Report

	sim5M.MiniCL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1989
# contigs (>= 5000 bp)	1617
# contigs (>= 10000 bp)	495
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16044610
Total length (>= 1000 bp)	16035946
Total length (>= 5000 bp)	14686425
Total length (>= 10000 bp)	6256754
Total length (>= 25000 bp)	25160
Total length (>= 50000 bp)	0
# contigs	1999
Largest contig	25160
Total length	16044187
Reference length	5000040
GC (%)	36.16
Reference GC (%)	35.84
N50	9117
NG50	13046
N75	6974
NG75	11731
L50	680
LG50	164
L75	1179
LG75	265
# misassemblies	7
# misassembled contigs	4
Misassembled contigs length	21941
# local misassemblies	35
# unaligned mis. contigs	1
# unaligned contigs	252 + 47 part
Unaligned length	2675640
Genome fraction (%)	91.389
Duplication ratio	2.926
# N's per 100 kbp	0.00
# mismatches per 100 kbp	167.02
# indels per 100 kbp	1308.09
Largest alignment	24005
Total aligned length	13362138
NA50	7939
NGA50	12004
NA75	4988
NGA75	10778
LA50	751
LGA50	177
LA75	1366
LGA75	287

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

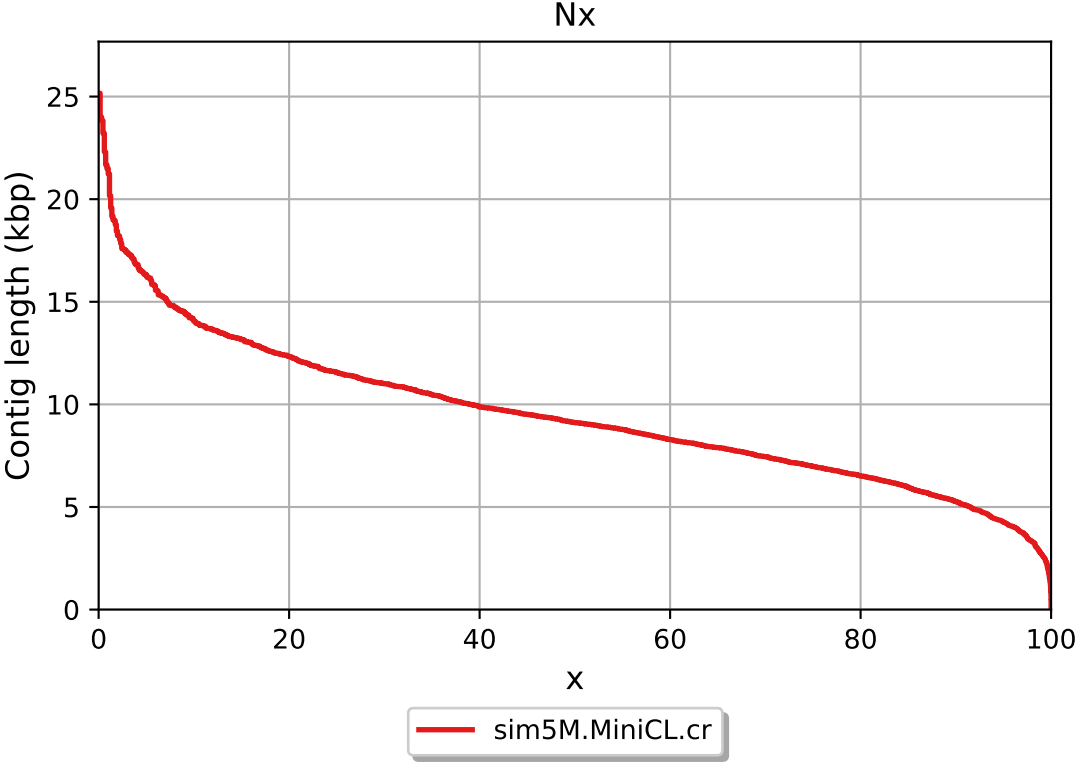
	sim5M.MiniCL.cr
# misassemblies	7
# relocations	5
# translocations	0
# inversions	2
# misassembled contigs	4
Misassembled contigs length	21941
# local misassemblies	35
# unaligned mis. contigs	1
# mismatches	7632
# indels	59773
# indels (<= 5 bp)	59733
# indels (> 5 bp)	40
Indels length	66570

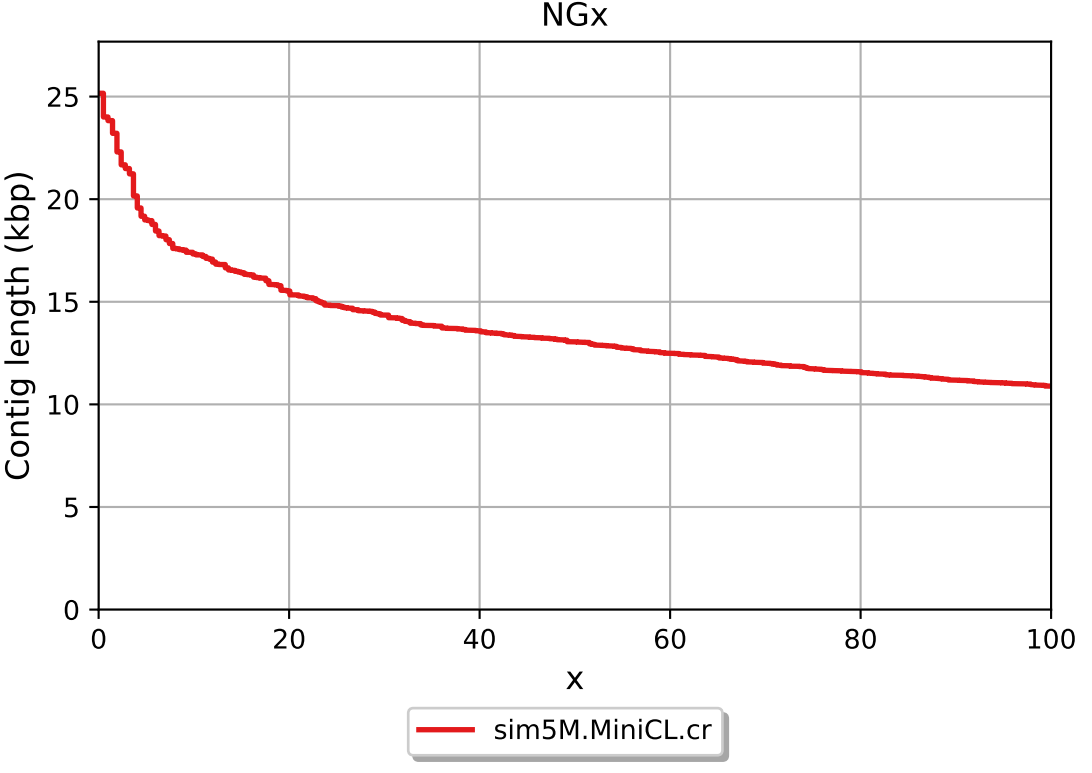
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

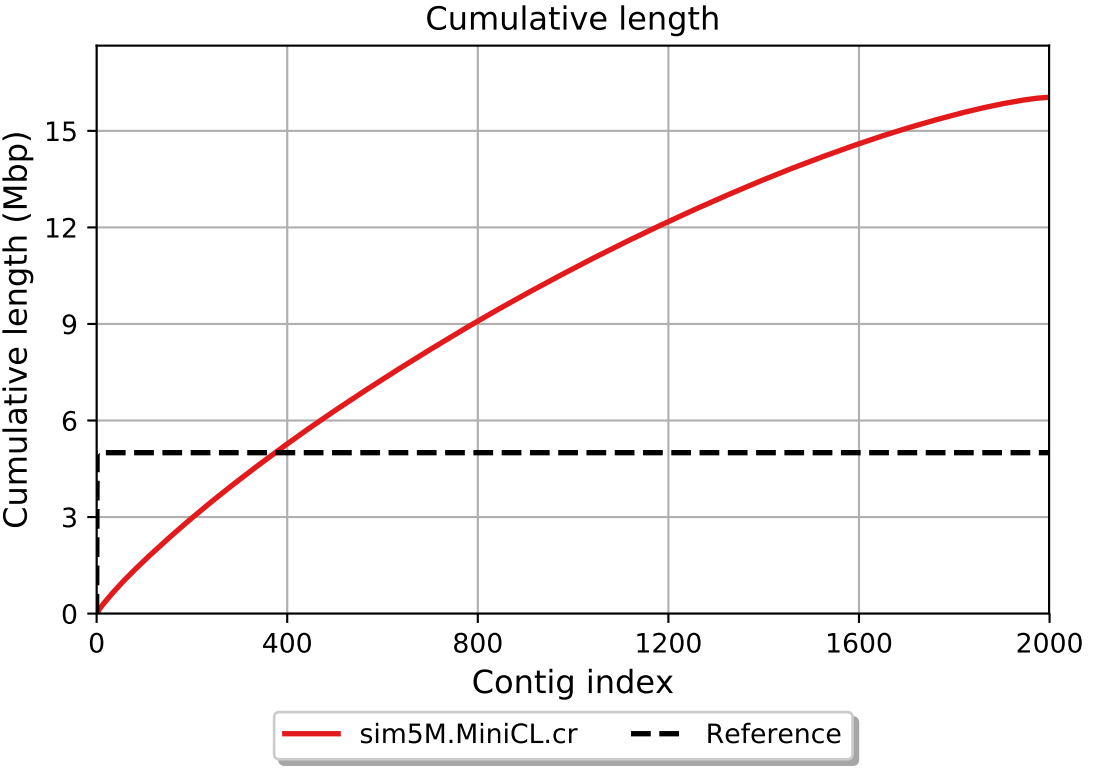
Unaligned report

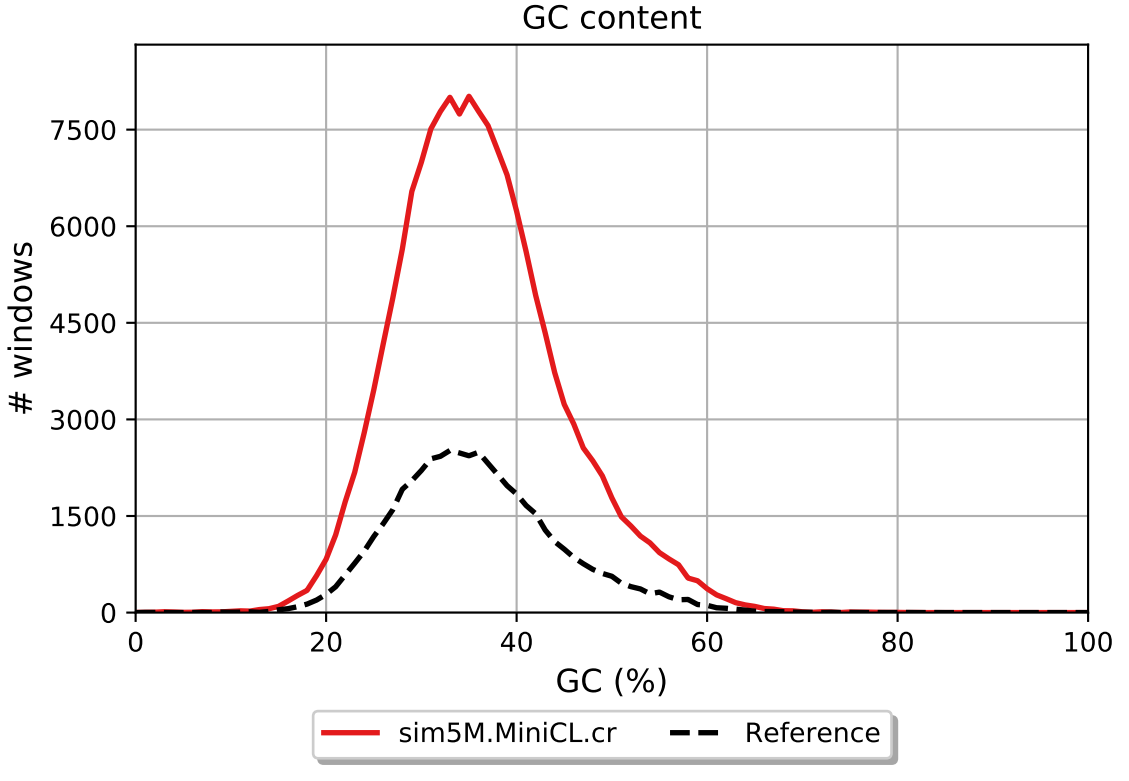
	sim5M.MiniCL.cr
# fully unaligned contigs	252
Fully unaligned length	2428027
# partially unaligned contigs	47
Partially unaligned length	247613
# N's	0

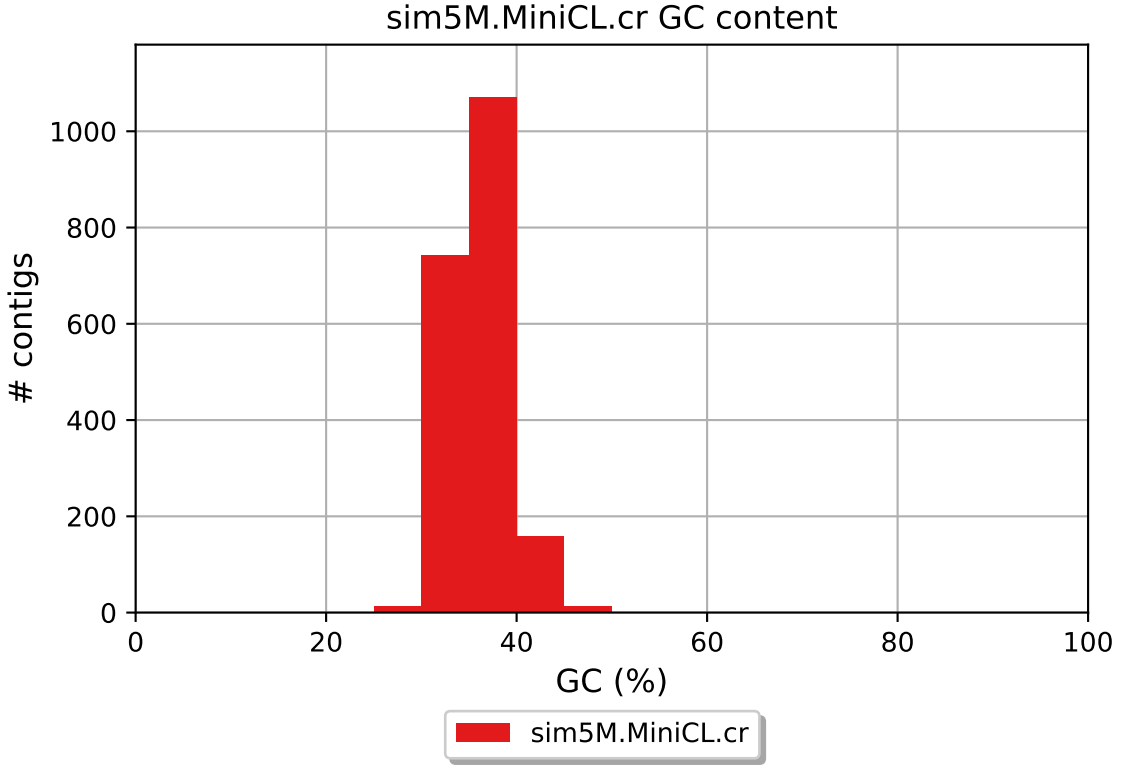
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


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

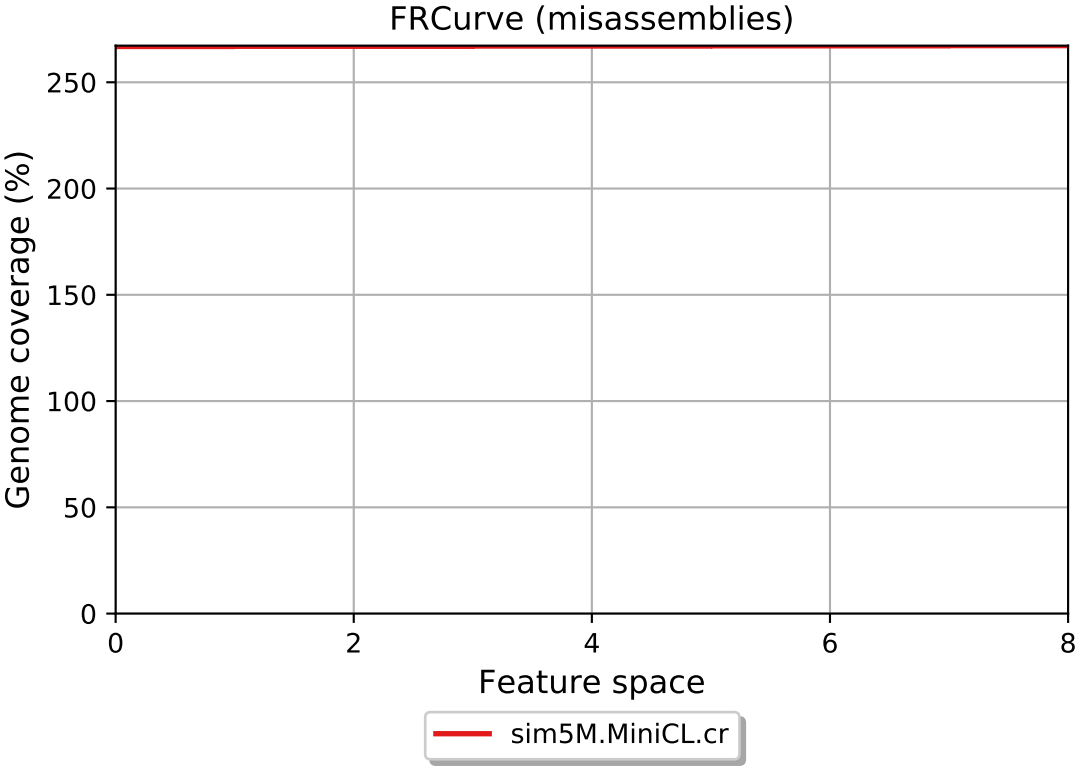

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.MiniCL.cr

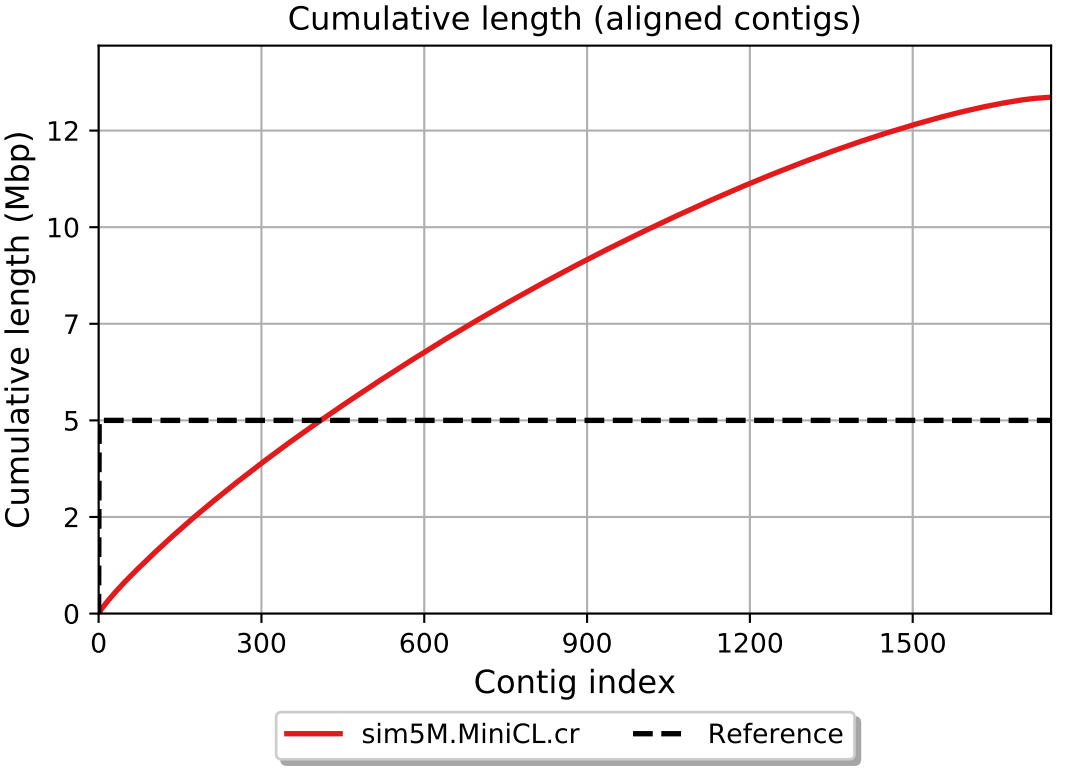

Cumulative length
Cumulative length (Mbp)
0
3
6
9
12
15
0
400
800
1200
1600
2000
Contig index
sim5M.MiniCL.cr
Reference

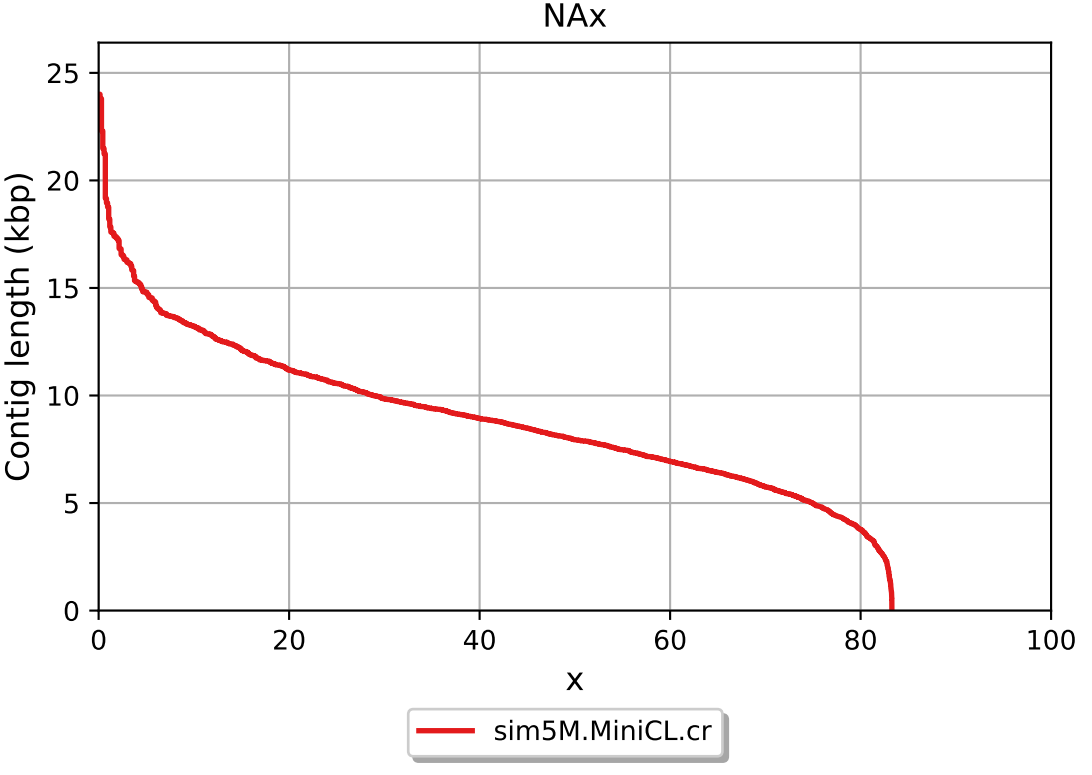

GC content
windows
7500
6000
4500
3000
1500
0
0
20
40
60
80
100
GC (%)
sim5M.MiniCL.cr
Reference

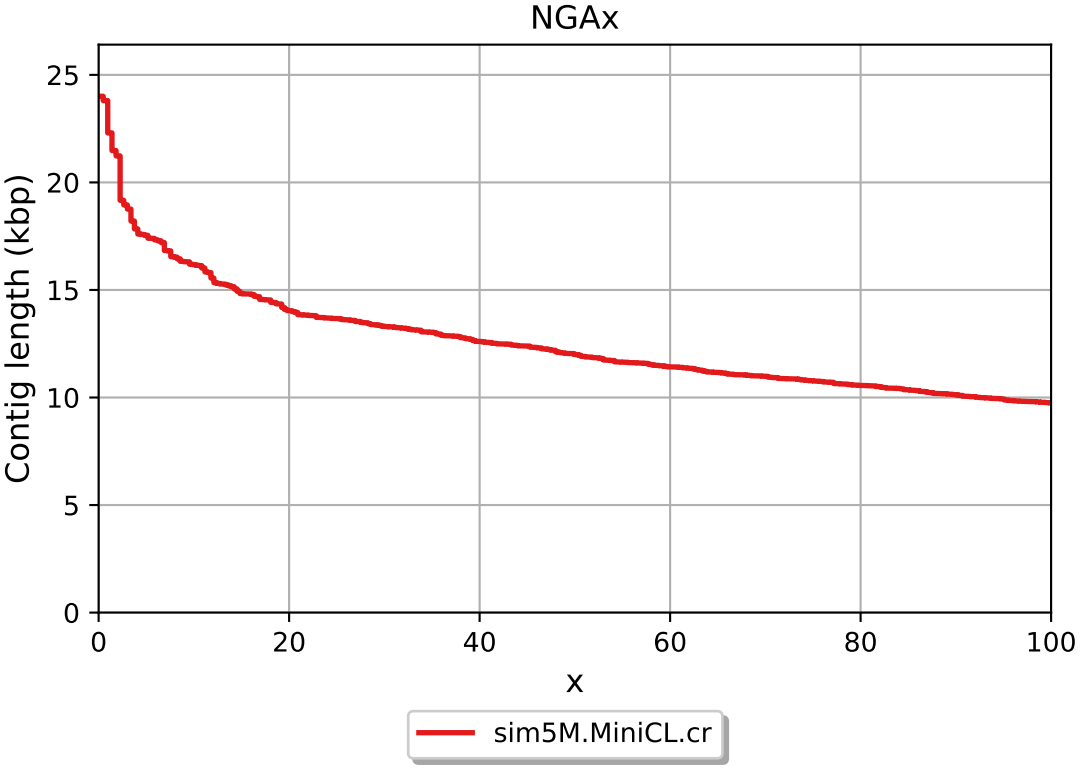

sim5M.MiniCL.cr GC content
contigs
0
200
400
600
800
1000
0
20
40
60
80
100
GC (%)
sim5M.MiniCL.cr

Misassemblies
8
6
4
2
0
sim5M.MiniCL.cr
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
250
200
150
100
50
0
0
2
4
6
8
Feature space
sim5M.MiniCL.cr


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
5
7
10
12
0
300
600
900
1200
1500
Contig index
sim5M.MiniCL.cr
Reference


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


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