Report

	sim25M.MiniCH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1989
# contigs (>= 5000 bp)	1581
# contigs (>= 10000 bp)	523
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	15898003
Total length (>= 1000 bp)	15890875
Total length (>= 5000 bp)	14417645
Total length (>= 10000 bp)	6507797
Total length (>= 25000 bp)	25098
Total length (>= 50000 bp)	0
# contigs	1998
Largest contig	25098
Total length	15897500
Reference length	25000020
GC (%)	43.95
Reference GC (%)	43.69
N50	9224
NG50	6578
N75	6953
L50	674
LG50	1250
L75	1165
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	16573
# local misassemblies	37
# unaligned mis. contigs	0
# unaligned contigs	72 + 28 part
Unaligned length	757088
Genome fraction (%)	45.445
Duplication ratio	1.333
# N's per 100 kbp	0.00
# mismatches per 100 kbp	86.65
# indels per 100 kbp	552.14
Largest alignment	25097
Total aligned length	15134318
NA50	8943
NGA50	6031
NA75	6506
LA50	689
LGA50	1296
LA75	1205

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

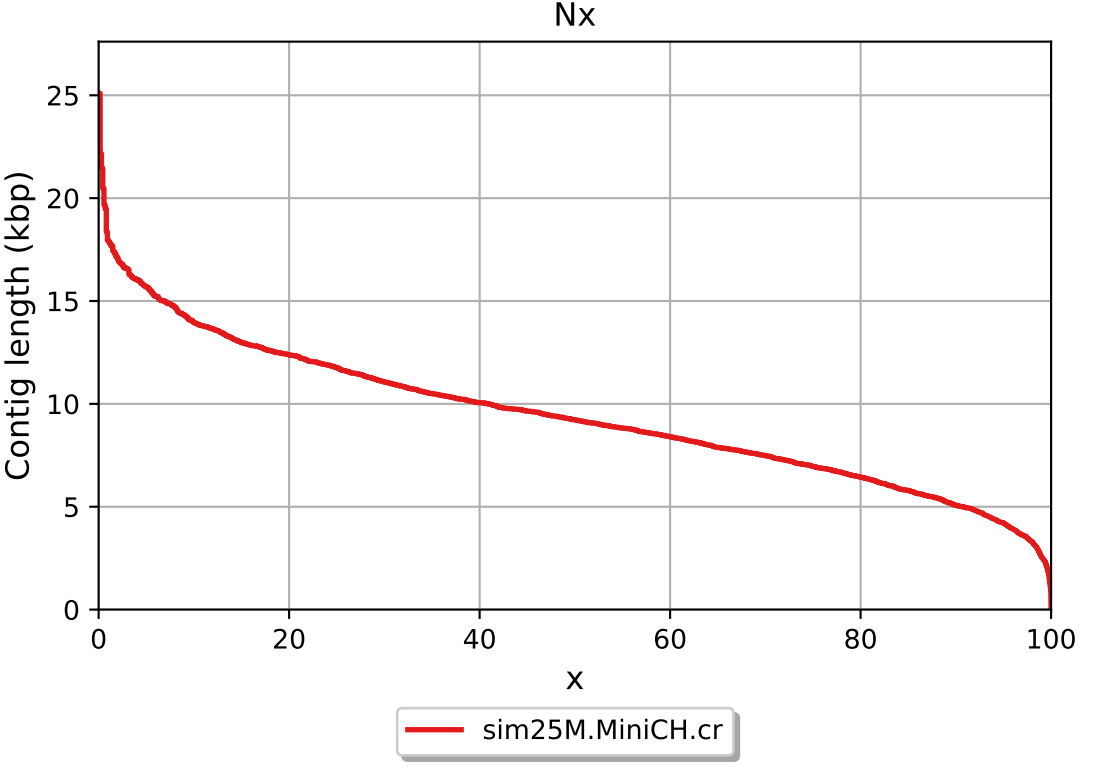
	sim25M.MiniCH.cr
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	16573
# local misassemblies	37
# unaligned mis. contigs	0
# mismatches	9845
# indels	62730
# indels (<= 5 bp)	62644
# indels (> 5 bp)	86
Indels length	73605

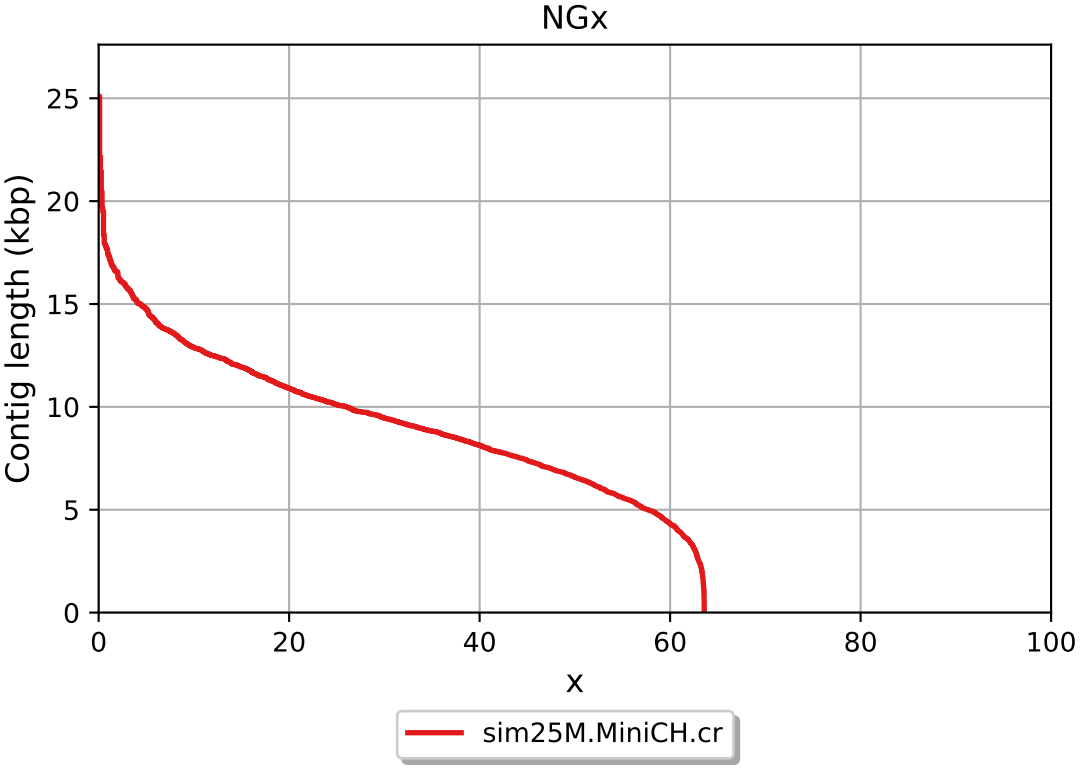
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

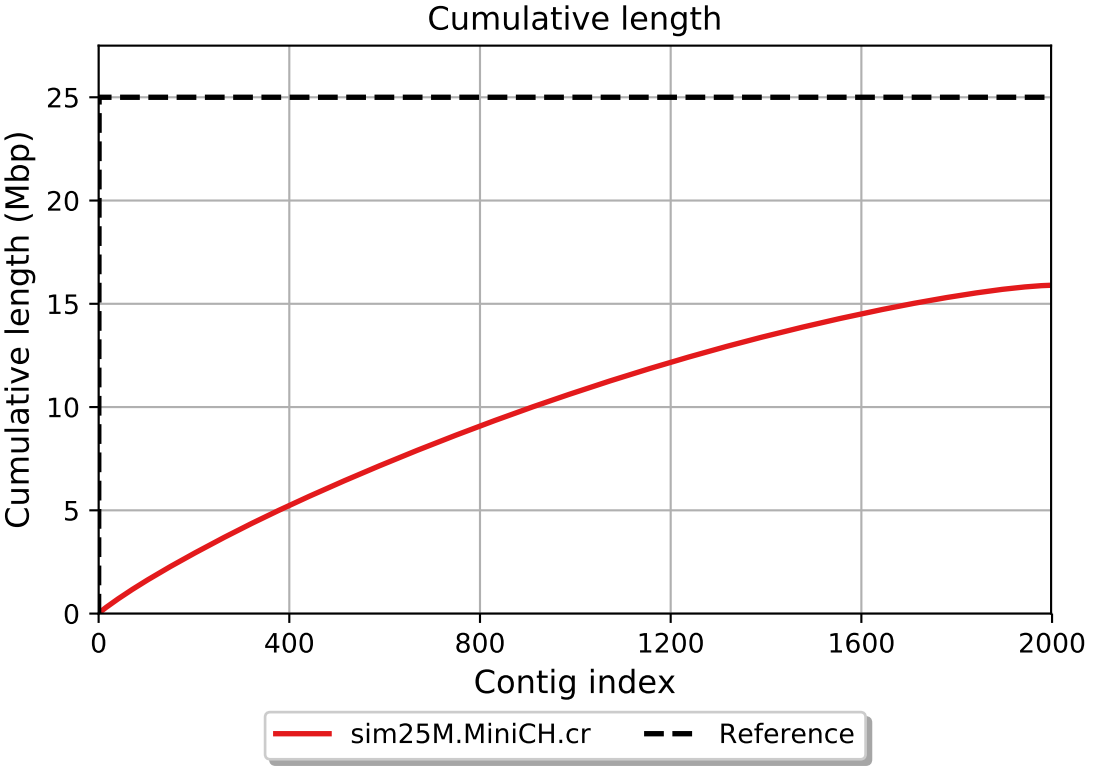
Unaligned report

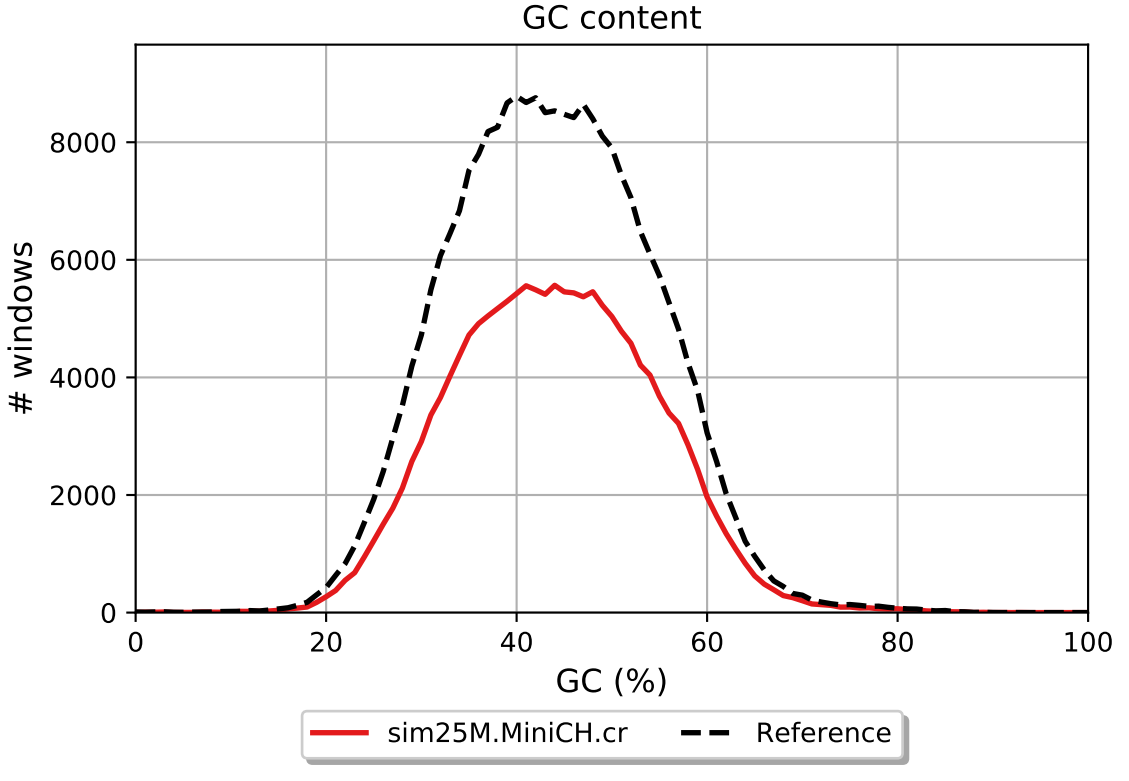
	sim25M.MiniCH.cr
# fully unaligned contigs	72
Fully unaligned length	684910
# partially unaligned contigs	28
Partially unaligned length	72178
# N's	0

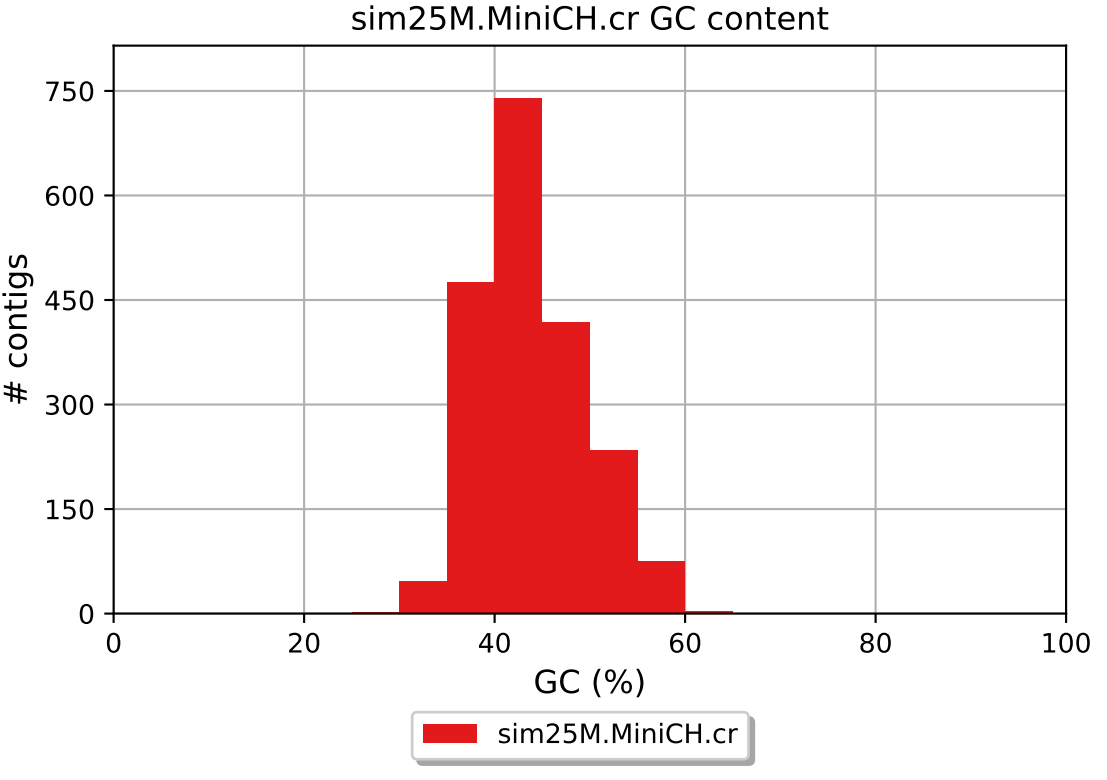
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

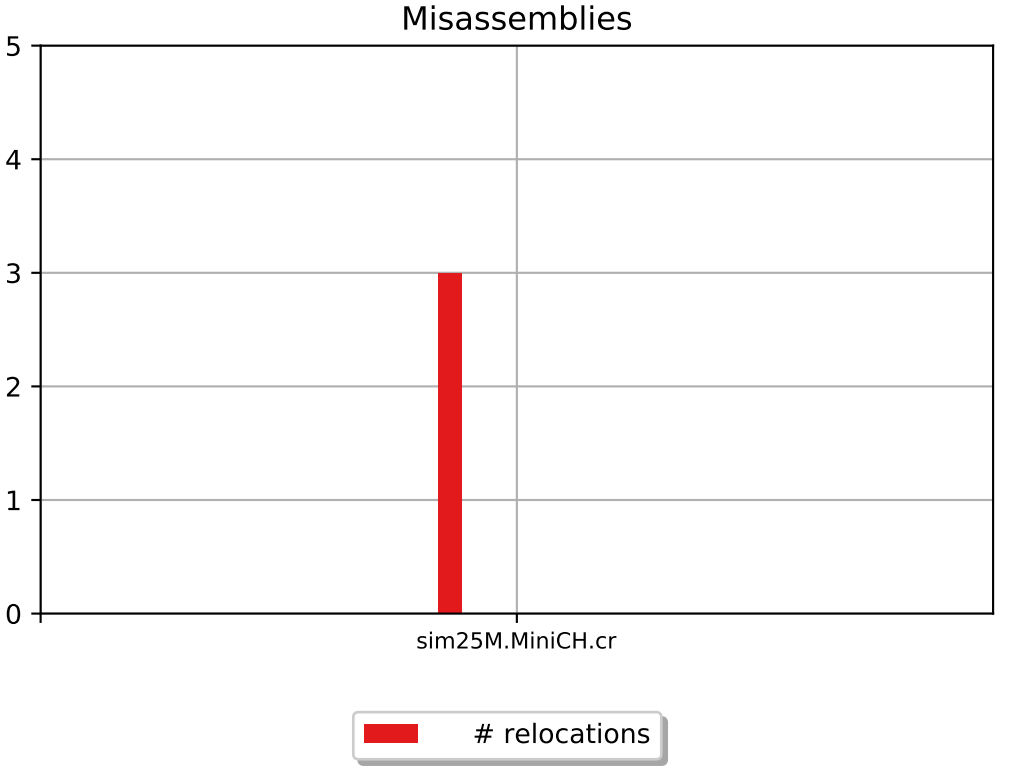

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim25M.MiniCH.cr

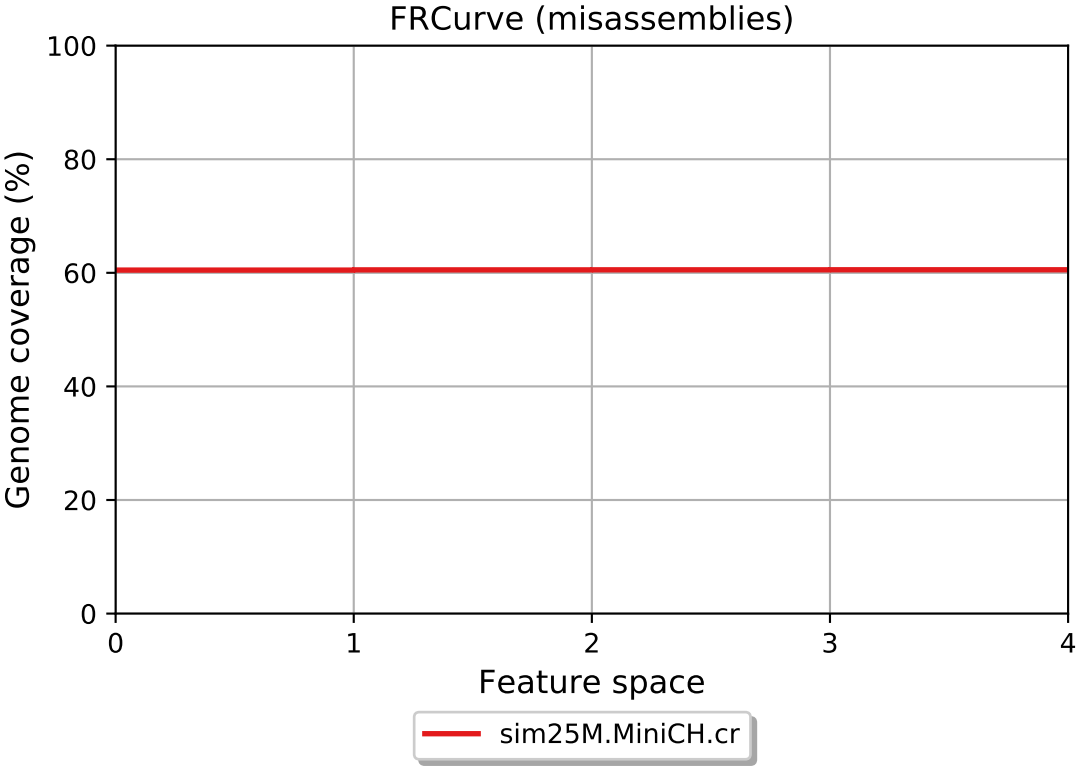

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim25M.MiniCH.cr

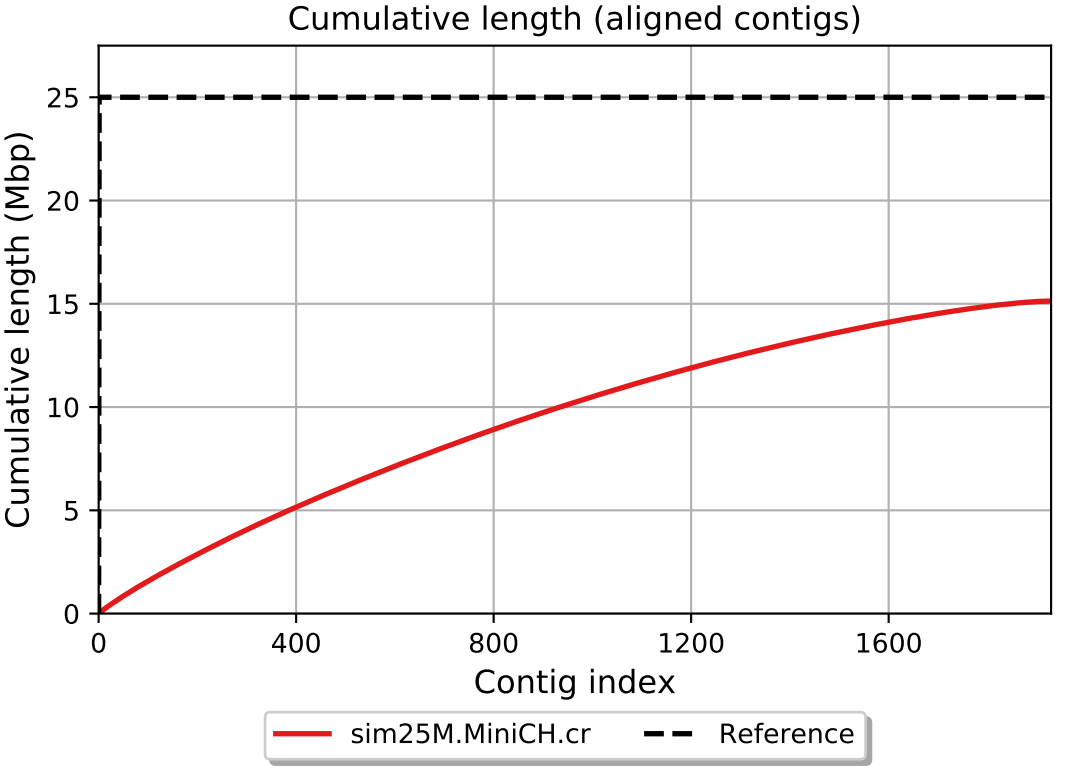

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
400
800
1200
1600
2000
Contig index
sim25M.MiniCH.cr
Reference

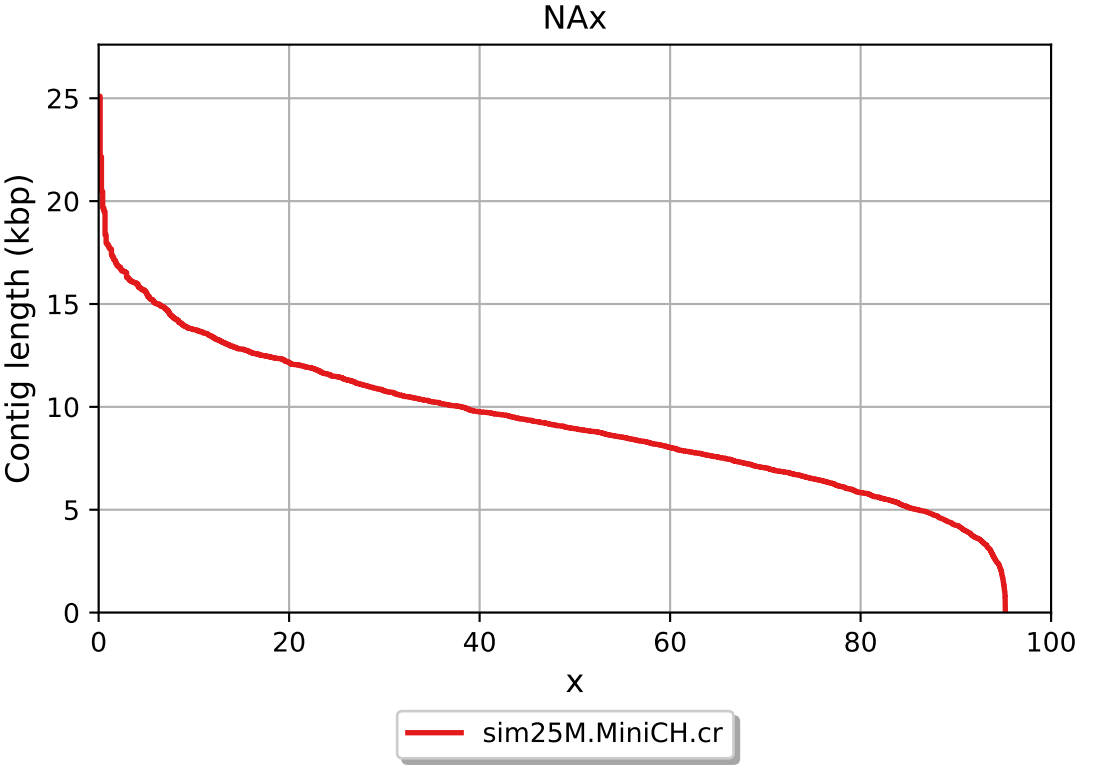

GC content
8000
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
sim25M.MiniCH.cr
Reference

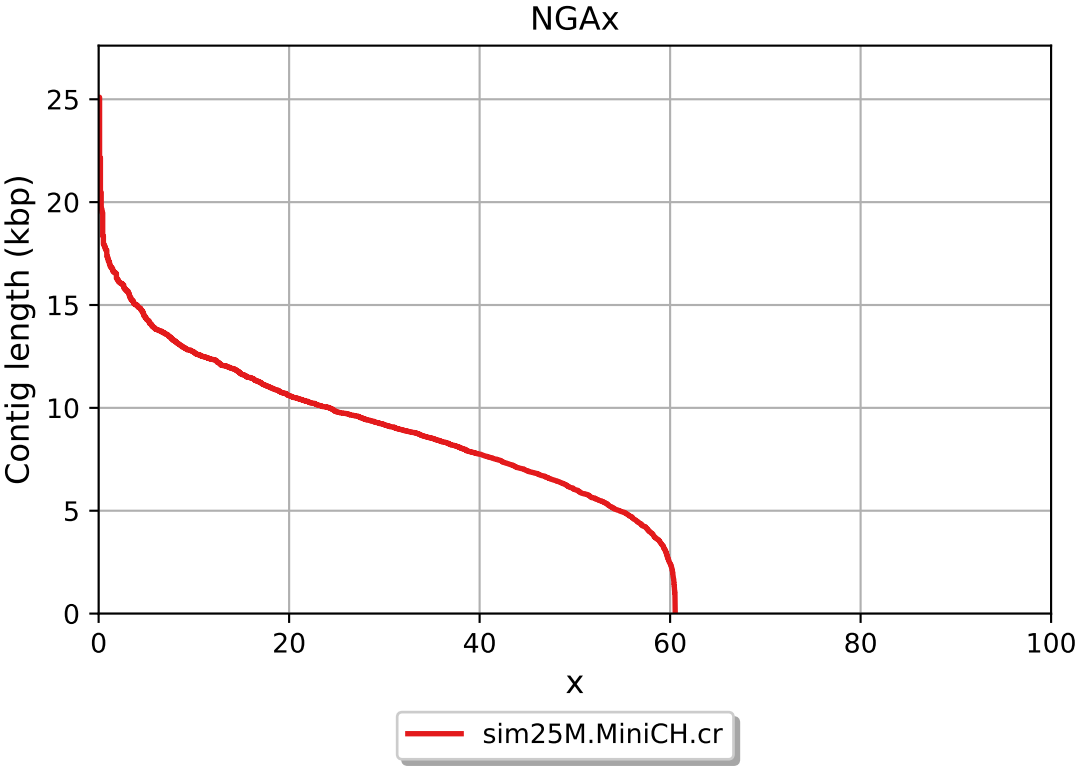

sim25M.MiniCH.cr GC content
contigs
0
150
300
450
600
750
0
20
40
60
80
100
GC (%)
sim25M.MiniCH.cr


Misassemblies
5
4
3
2
1
0
sim25M.MiniCH.cr
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
Feature space
sim25M.MiniCH.cr


Cumulative length (aligned contigs)
Cumulative length (Mbp)
25
20
15
10
5
0
0
400
800
1200
1600
Contig index
sim25M.MiniCH.cr
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim25M.MiniCH.cr


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim25M.MiniCH.cr