Report

	sim25M.MiniL
# contigs (>= 0 bp)	35
# contigs (>= 1000 bp)	35
# contigs (>= 5000 bp)	35
# contigs (>= 10000 bp)	35
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	24726068
Total length (>= 1000 bp)	24726068
Total length (>= 5000 bp)	24726068
Total length (>= 10000 bp)	24726068
Total length (>= 25000 bp)	24726068
Total length (>= 50000 bp)	24638686
# contigs	35
Largest contig	2770879
Total length	24726068
Reference length	25000020
GC (%)	43.74
Reference GC (%)	43.69
N50	1264603
NG50	1264603
N75	988893
NG75	938279
L50	8
LG50	8
L75	13
LG75	14
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3963246
# local misassemblies	4
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	20609
Genome fraction (%)	98.411
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.53
# indels per 100 kbp	211.38
Largest alignment	2561227
Total aligned length	24705328
NA50	1264603
NGA50	1264603
NA75	938277
NGA75	938277
LA50	8
LGA50	8
LA75	14
LGA75	14

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

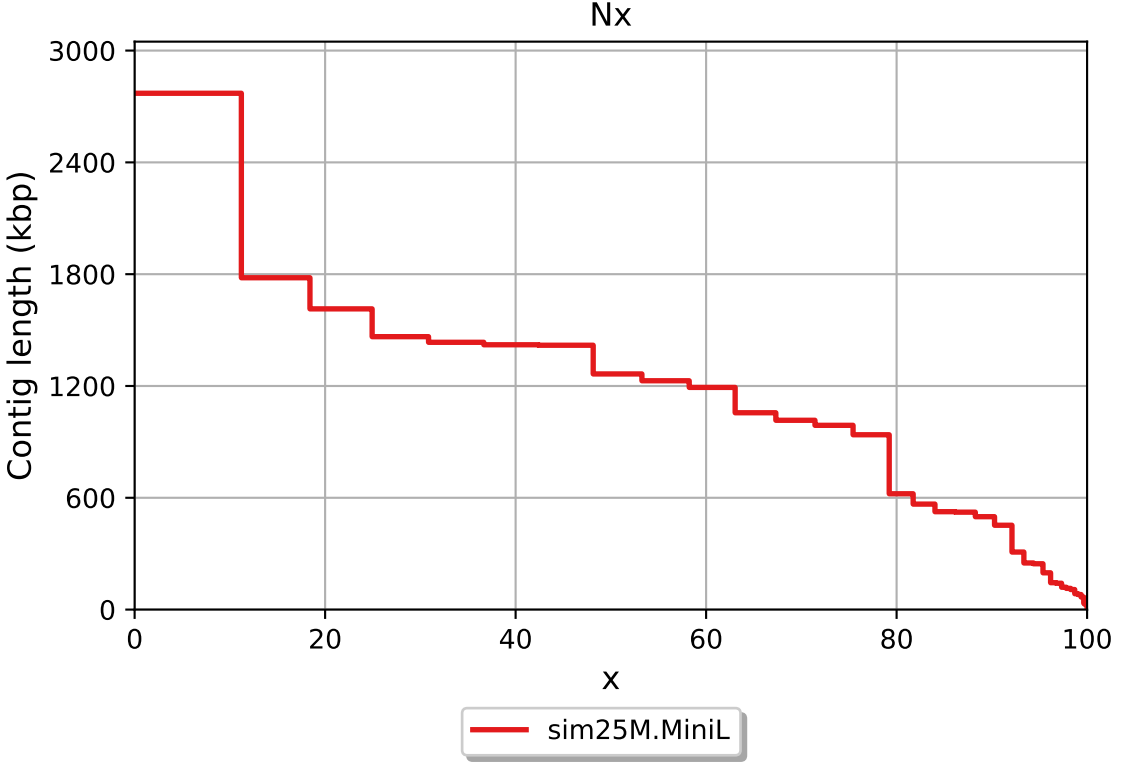
	sim25M.MiniL
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	3963246
# local misassemblies	4
# unaligned mis. contigs	0
# mismatches	2345
# indels	52005
# indels (<= 5 bp)	51932
# indels (> 5 bp)	73
Indels length	67434

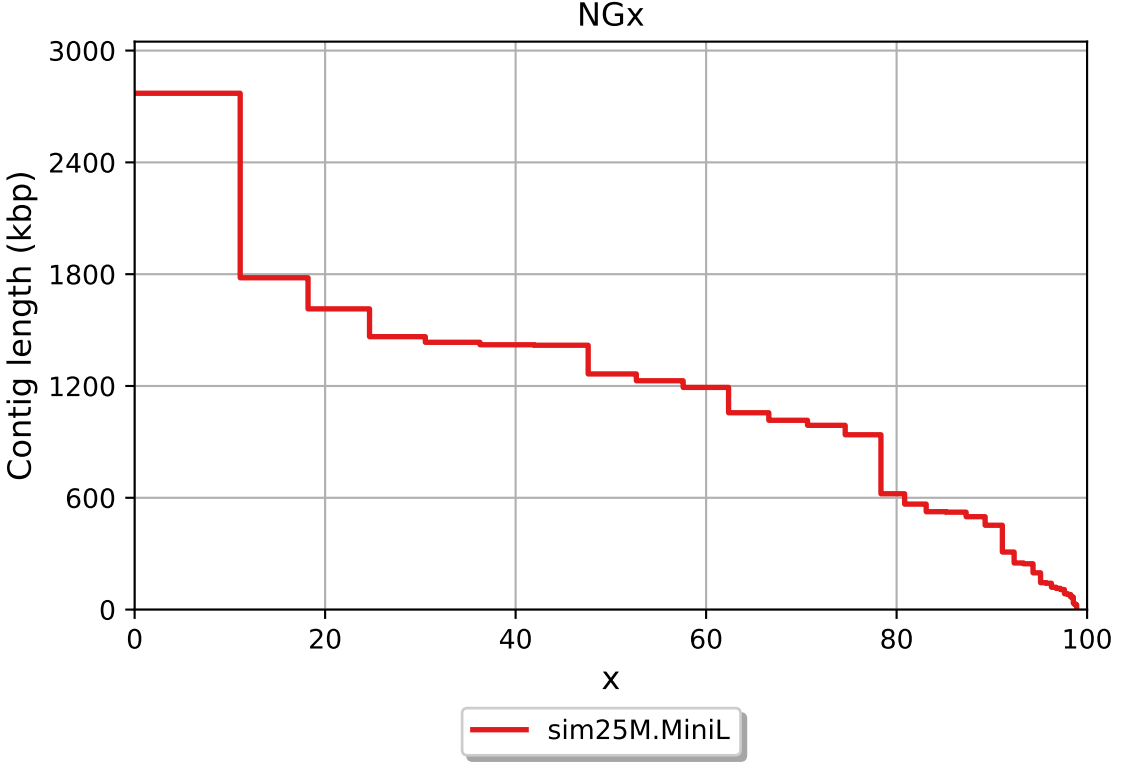
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

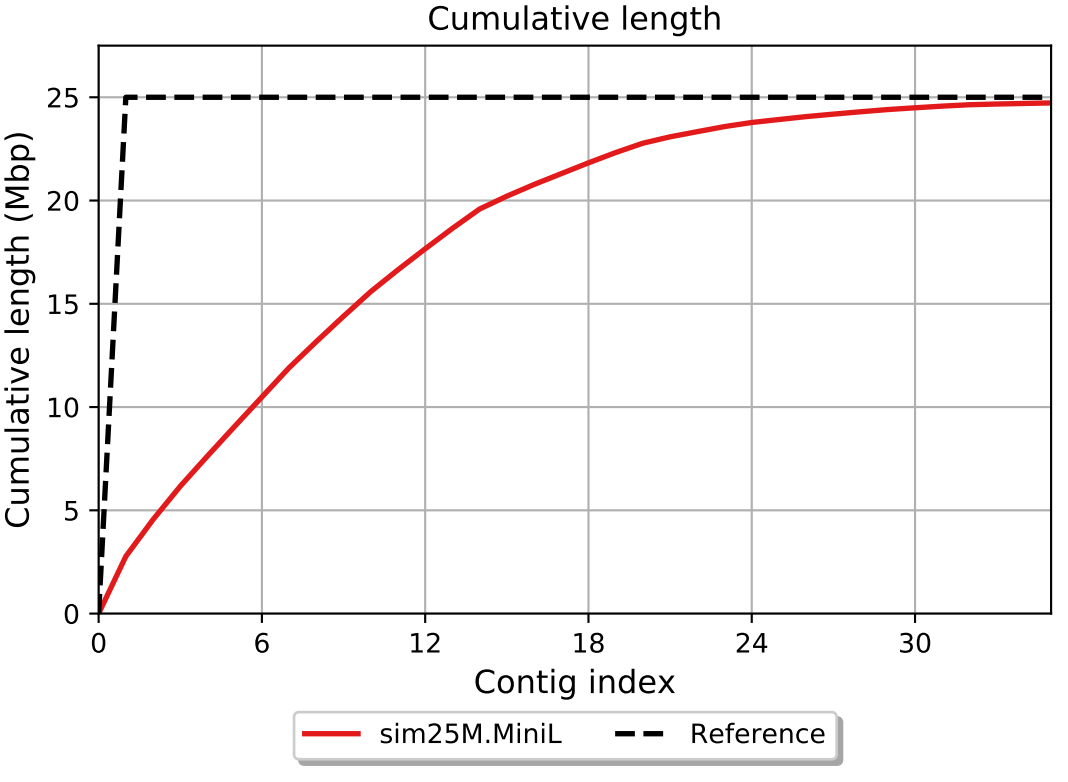
Unaligned report

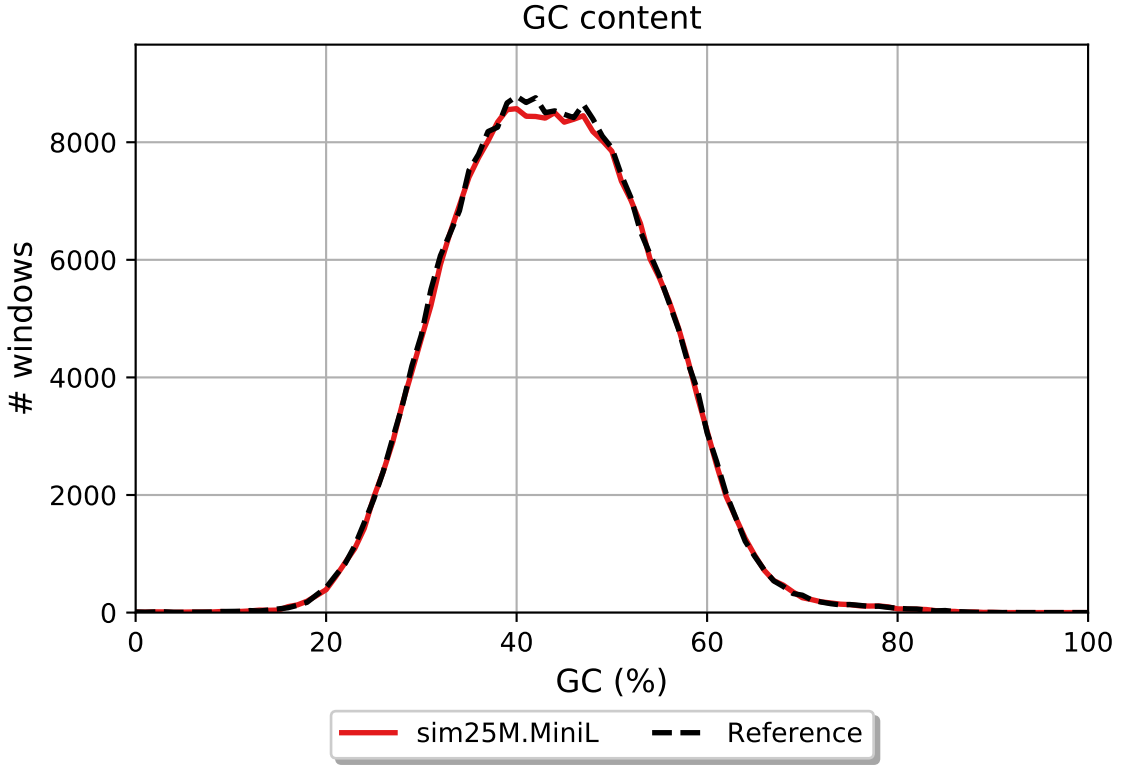
	sim25M.MiniL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	20609
# N's	0

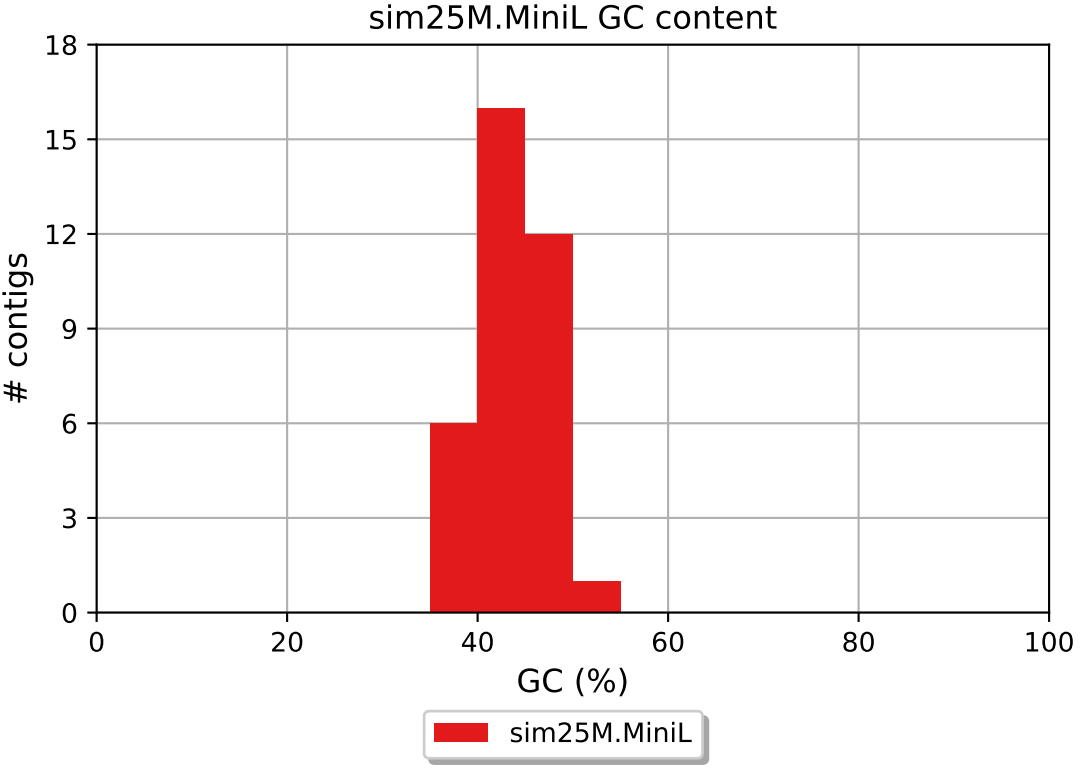
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

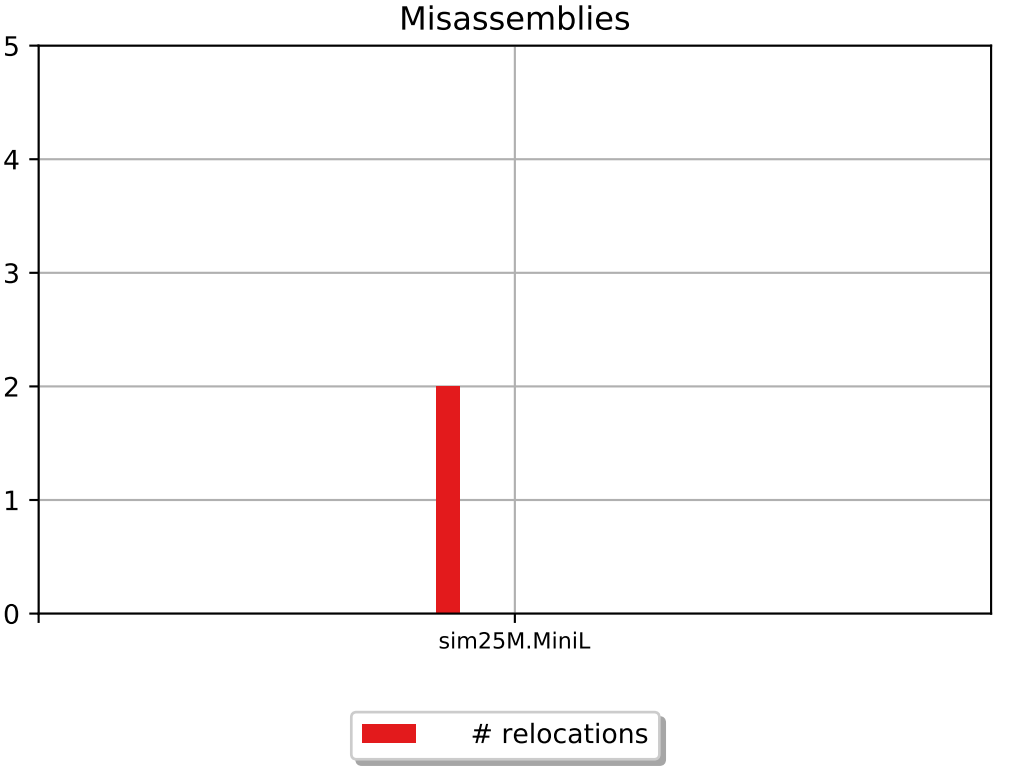

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
sim25M.MiniL

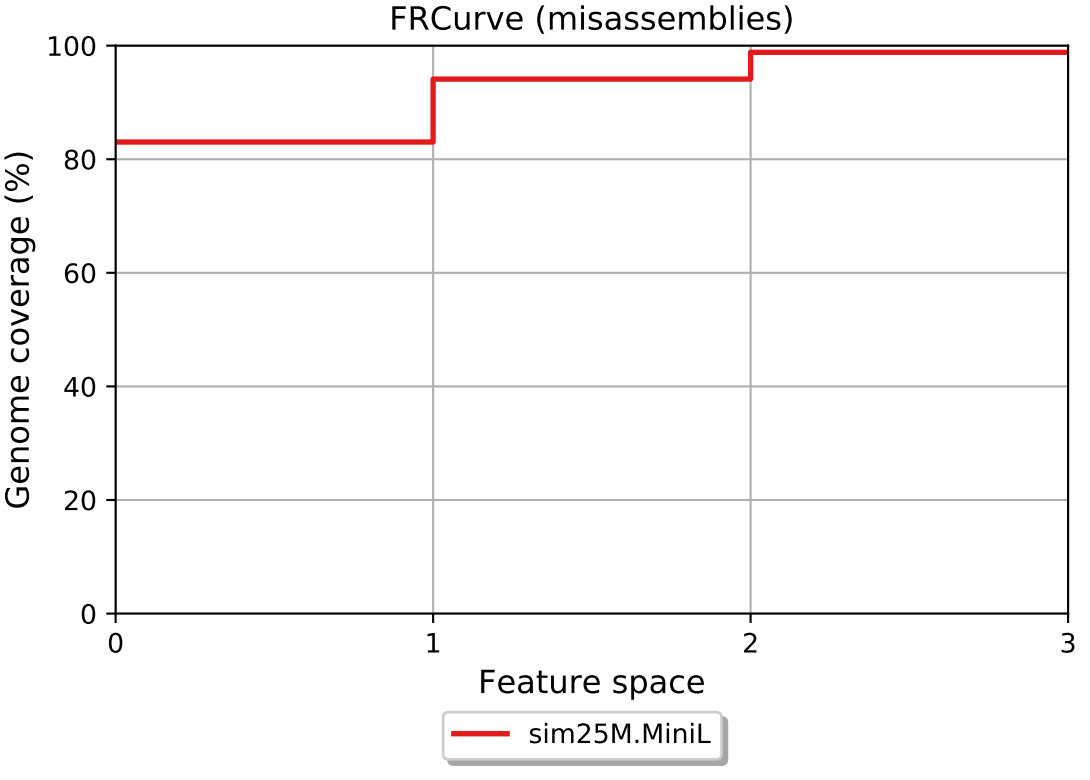

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
sim25M.MiniL

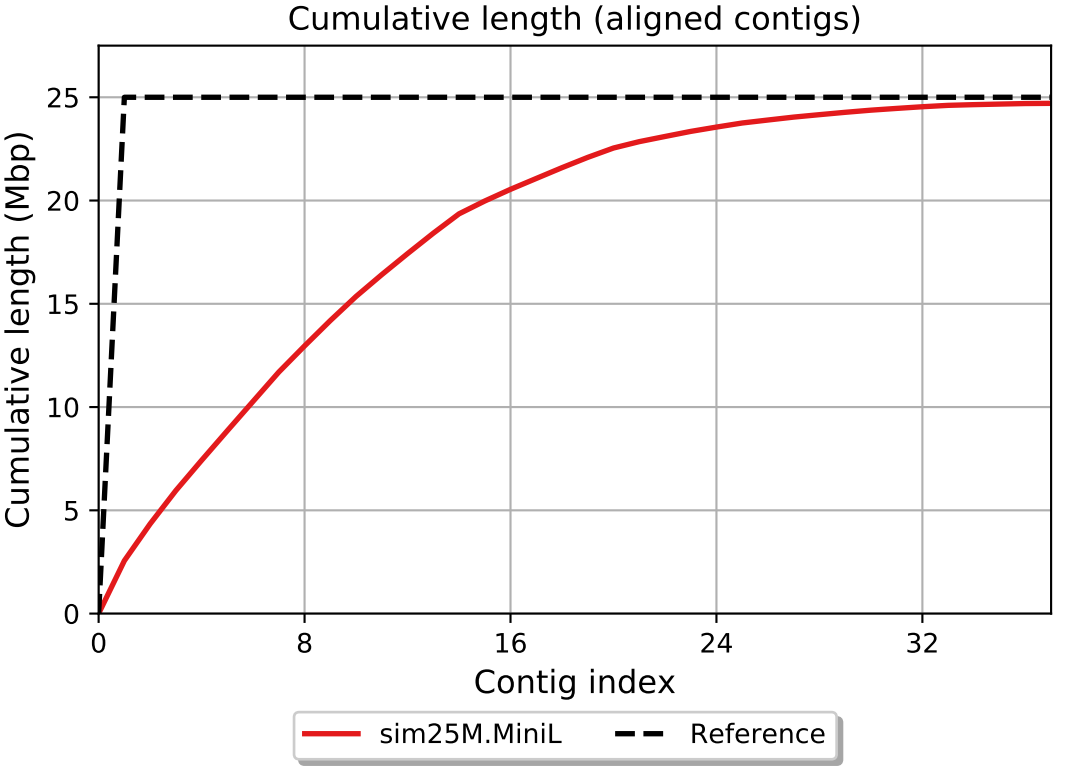

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
6
12
18
24
30
Contig index
sim25M.MiniL
Reference

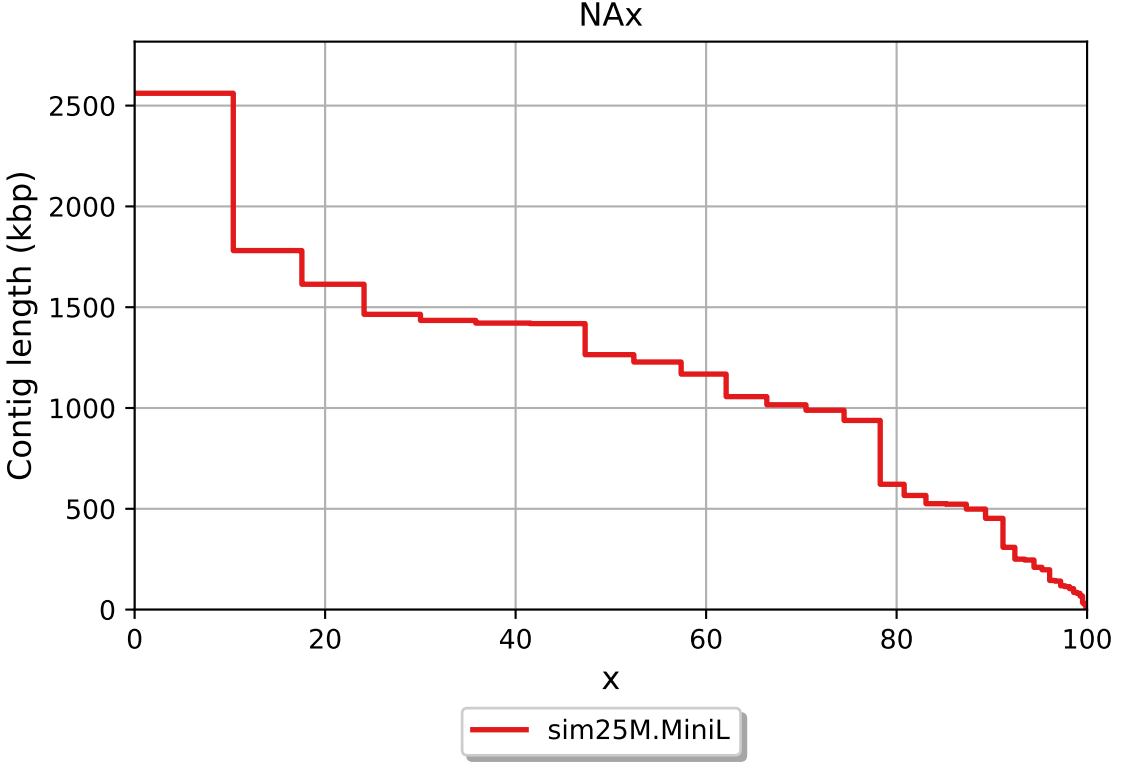

GC content
windows
8000
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
sim25M.MiniL
Reference

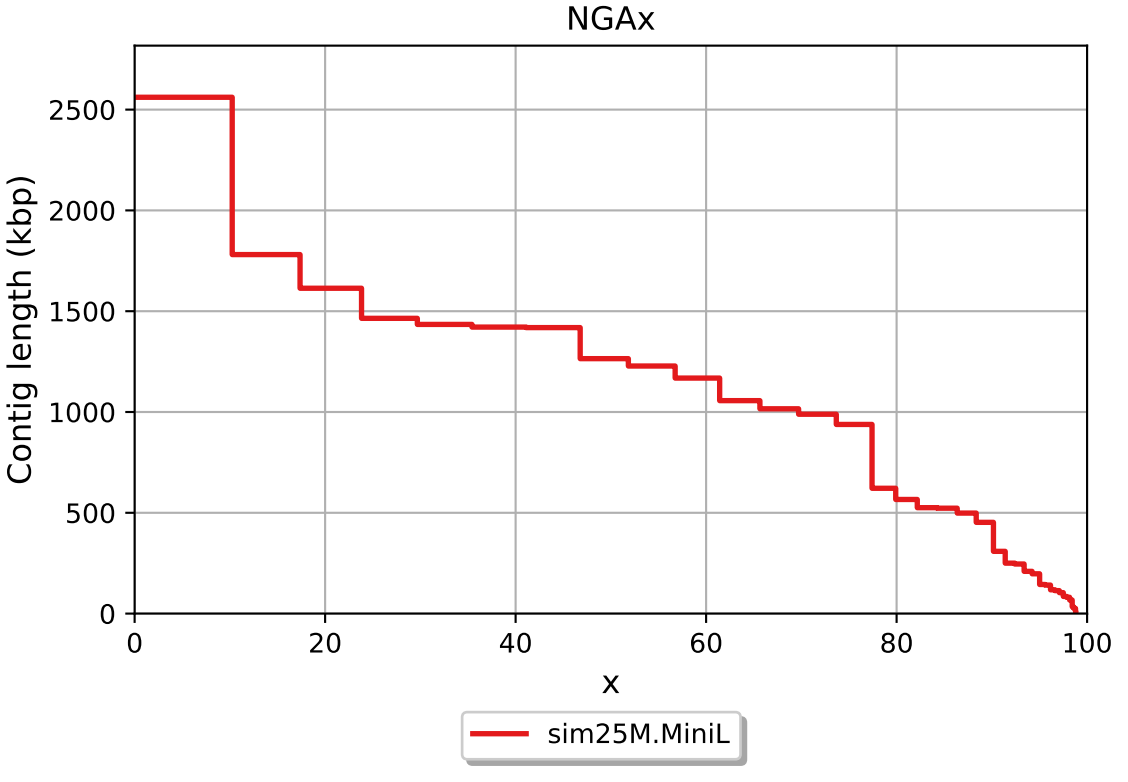

sim25M.MiniL GC content
contigs
GC (%)
0
3
6
9
12
15
18
0
20
40
60
80
100
sim25M.MiniL


Misassemblies
5
4
3
2
1
0
sim25M.MiniL
relocations


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
25
20
15
10
5
0
0
8
16
24
32
Contig index
sim25M.MiniL
Reference


NAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
sim25M.MiniL


NGAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
sim25M.MiniL