Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	8	12	1	19	19	5	5	4
# contigs (>= 5000 bp)	6	9	1	13	14	5	4	0
# contigs (>= 10000 bp)	6	3	1	11	11	5	4	0
# contigs (>= 25000 bp)	6	0	1	5	1	4	3	0
# contigs (>= 50000 bp)	6	0	1	3	0	3	1	0
Total length (>= 1000 bp)	1083384	90584	4884705	619640	200840	422524	239113	9557
Total length (>= 5000 bp)	1080880	82098	4884705	604170	186763	422524	235138	0
Total length (>= 10000 bp)	1080880	40108	4884705	588332	162584	422524	235138	0
Total length (>= 25000 bp)	1080880	0	4884705	500651	31085	409276	211189	0
Total length (>= 50000 bp)	1080880	0	4884705	409801	0	381527	152387	0
# contigs	12	12	1	22	20	5	6	6
Largest contig	236311	17986	4884705	189776	31085	156872	152387	4952
Total length	1086044	90584	4884705	621539	201473	422524	239617	11236
Reference length	5083	5083	5083	5083	5083	5083	5083	5083
GC (%)	45.89	46.04	46.03	45.35	45.41	46.21	45.54	46.37
Reference GC (%)	59.49	59.49	59.49	59.49	59.49	59.49	59.49	59.49
N50	226018	8561	4884705	161522	12296	143938	152387	1784
NG50	236311	17986	4884705	189776	31085	156872	152387	4952
N75	226018	5493	4884705	42104	10525	80717	29729	1133
NG75	236311	17986	4884705	189776	31085	156872	152387	4952
L50	3	4	1	2	6	2	1	2
LG50	1	1	1	1	1	1	1	1
L75	4	7	1	5	10	3	2	4
LG75	1	1	1	1	1	1	1	1
# misassemblies	0	0	0	2	0	0	0	0
# misassembled contigs	0	0	0	2	0	0	0	0
Misassembled contigs length	0	0	0	1048	0	0	0	0
# local misassemblies	2	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	2	1	1	3	0	1	0	0
# unaligned contigs	0 + 8 part	0 + 12 part	0 + 1 part	0 + 19 part	0 + 19 part	0 + 5 part	0 + 5 part	0 + 6 part
Unaligned length	1077474	84149	4879622	611497	193325	418867	236583	9148
Genome fraction (%)	73.028	62.620	100.000	80.327	72.280	70.195	59.433	41.078
Duplication ratio	2.309	2.022	1.000	2.459	2.218	1.025	1.004	1.000
# N's per 100 kbp	0.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2047.41	377.00	0.00	2253.25	816.55	0.00	529.63	766.28
# indels per 100 kbp	53.88	0.00	0.00	24.49	0.00	0.00	33.10	0.00
Largest alignment	637	944	3110	955	663	1003	693	554
Total aligned length	8320	6435	5083	10087	8148	3657	3034	2088
NGA50	571	759	3110	581	593	765	347	-
NGA75	543	594	816	552	516	-	-	-
LGA50	5	3	1	4	5	3	5	-
LGA75	7	5	2	6	7	-	-	-

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

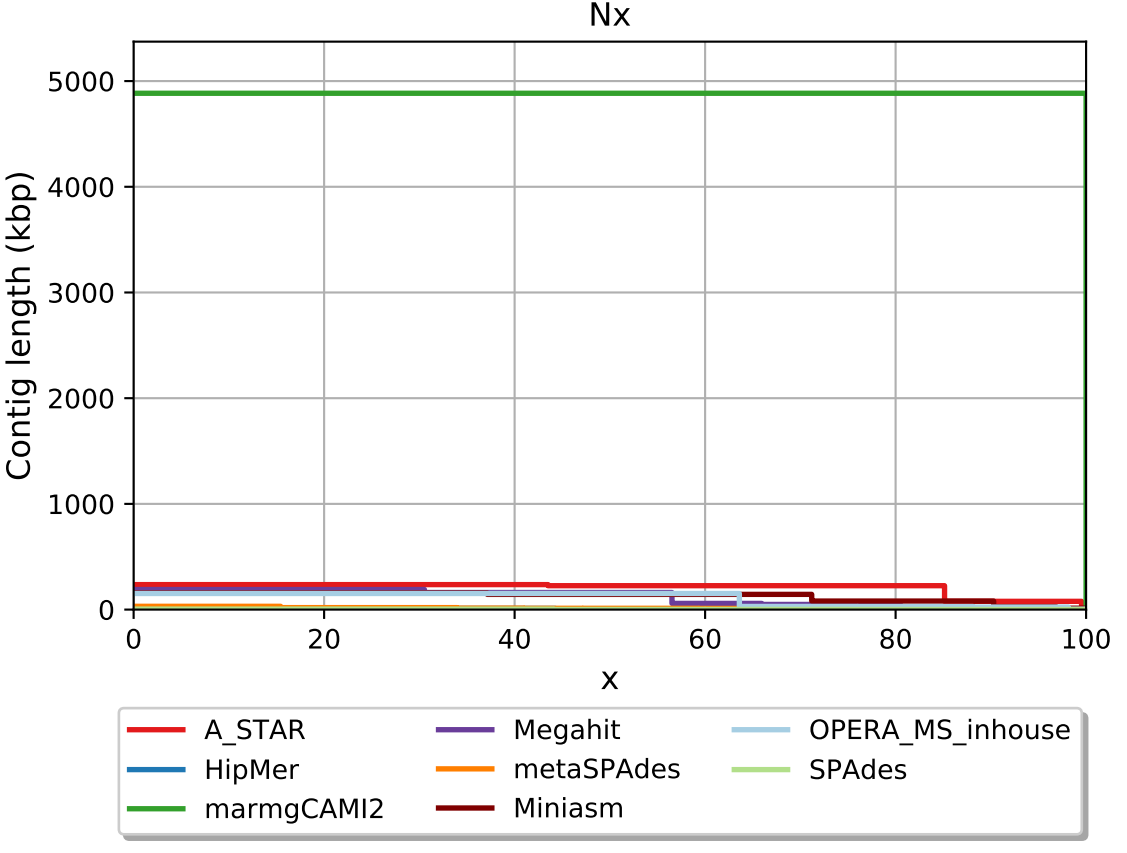
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	2	0	0	0	0
# contig misassemblies	0	0	0	2	0	0	0	0
# c. relocations	0	0	0	1	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	1	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	2	0	0	0	0
Misassembled contigs length	0	0	0	1048	0	0	0	0
# possibly misassembled contigs	6	11	0	15	19	4	4	6
# possible misassemblies	10	13	0	17	22	5	6	7
# local misassemblies	2	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	2	1	1	3	0	1	0	0
# mismatches	76	12	0	92	30	0	16	16
# indels	2	0	0	1	0	0	1	0
# indels (<= 5 bp)	0	0	0	0	0	0	0	0
# indels (> 5 bp)	2	0	0	1	0	0	1	0
Indels length	108	0	0	54	0	0	13	0

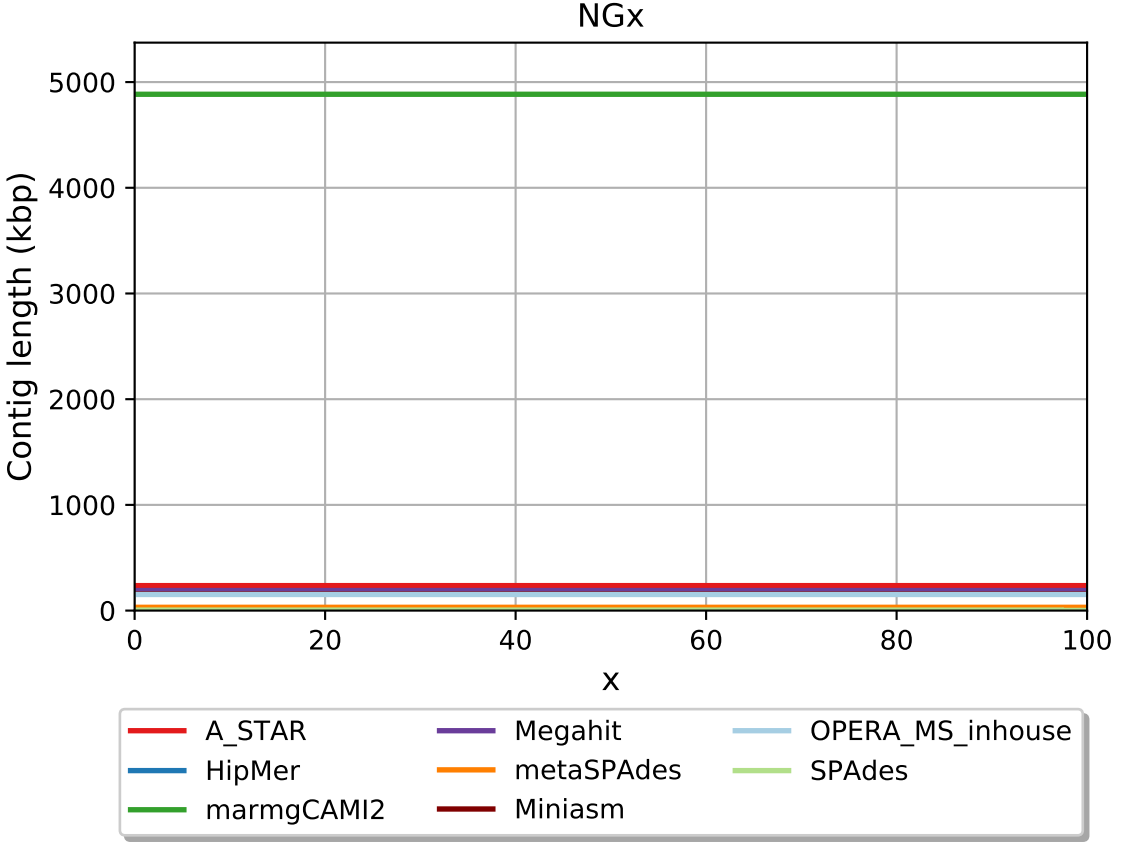
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

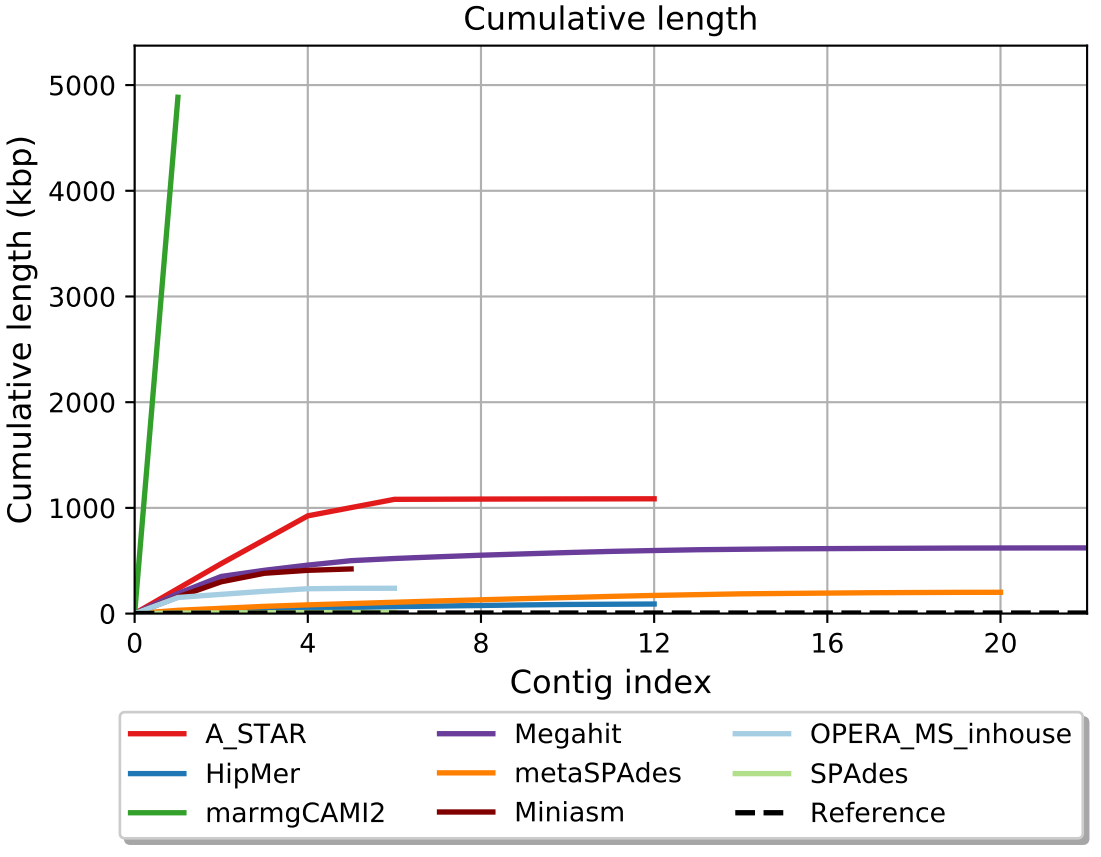
Unaligned report

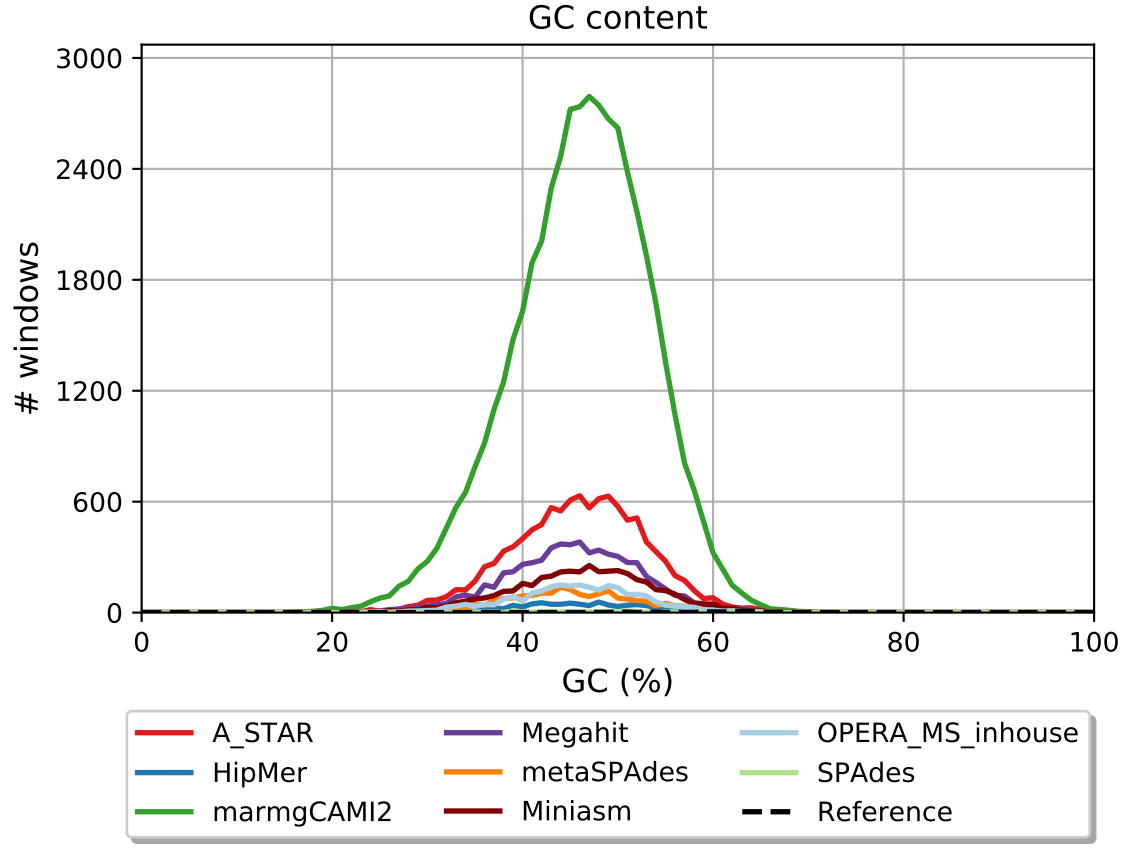
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	8	12	1	19	19	5	5	6
Partially unaligned length	1077474	84149	4879622	611497	193325	418867	236583	9148
# N's	6	0	0	0	0	0	0	0

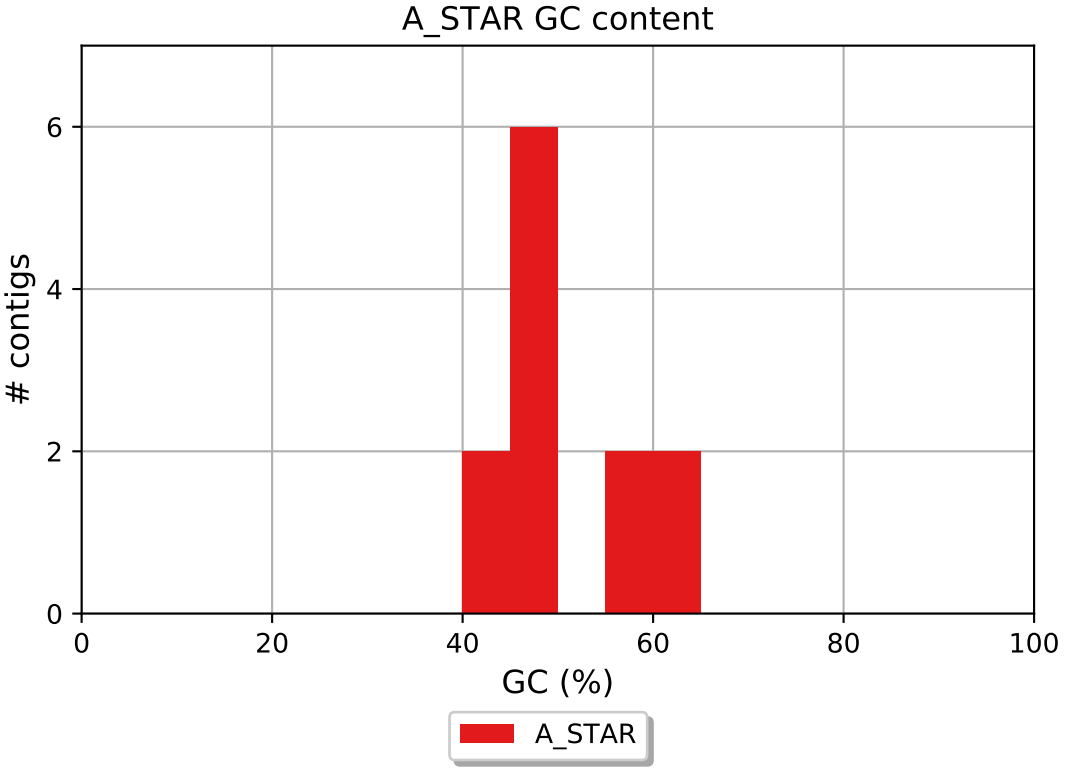
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

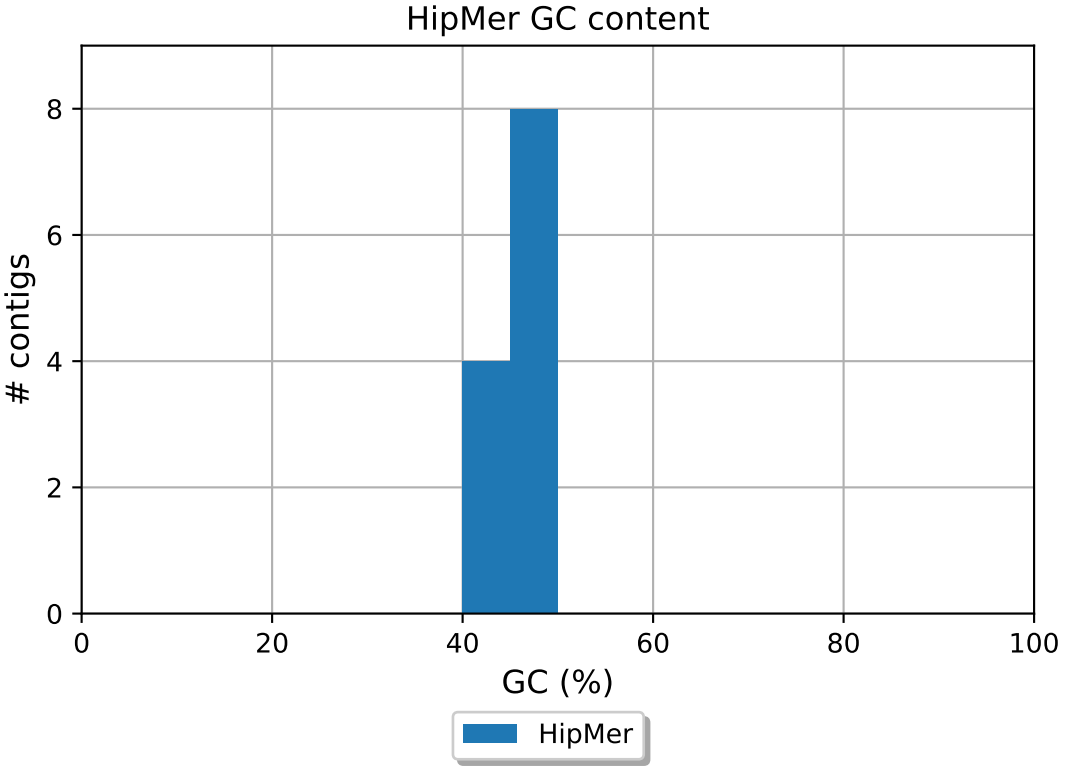

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

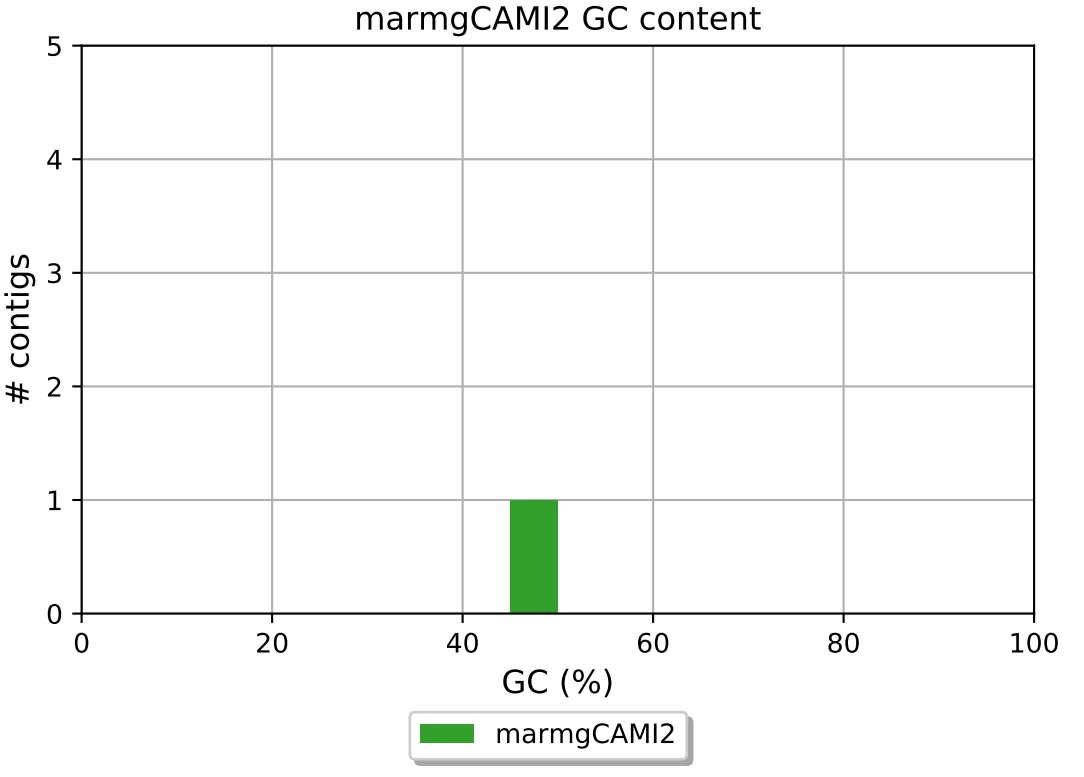

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes

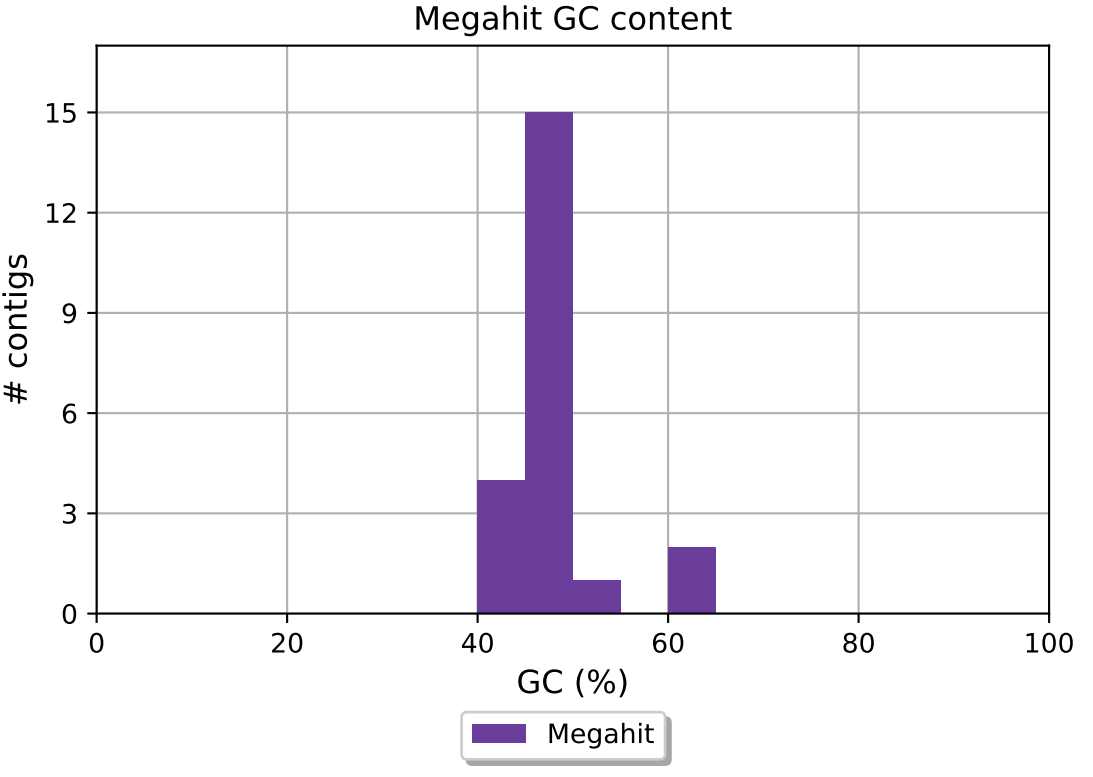

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

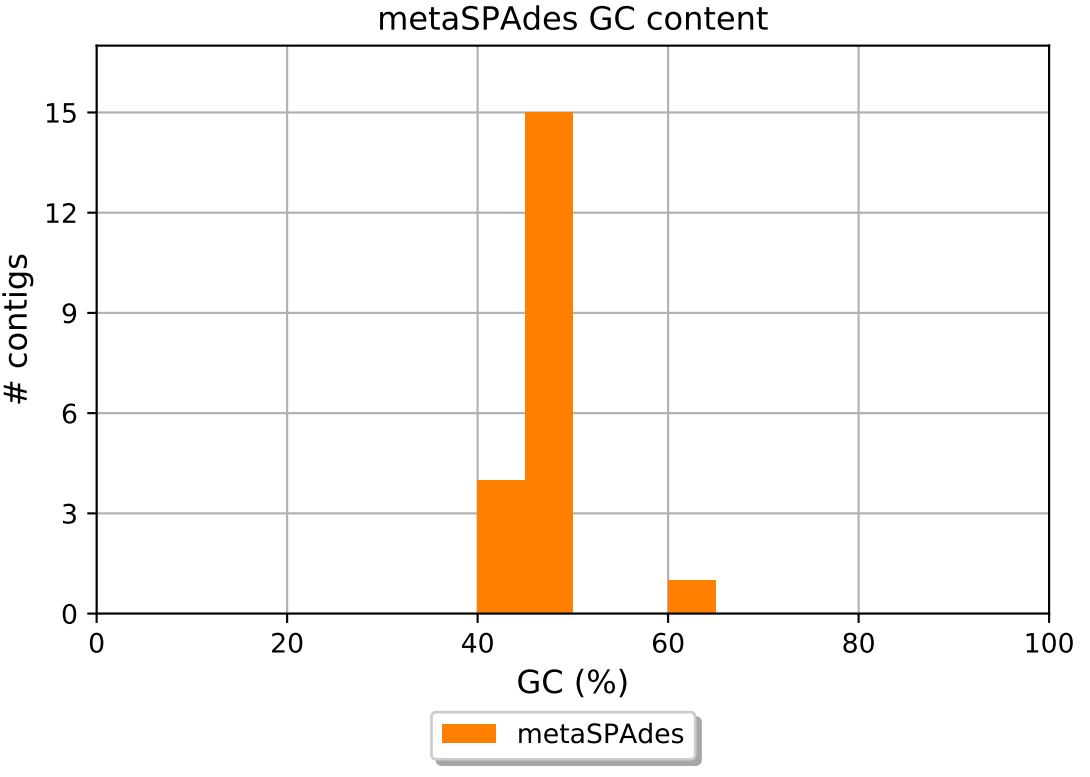

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference

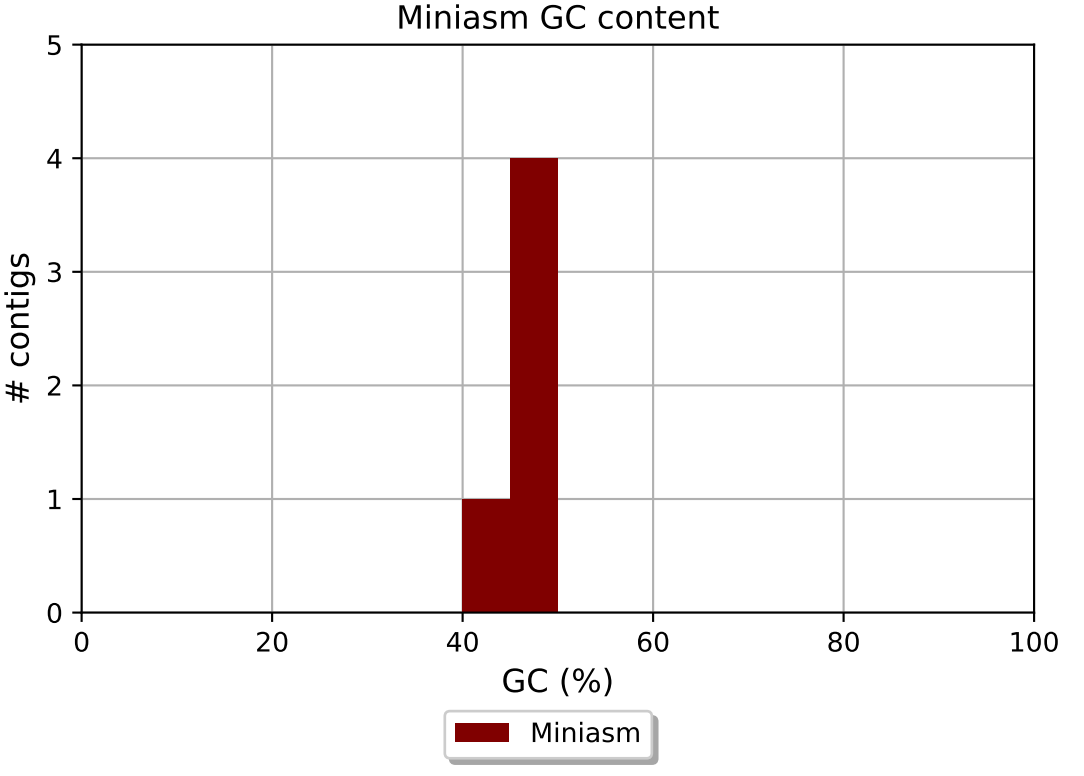

A_STAR GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
A_STAR

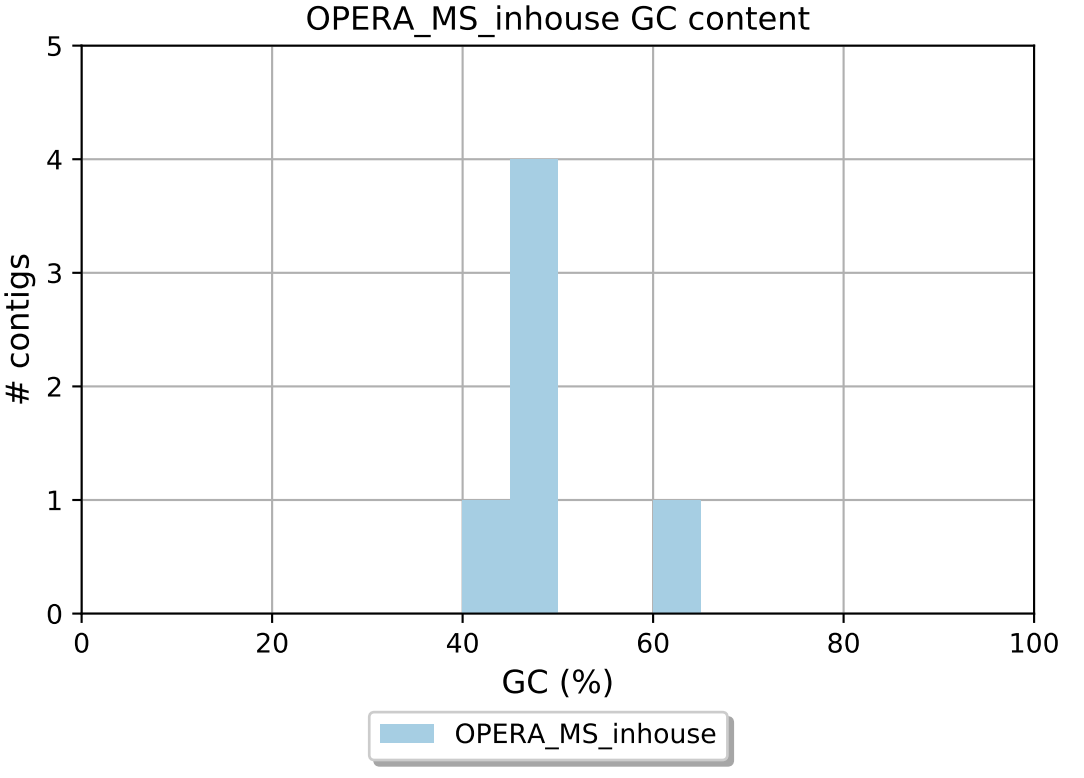

HipMer GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
HipMer

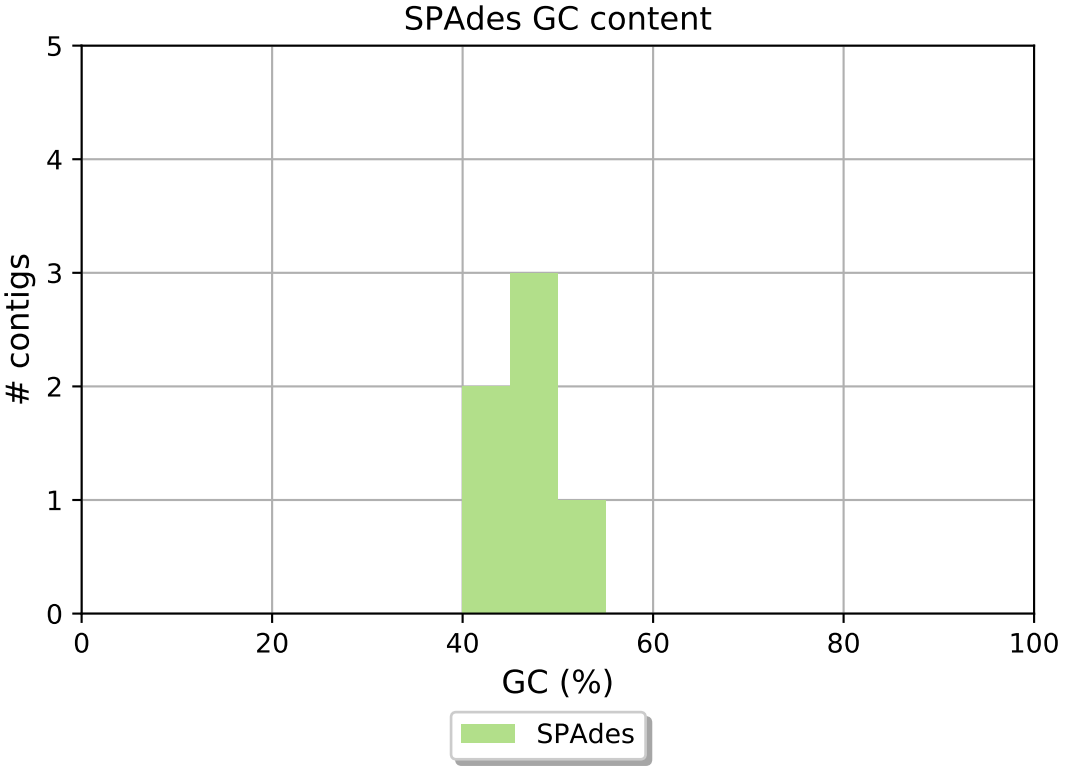

marmgCAMI2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
marmgCAMI2

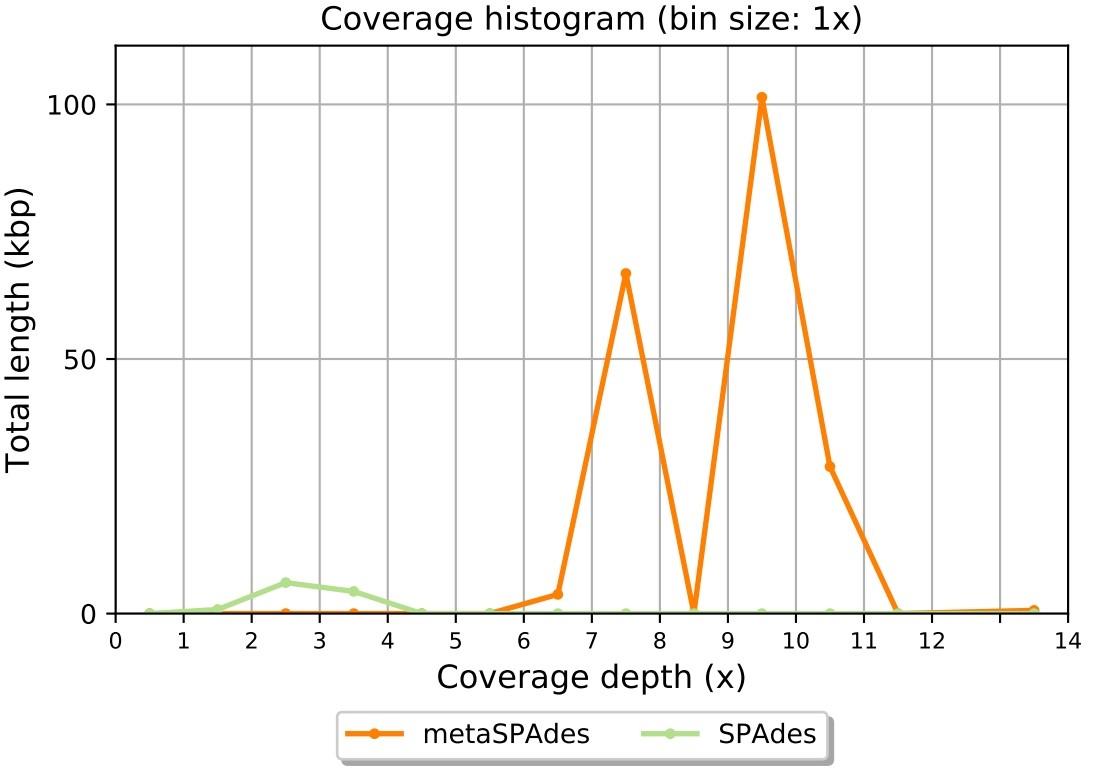

Megahit GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
Megahit

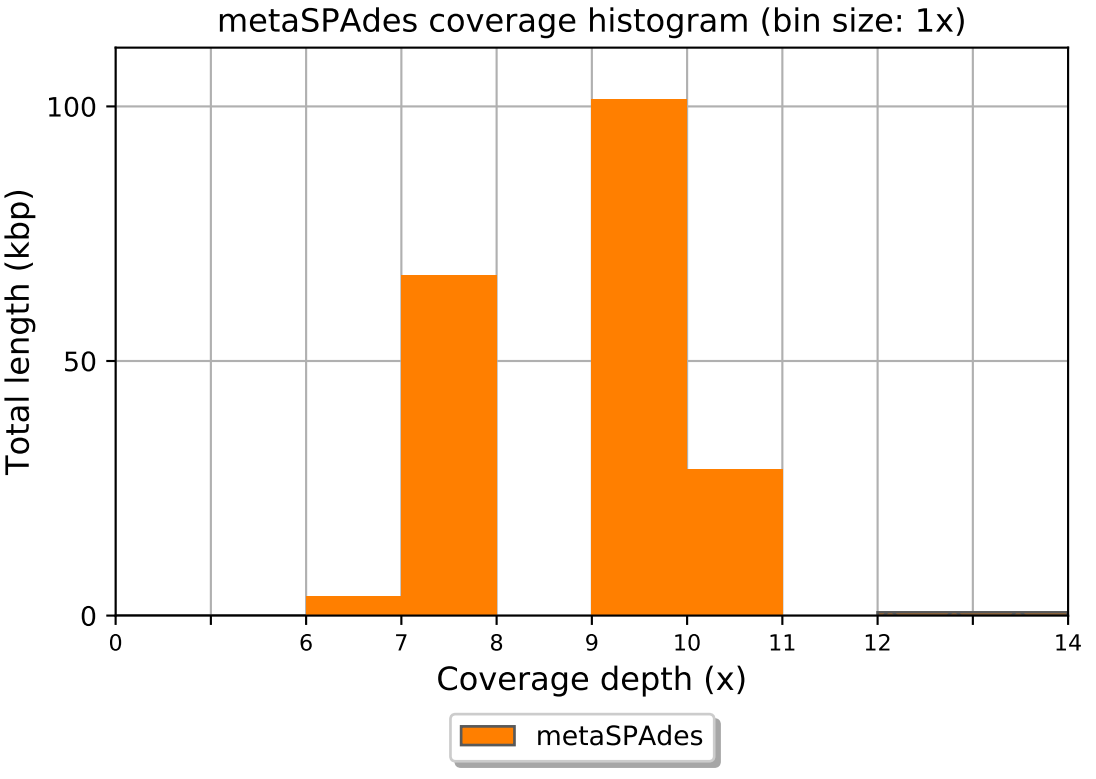

metaSPAdes GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
metaSPAdes

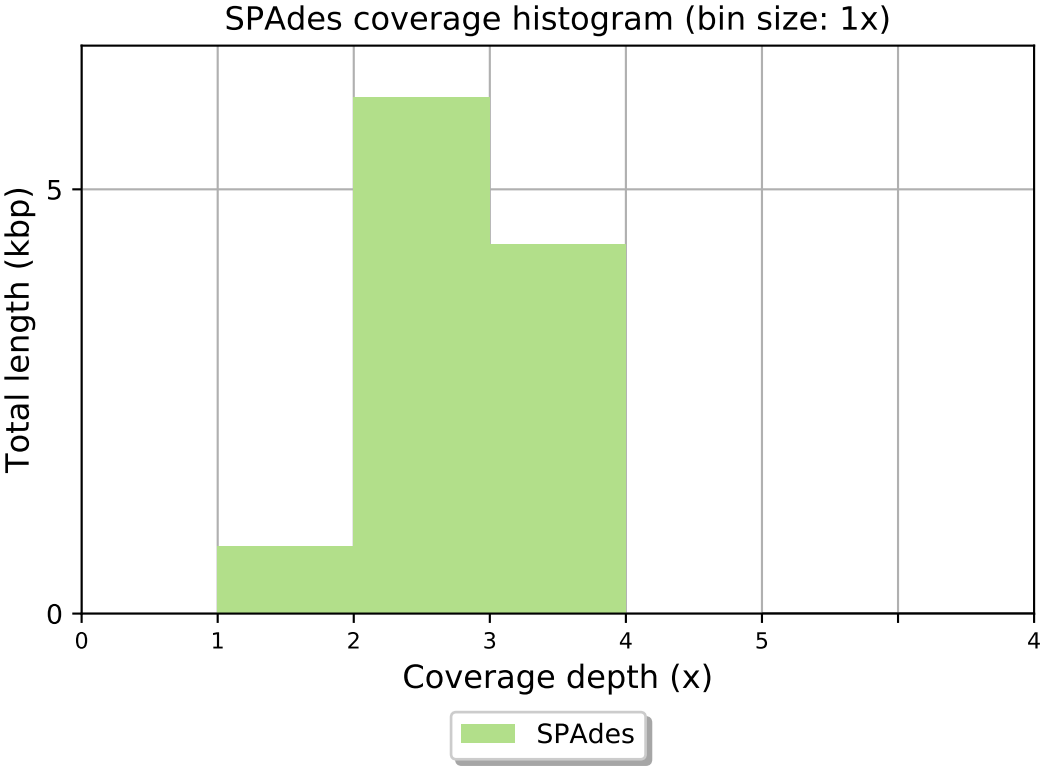

Miniasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Miniasm

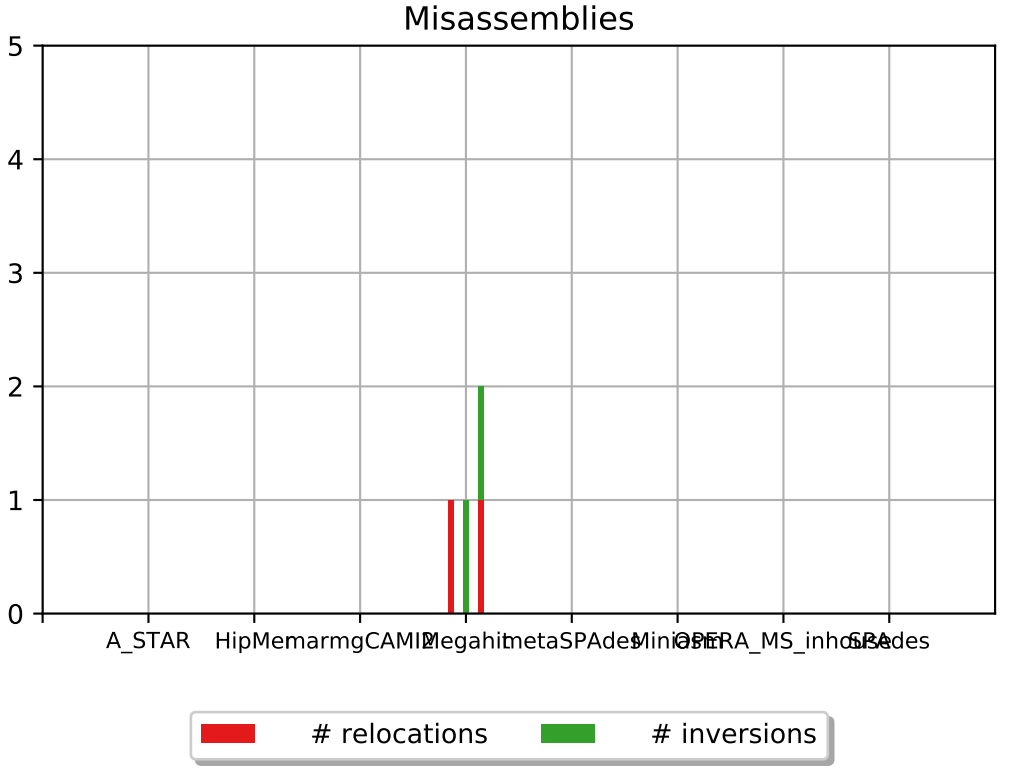

OPERA_MS_inhouse GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
OPERA_MS_inhouse

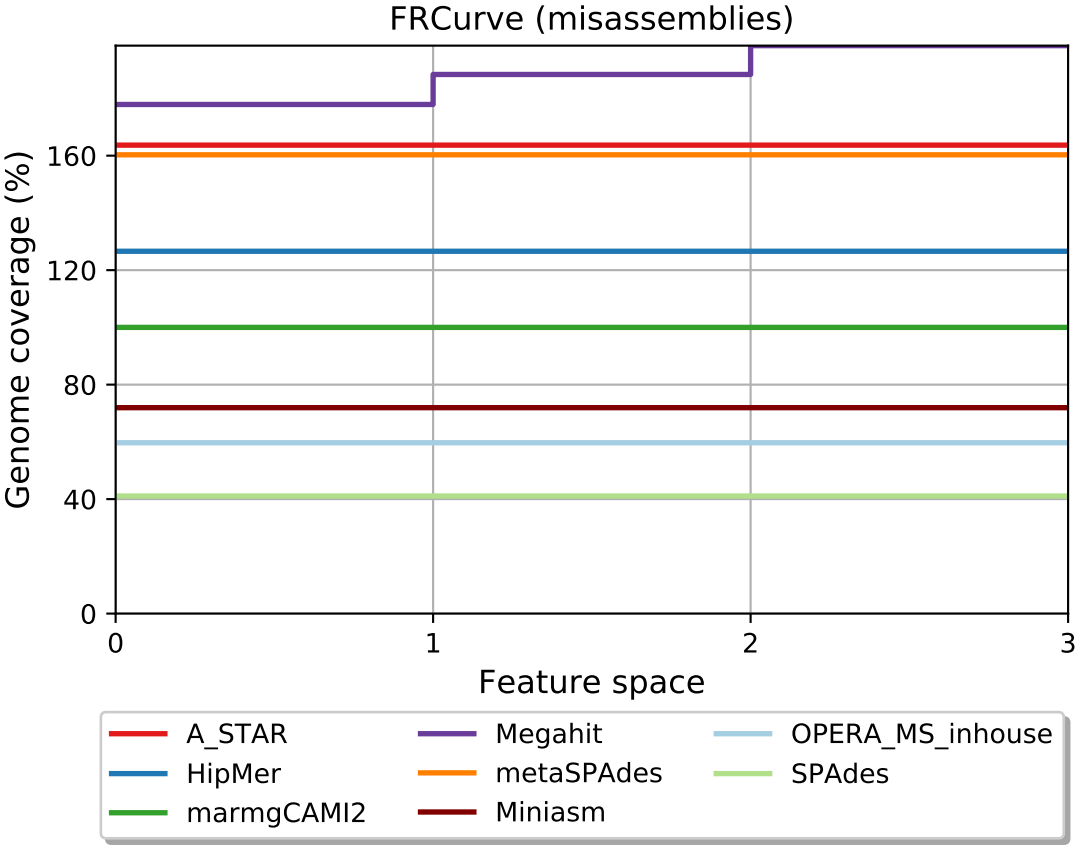

SPAdes GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes

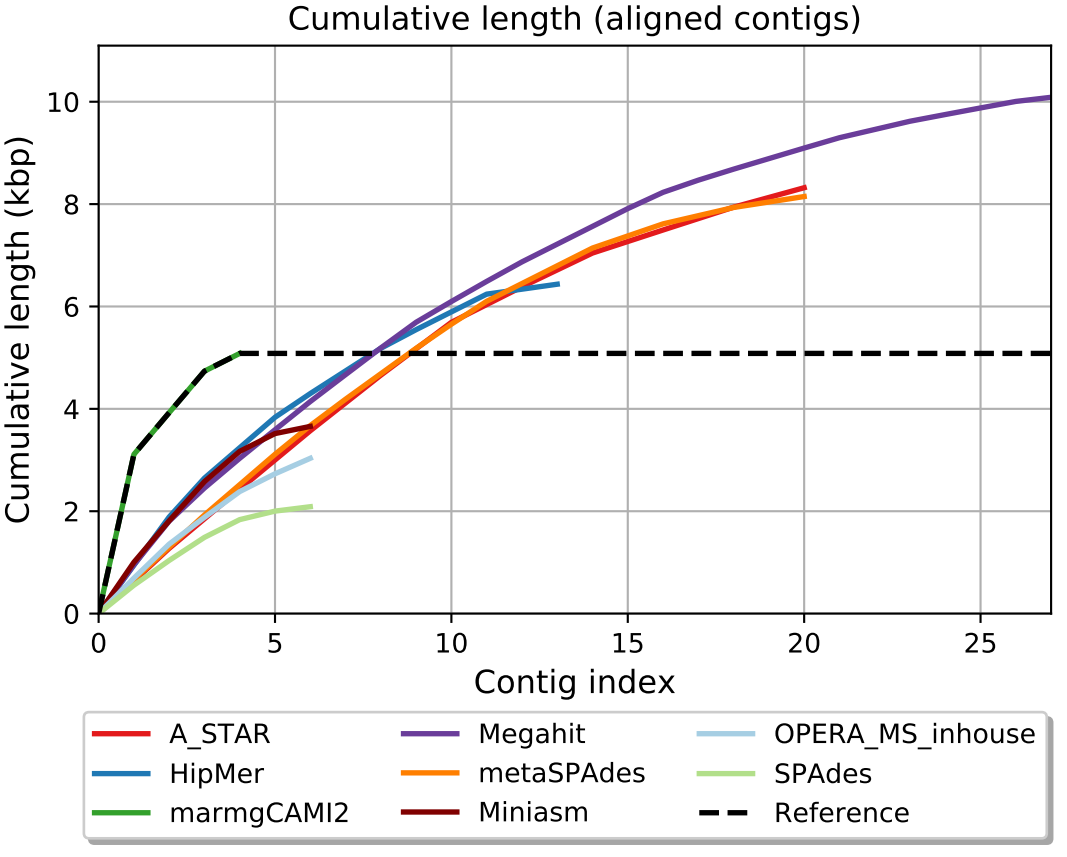

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
1
2
3
4
5
6
7
8
9
10
11
12
14
Coverage depth (x)
metaSPAdes
SPAdes

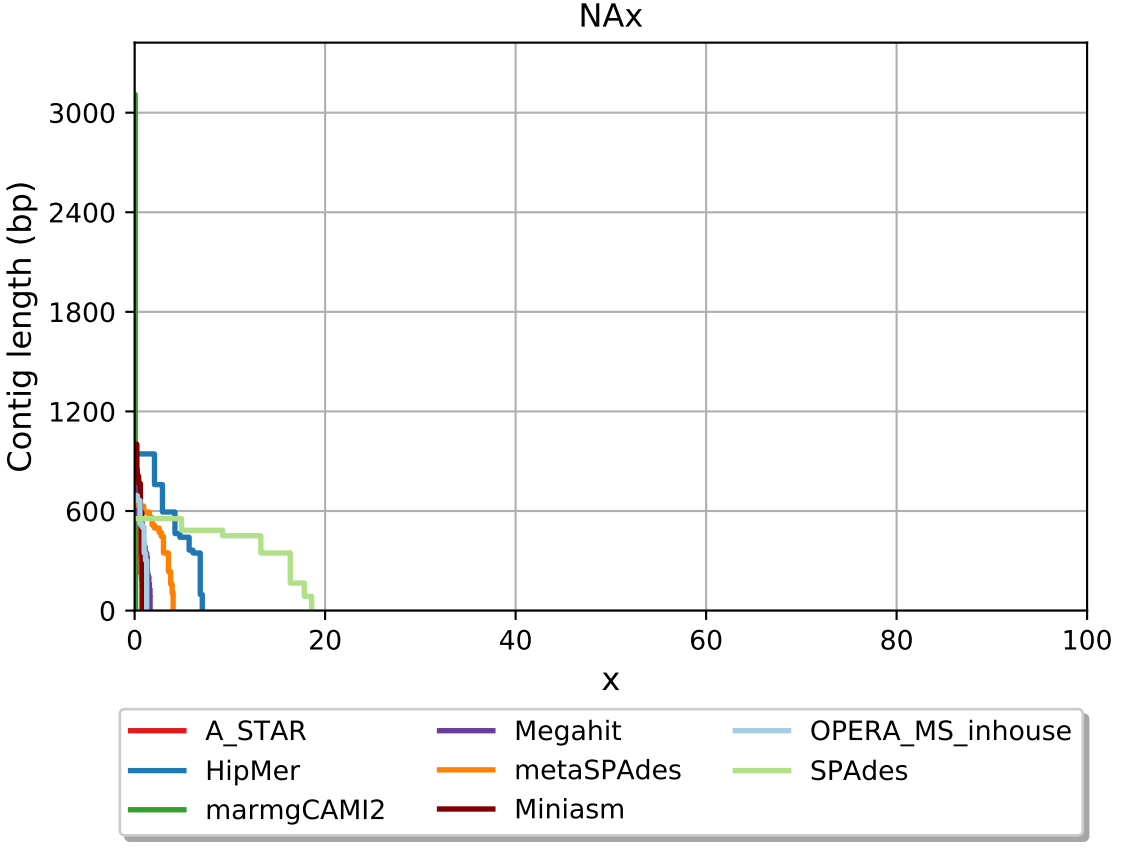

metaSPAdes coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
6
7
8
9
10
11
12
14
Coverage depth (x)
metaSPAdes

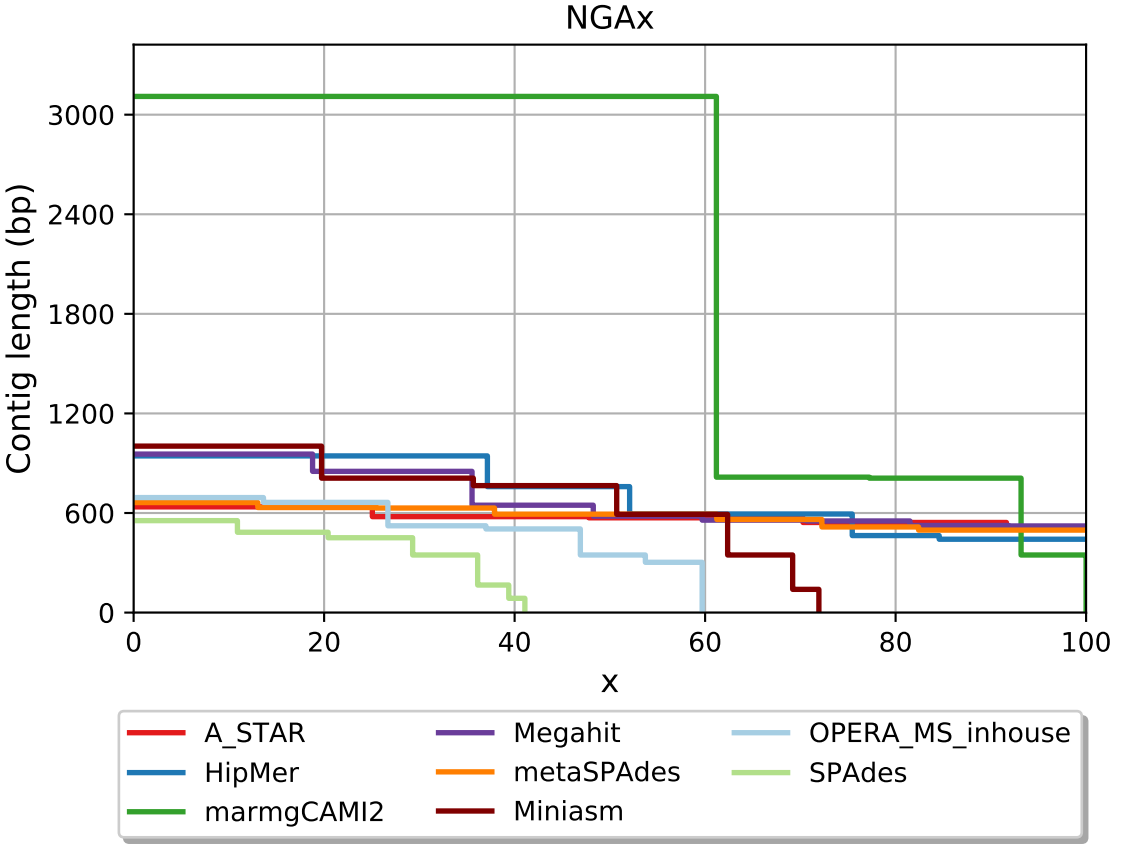

SPAdes coverage histogram (bin size: 1x)
Total length (kbp)
5
0
0
1
2
3
4
5
4
Coverage depth (x)
SPAdes

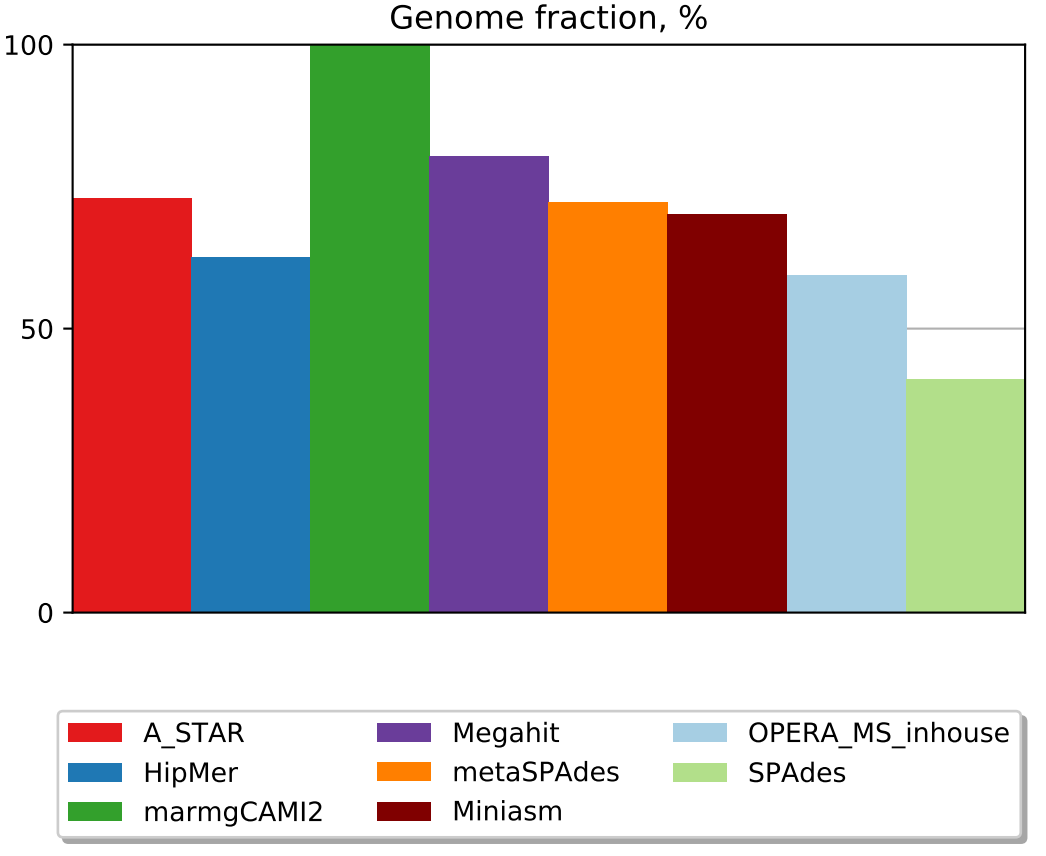

Misassemblies
5
4
3
2
1
0
A_STAR
HipMemarmgCAMIL
Megahit
metaSPAdes
MiniasmOPERA_MS_inhouse
SPAdes
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
40
80
120
160
0
1
2
3
Feature space
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
2
4
6
8
10
0
5
10
15
20
25
Contig index
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes
Reference


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
A_STAR
HipMer
marmgCAMI2
Megahit
metaSPAdes
Miniasm
OPERA_MS_inhouse
SPAdes


NGAx
Contig length (bp)
3000
2400
1800
1200
600
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