Report

	sim5M.SGAH
# contigs (>= 0 bp)	2355
# contigs (>= 1000 bp)	729
# contigs (>= 5000 bp)	339
# contigs (>= 10000 bp)	157
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5202931
Total length (>= 1000 bp)	4737537
Total length (>= 5000 bp)	3717968
Total length (>= 10000 bp)	2446369
Total length (>= 25000 bp)	342120
Total length (>= 50000 bp)	0
# contigs	871
Largest contig	43317
Total length	4839182
Reference length	5000040
GC (%)	35.67
Reference GC (%)	35.84
N50	10025
NG50	9782
N75	5308
NG75	4947
L50	155
LG50	163
L75	322
LG75	346
# 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 (%)	95.891
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.04
Largest alignment	43317
Total aligned length	4839182
NA50	10025
NGA50	9782
NA75	5308
NGA75	4947
LA50	155
LGA50	163
LA75	322
LGA75	346

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

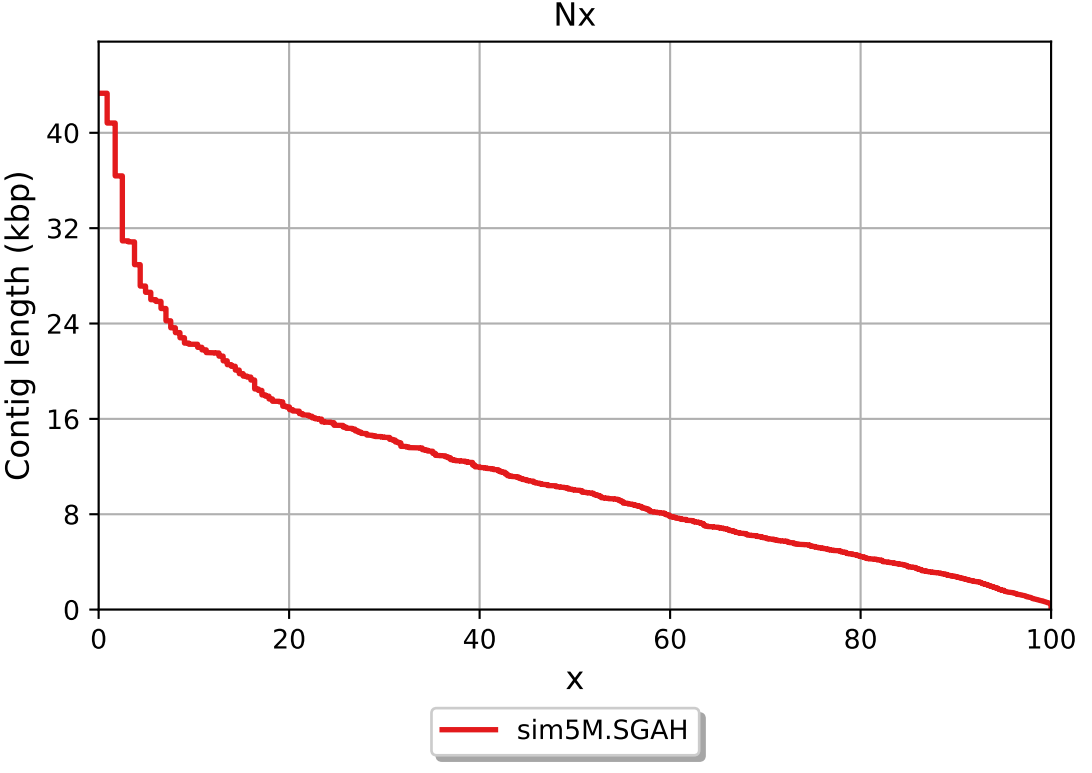
	sim5M.SGAH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	2
# indels (<= 5 bp)	0
# indels (> 5 bp)	2
Indels length	66

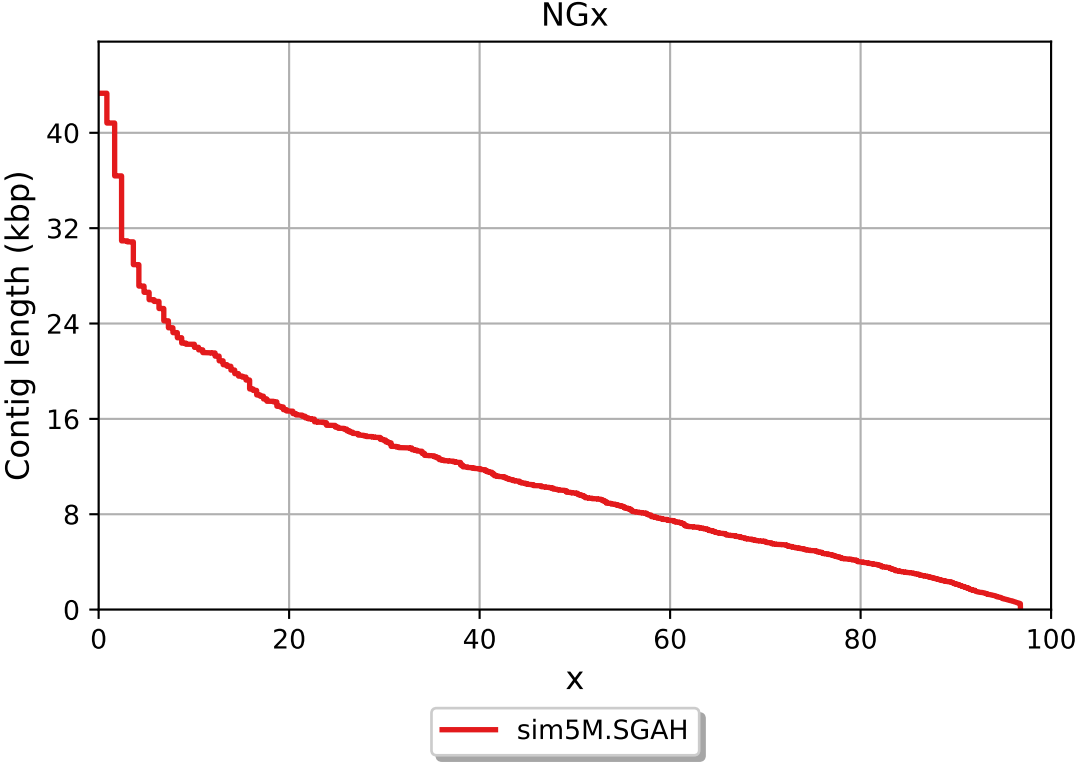
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

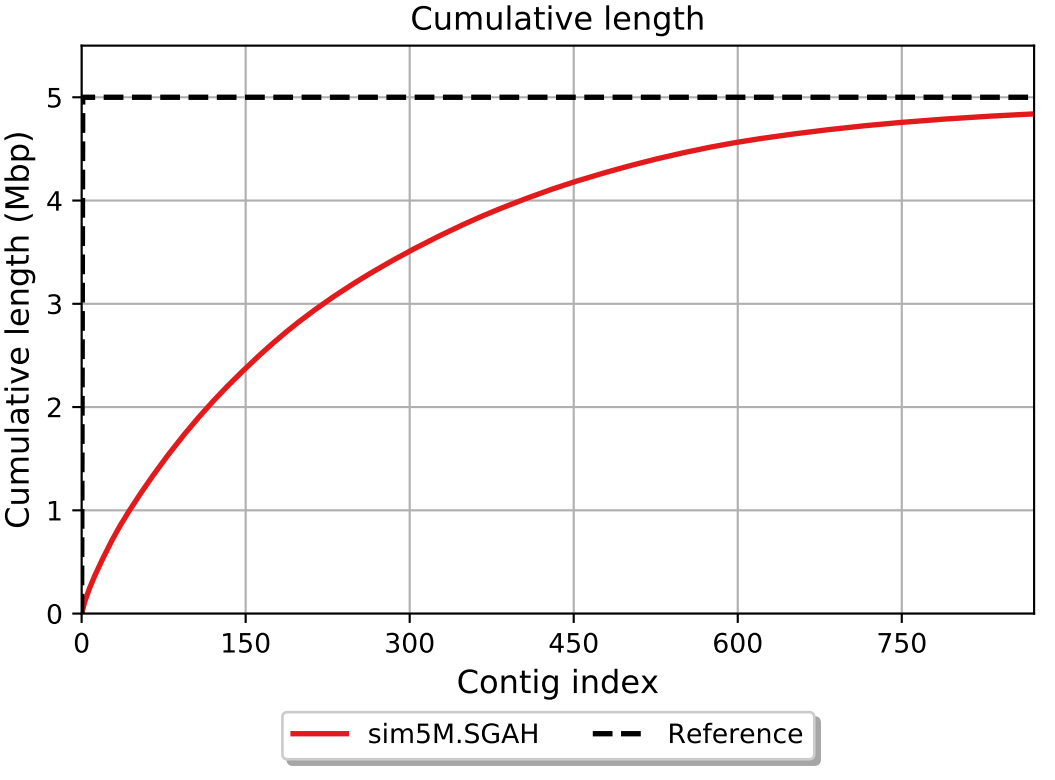
Unaligned report

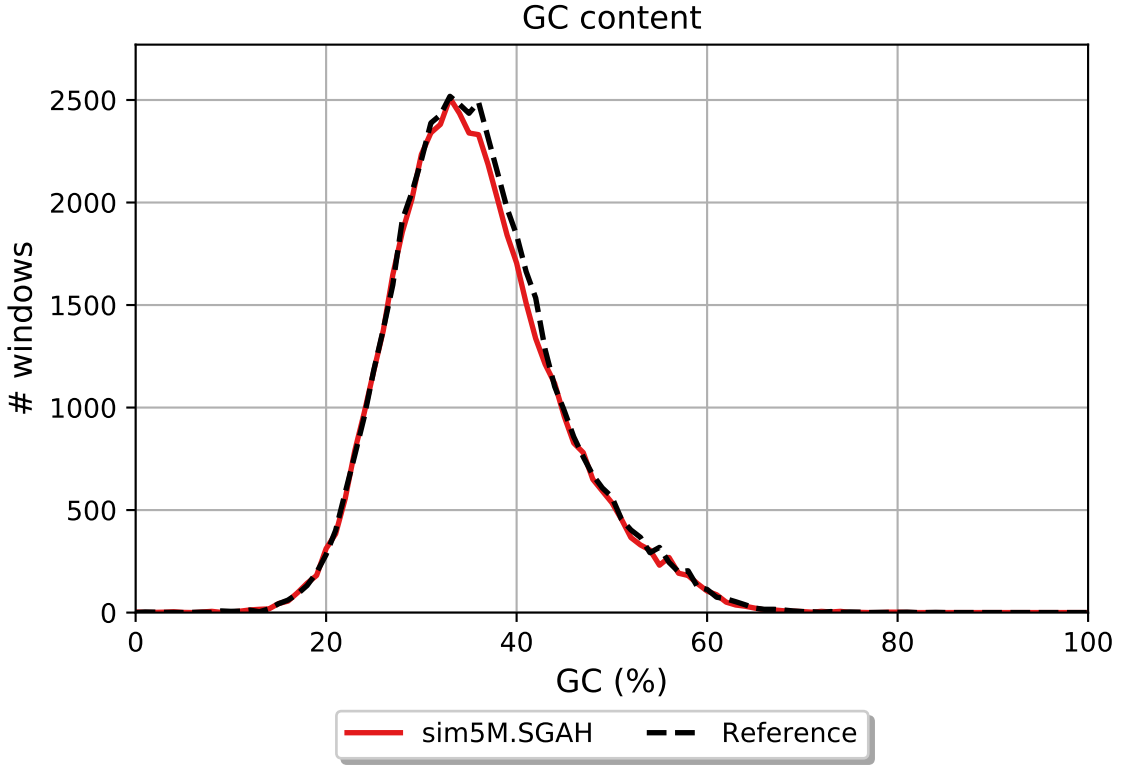
	sim5M.SGAH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

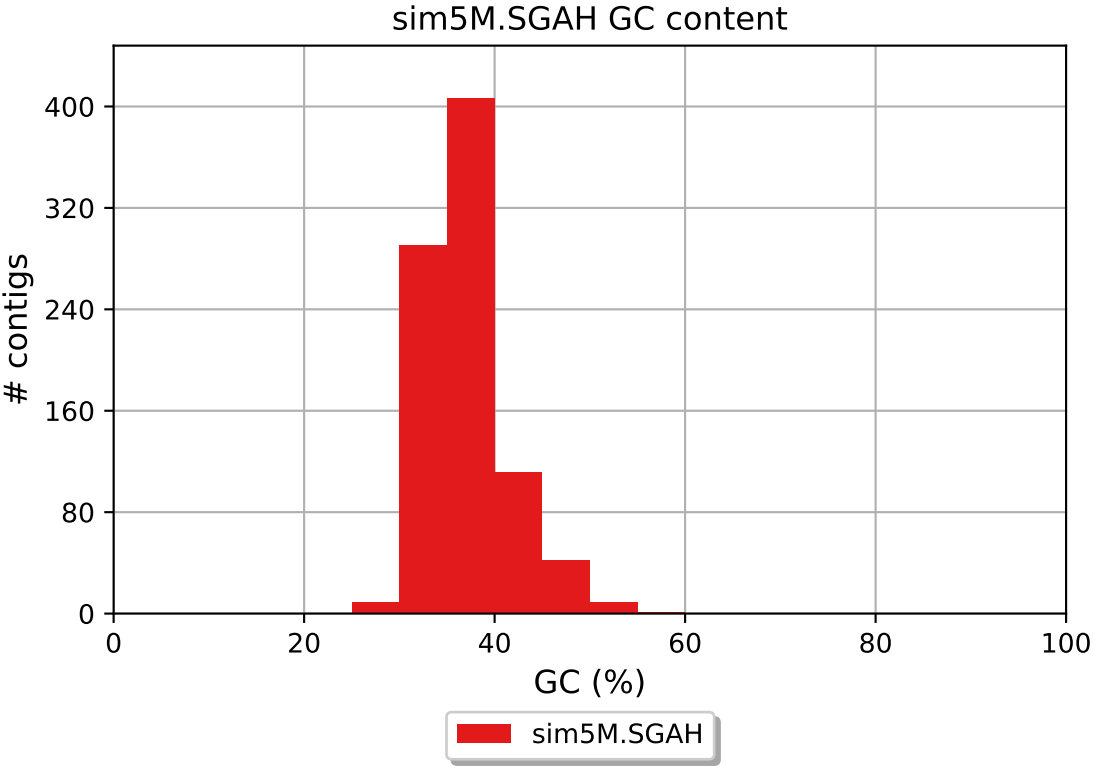
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

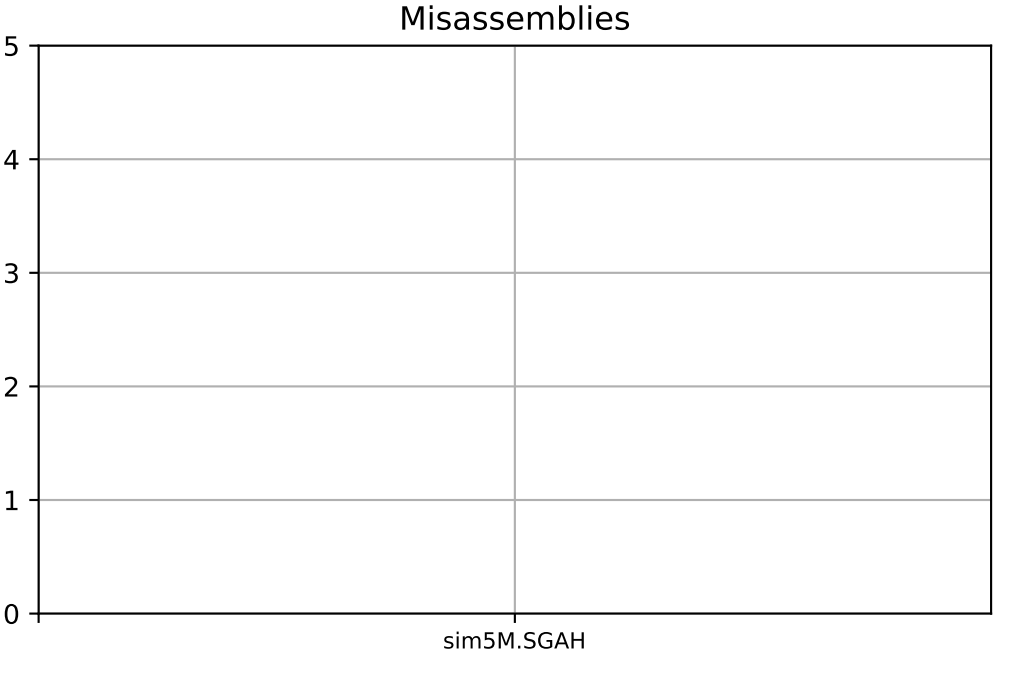

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim5M.SGAH

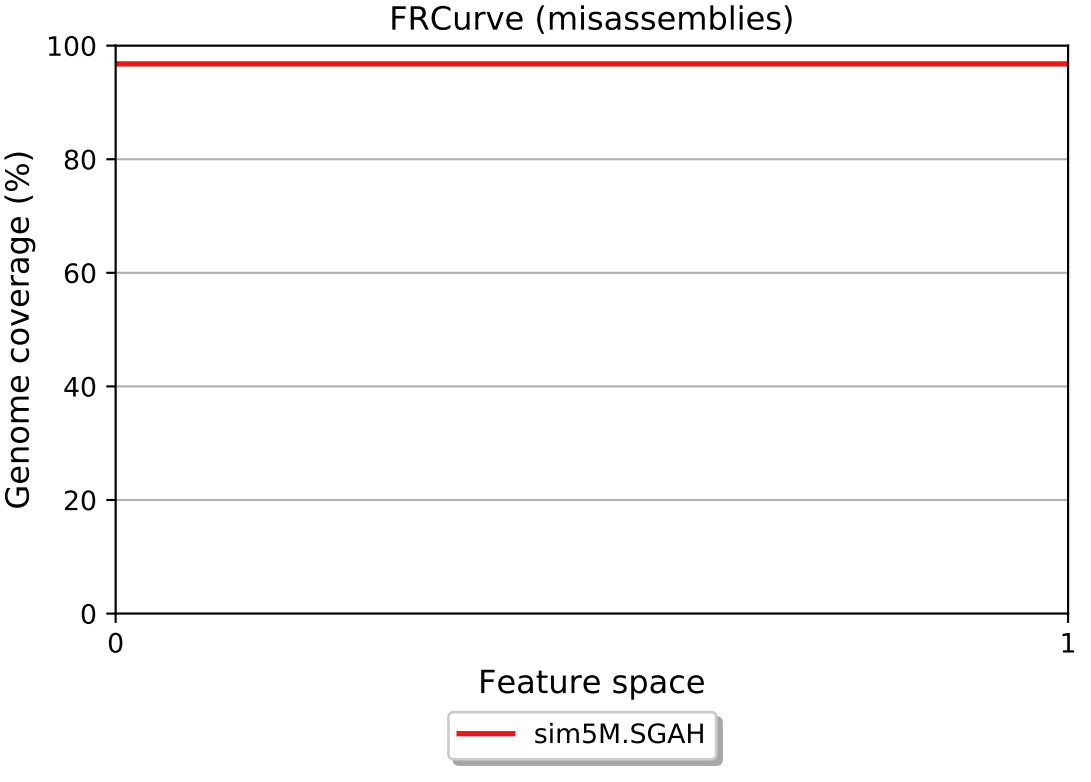

NGx
Contig length (kbp)
0
8
16
24
32
40
0
20
40
60
80
100
x
sim5M.SGAH

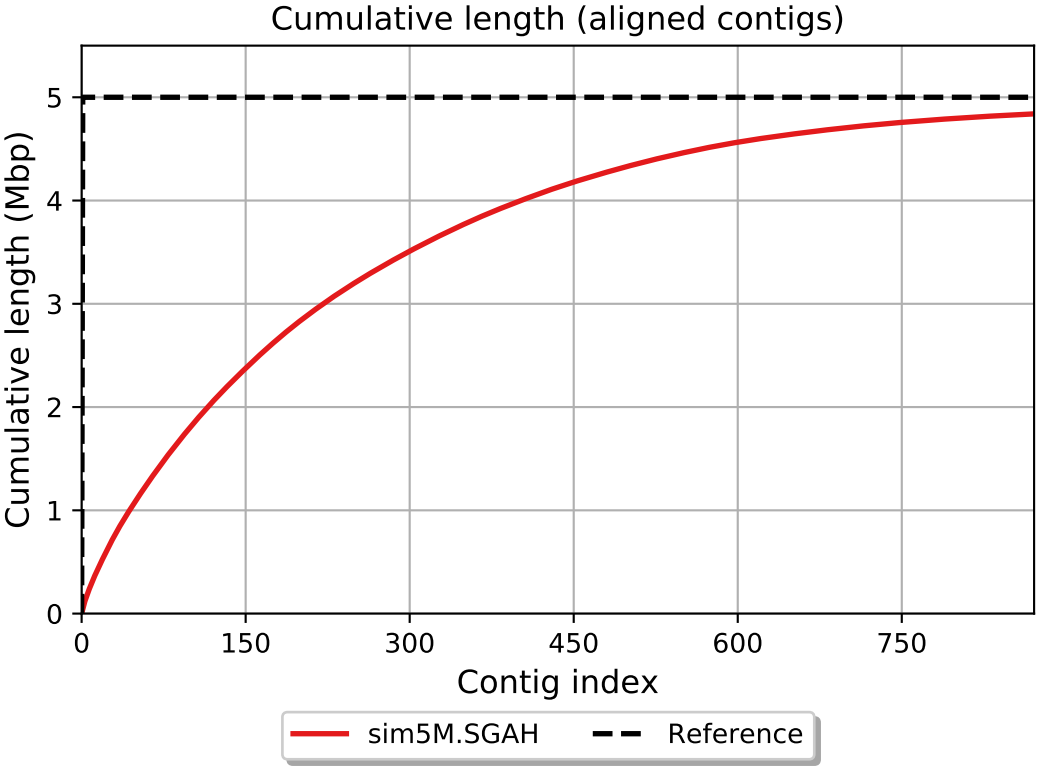

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
150
300
450
600
750
Contig index
sim5M.SGAH
Reference

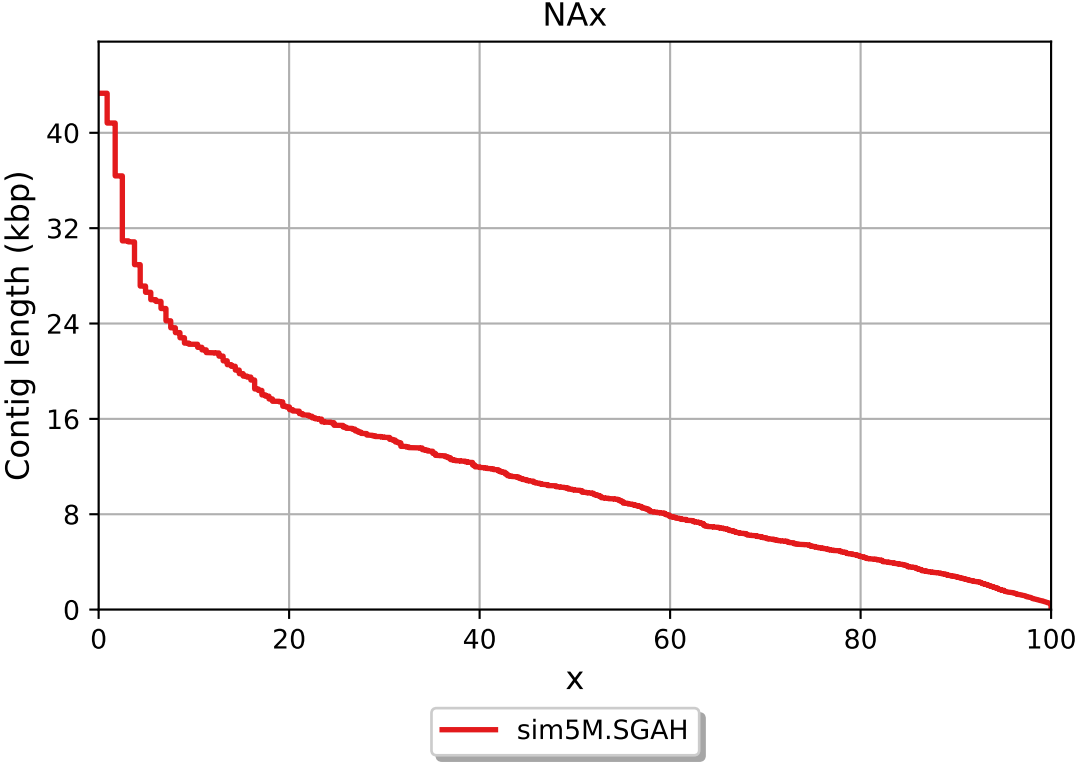

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
0
20
40
60
80
100
sim5M.SGAH
Reference

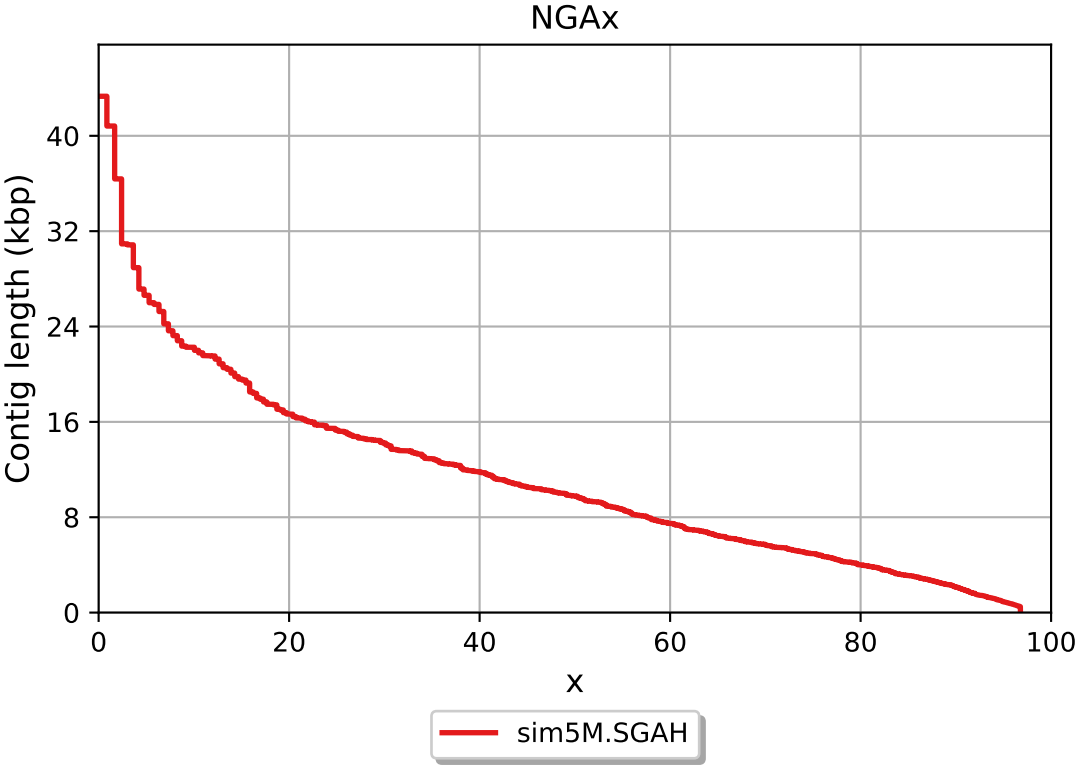

sim5M.SGAH GC content
contigs
400
320
240
160
80
0
0
20
40
60
80
100
GC (%)
sim5M.SGAH


Misassemblies
5
4
3
2
1
0
sim5M.SGAH


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
150
300
450
600
750
Contig index
sim5M.SGAH
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim5M.SGAH


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim5M.SGAH