Report

	sim5M.MiniCH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1990
# contigs (>= 5000 bp)	1607
# contigs (>= 10000 bp)	474
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	15688889
Total length (>= 1000 bp)	15681889
Total length (>= 5000 bp)	14295341
Total length (>= 10000 bp)	5879882
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1998
Largest contig	23137
Total length	15688017
Reference length	5000040
GC (%)	35.91
Reference GC (%)	35.84
N50	8894
NG50	12626
N75	6845
NG75	11468
L50	683
LG50	171
L75	1185
LG75	275
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	33833
# local misassemblies	17
# unaligned mis. contigs	0
# unaligned contigs	119 + 25 part
Unaligned length	1266588
Genome fraction (%)	93.857
Duplication ratio	3.073
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.46
# indels per 100 kbp	545.91
Largest alignment	23137
Total aligned length	14415597
NA50	8305
NGA50	12208
NA75	6064
NGA75	11069
LA50	714
LGA50	175
LA75	1260
LGA75	283

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

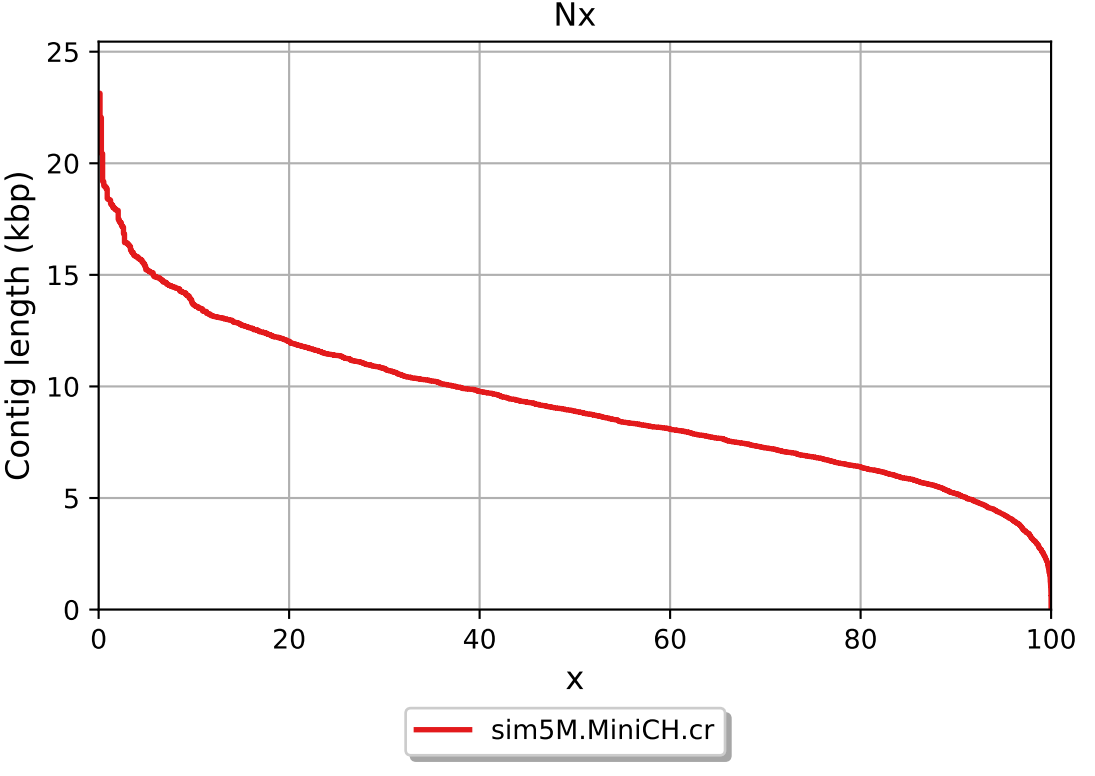
	sim5M.MiniCH.cr
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	33833
# local misassemblies	17
# unaligned mis. contigs	0
# mismatches	2931
# indels	25619
# indels (<= 5 bp)	25602
# indels (> 5 bp)	17
Indels length	30169

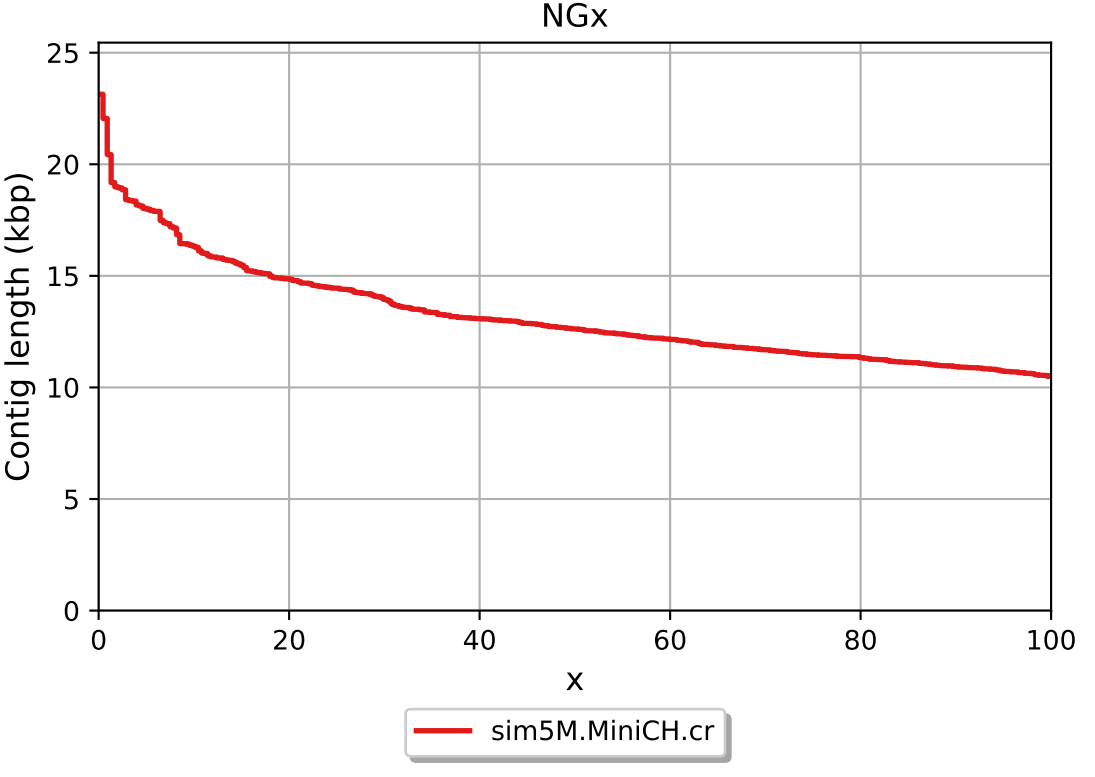
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

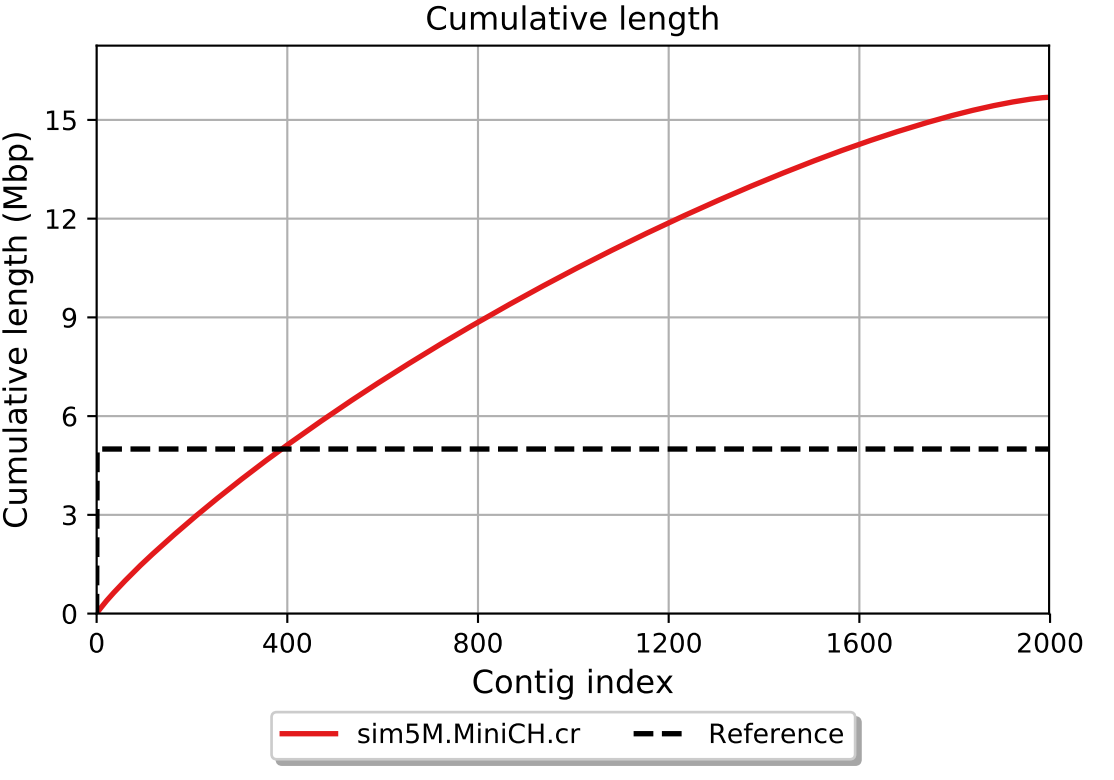
Unaligned report

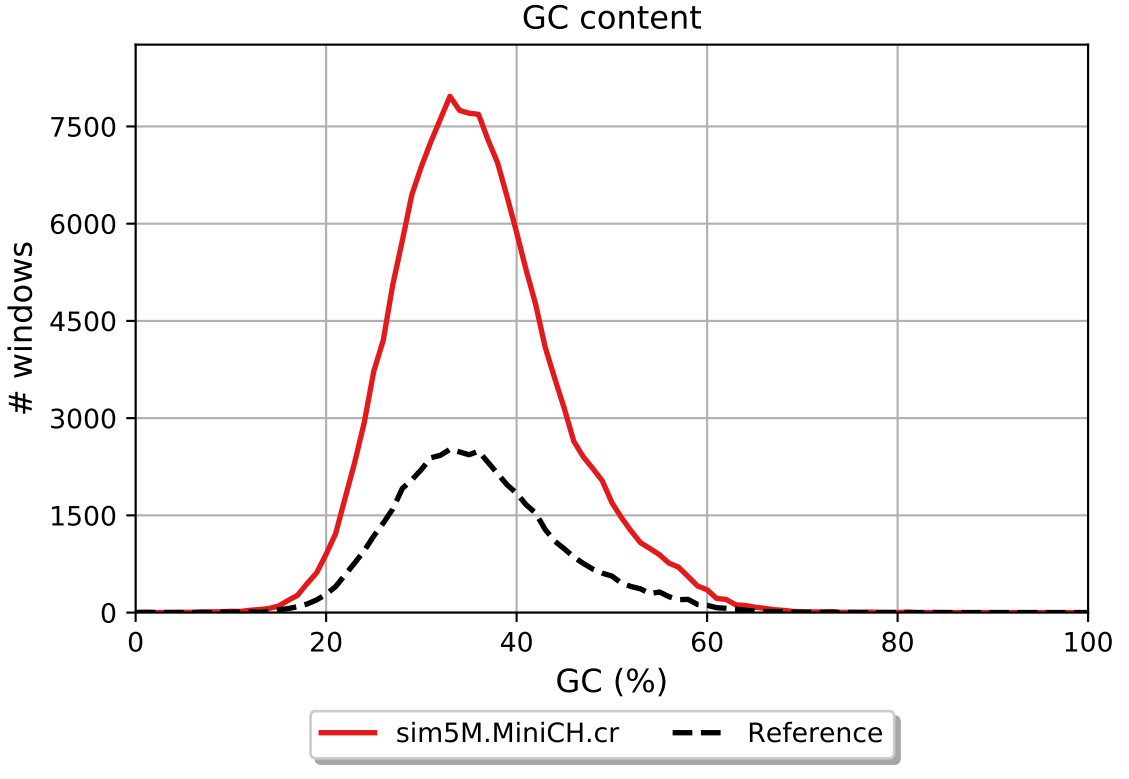
	sim5M.MiniCH.cr
# fully unaligned contigs	119
Fully unaligned length	1157463
# partially unaligned contigs	25
Partially unaligned length	109125
# N's	0

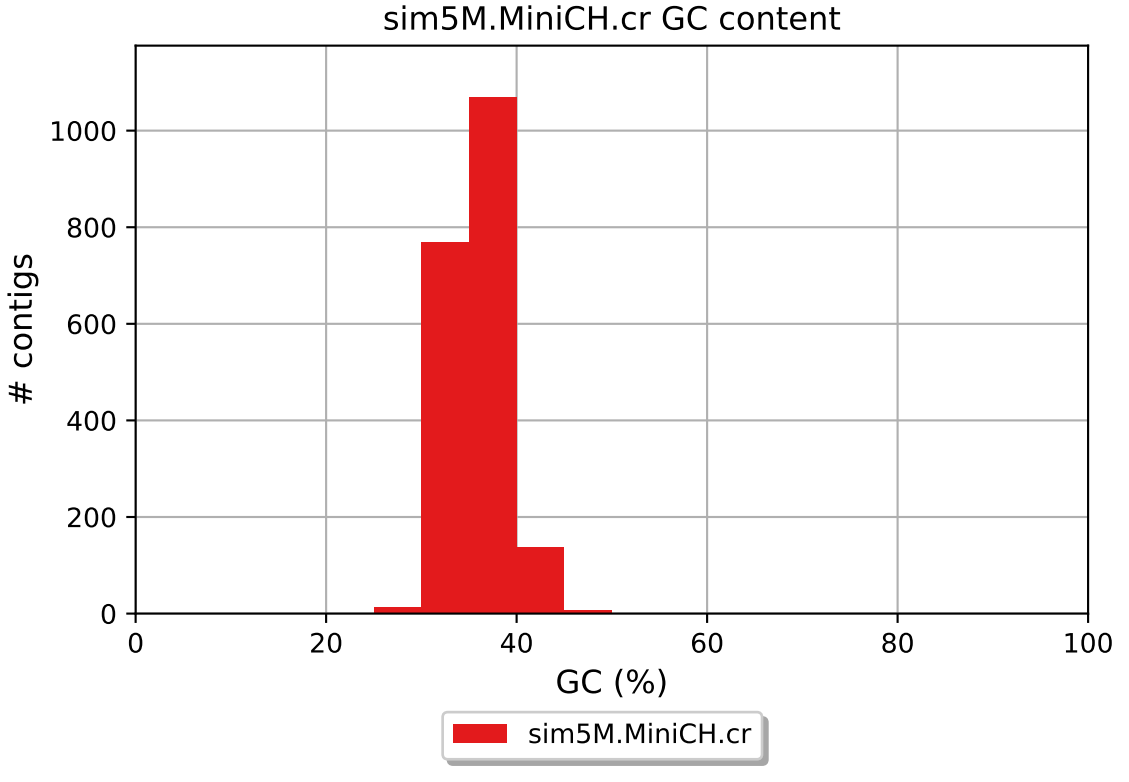
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

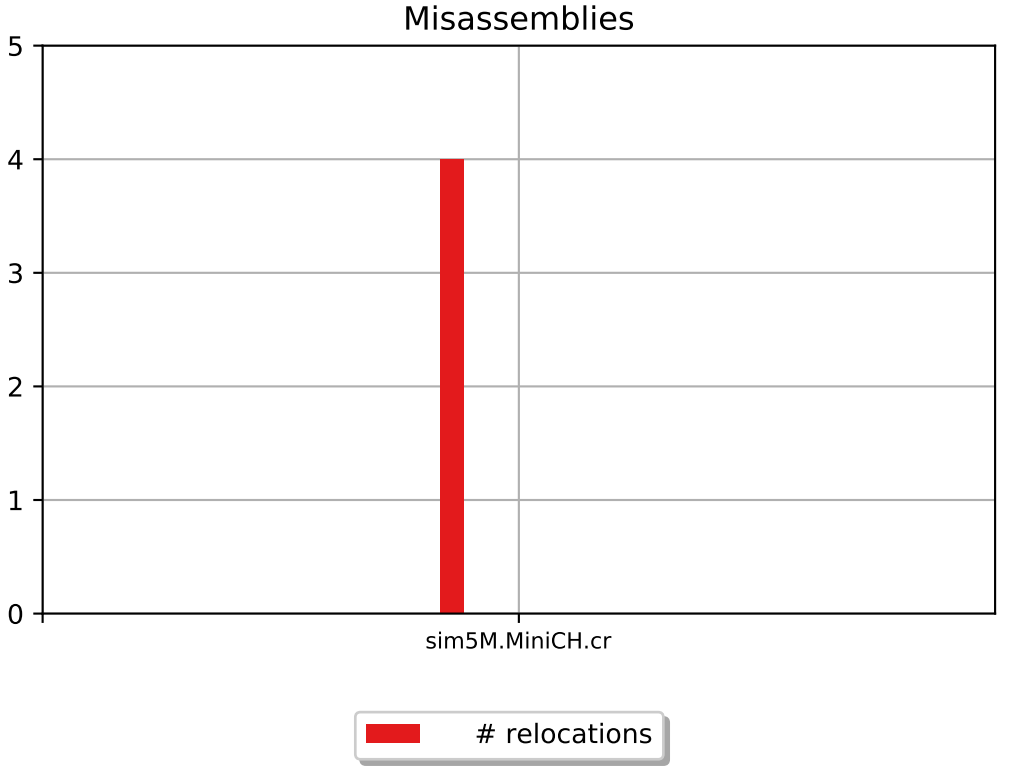

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.MiniCH.cr

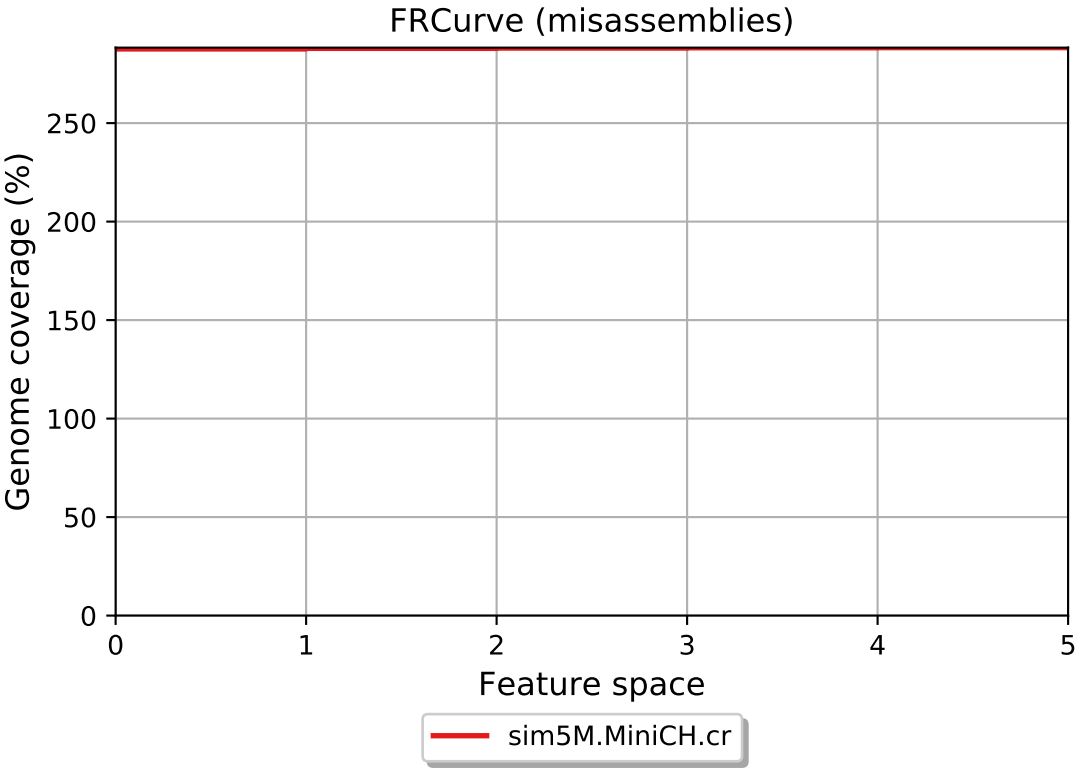

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.MiniCH.cr

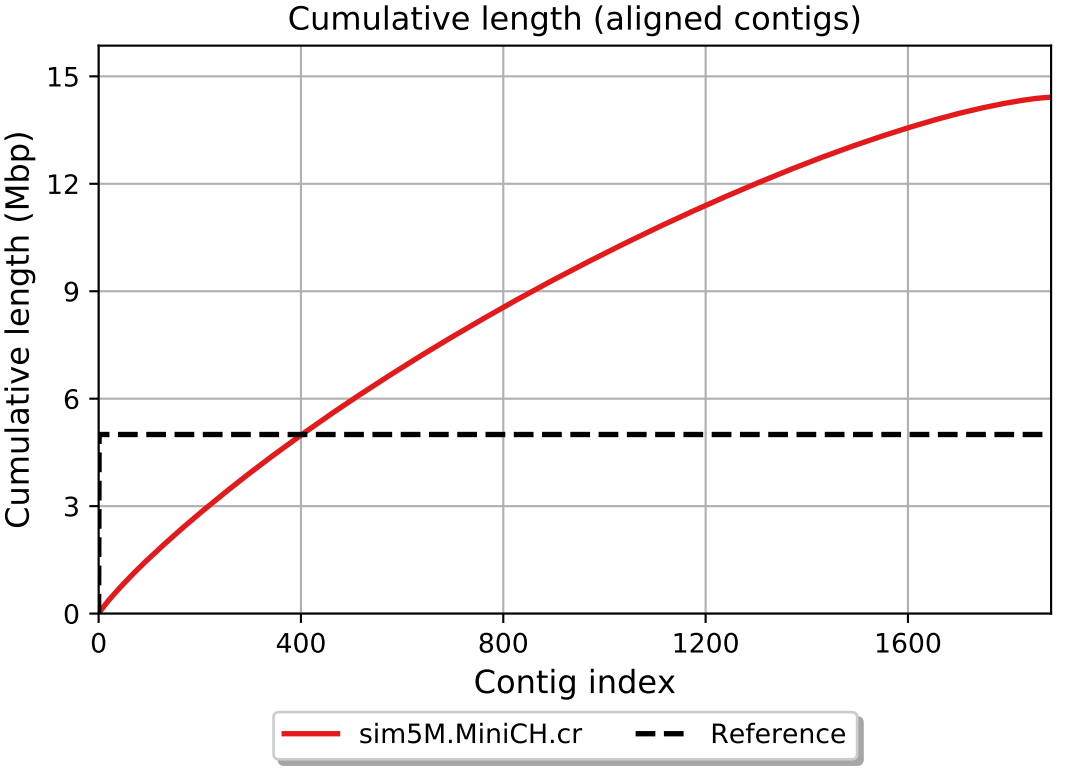

Cumulative length
Cumulative length (Mbp)
0
3
6
9
12
15
0
400
800
1200
1600
2000
Contig index
sim5M.MiniCH.cr
Reference

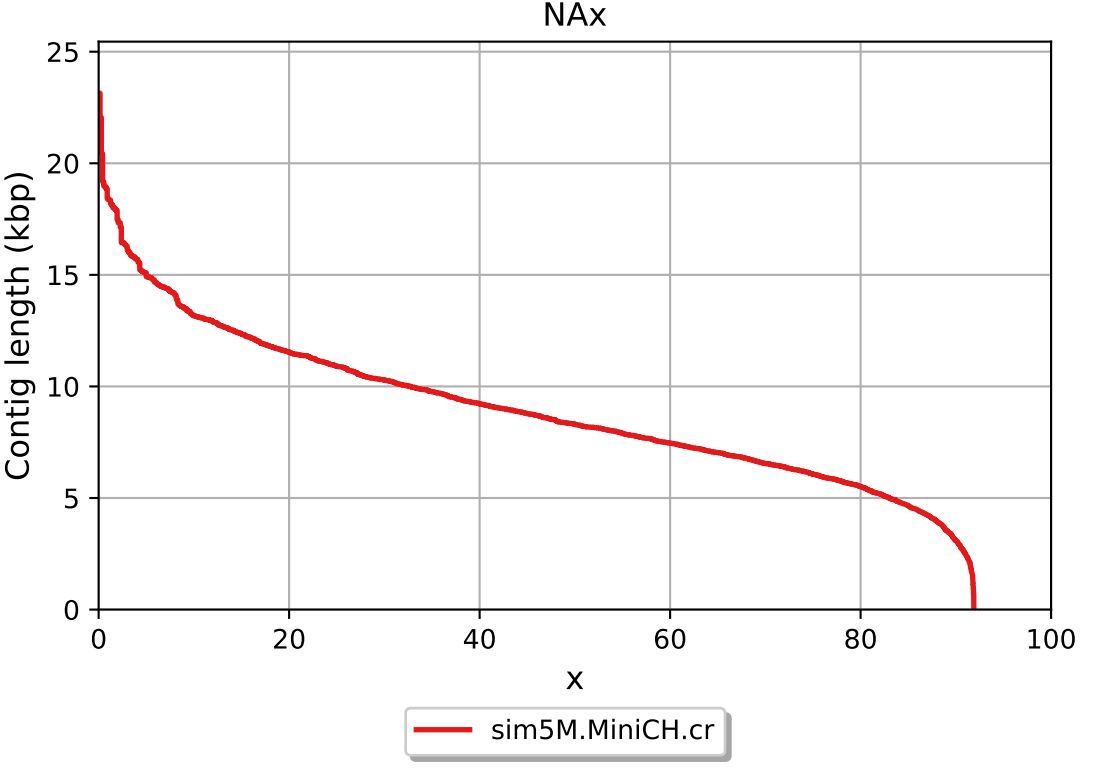

GC content
windows
7500
6000
4500
3000
1500
0
0
20
40
60
80
100
GC (%)
sim5M.MiniCH.cr
Reference

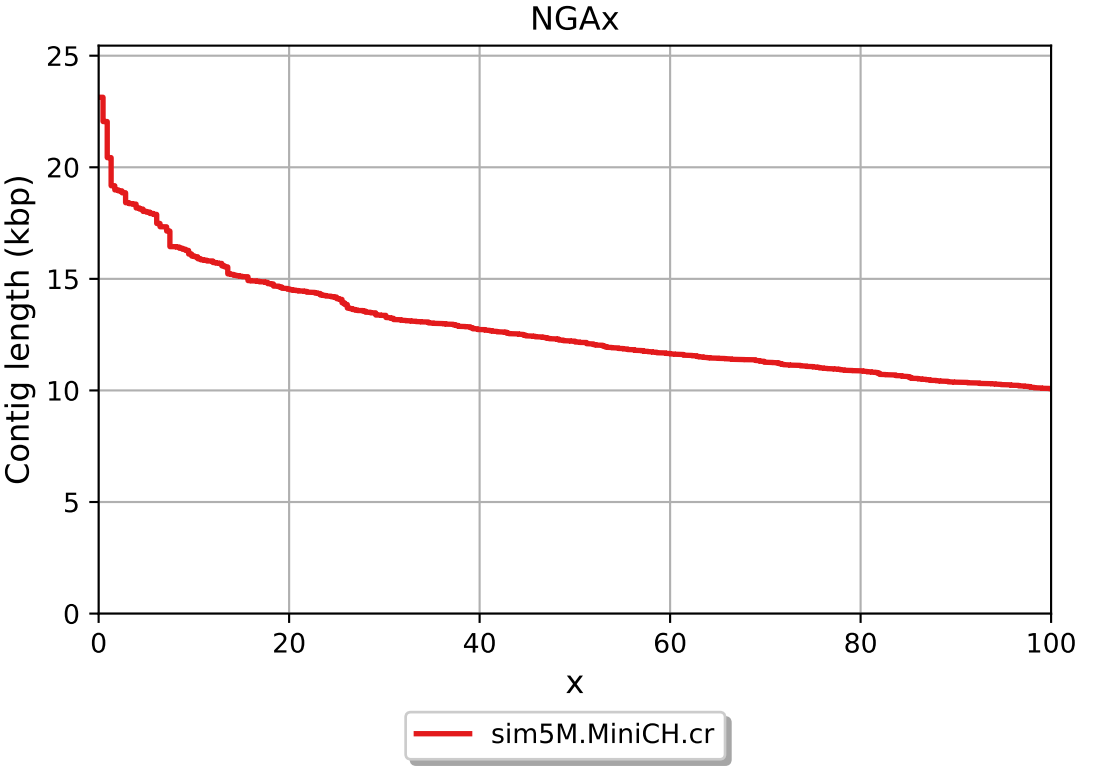

sim5M.MiniCH.cr GC content
contigs
0
200
400
600
800
1000
0
20
40
60
80
100
GC (%)
sim5M.MiniCH.cr


Misassemblies
5
4
3
2
1
0
sim5M.MiniCH.cr
relocations


FRCurve (misassemblies)
Genome coverage (%)
250
200
150
100
50
0
0
1
2
3
4
5
Feature space
sim5M.MiniCH.cr


Cumulative length (aligned contigs)
Cumulative length (Mbp)
15
12
9
6
3
0
0
400
800
1200
1600
Contig index
sim5M.MiniCH.cr
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.MiniCH.cr


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.MiniCH.cr