Report

	sim5M.MiniH.p3
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	4983308
Total length (>= 1000 bp)	4983308
Total length (>= 5000 bp)	4983308
Total length (>= 10000 bp)	4983308
Total length (>= 25000 bp)	4983308
Total length (>= 50000 bp)	4983308
# contigs	3
Largest contig	2861751
Total length	4983308
Reference length	5000040
GC (%)	35.83
Reference GC (%)	35.84
N50	2861751
NG50	2861751
N75	1154416
NG75	1154416
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.632
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.68
# indels per 100 kbp	2.67
Largest alignment	2861745
Total aligned length	4983301
NA50	2861745
NGA50	2861745
NA75	1154415
NGA75	1154415
LA50	1
LGA50	1
LA75	2
LGA75	2

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

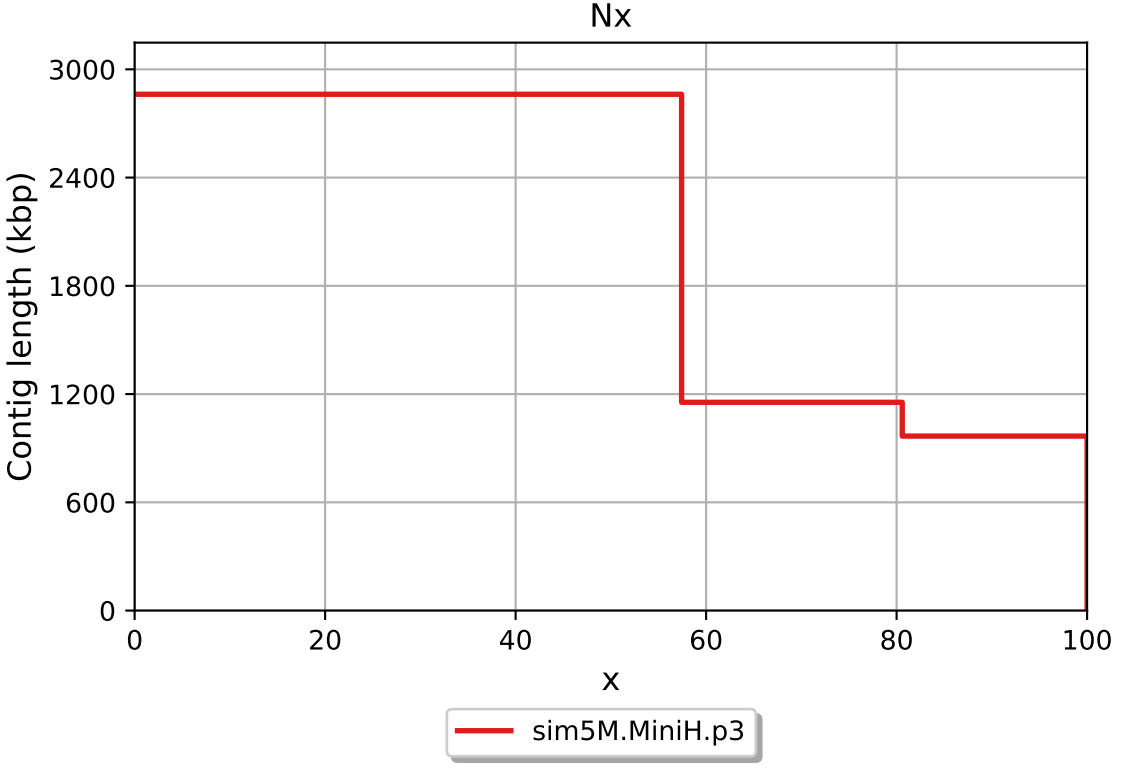
	sim5M.MiniH.p3
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	34
# indels	133
# indels (<= 5 bp)	133
# indels (> 5 bp)	0
Indels length	158

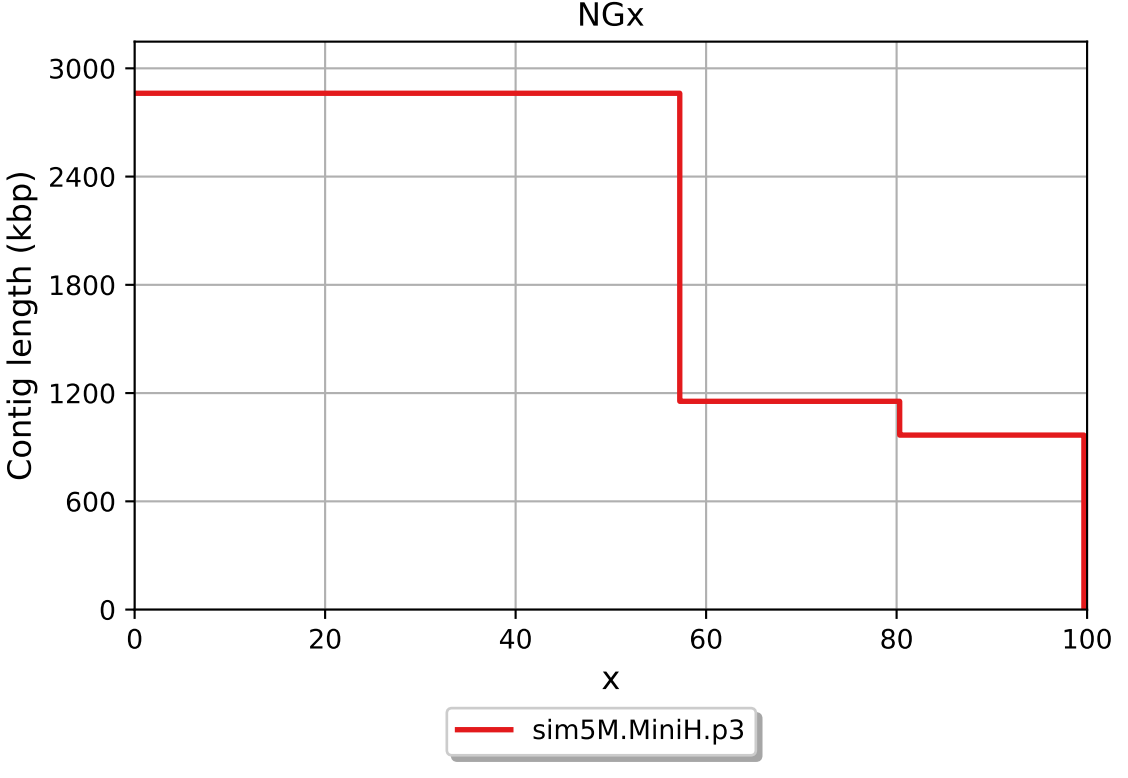
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

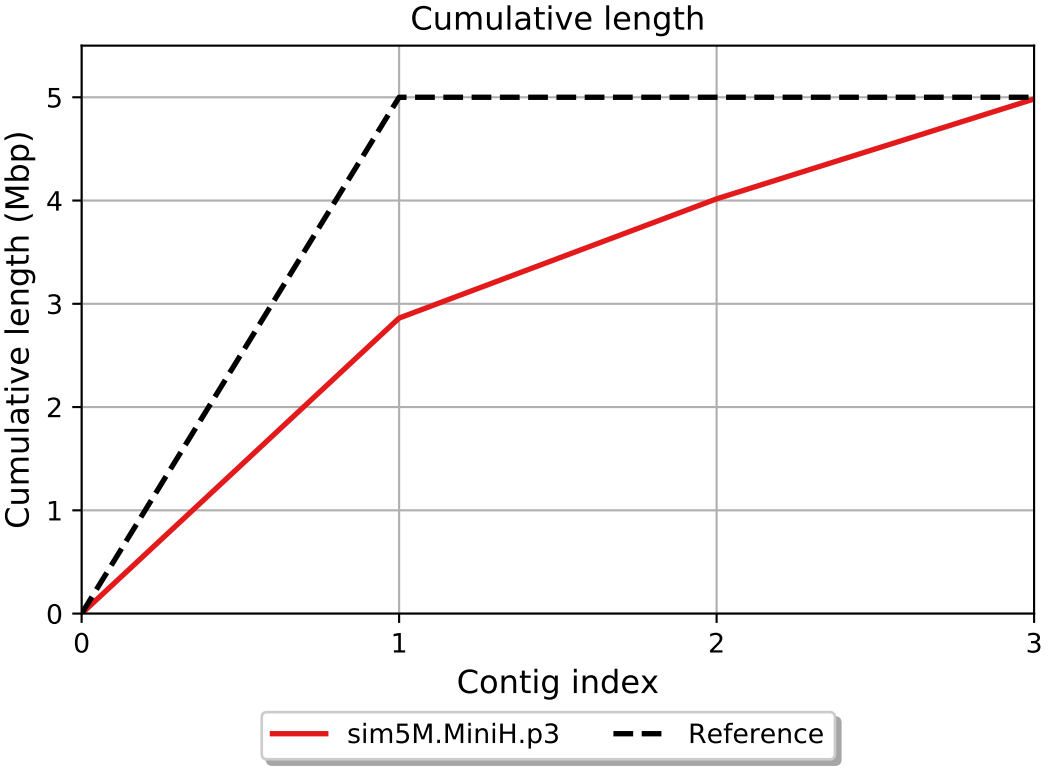
Unaligned report

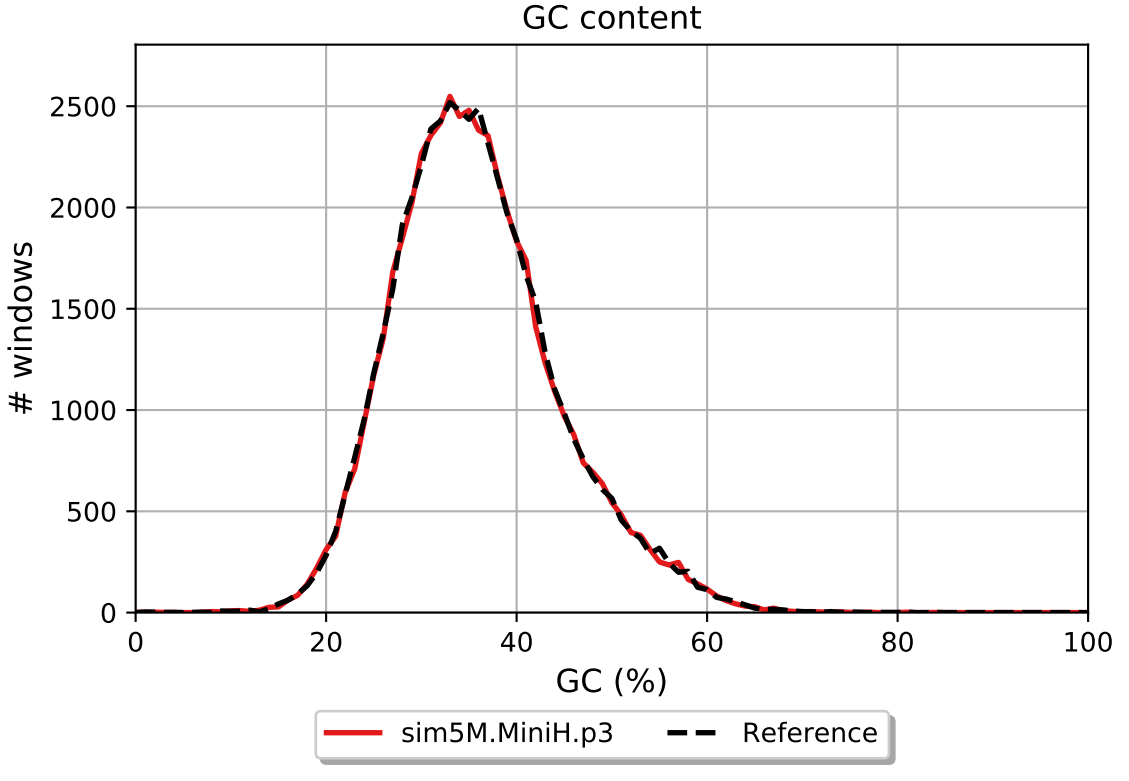
	sim5M.MiniH.p3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

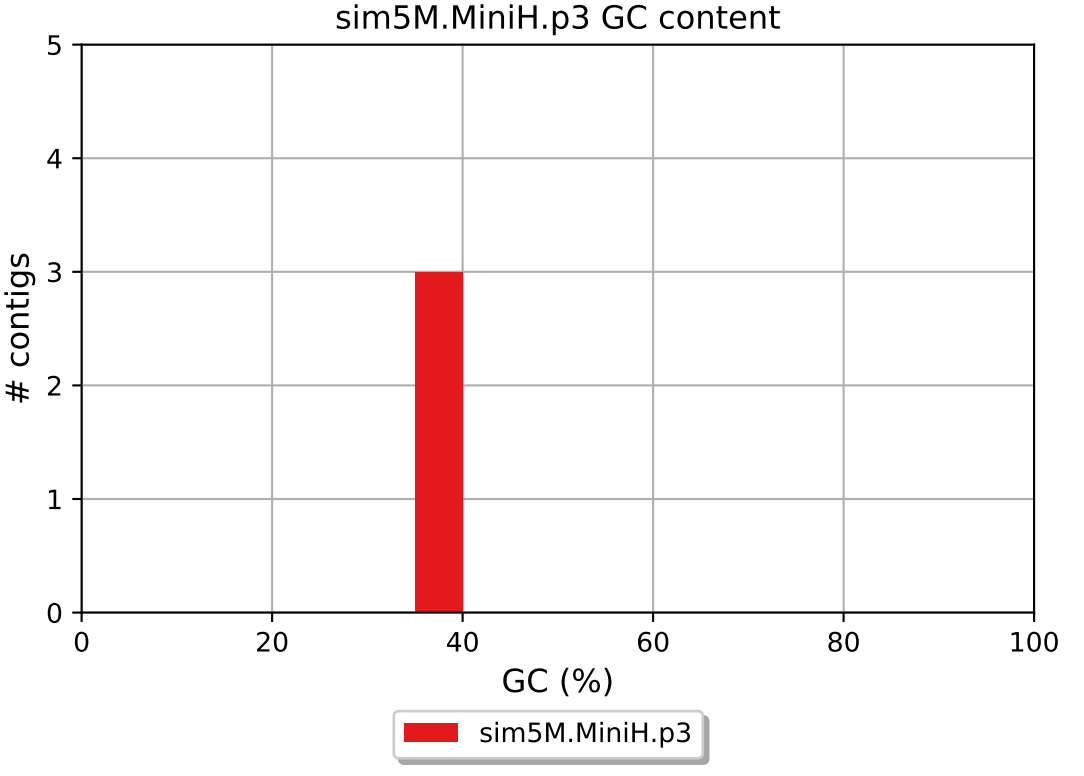
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

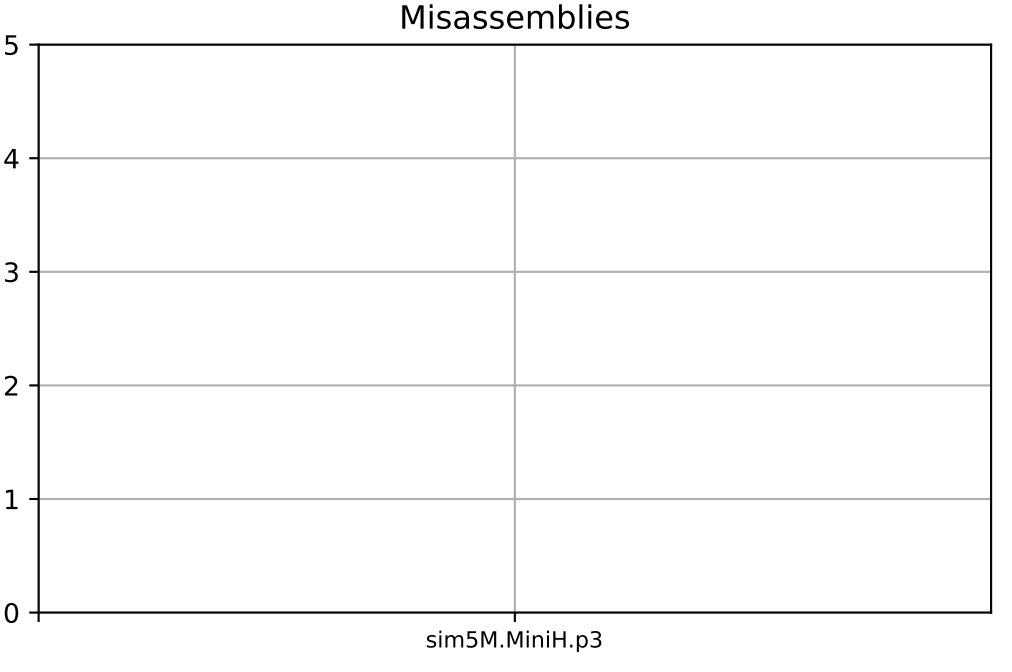

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim5M.MiniH.p3

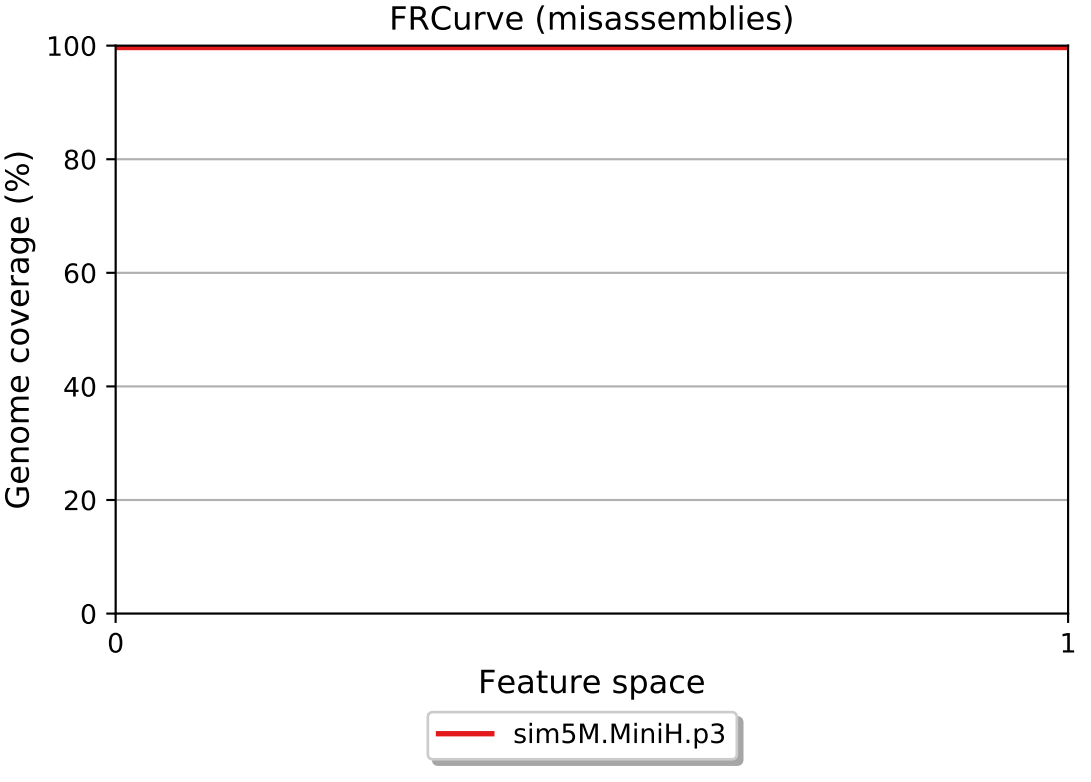

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim5M.MiniH.p3

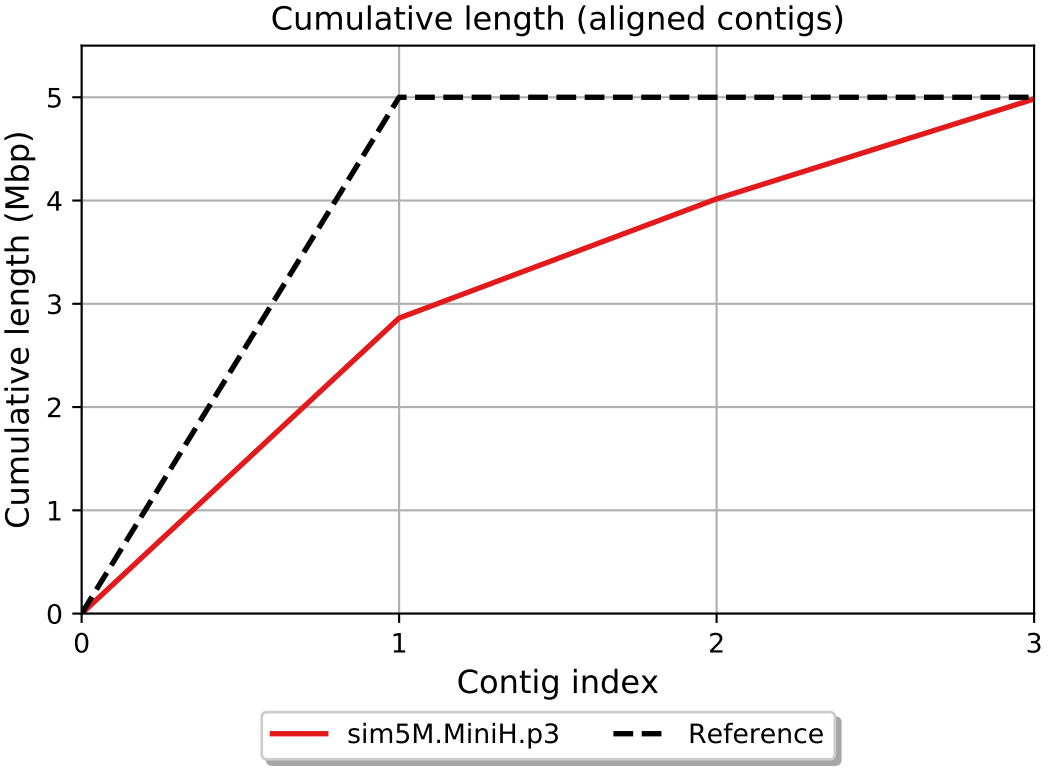

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
1
2
3
Contig index
sim5M.MiniH.p3
Reference

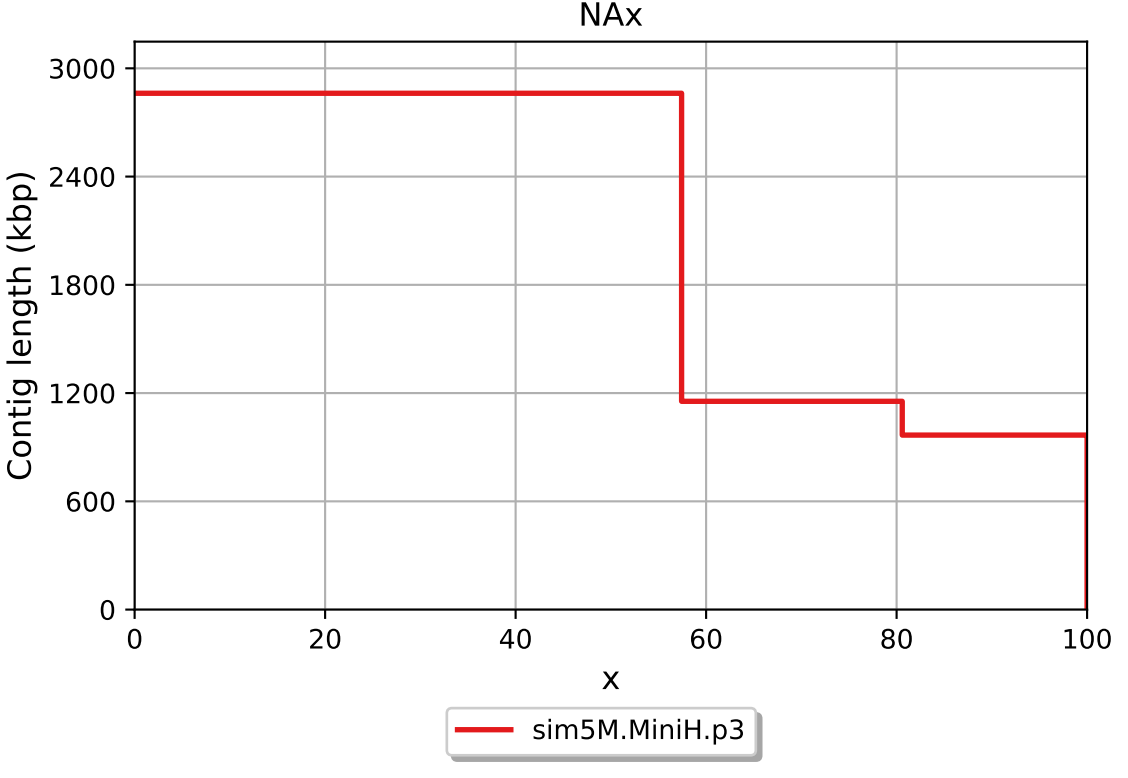

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
sim5M.MiniH.p3
Reference

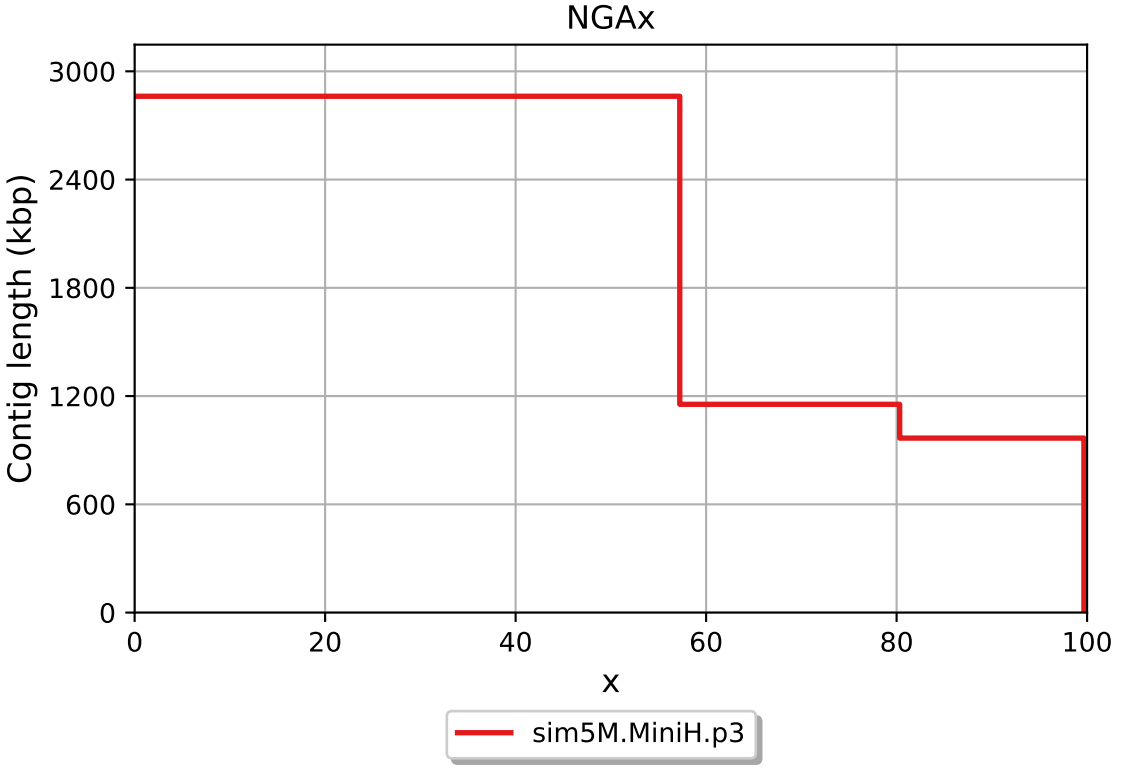

sim5M.MiniH.p3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
sim5M.MiniH.p3


Misassemblies
5
4
3
2
1
0
sim5M.MiniH.p3


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
sim5M.MiniH.p3


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
1
2
3
Contig index
sim5M.MiniH.p3
Reference


NAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim5M.MiniH.p3


NGAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim5M.MiniH.p3