Report

	sim5M.MiniH
# 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)	4996359
Total length (>= 1000 bp)	4996359
Total length (>= 5000 bp)	4996359
Total length (>= 10000 bp)	4996359
Total length (>= 25000 bp)	4996359
Total length (>= 50000 bp)	4996359
# contigs	3
Largest contig	2869036
Total length	4996359
Reference length	5000040
GC (%)	35.83
Reference GC (%)	35.84
N50	2869036
NG50	2869036
N75	1157358
NG75	1157358
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	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.51
# indels per 100 kbp	195.42
Largest alignment	2869030
Total aligned length	4996352
NA50	2869030
NGA50	2869030
NA75	1157357
NGA75	1157357
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

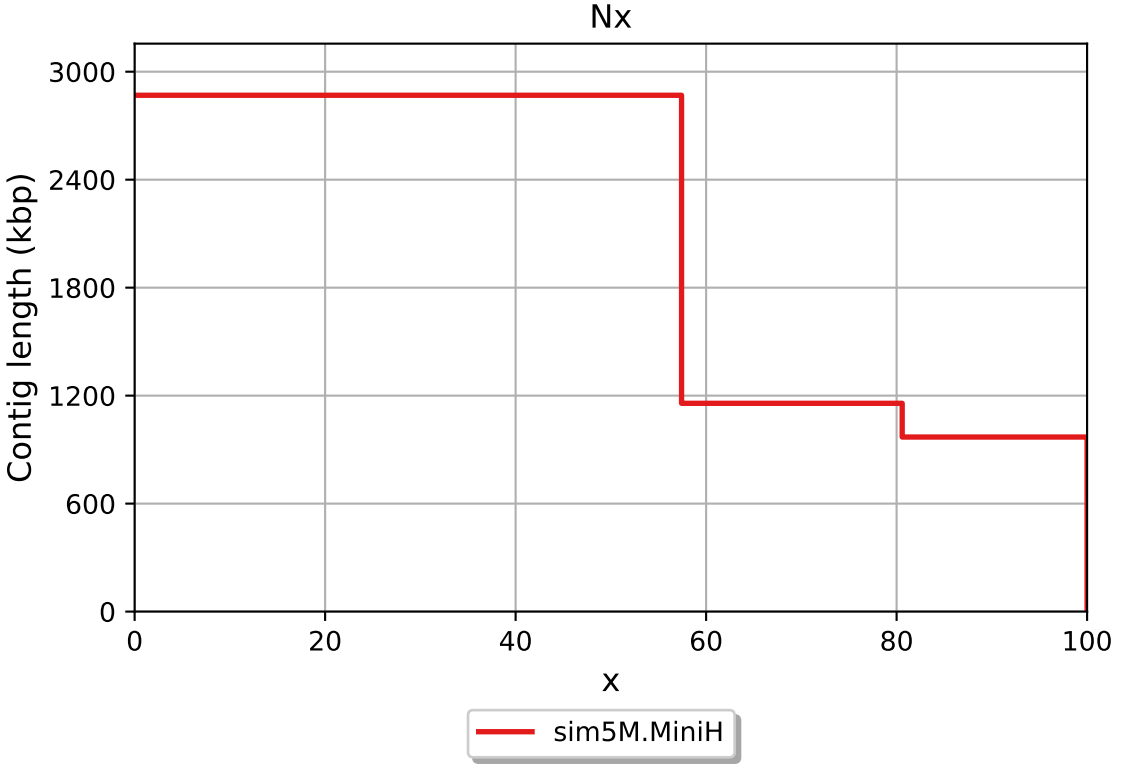
	sim5M.MiniH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	75
# indels	9735
# indels (<= 5 bp)	9729
# indels (> 5 bp)	6
Indels length	13315

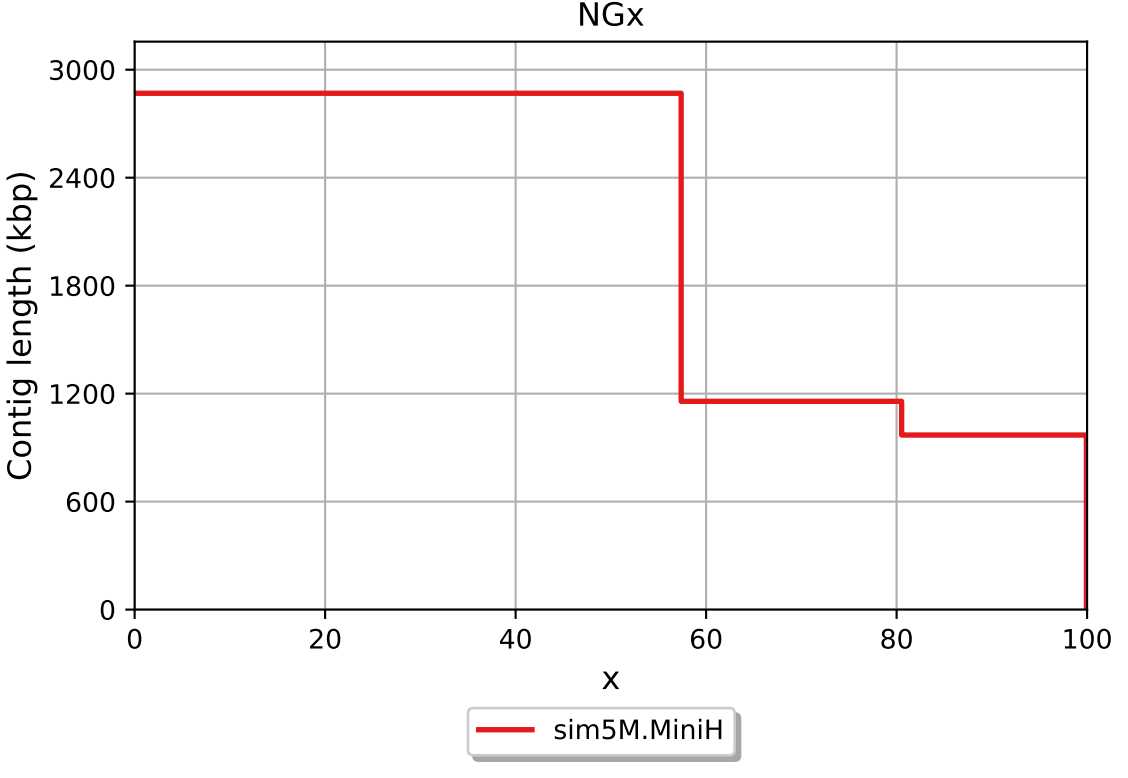
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

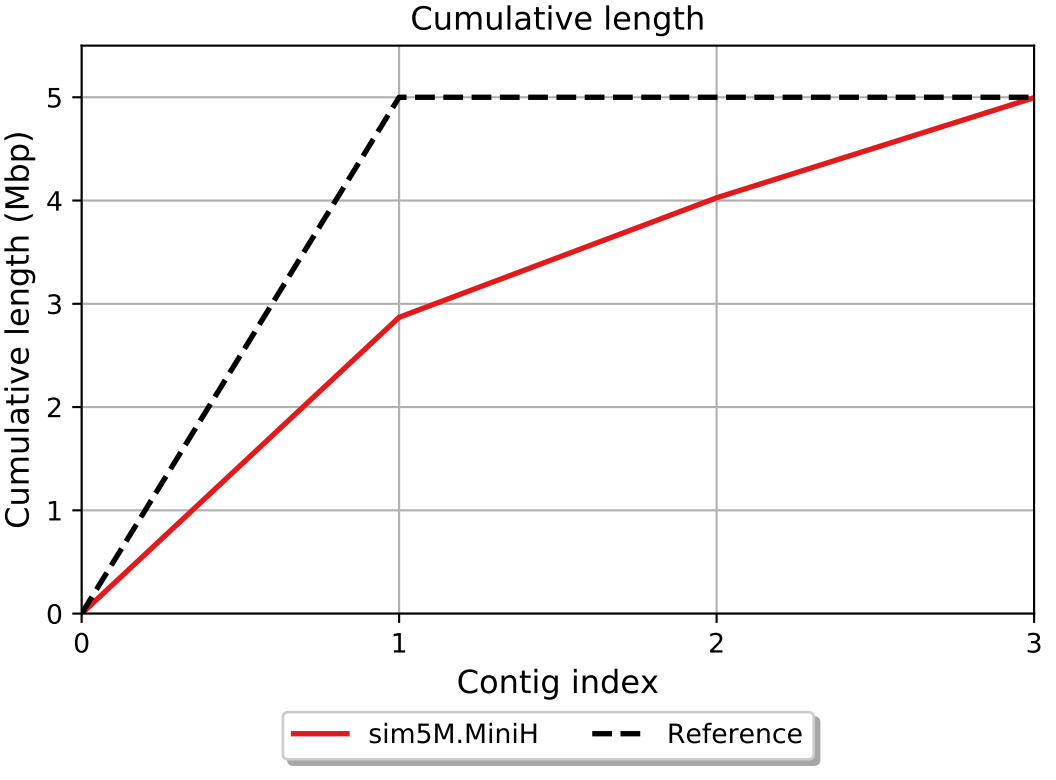
Unaligned report

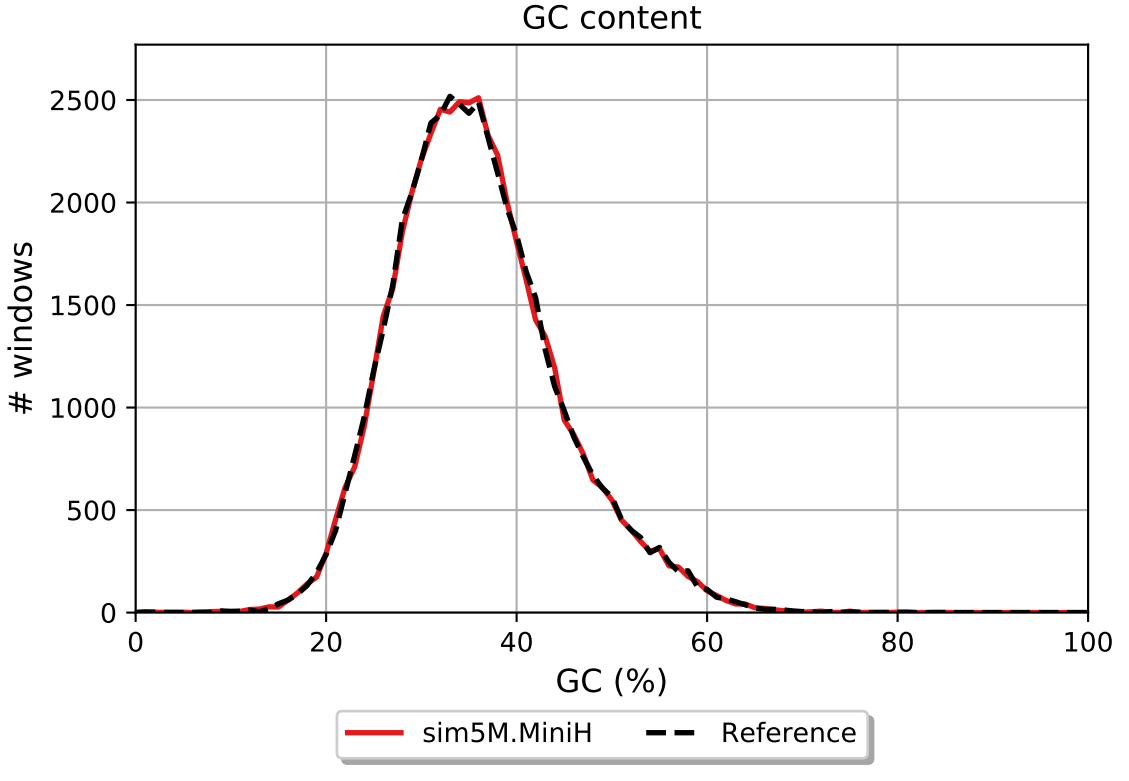
	sim5M.MiniH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

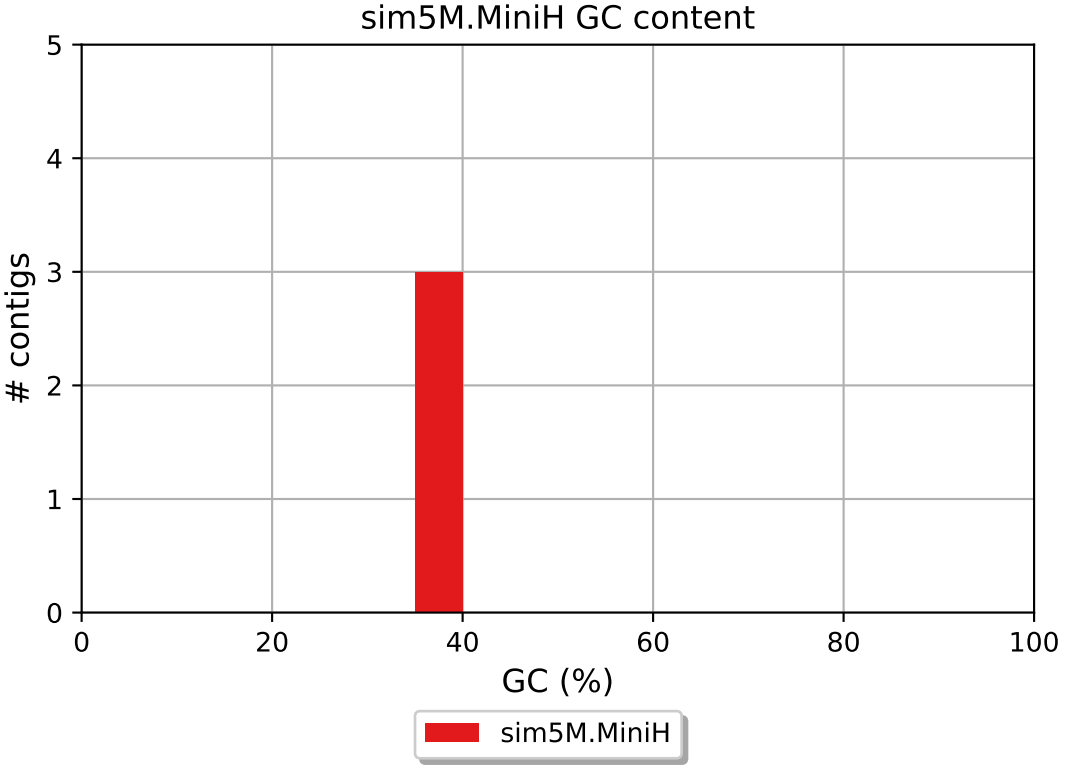
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

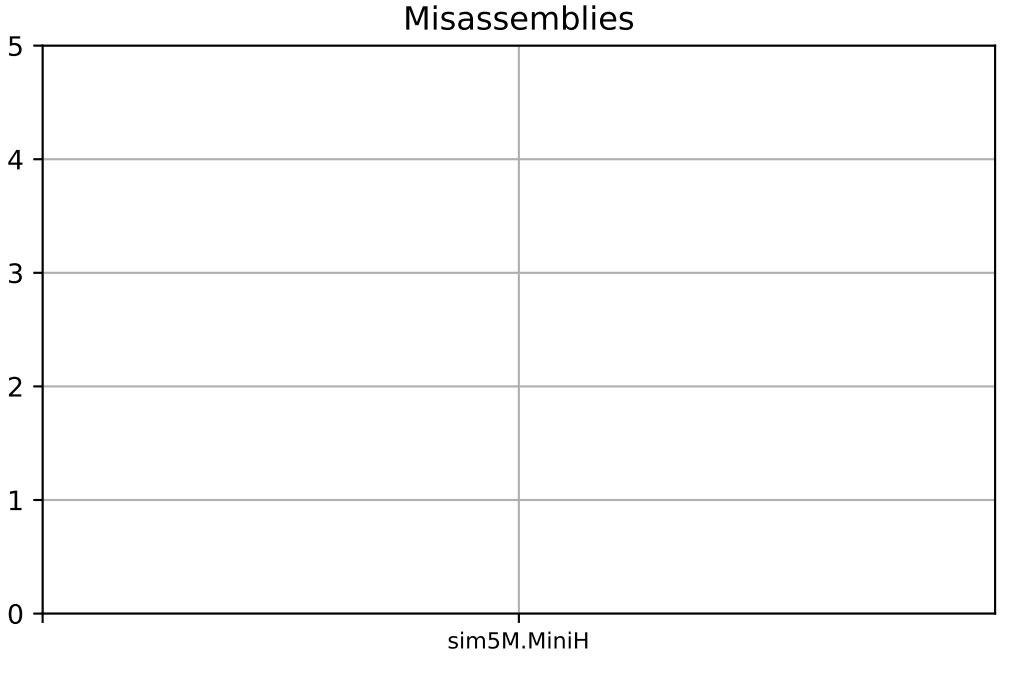

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim5M.MiniH

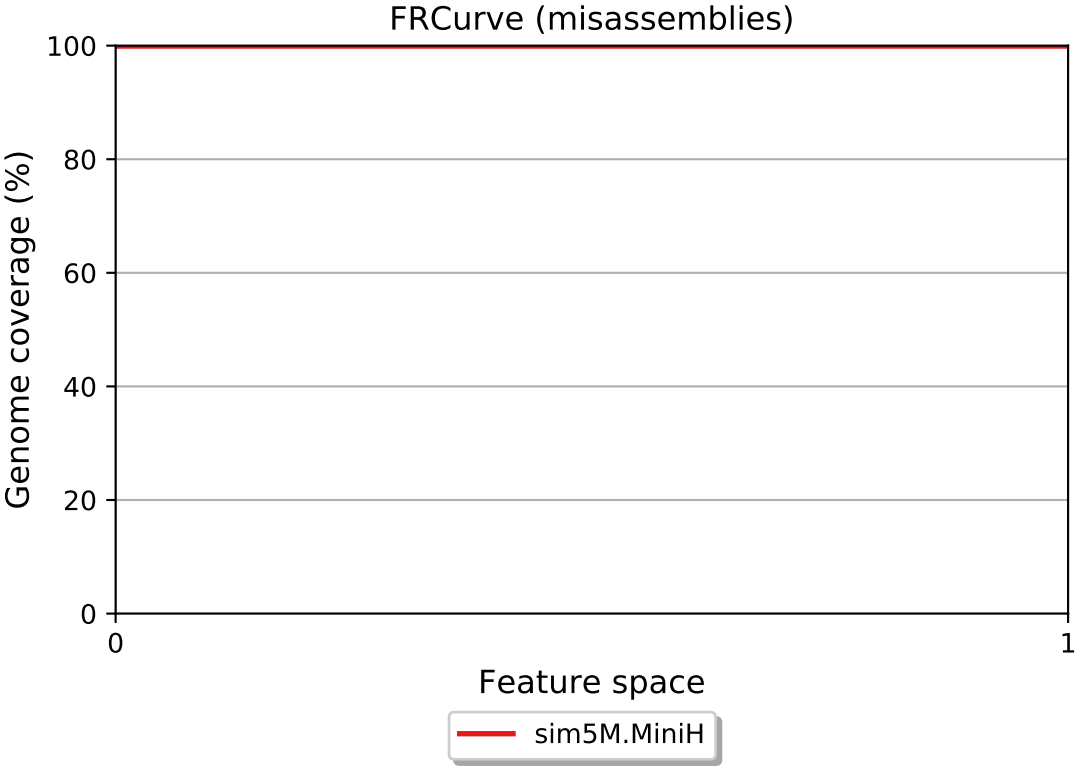

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim5M.MiniH

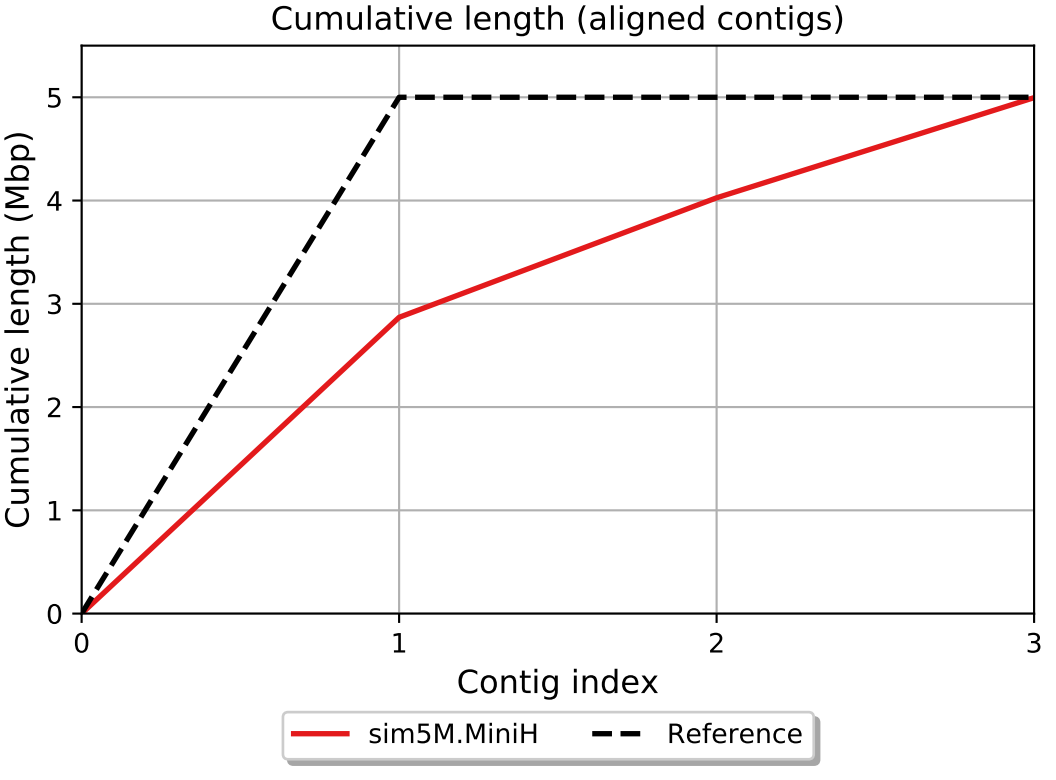

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
1
2
3
Contig index
sim5M.MiniH
Reference

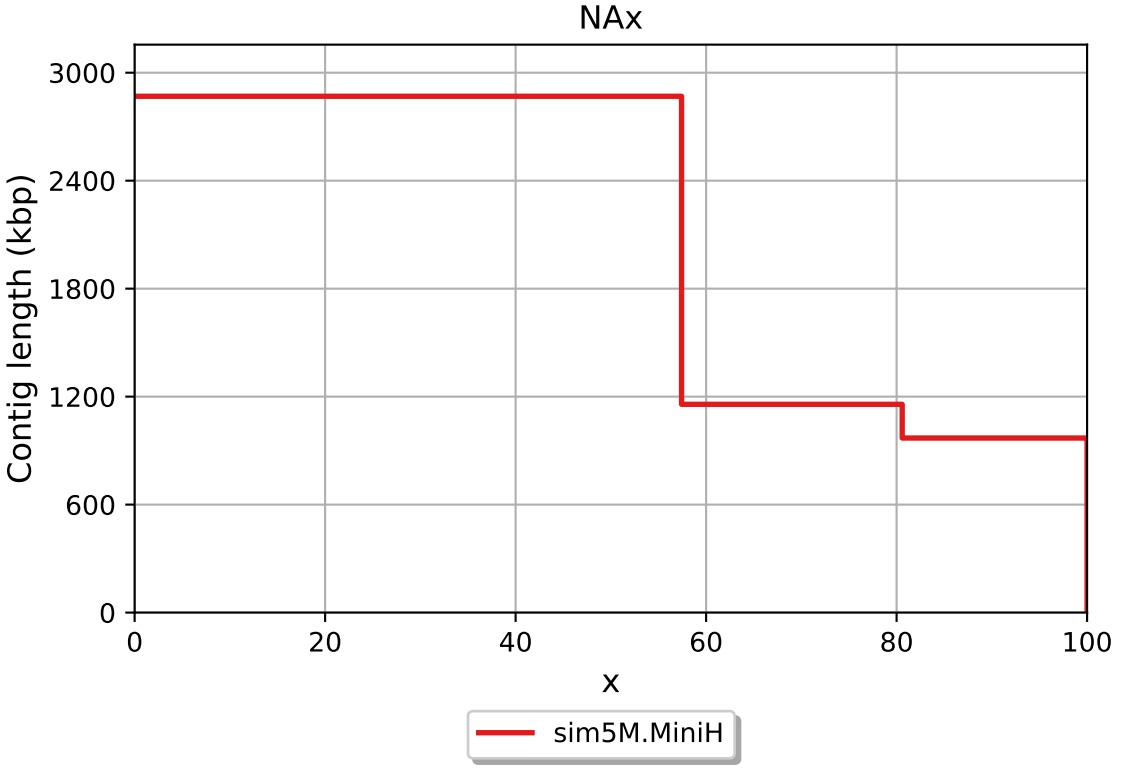

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
sim5M.MiniH
Reference

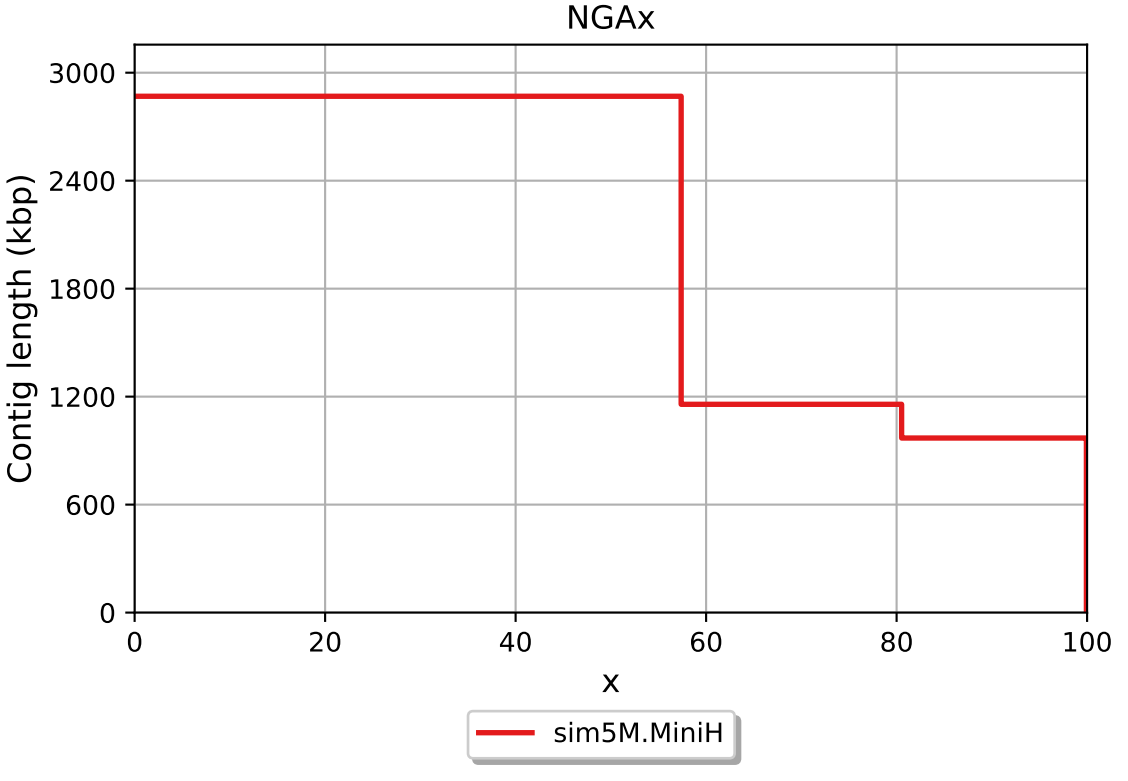

sim5M.MiniH GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
sim5M.MiniH


Misassemblies
5
4
3
2
1
0
sim5M.MiniH


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


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


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


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