Report

	hifiasm
# contigs (>= 0 bp)	302
# contigs (>= 1000 bp)	302
# contigs (>= 5000 bp)	301
# contigs (>= 10000 bp)	298
# contigs (>= 25000 bp)	258
# contigs (>= 50000 bp)	215
Total length (>= 0 bp)	2143853045
Total length (>= 1000 bp)	2143853045
Total length (>= 5000 bp)	2143848428
Total length (>= 10000 bp)	2143827229
Total length (>= 25000 bp)	2143071830
Total length (>= 50000 bp)	2141533709
# contigs	302
Largest contig	160459971
Total length	2143853045
Reference length	2182786008
GC (%)	46.79
Reference GC (%)	46.77
N50	63673969
NG50	63673969
N75	32553861
NG75	30949767
L50	12
LG50	12
L75	23
LG75	24
# misassemblies	157
# misassembled contigs	93
Misassembled contigs length	905390237
# local misassemblies	78
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 38 part
Unaligned length	1235063
Genome fraction (%)	98.285
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.59
# indels per 100 kbp	0.34
Largest alignment	128858610
Total aligned length	2141466821
NA50	56635102
NGA50	56635102
NA75	24244347
NGA75	24008378
LA50	14
LGA50	14
LA75	28
LGA75	29

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

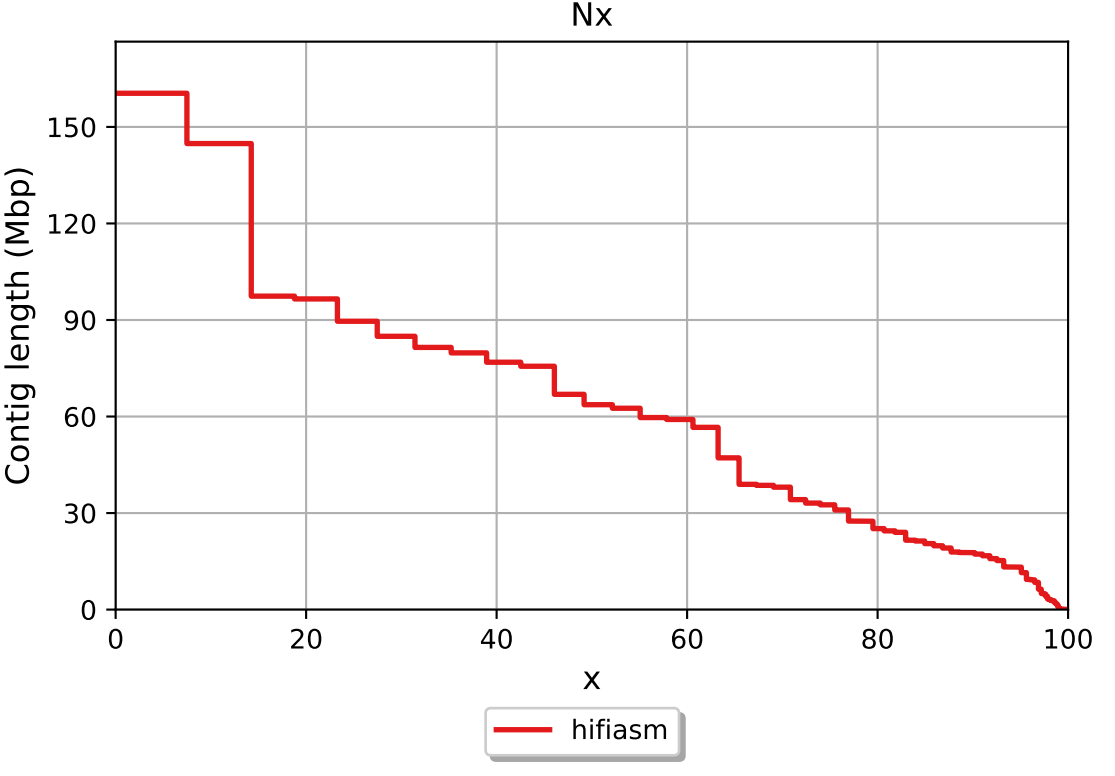
	hifiasm
# misassemblies	157
# contig misassemblies	157
# c. relocations	36
# c. translocations	121
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	93
Misassembled contigs length	905390237
# local misassemblies	78
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	0
# possible TEs	0
# unaligned mis. contigs	0
# mismatches	12558
# indels	7205
# indels (<= 5 bp)	6902
# indels (> 5 bp)	303
Indels length	1044739

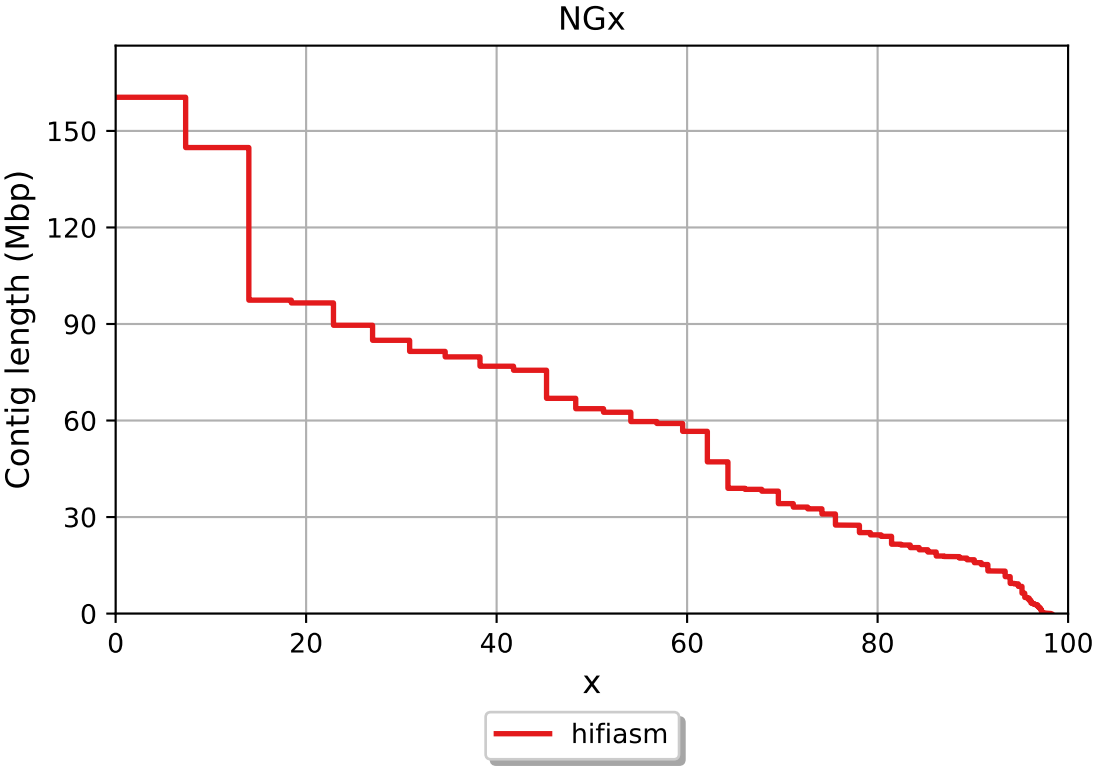
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

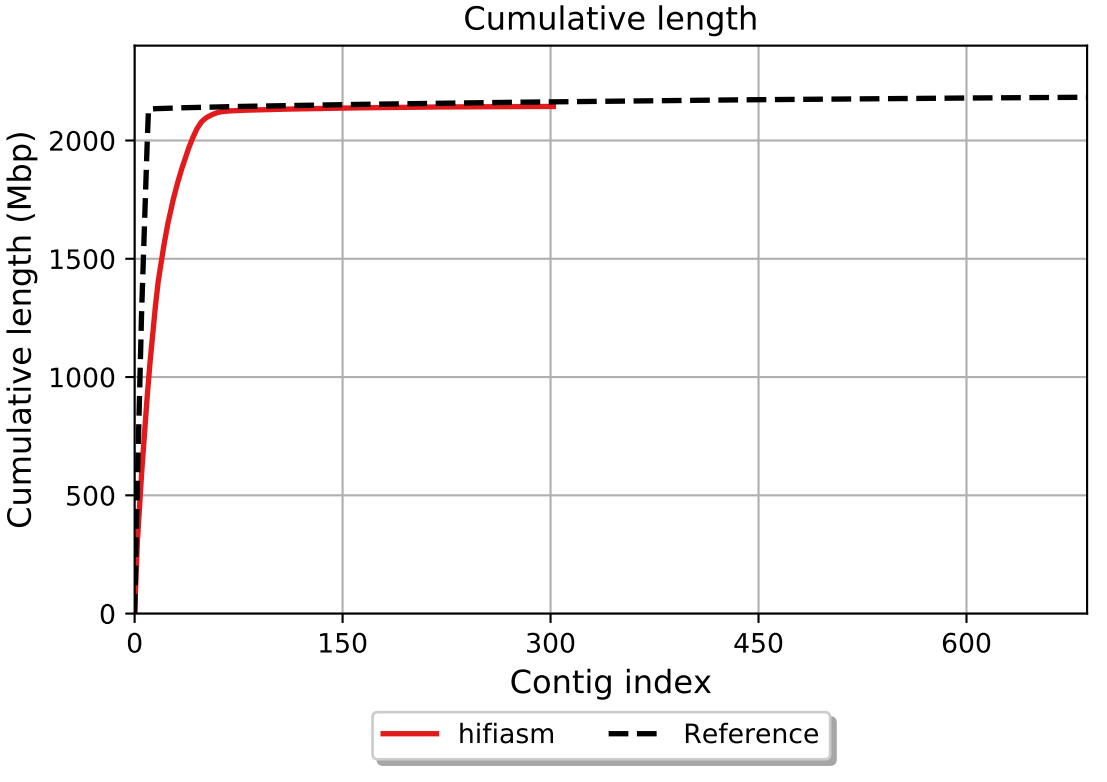
Unaligned report

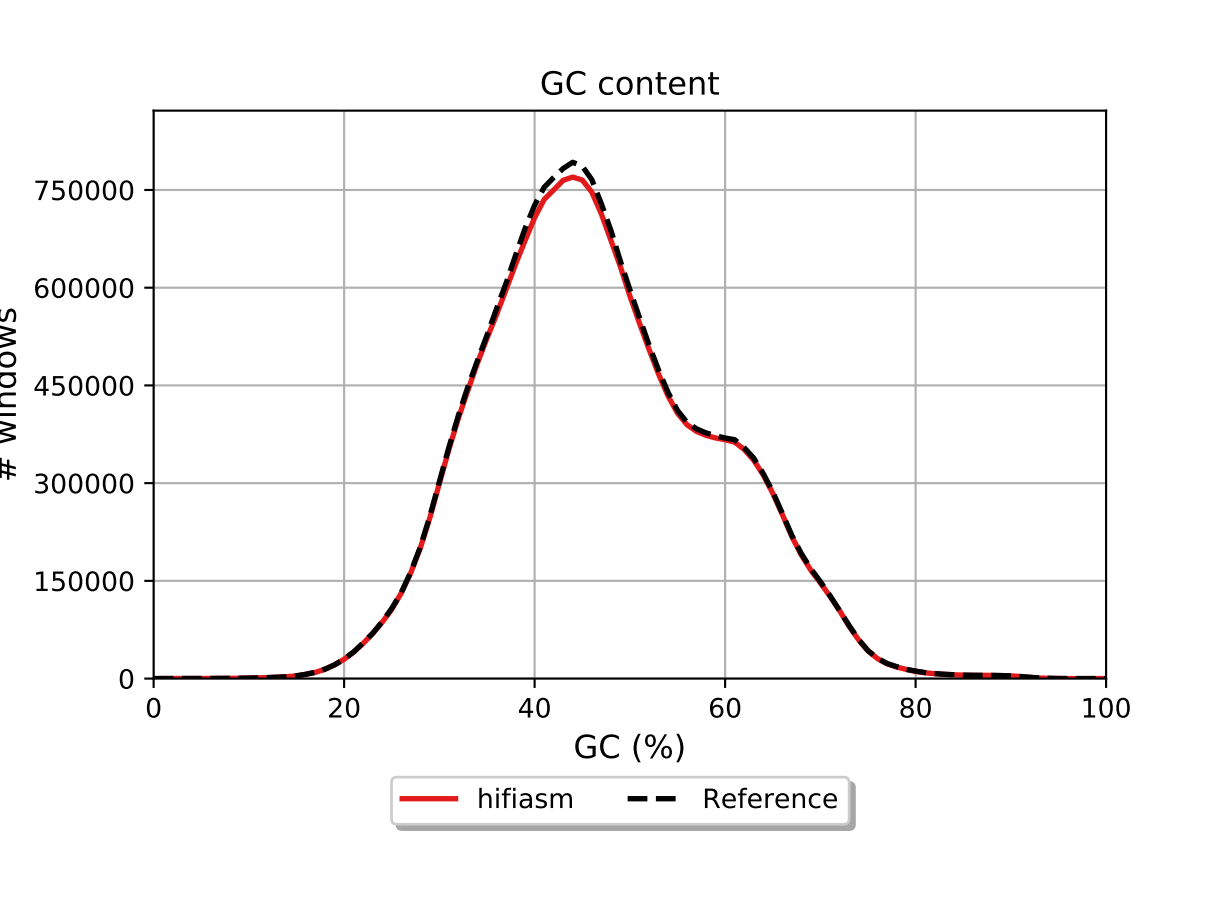
	hifiasm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	38
Partially unaligned length	1235063
# N's	0

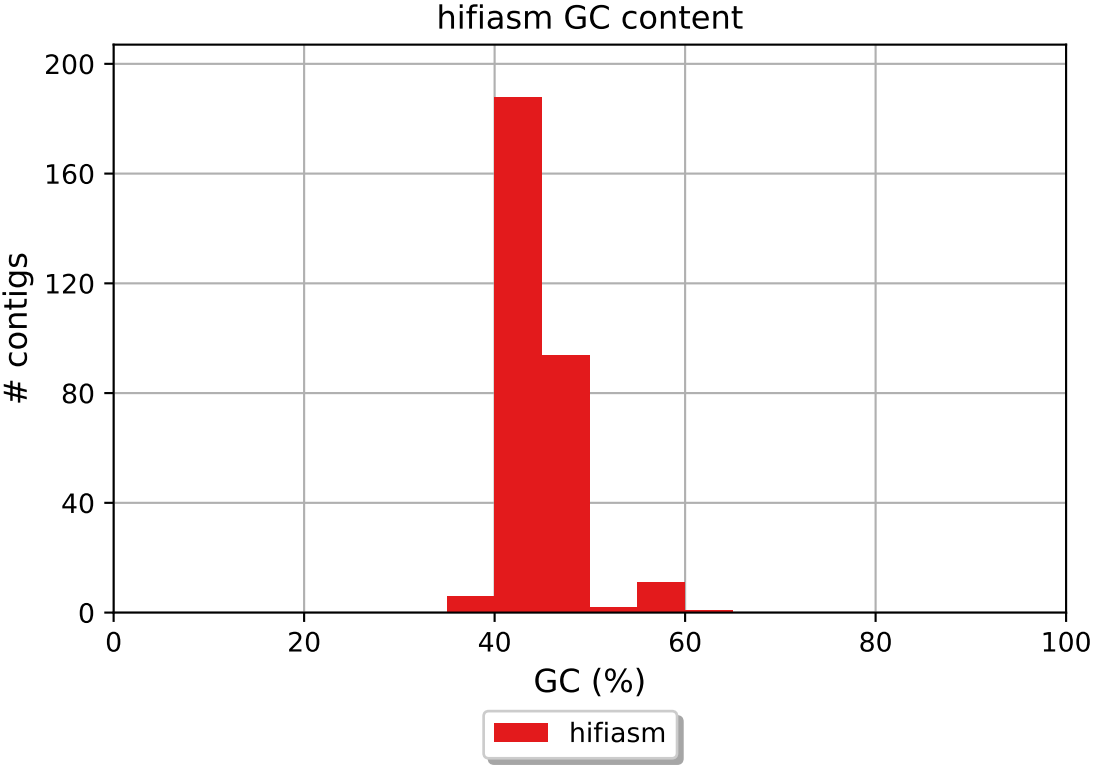
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

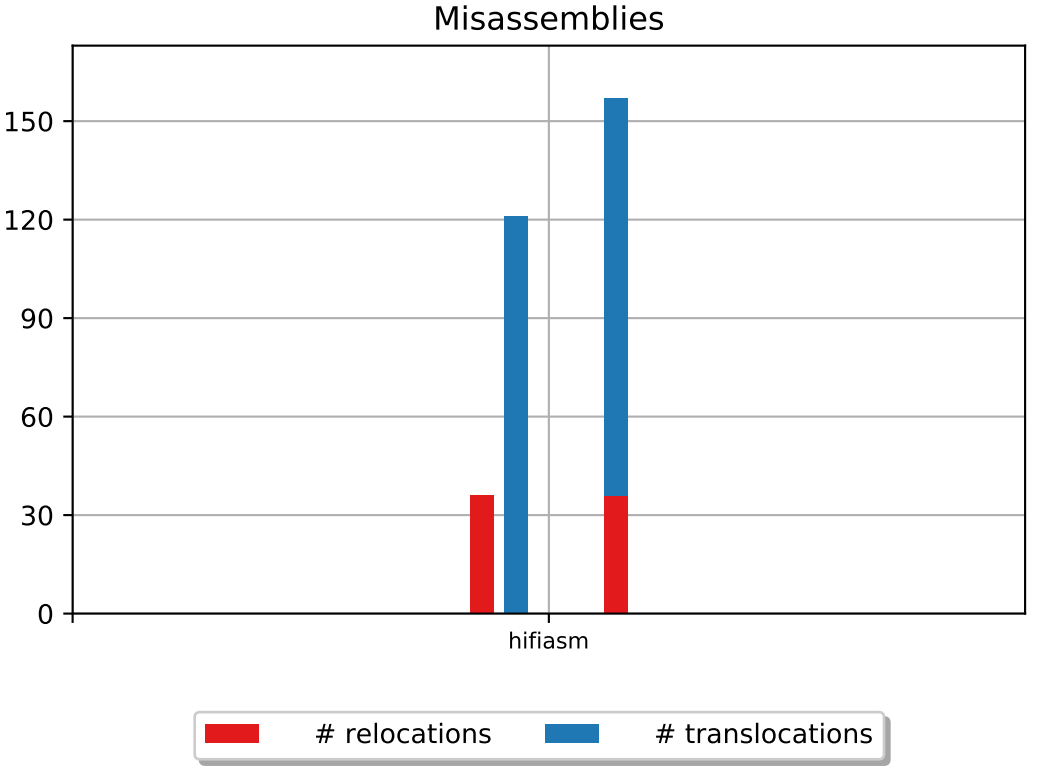

Nx
Contig length (Mbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
hifiasm

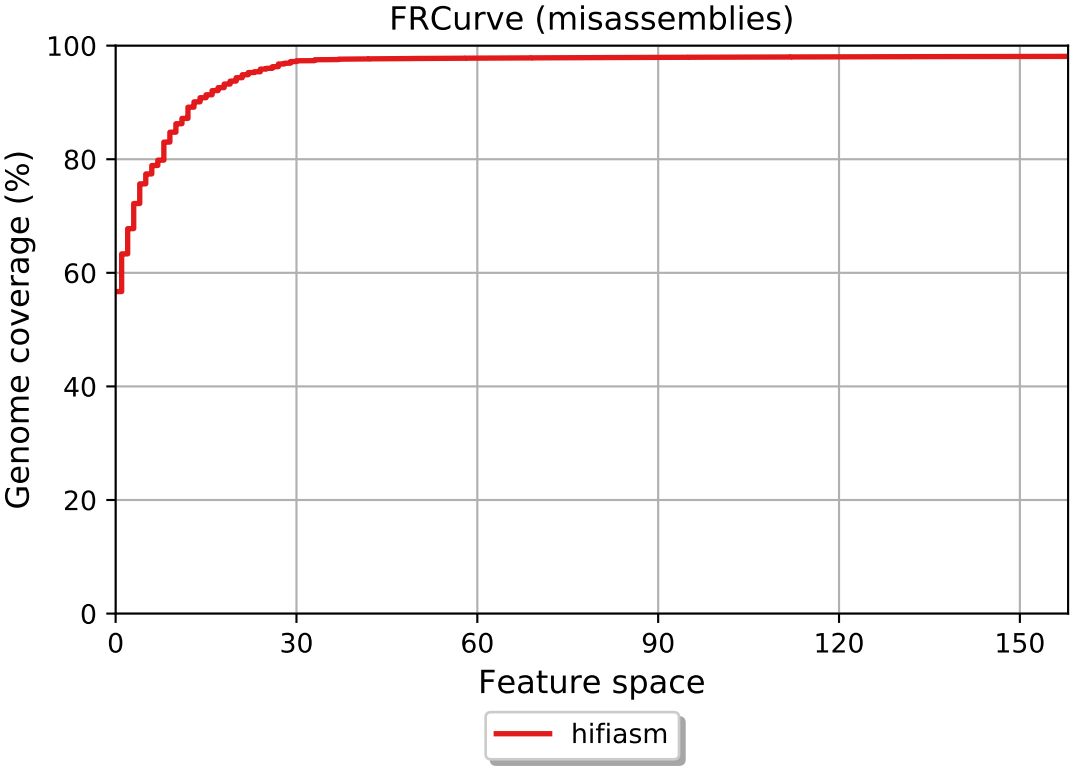

NGx
Contig length (Mbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
hifiasm

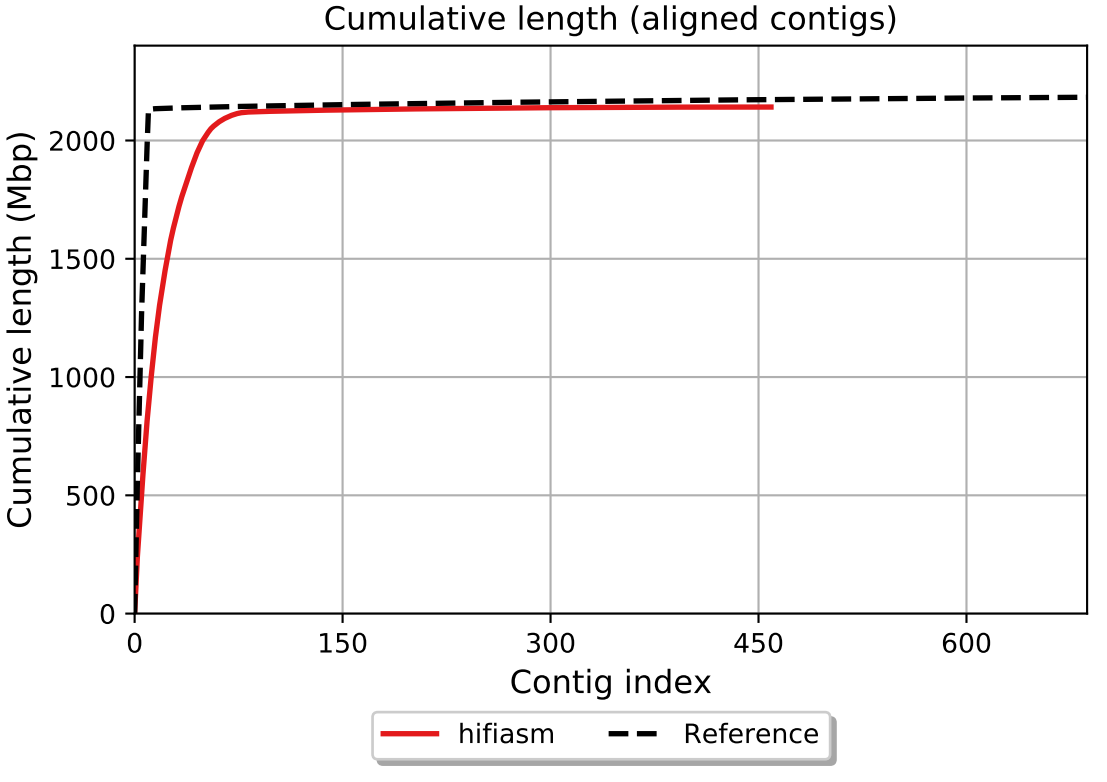

Cumulative length
Cumulative length (Mbp)
2000
1500
1000
500
0
0
150
300
450
600
Contig index
hifiasm
Reference

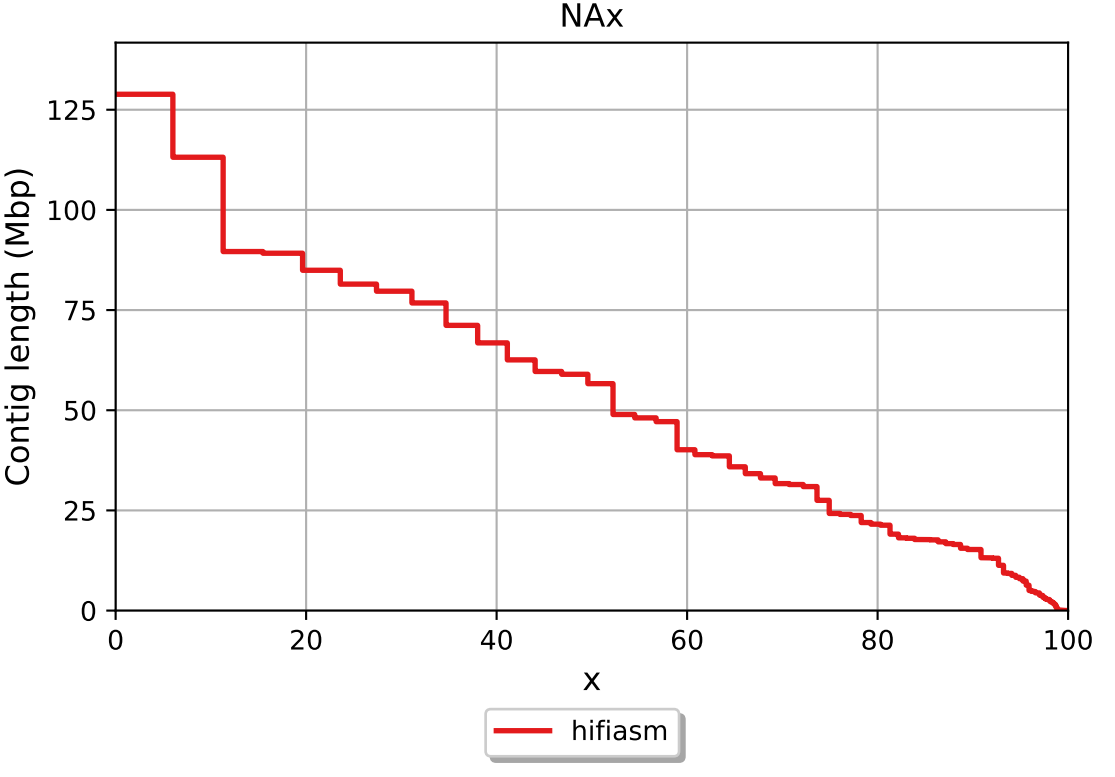

GC content
windows
750000
600000
450000
300000
150000
0
0
20
40
60
80
100
GC (%)
hifiasm
Reference

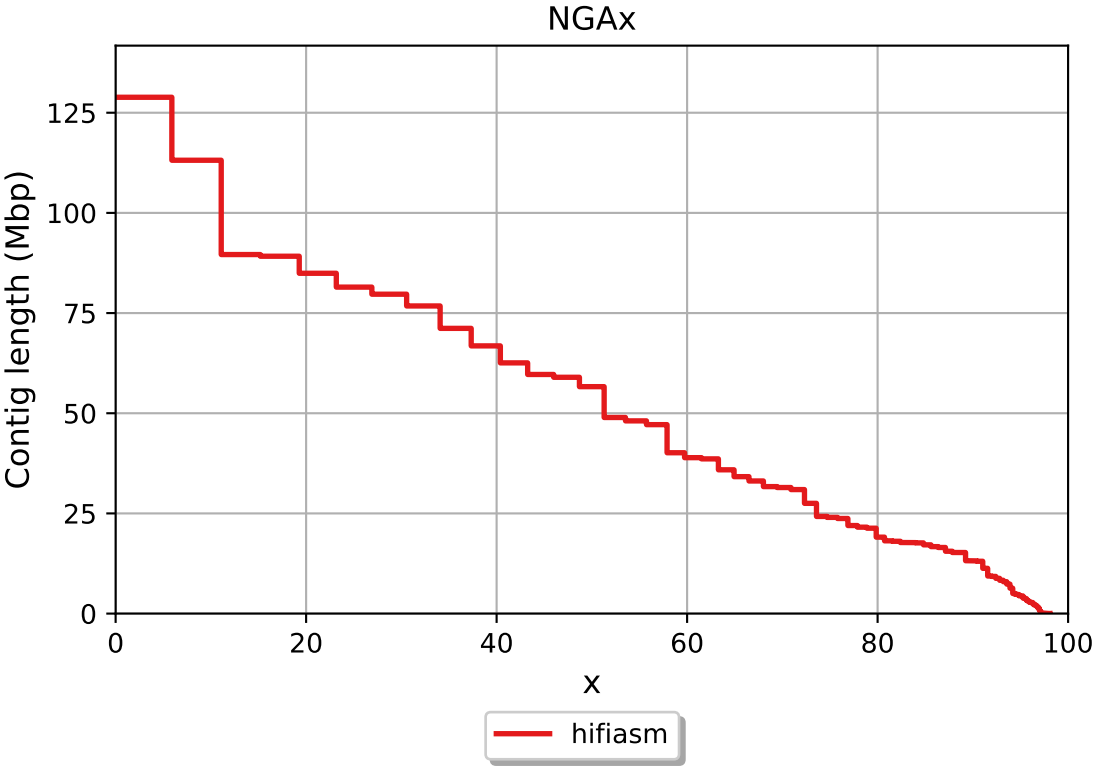

hifiasm GC content
contigs
GC (%)
hifiasm
0
40
80
120
160
200
0
20
40
60
80
100


Misassemblies
150
120
90
60
30
0
hifiasm
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
30
60
90
120
150
Feature space
hifiasm


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
500
1000
1500
2000
0
150
300
450
600
Contig index
hifiasm
Reference


NAx
Contig length (Mbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
hifiasm


NGAx
Contig length (Mbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
hifiasm