Report

	sim25M.MiniH
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	11
Total length (>= 0 bp)	25094927
Total length (>= 1000 bp)	25094927
Total length (>= 5000 bp)	25094927
Total length (>= 10000 bp)	25094927
Total length (>= 25000 bp)	25077342
Total length (>= 50000 bp)	25036692
# contigs	13
Largest contig	7666928
Total length	25094927
Reference length	25000020
GC (%)	43.71
Reference GC (%)	43.69
N50	7138142
NG50	7138142
N75	1757646
NG75	1757646
L50	2
LG50	2
L75	4
LG75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	1078
Genome fraction (%)	99.790
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.00
# indels per 100 kbp	201.47
Largest alignment	7665207
Total aligned length	25089836
NA50	7138139
NGA50	7138139
NA75	1757645
NGA75	1757645
LA50	2
LGA50	2
LA75	4
LGA75	4

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

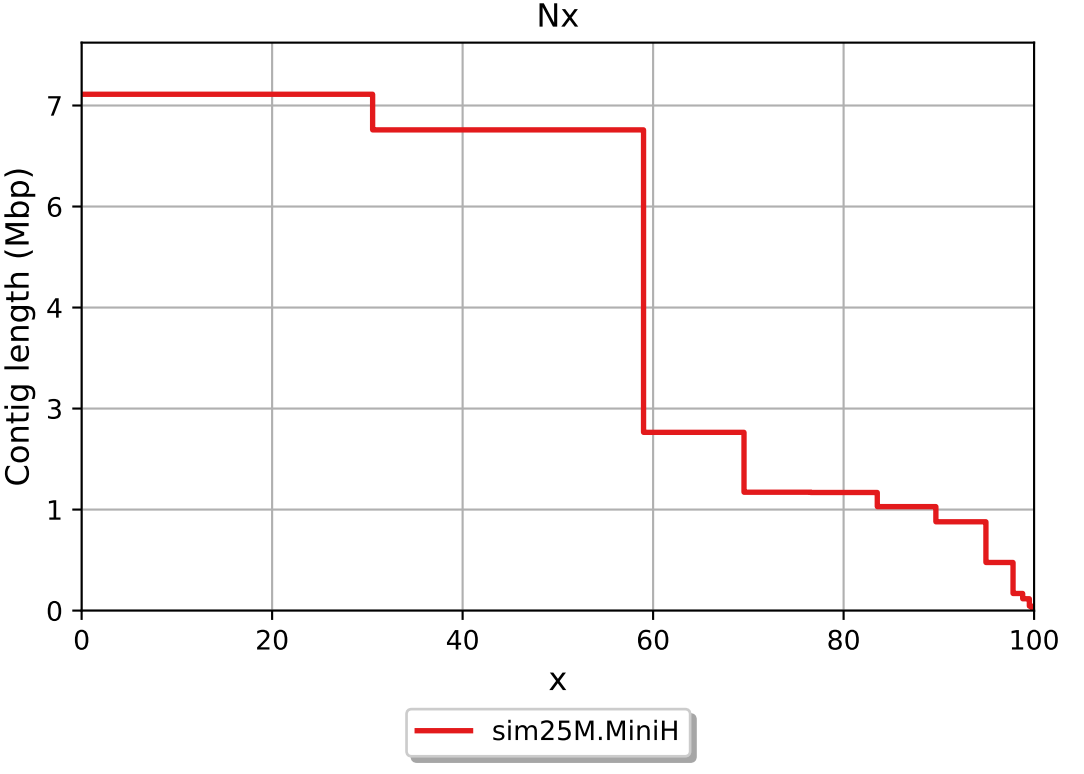
	sim25M.MiniH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	748
# indels	50261
# indels (<= 5 bp)	50207
# indels (> 5 bp)	54
Indels length	68922

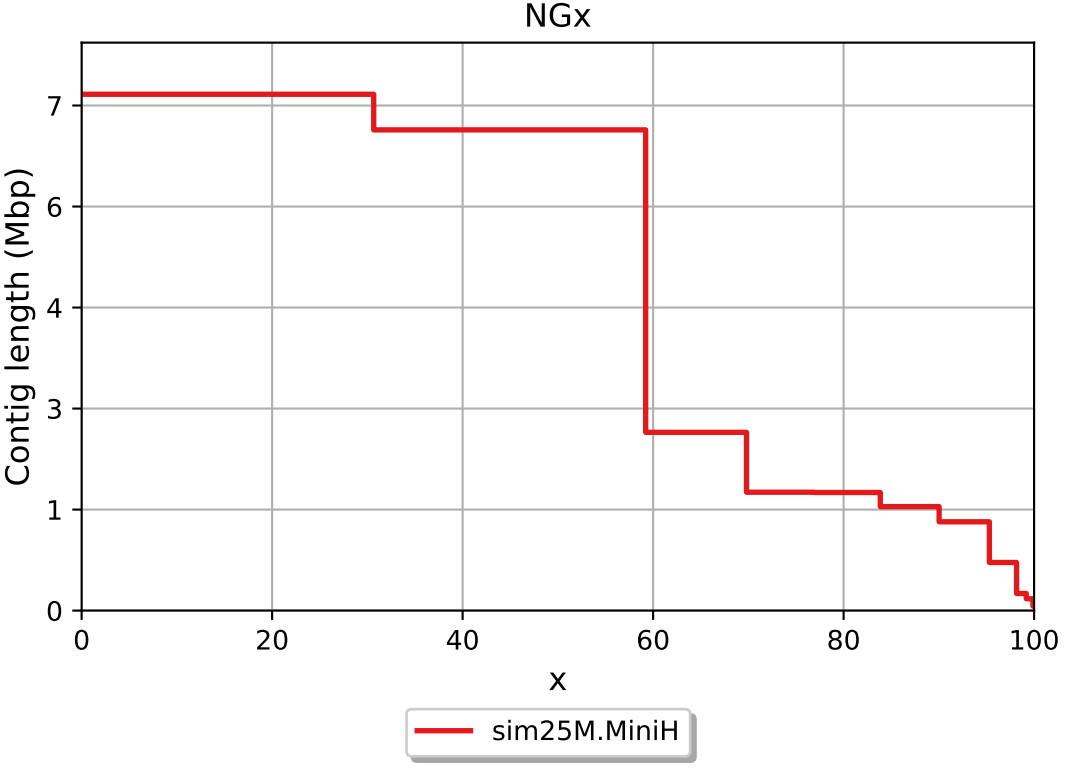
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

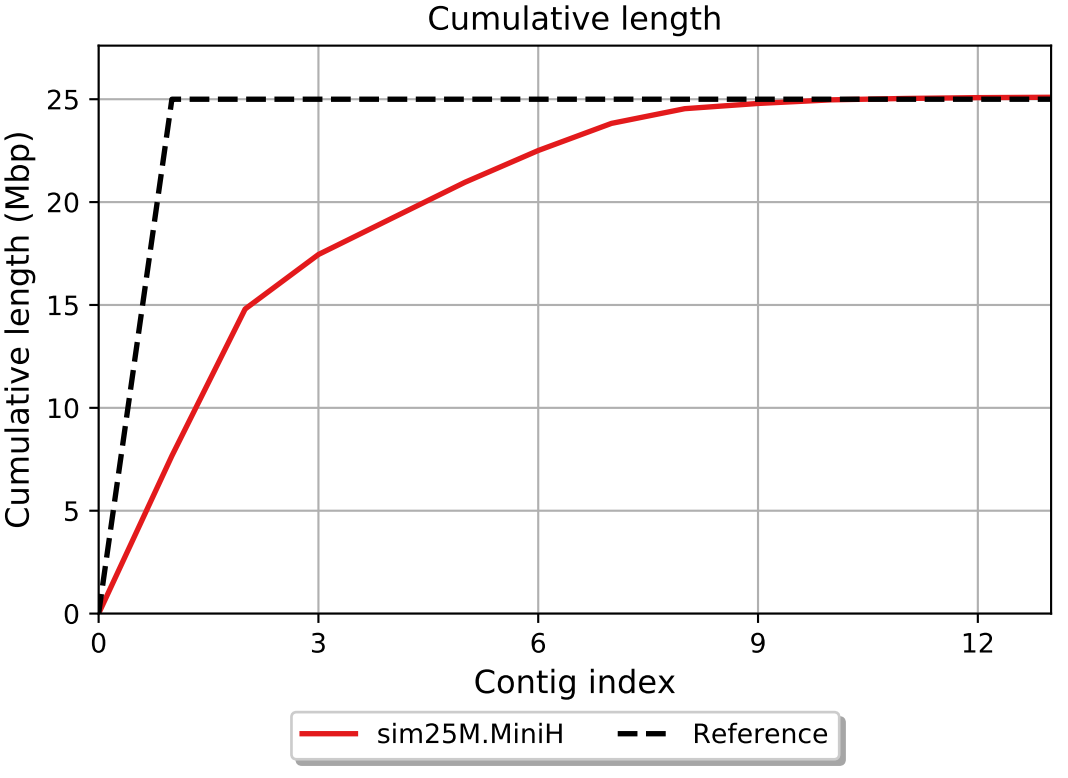
Unaligned report

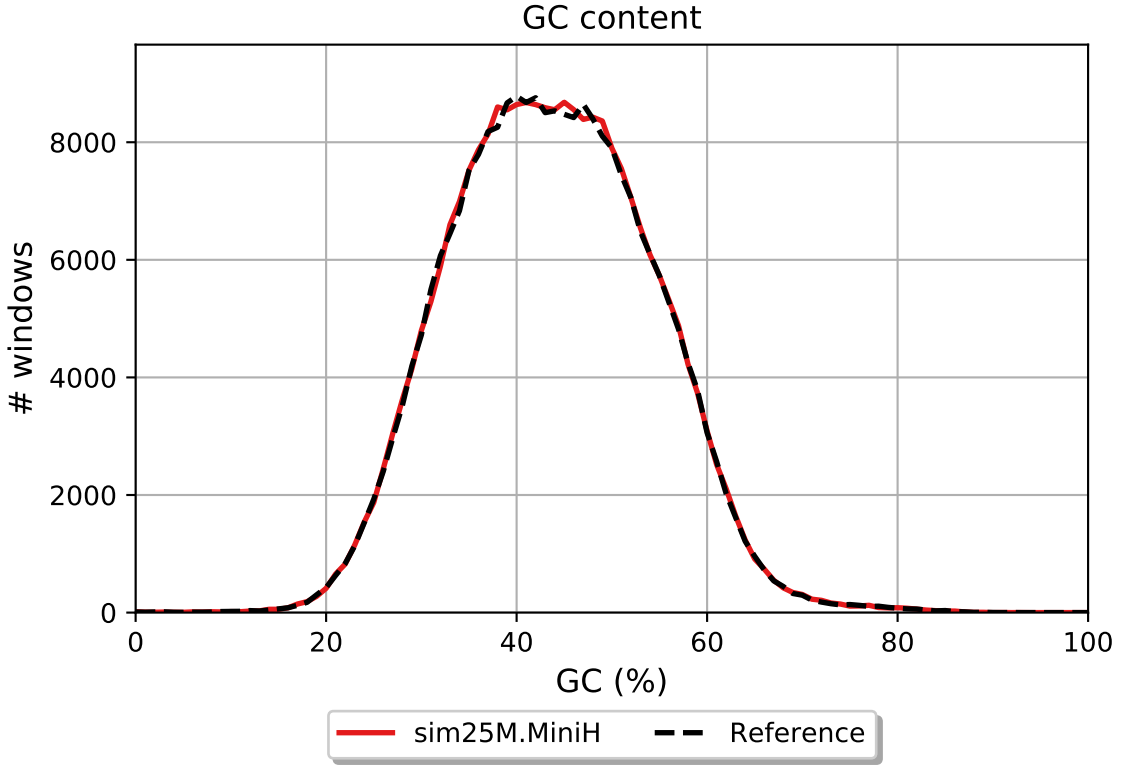
	sim25M.MiniH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	1078
# N's	0

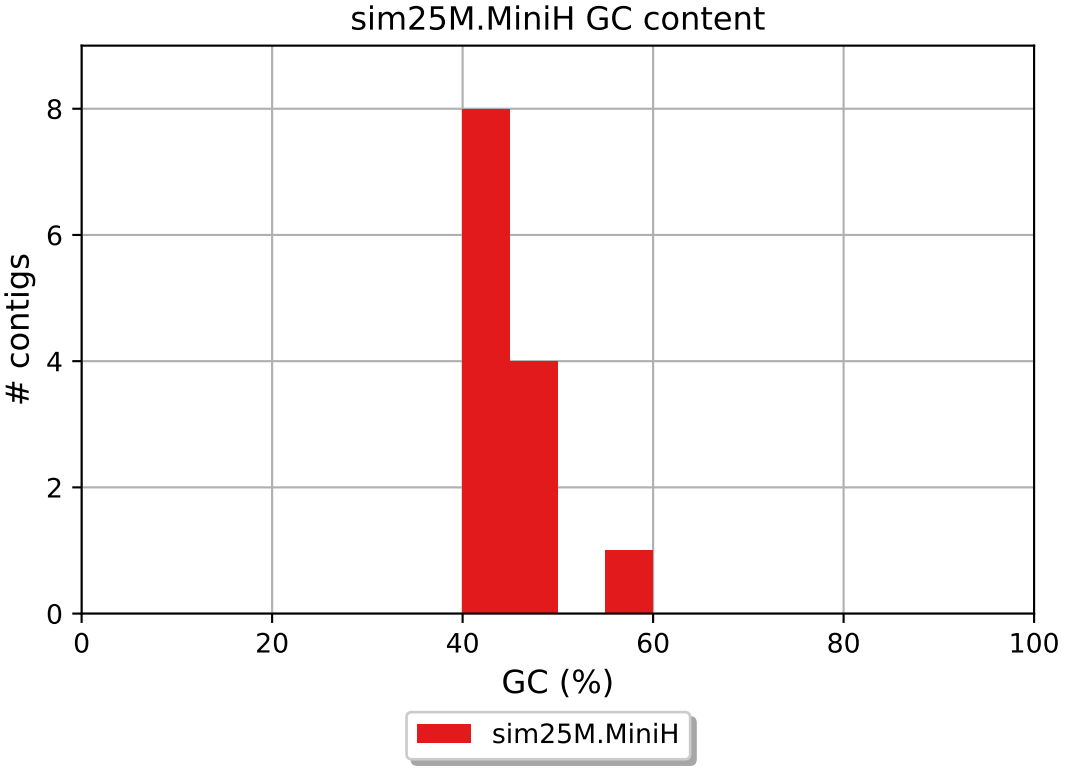
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

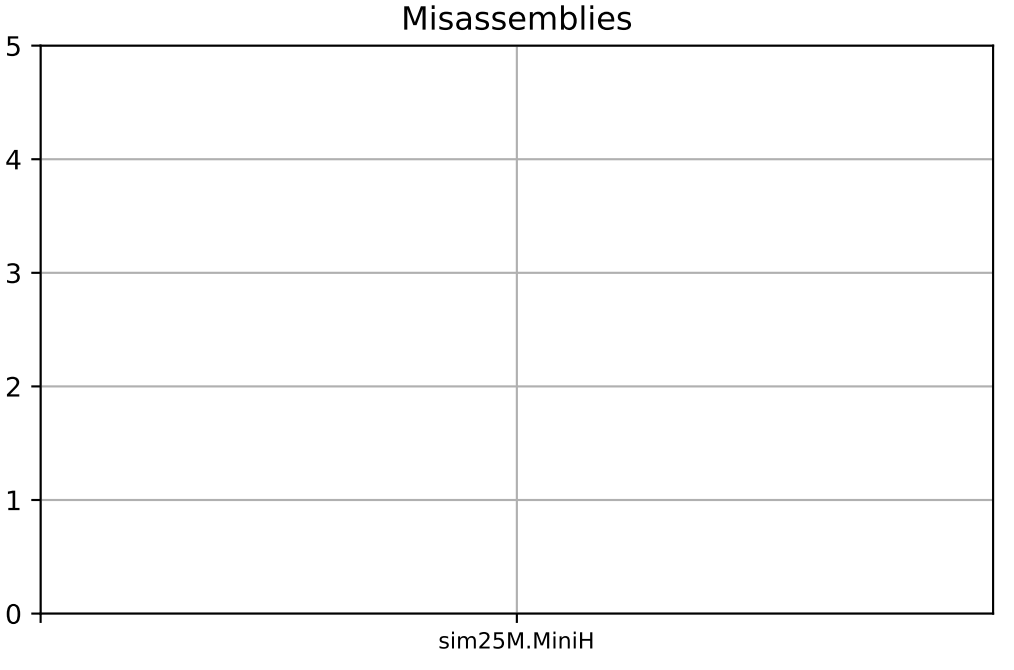

Nx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
sim25M.MiniH

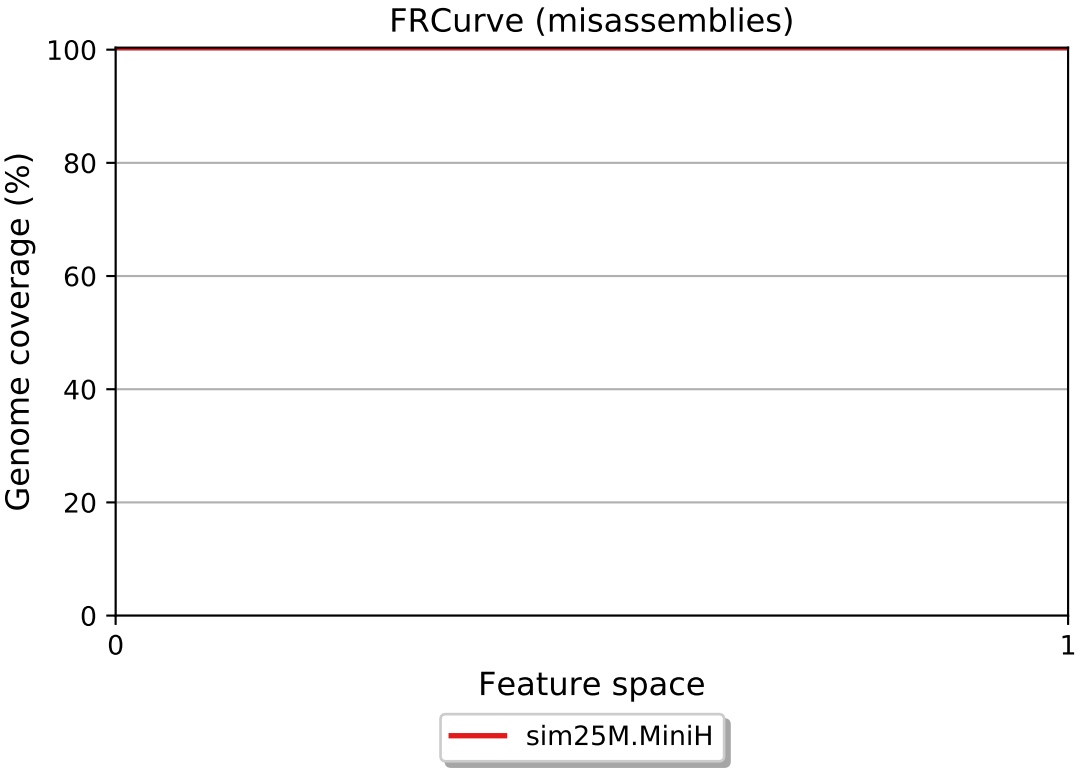

NGx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
sim25M.MiniH

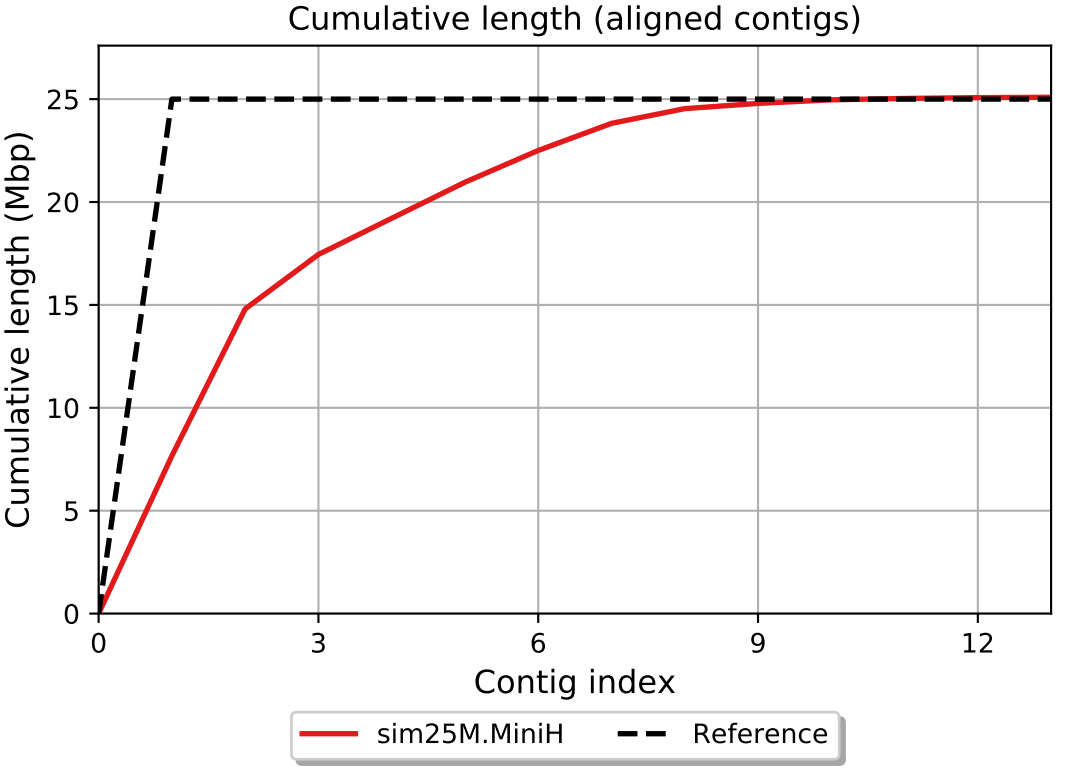

Cumulative length
Cumulative length (Mbp)
0
5
10
15
20
25
0
3
6
9
12
Contig index
sim25M.MiniH
Reference

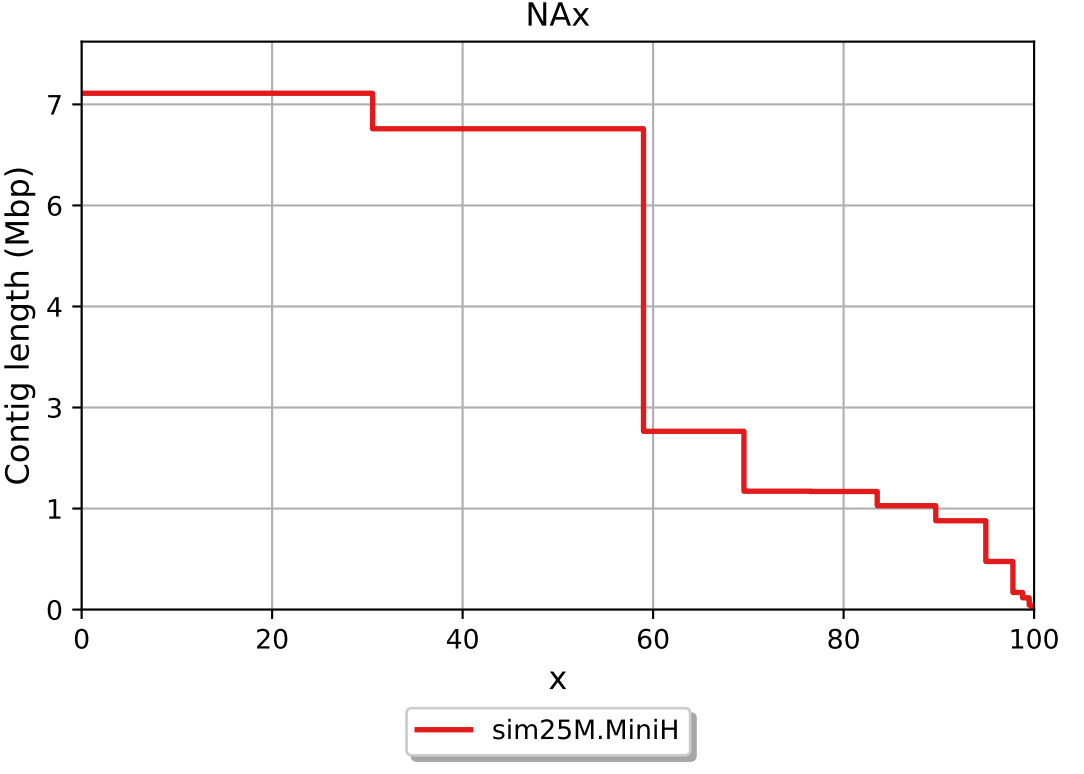

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
sim25M.MiniH
Reference

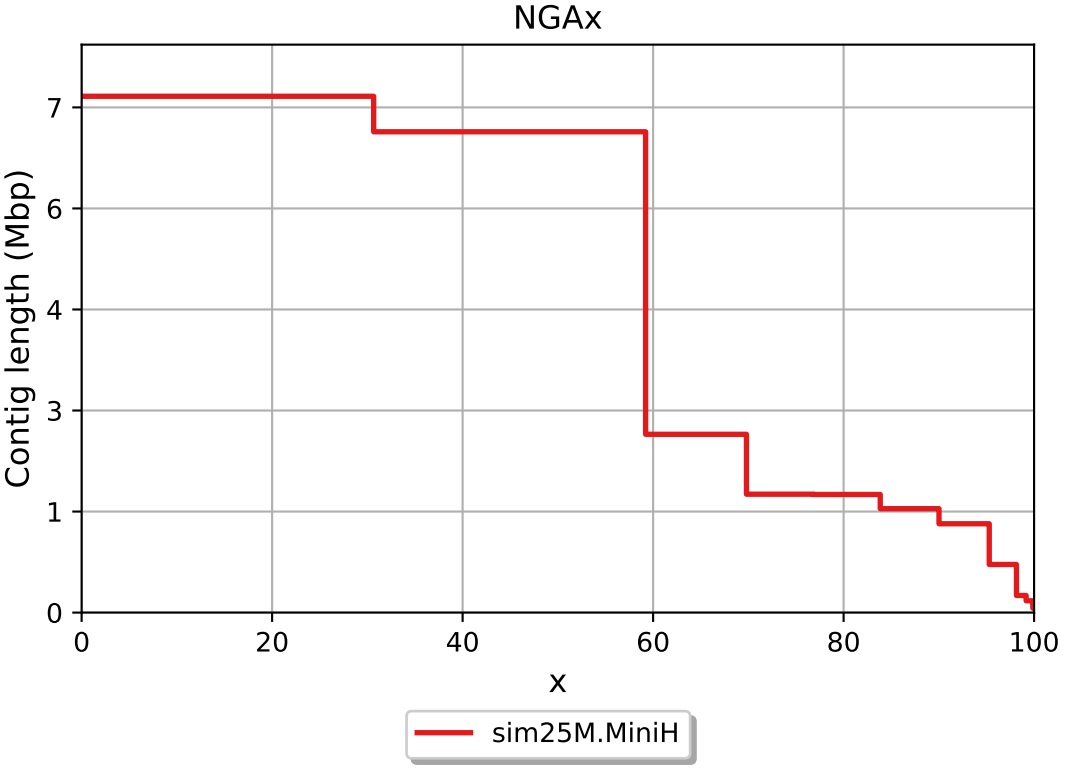

sim25M.MiniH GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
sim25M.MiniH


Misassemblies
5
4
3
2
1
0
sim25M.MiniH


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
sim25M.MiniH


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
5
10
15
20
25
0
3
6
9
12
Contig index
sim25M.MiniH
Reference


NAx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
sim25M.MiniH


NGAx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
sim25M.MiniH