Report

	sim25M.SGAH
# contigs (>= 0 bp)	26181
# contigs (>= 1000 bp)	5906
# contigs (>= 5000 bp)	1130
# contigs (>= 10000 bp)	301
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	27121893
Total length (>= 1000 bp)	20737206
Total length (>= 5000 bp)	10197192
Total length (>= 10000 bp)	4447052
Total length (>= 25000 bp)	331914
Total length (>= 50000 bp)	0
# contigs	8661
Largest contig	42930
Total length	22720373
Reference length	25000020
GC (%)	43.39
Reference GC (%)	43.69
N50	4302
NG50	3755
N75	2033
NG75	1511
L50	1381
LG50	1664
L75	3317
LG75	4296
# 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 (%)	89.996
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.10
# indels per 100 kbp	0.03
Largest alignment	42930
Total aligned length	22720373
NA50	4302
NGA50	3755
NA75	2033
NGA75	1511
LA50	1381
LGA50	1664
LA75	3317
LGA75	4296

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

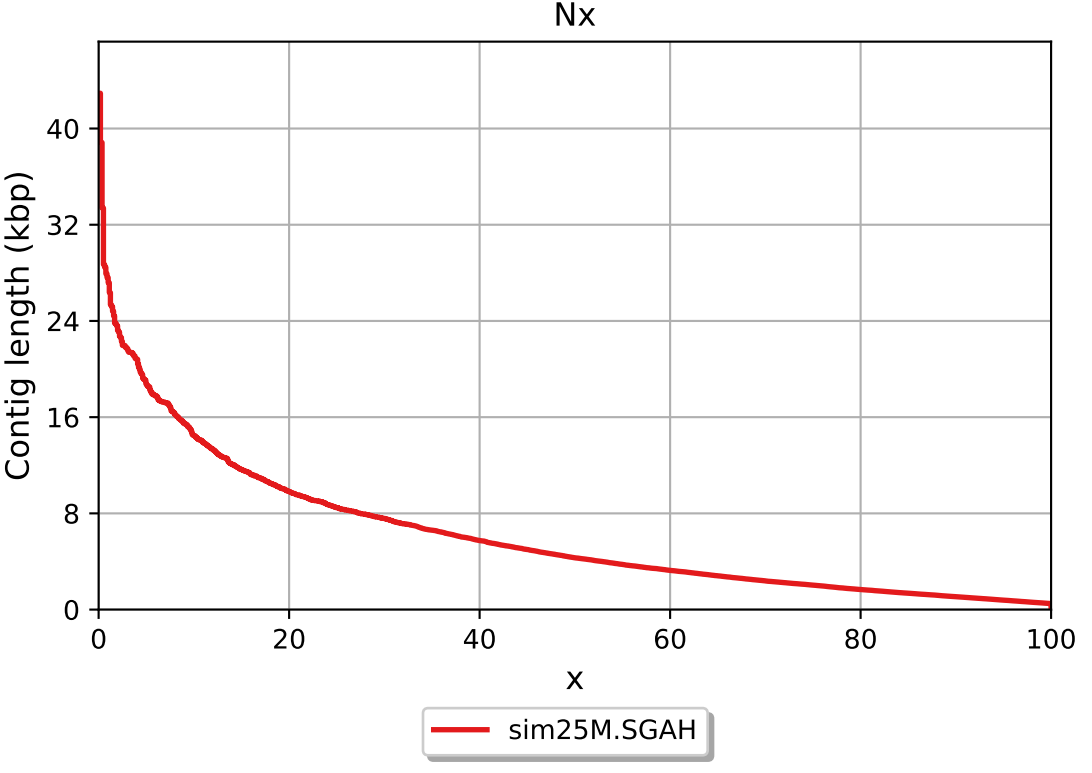
	sim25M.SGAH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	22
# indels	7
# indels (<= 5 bp)	2
# indels (> 5 bp)	5
Indels length	177

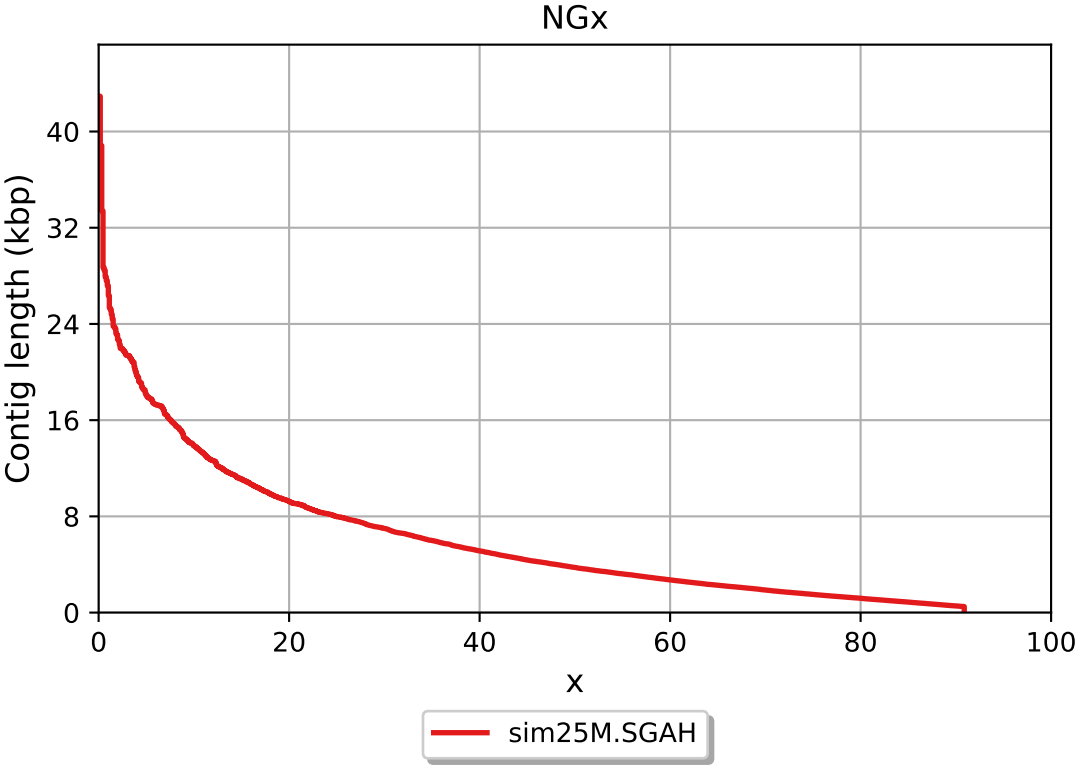
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

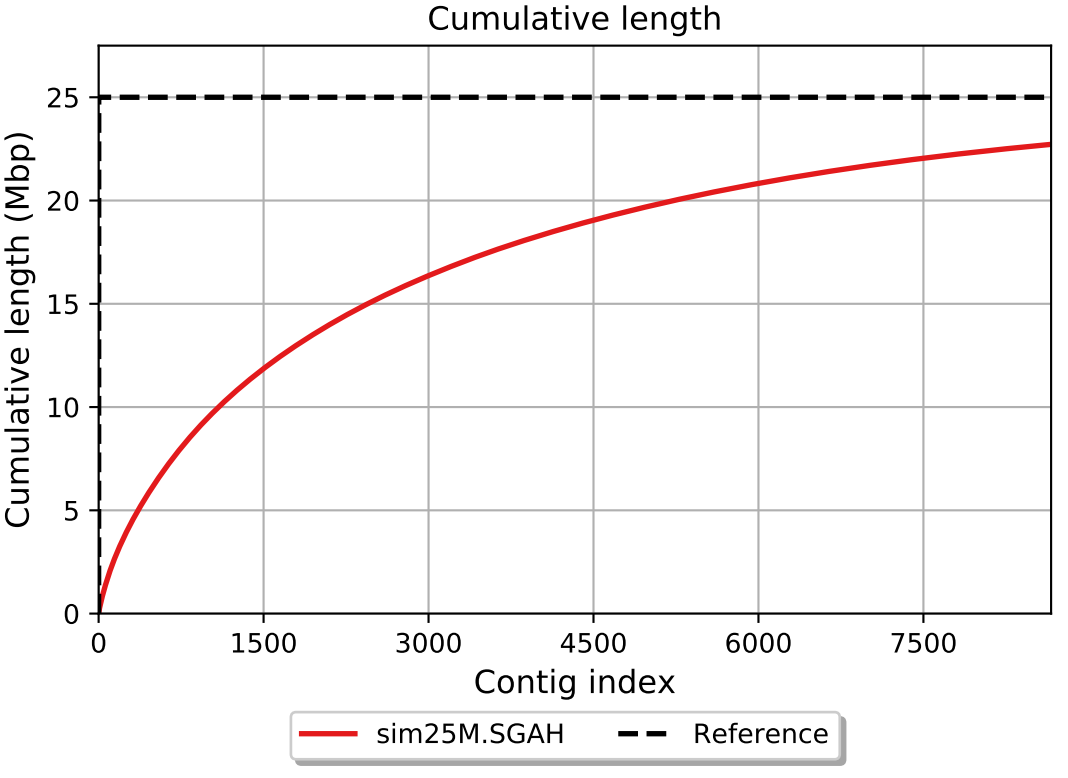
Unaligned report

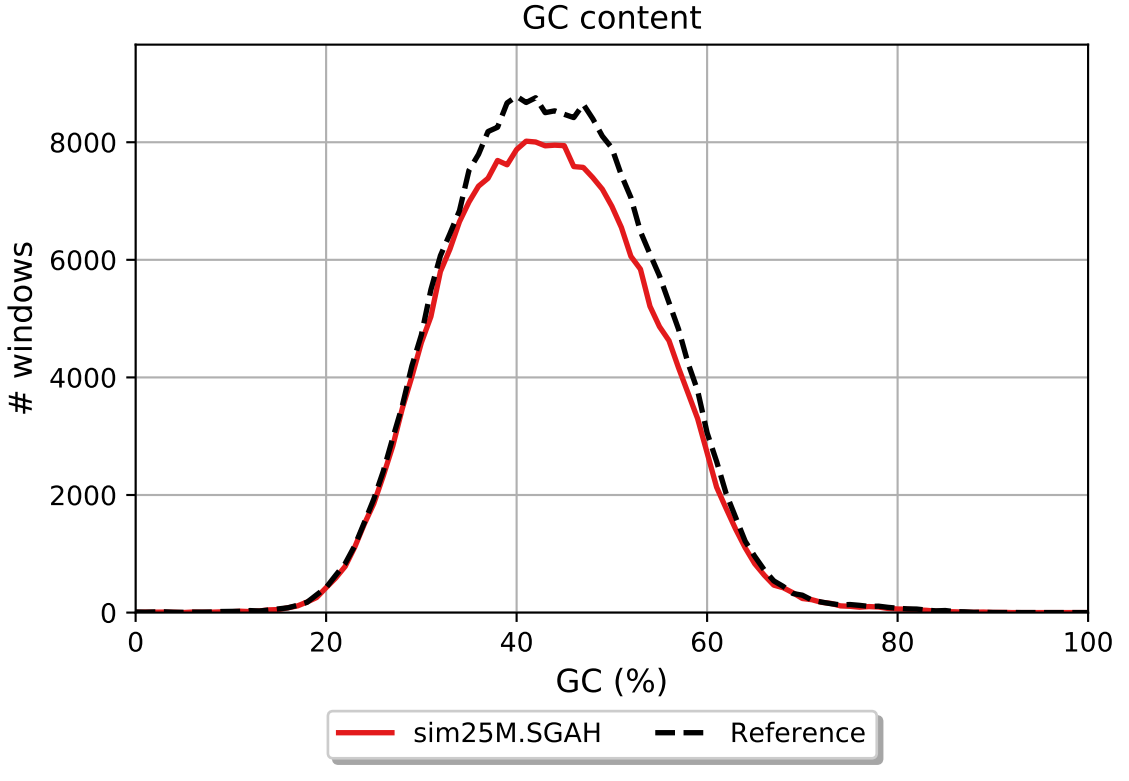
	sim25M.SGAH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

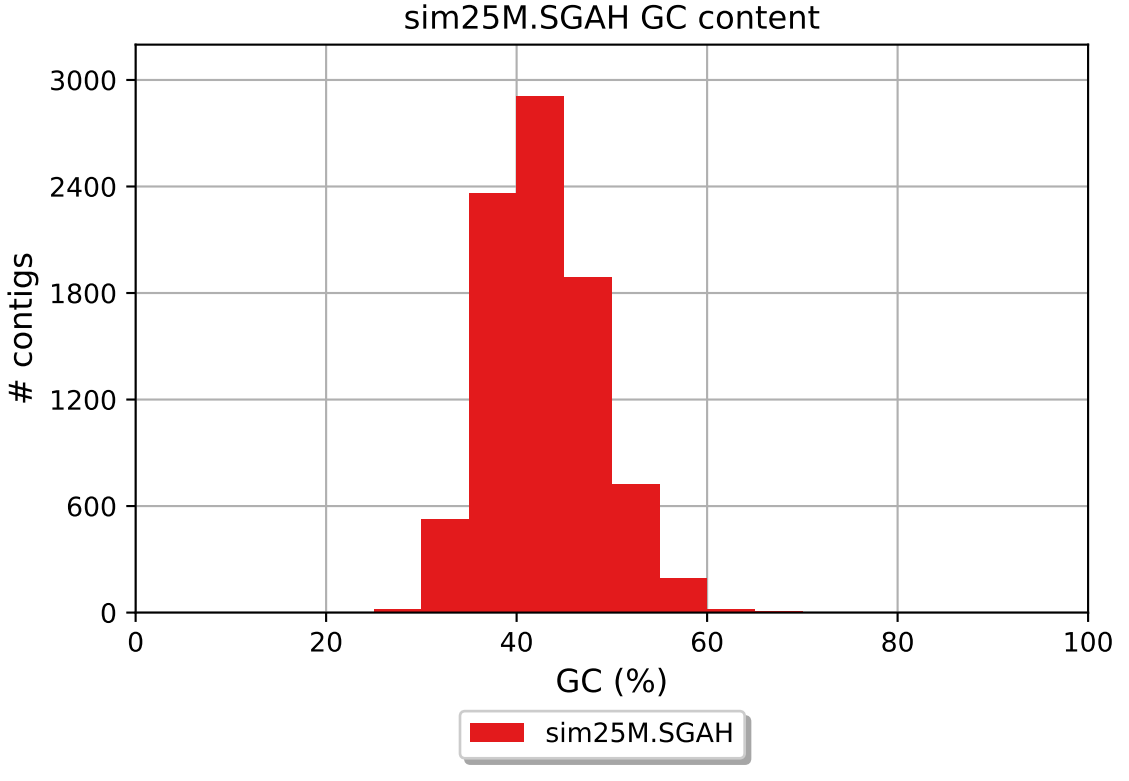
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SGAH

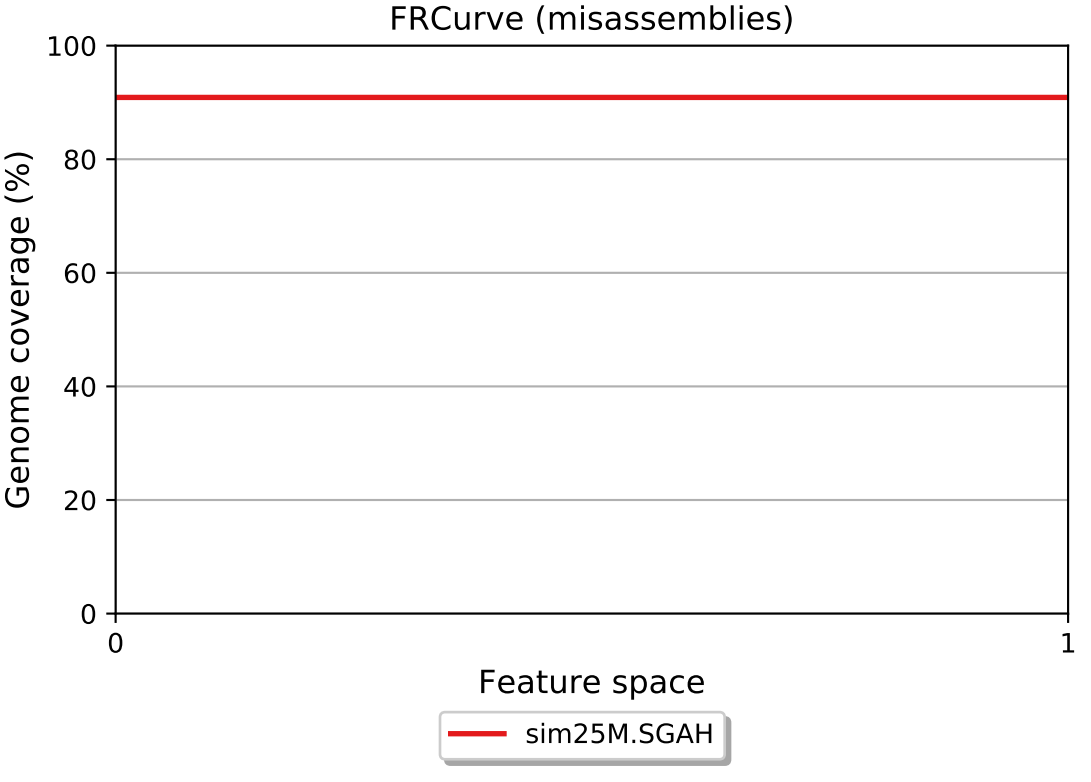

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SGAH

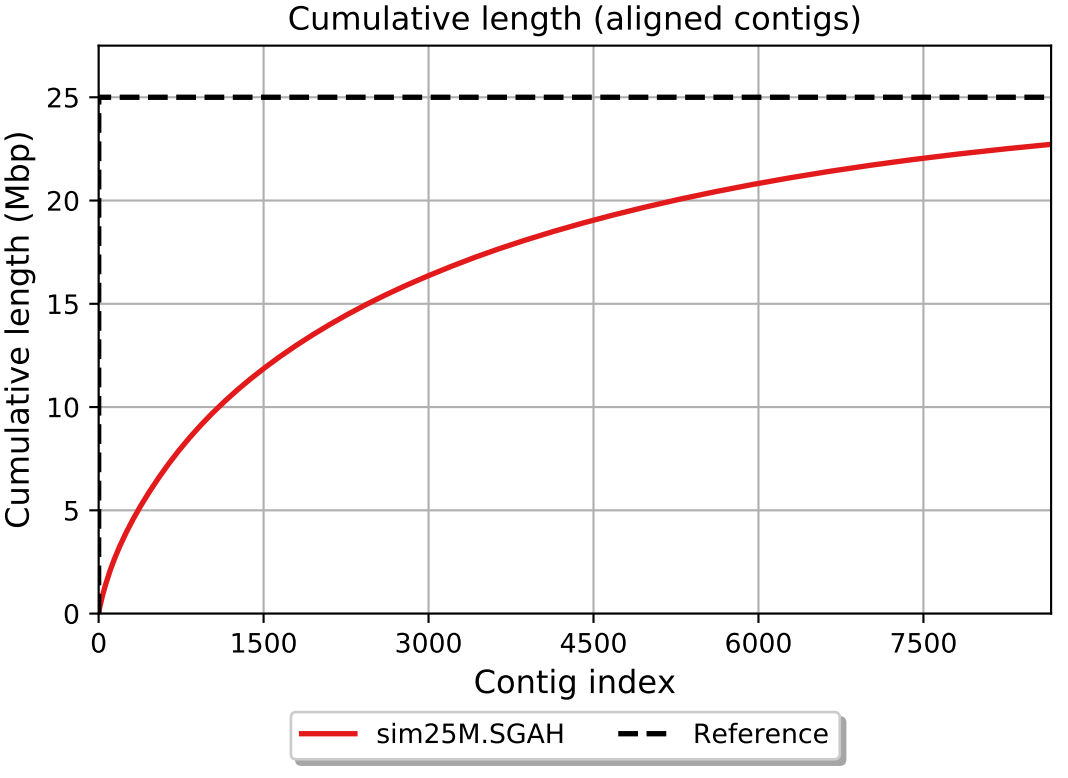

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
1500
3000
4500
6000
7500
Contig index
sim25M.SGAH
Reference

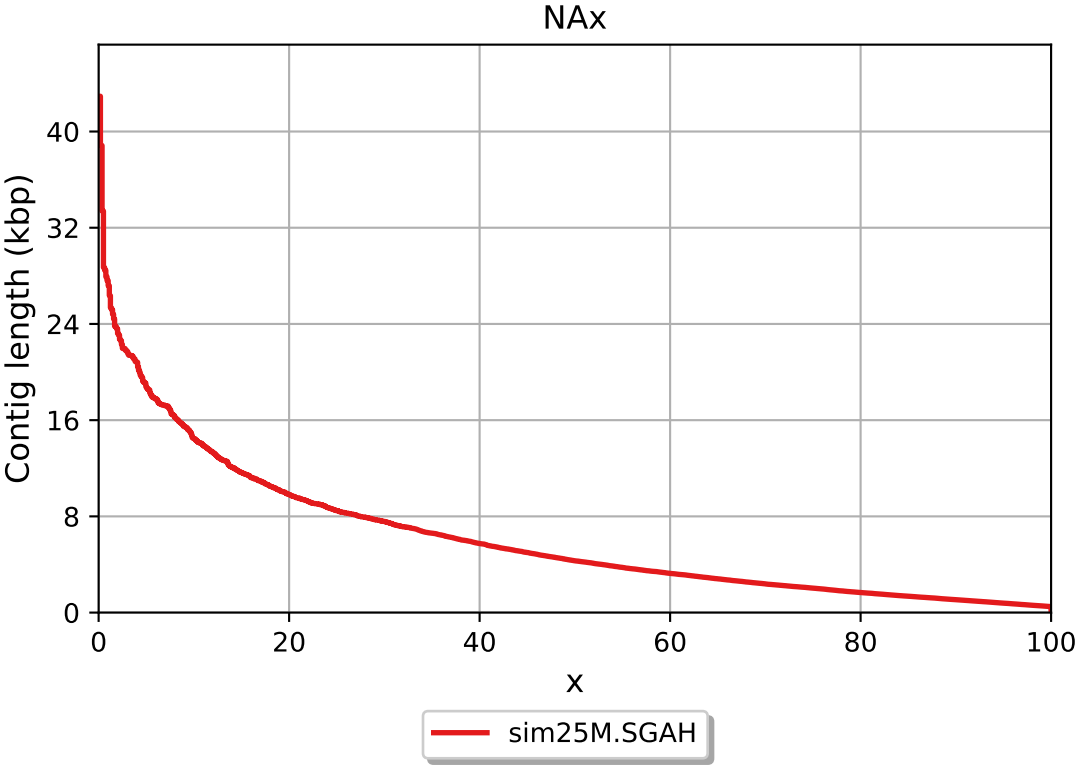

GC content
windows
8000
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
sim25M.SGAH
Reference

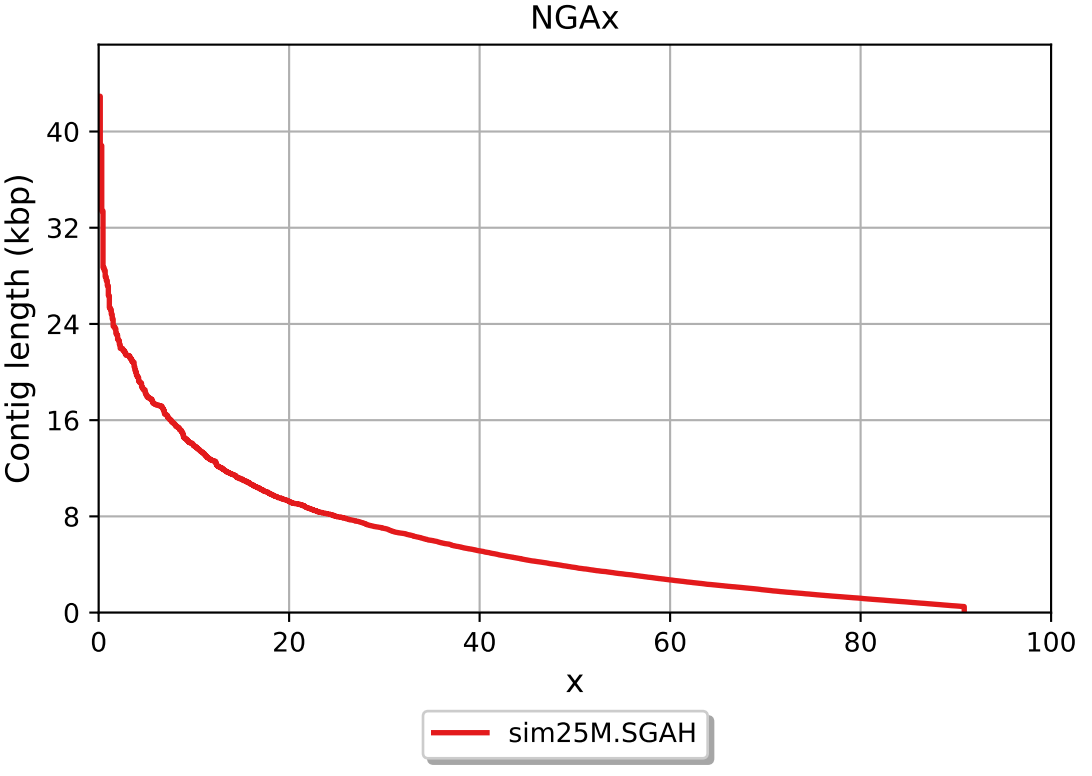

sim25M.SGAH GC content
3000
2400
1800
1200
600
0
contigs
0
20
40
60
80
100
GC (%)
sim25M.SGAH

Misassemblies
5
4
3
2
1
0
sim25M.SGAH


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
5
10
15
20
25
0
1500
3000
4500
6000
7500
Contig index
sim25M.SGAH
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SGAH


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SGAH