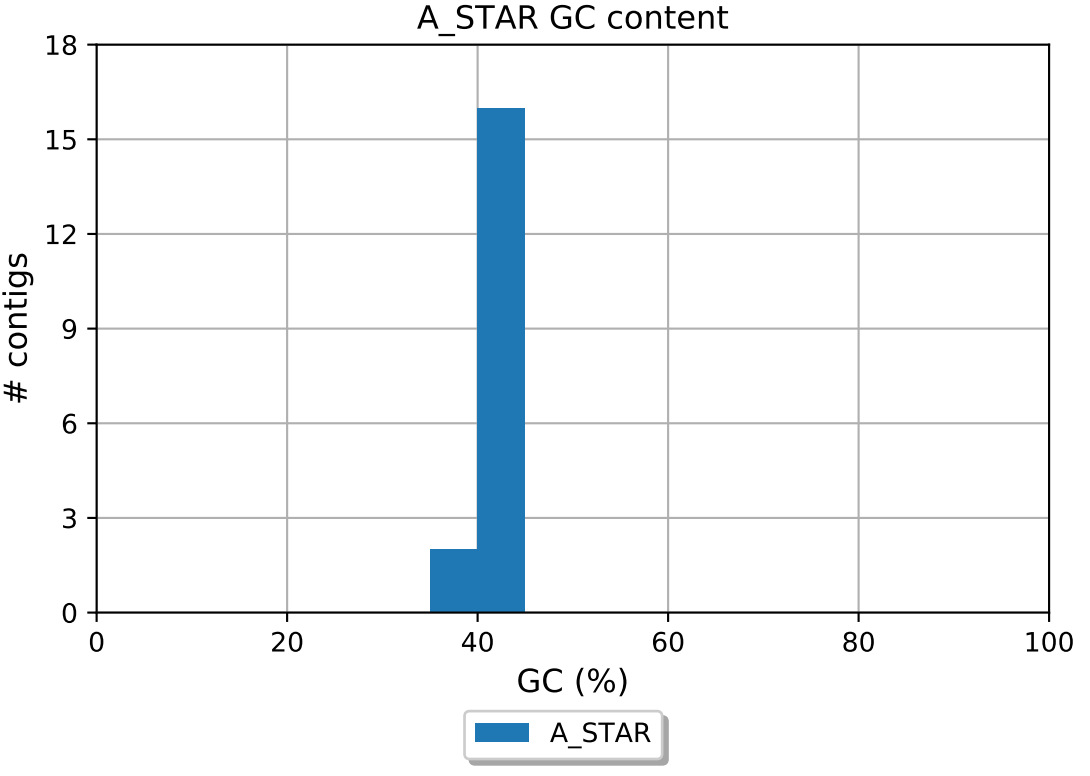

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

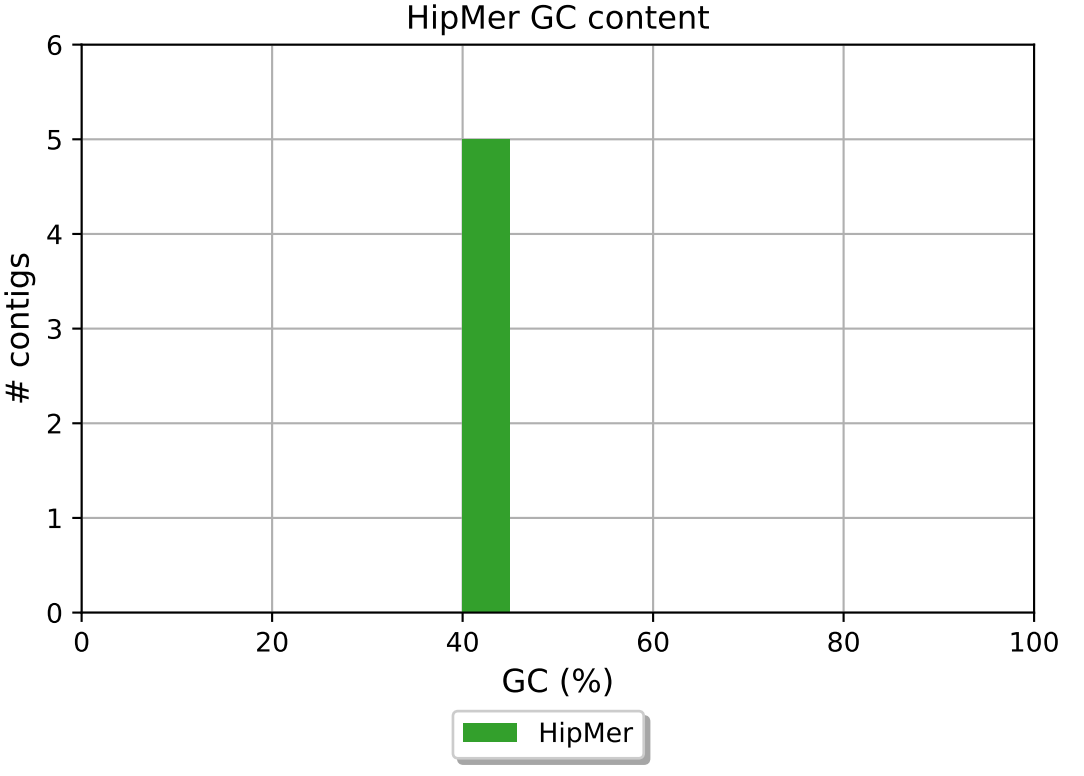

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

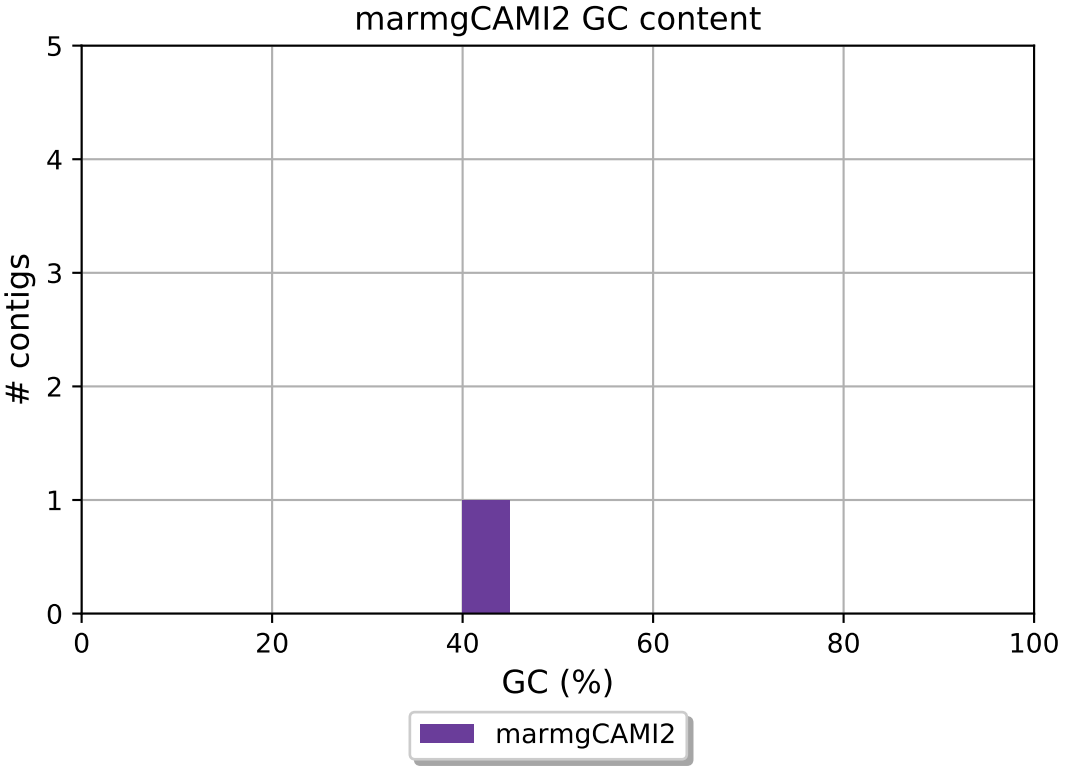

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
0
3
6
9
12
15
18
Contig index
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

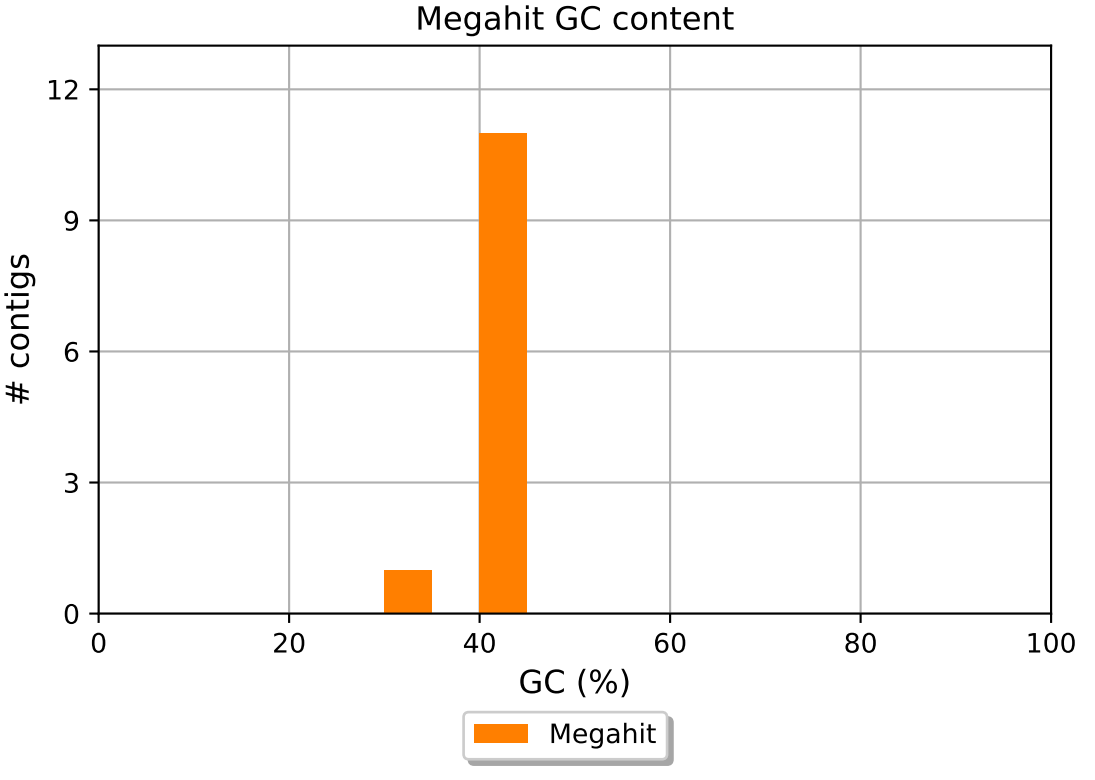

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

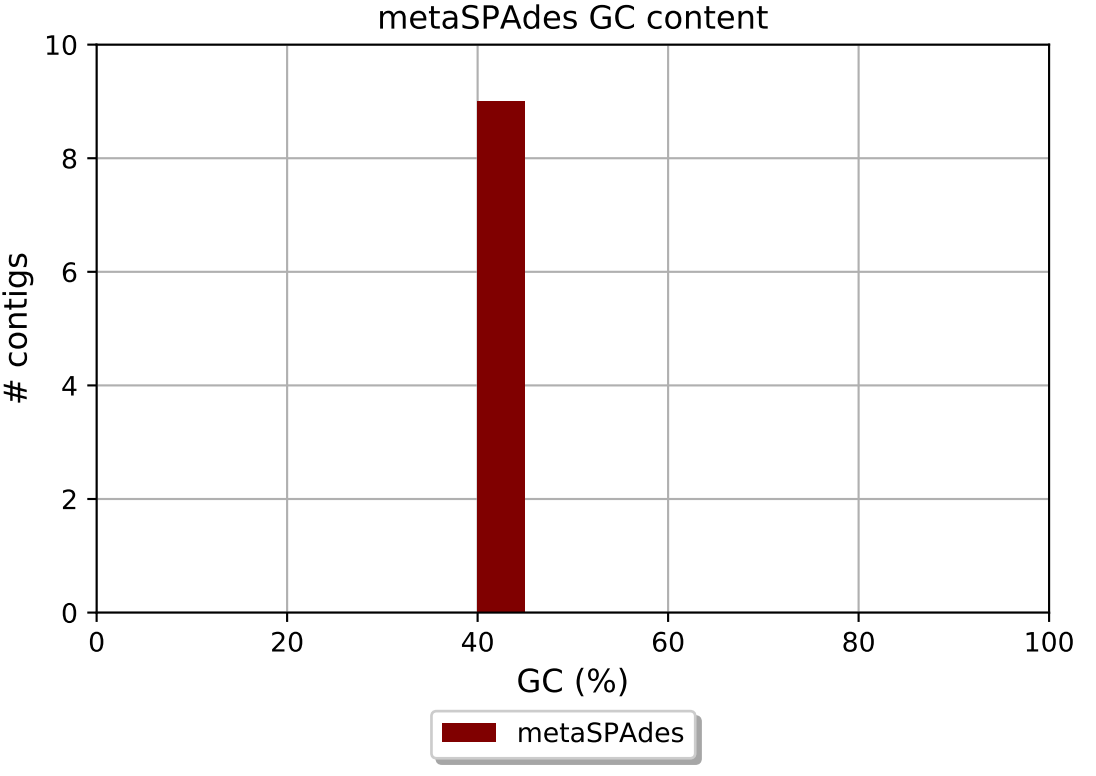

ABySS GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
ABySS

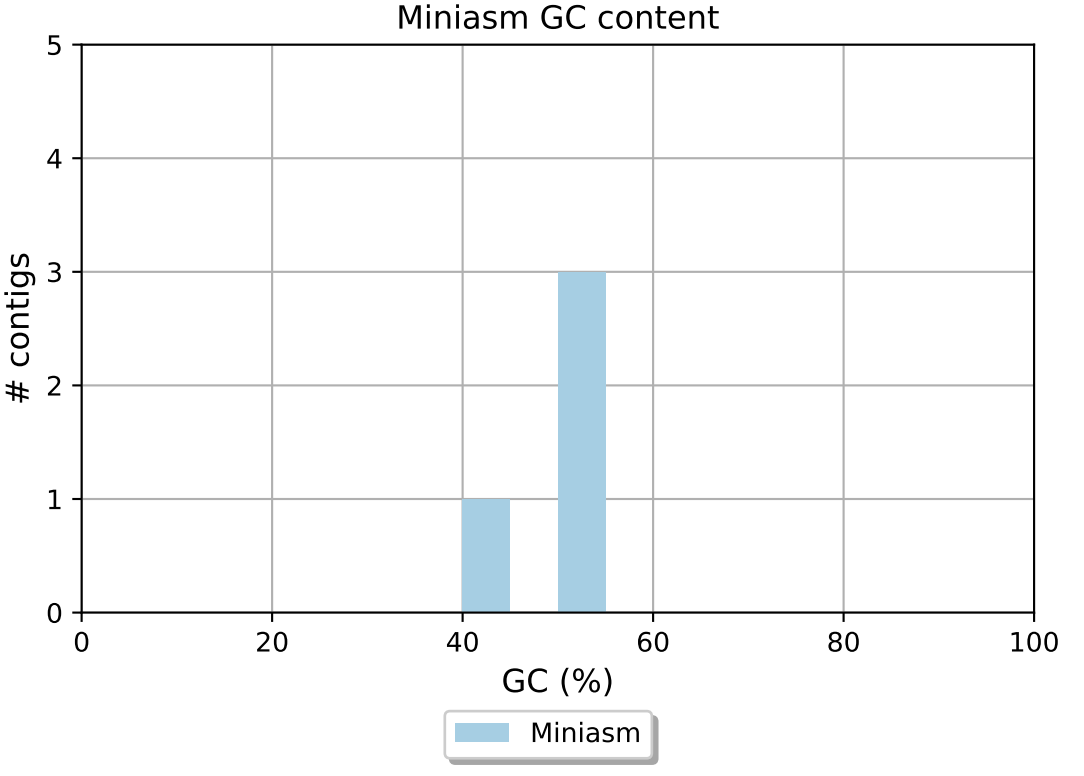

A_STAR GC content
18
15
12
9
6
3
0
contigs
0
20
40
60
80
100
GC (%)
A_STAR

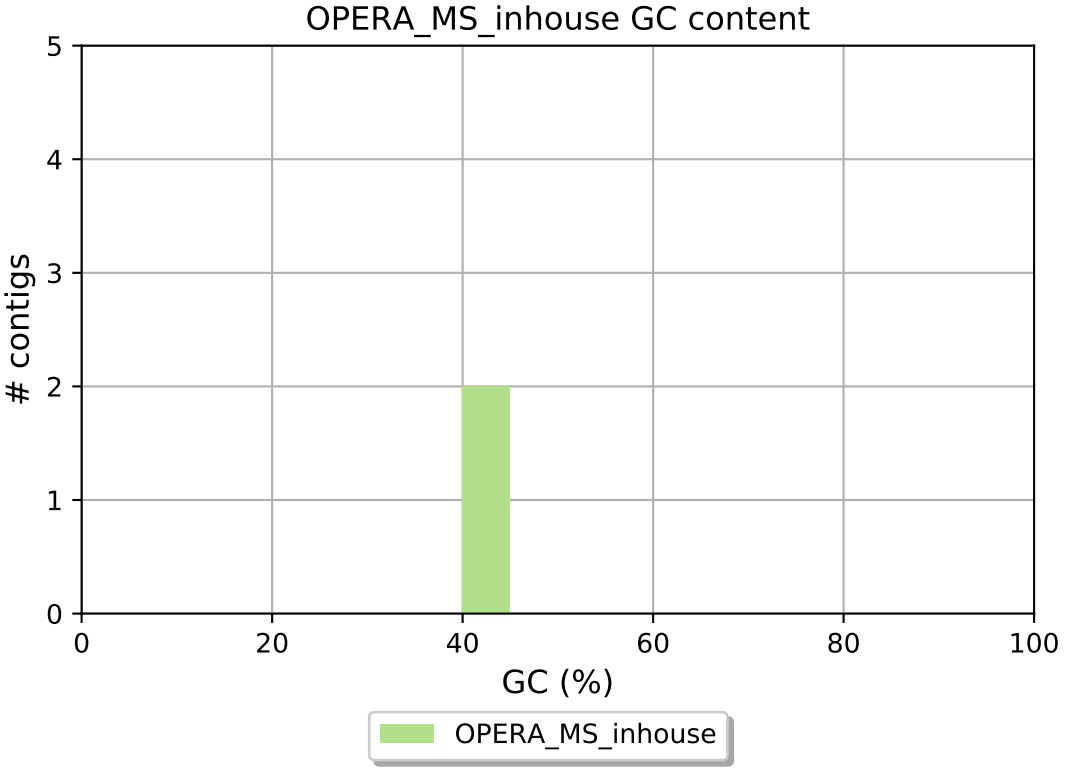

HipMer GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
HipMer

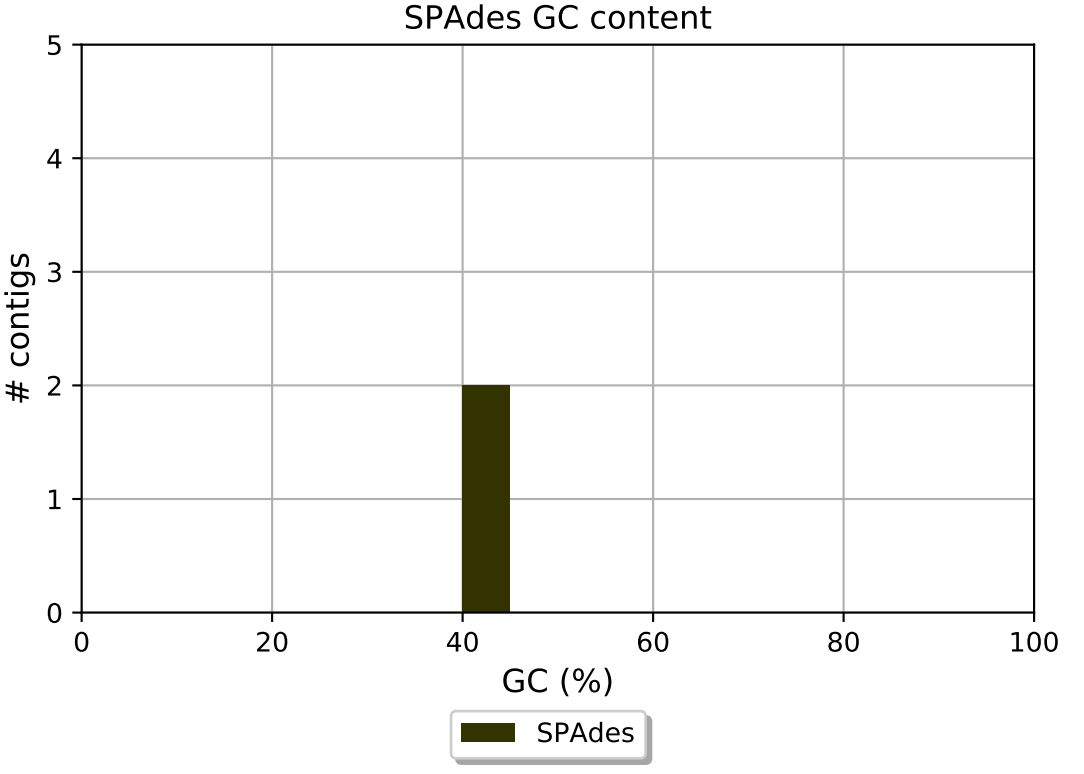

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

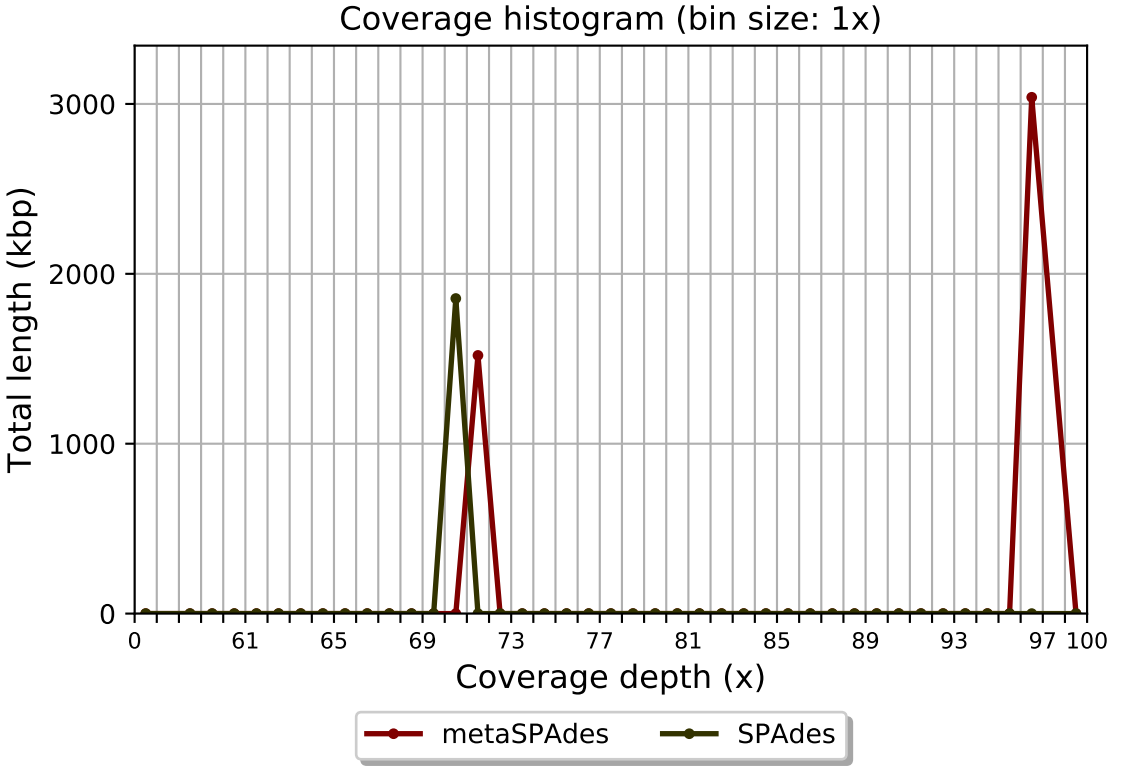

Megahit GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
Megahit

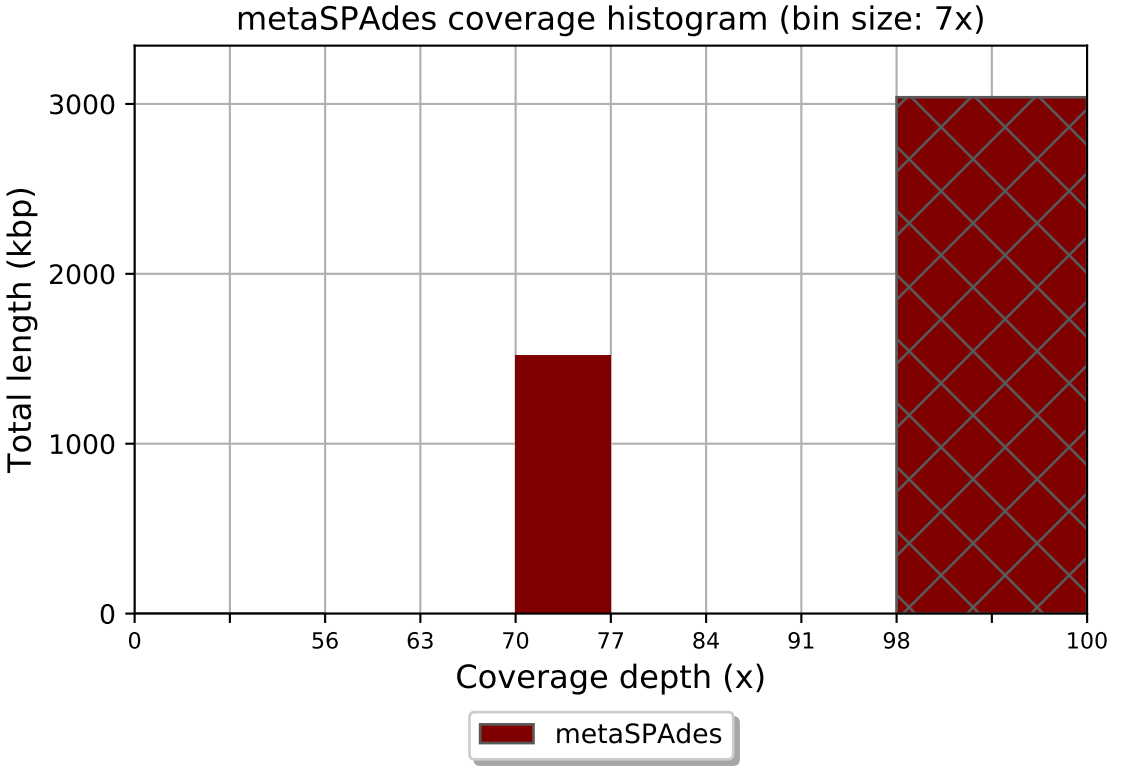

metaSPAdes GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
metaSPAdes

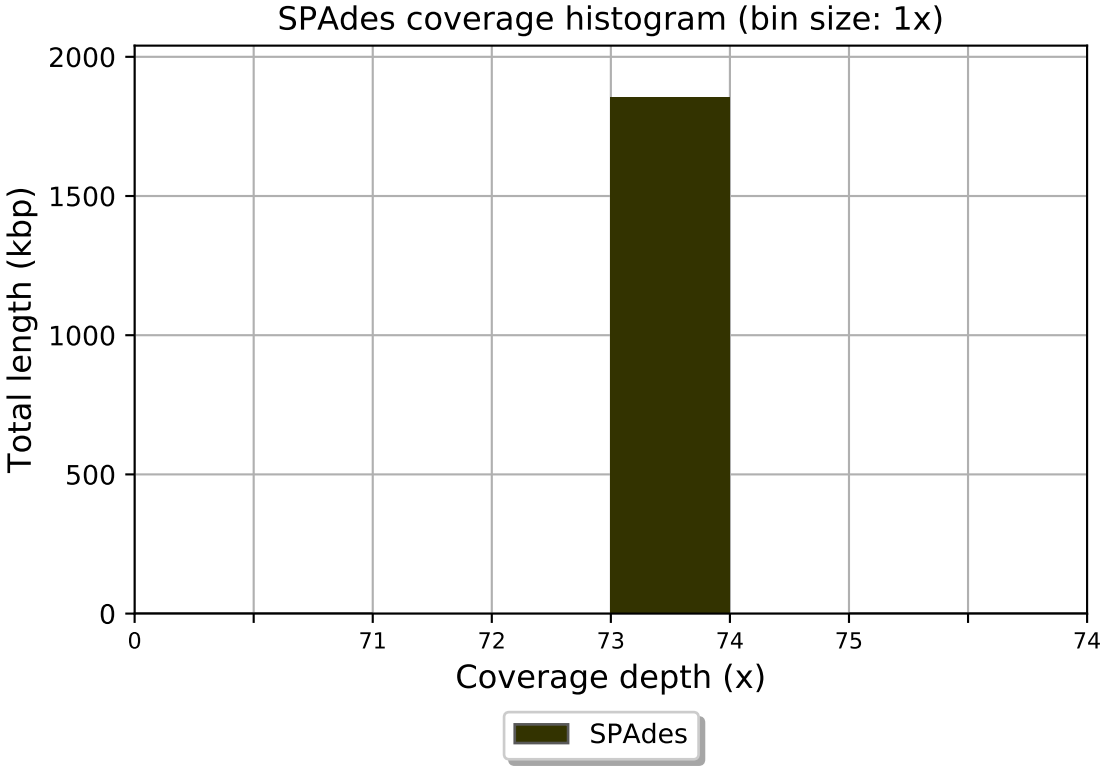

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

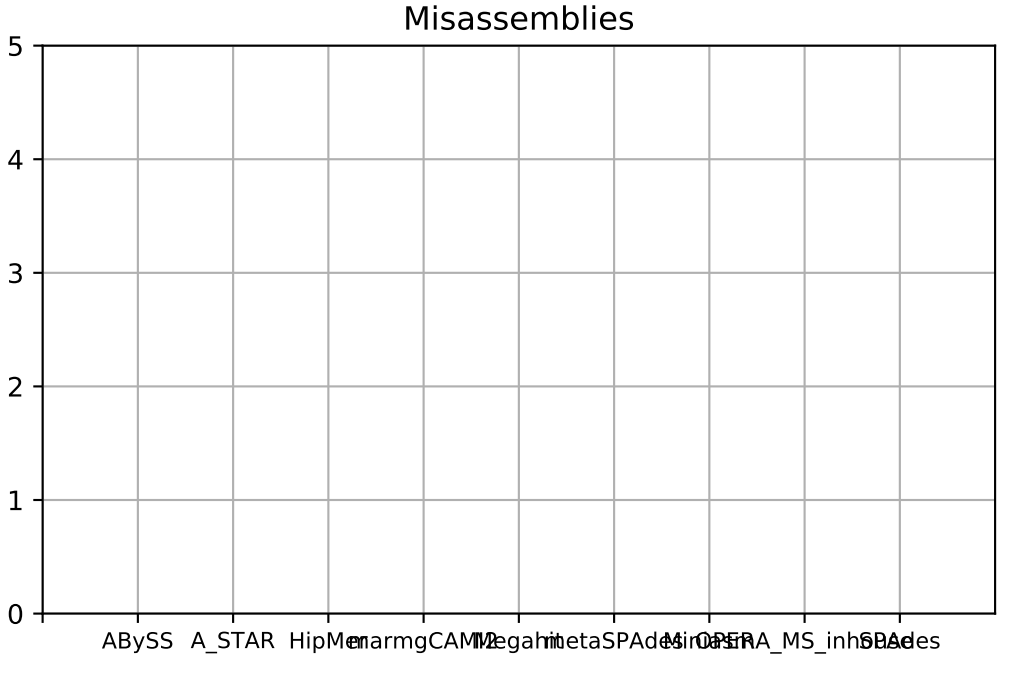

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

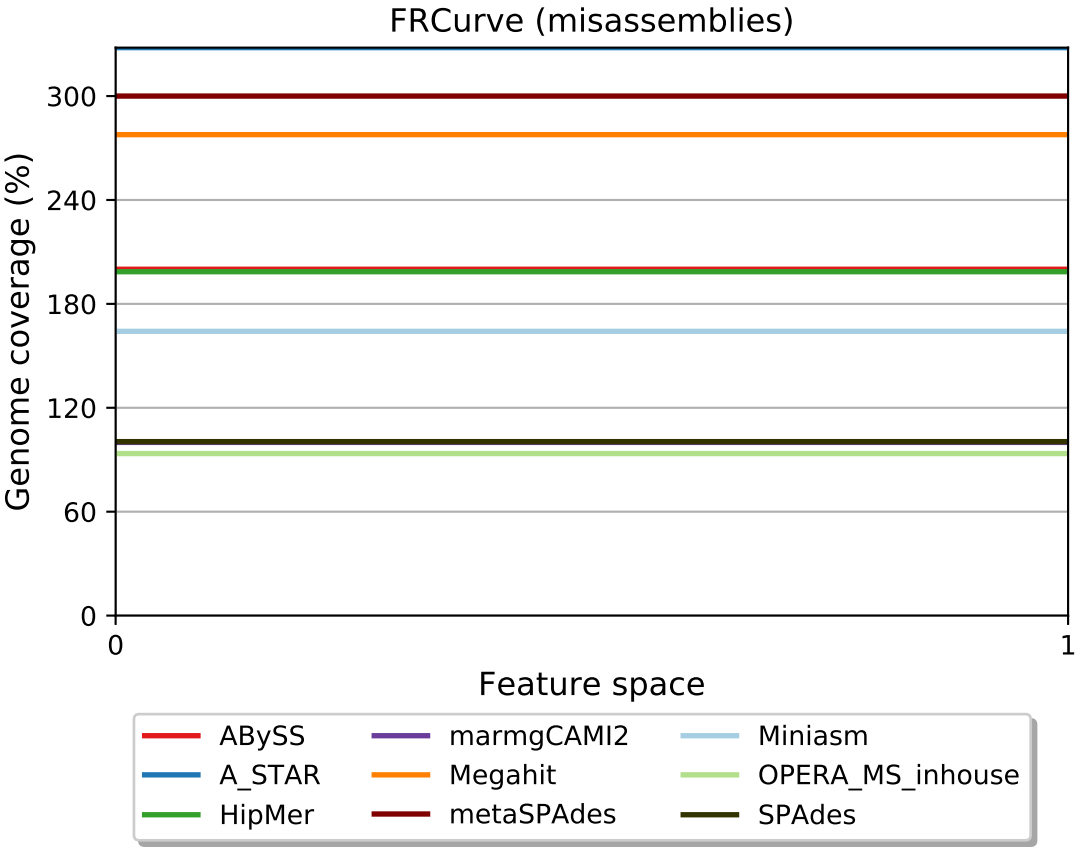

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

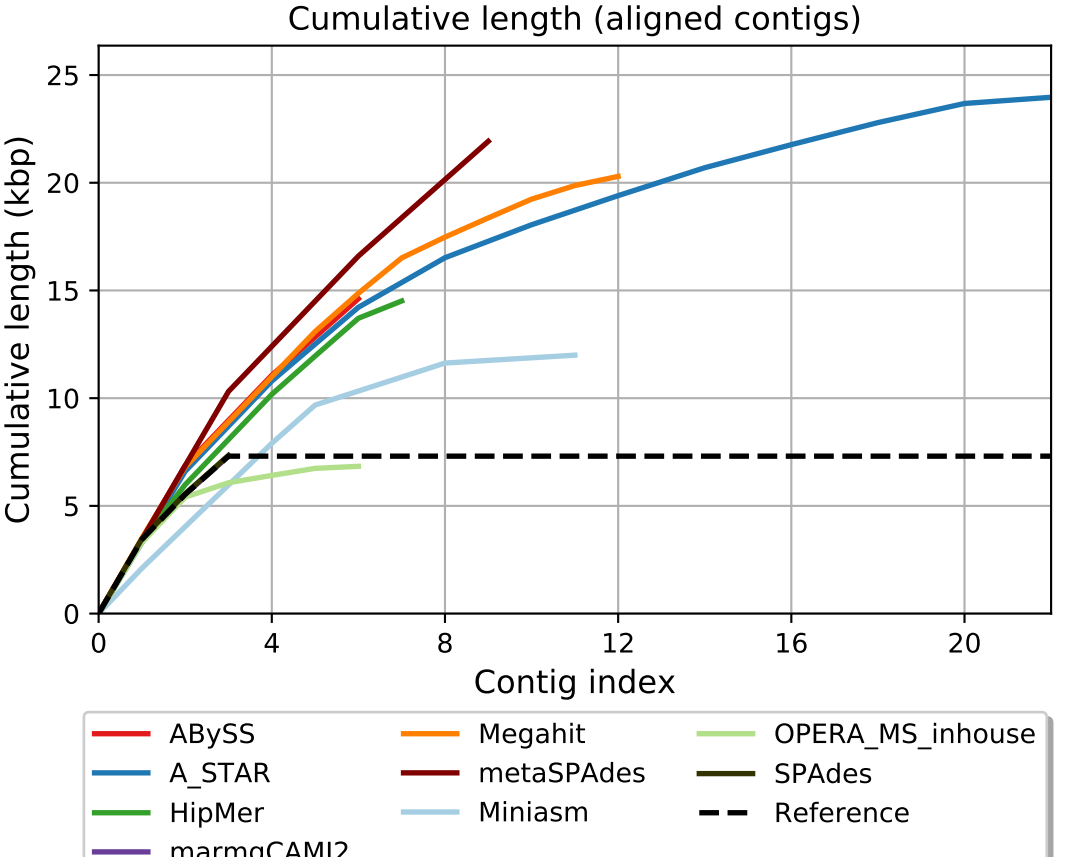

Coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
61
65
69
73
77
81
85
89
93
97
100
Coverage depth (x)
metaSPAdes
SPAdes

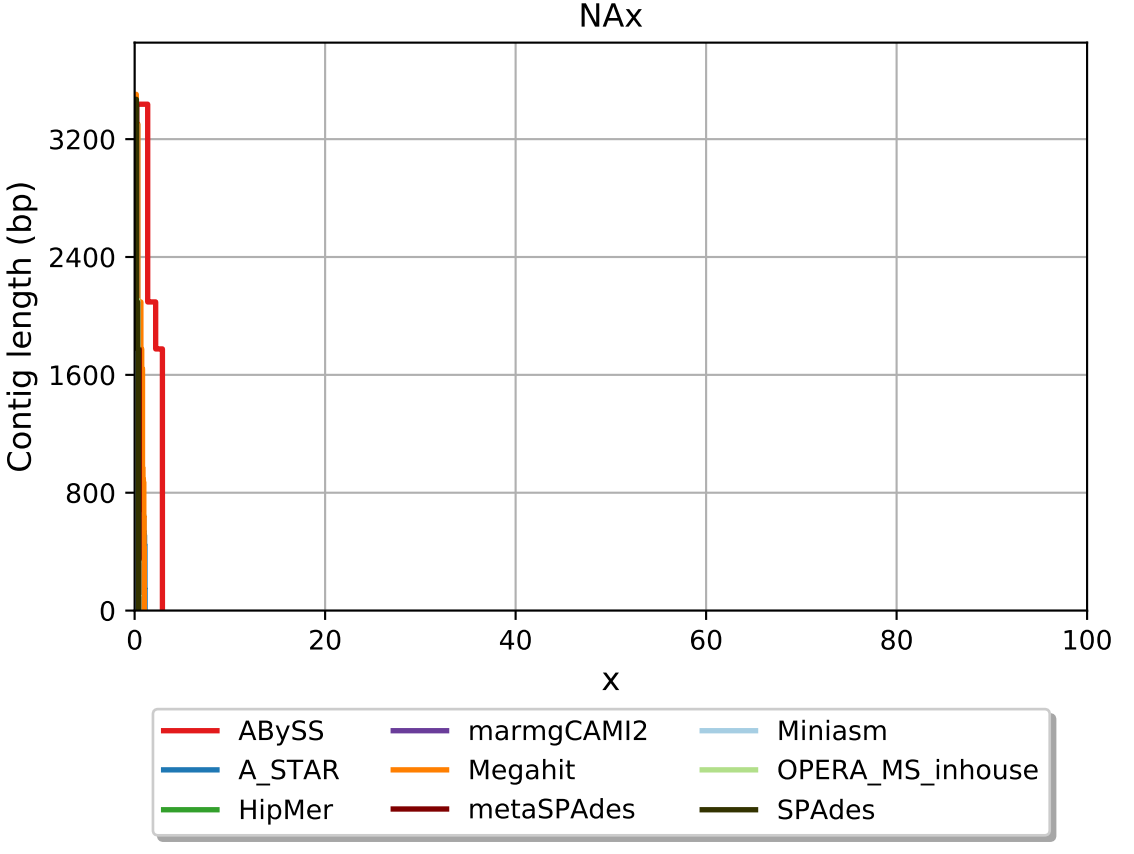

metaSPAdes coverage histogram (bin size: 7x)
Total length (kbp)
3000
2000
1000
0
0
56
63
70
77
84
91
98
100
Coverage depth (x)
metaSPAdes

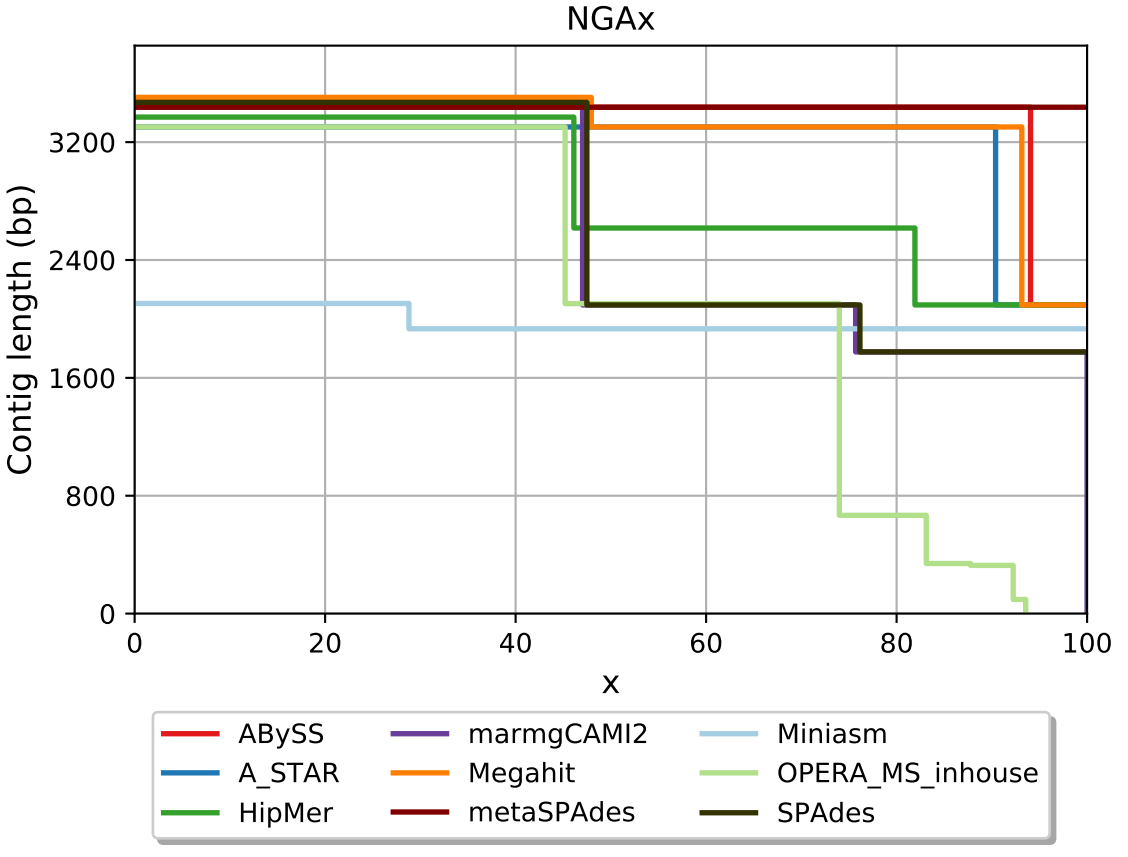

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
71
72
73
74
75
74
Coverage depth (x)
SPAdes

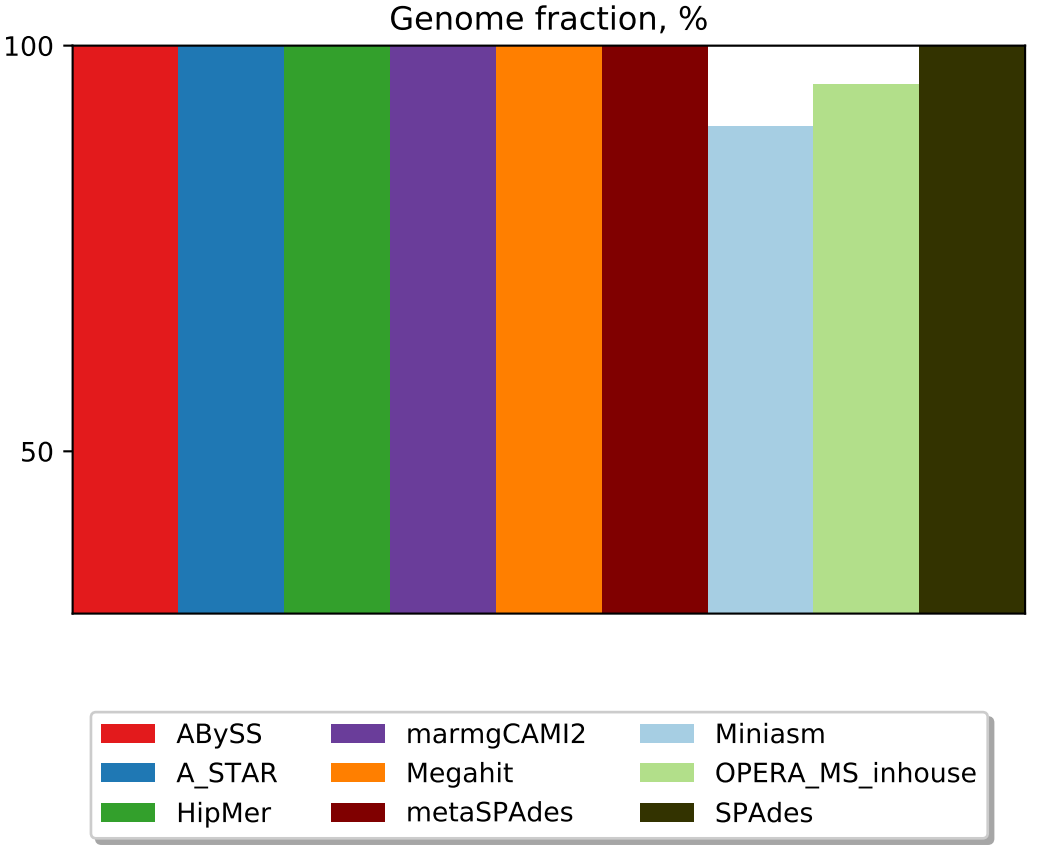

Misassemblies
5
4
3
2
1
0
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
MinoPER
A_MS_inhouse
SPAdes


FRCurve (misassemblies)
Genome coverage (%)
300
240
180
120
60
0
0
1
Feature space
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
5
10
15
20
25
0
4
8
12
16
20
ABySS
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


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


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


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