Report

	sim25M.SGAL
# contigs (>= 0 bp)	21366
# contigs (>= 1000 bp)	5935
# contigs (>= 5000 bp)	1201
# contigs (>= 10000 bp)	328
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	26598754
Total length (>= 1000 bp)	21480767
Total length (>= 5000 bp)	10834917
Total length (>= 10000 bp)	4790298
Total length (>= 25000 bp)	504137
Total length (>= 50000 bp)	0
# contigs	8469
Largest contig	38190
Total length	23298318
Reference length	25000020
GC (%)	43.52
Reference GC (%)	43.69
N50	4598
NG50	4134
N75	2163
NG75	1755
L50	1372
LG50	1567
L75	3239
LG75	3893
# 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 (%)	92.125
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.18
# indels per 100 kbp	0.05
Largest alignment	38190
Total aligned length	23298298
NA50	4598
NGA50	4134
NA75	2163
NGA75	1755
LA50	1372
LGA50	1567
LA75	3239
LGA75	3893

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

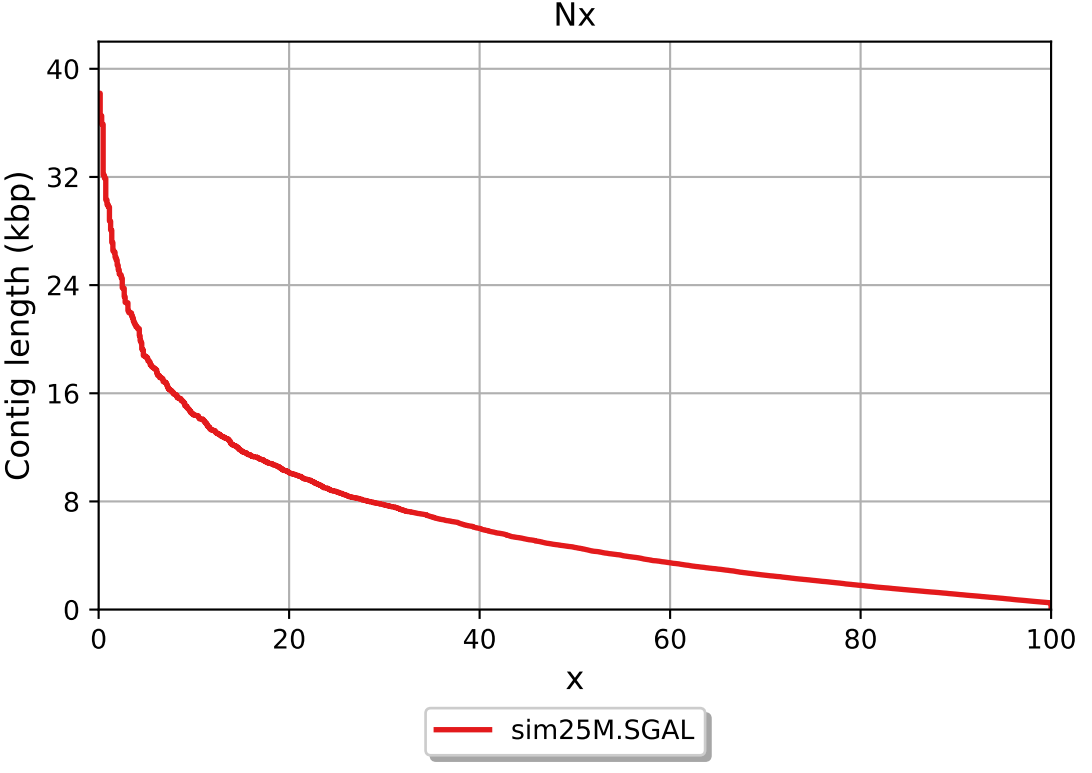
	sim25M.SGAL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	41
# indels	11
# indels (<= 5 bp)	4
# indels (> 5 bp)	7
Indels length	300

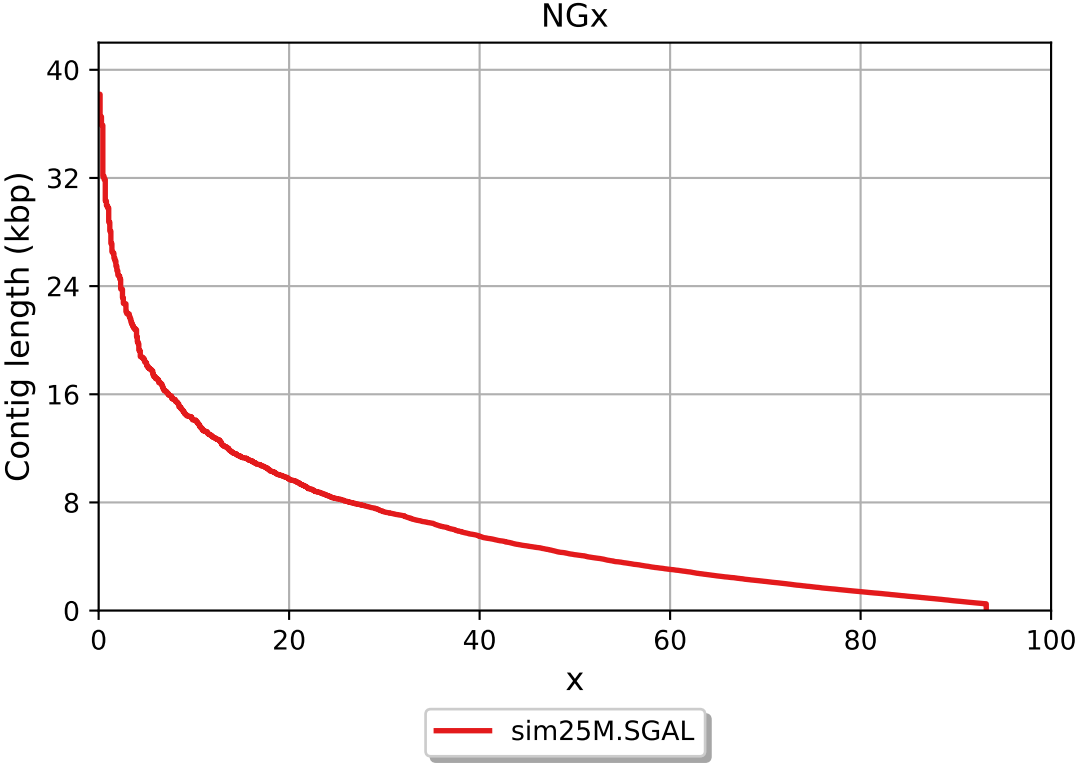
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

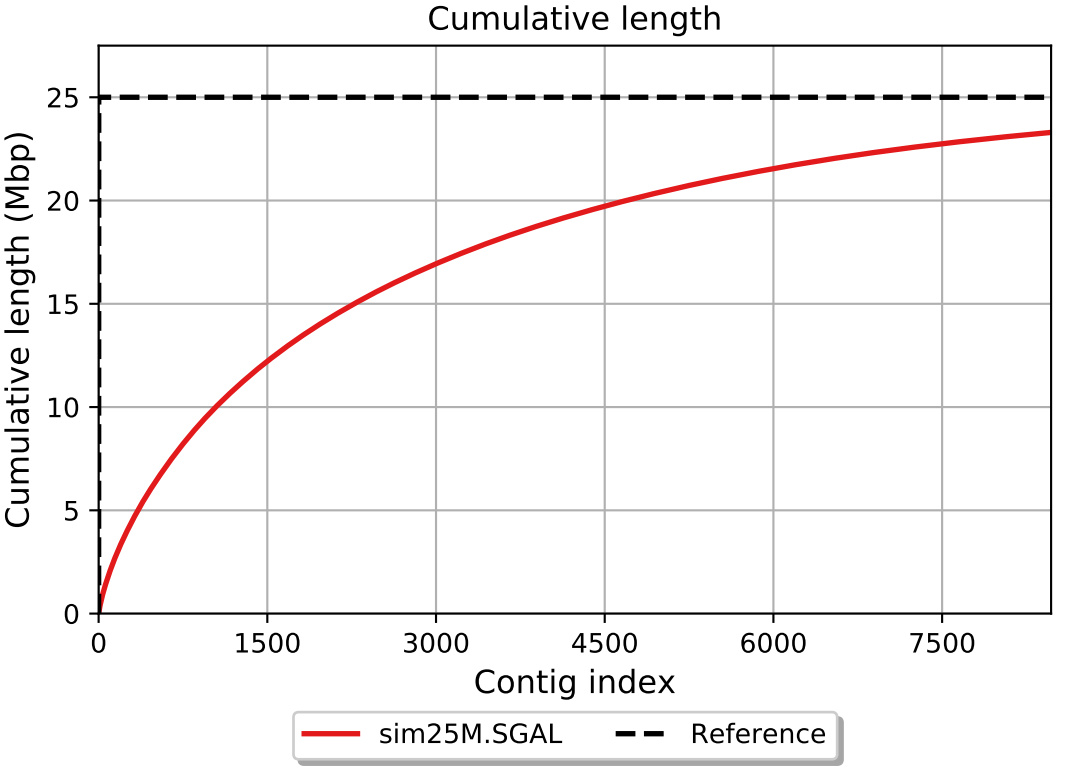
Unaligned report

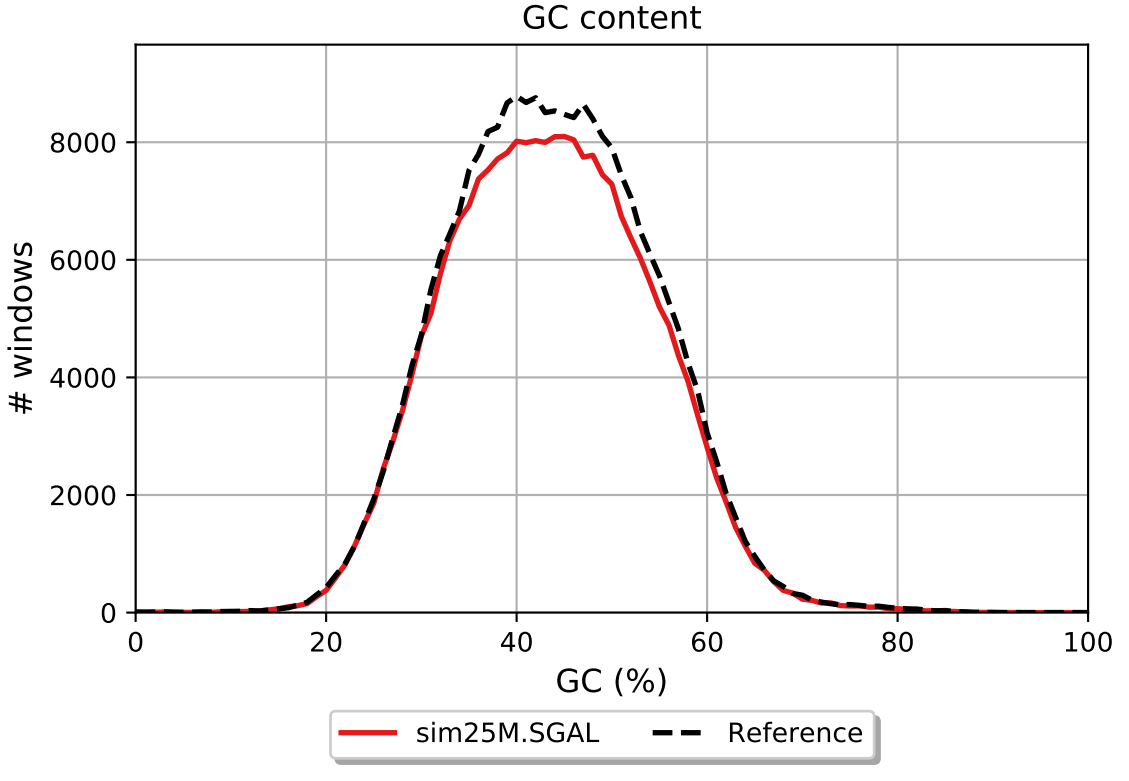
	sim25M.SGAL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

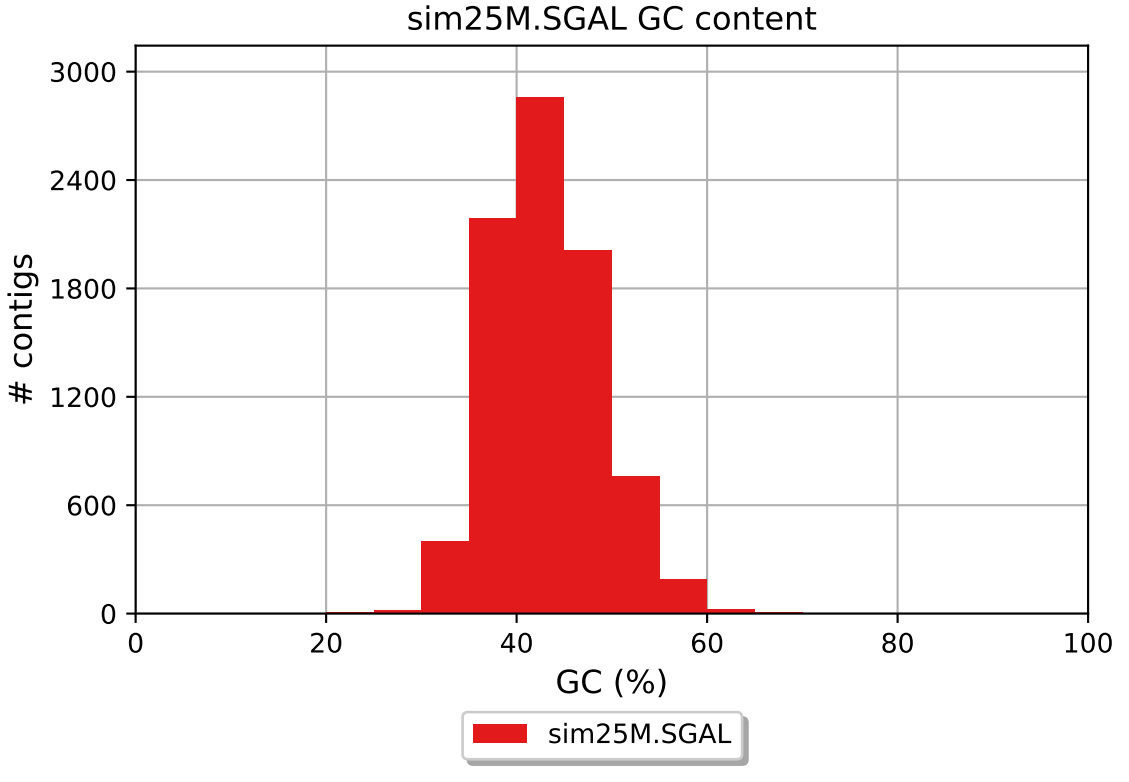
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

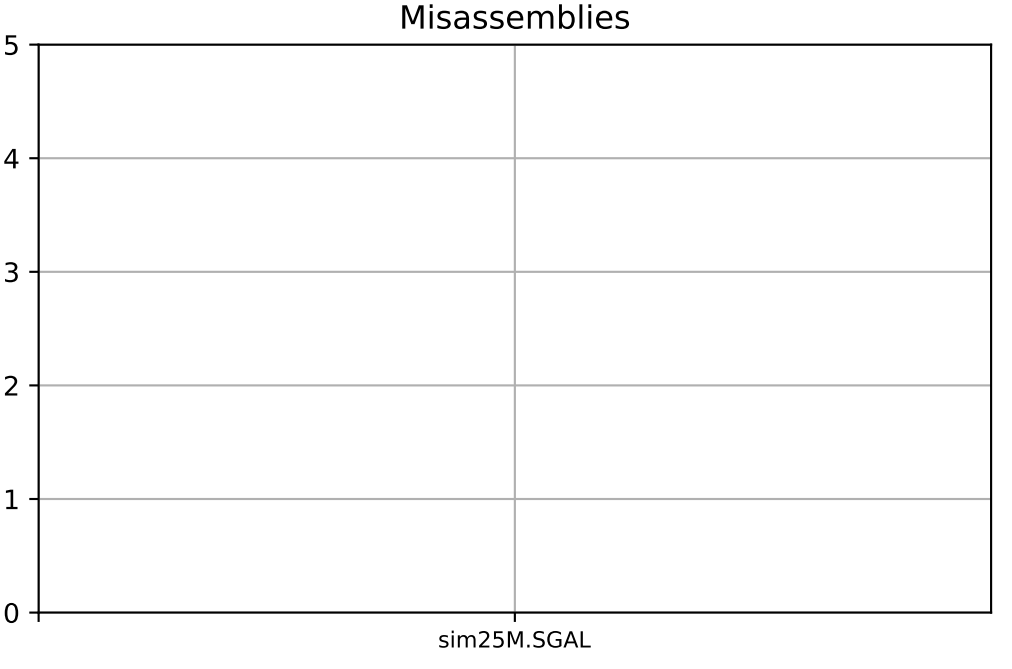

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SGAL

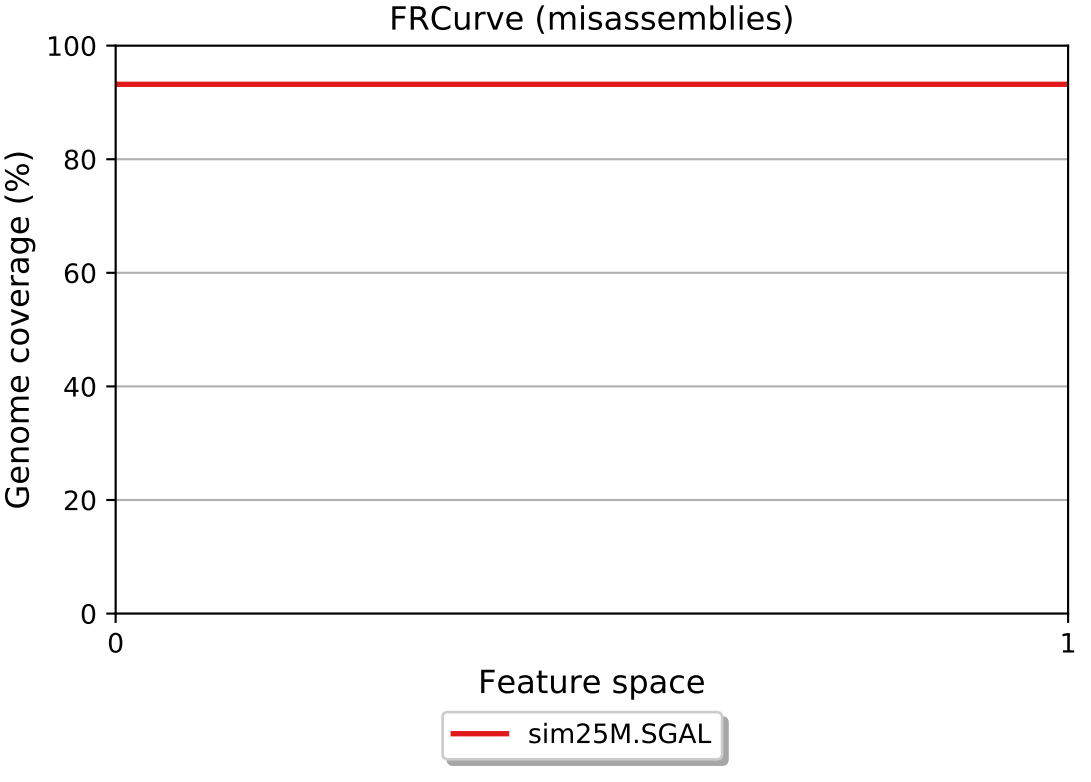

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SGAL

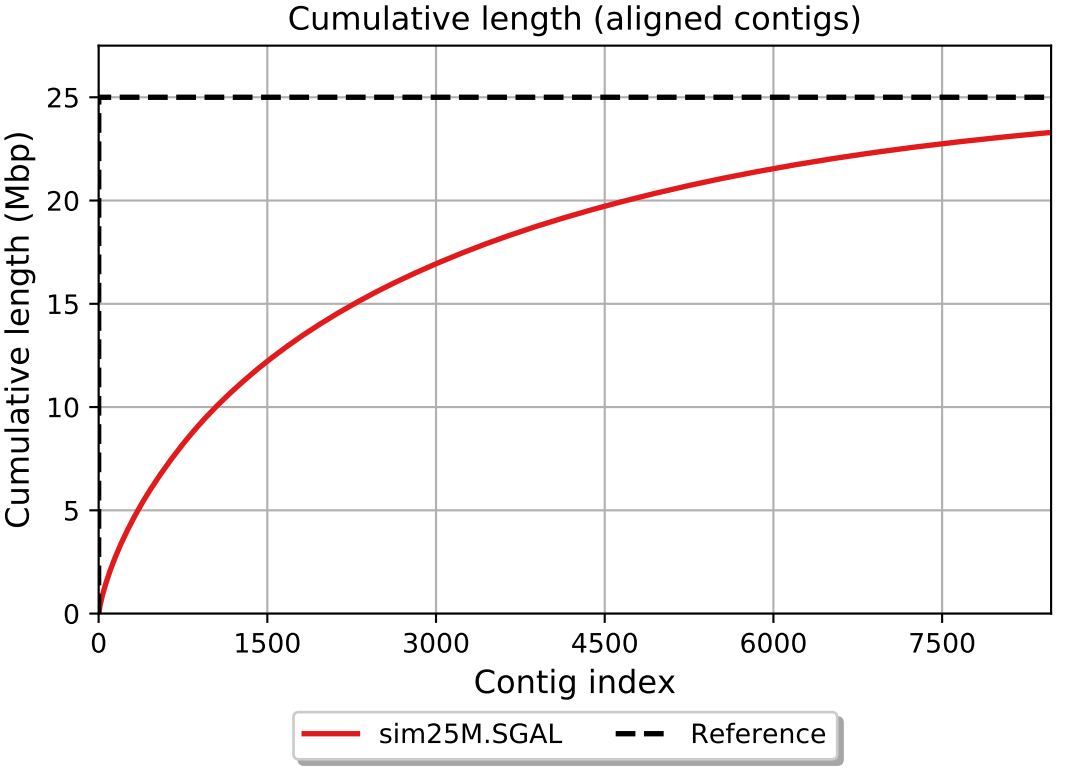

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
1500
3000
4500
6000
7500
Contig index
sim25M.SGAL
Reference

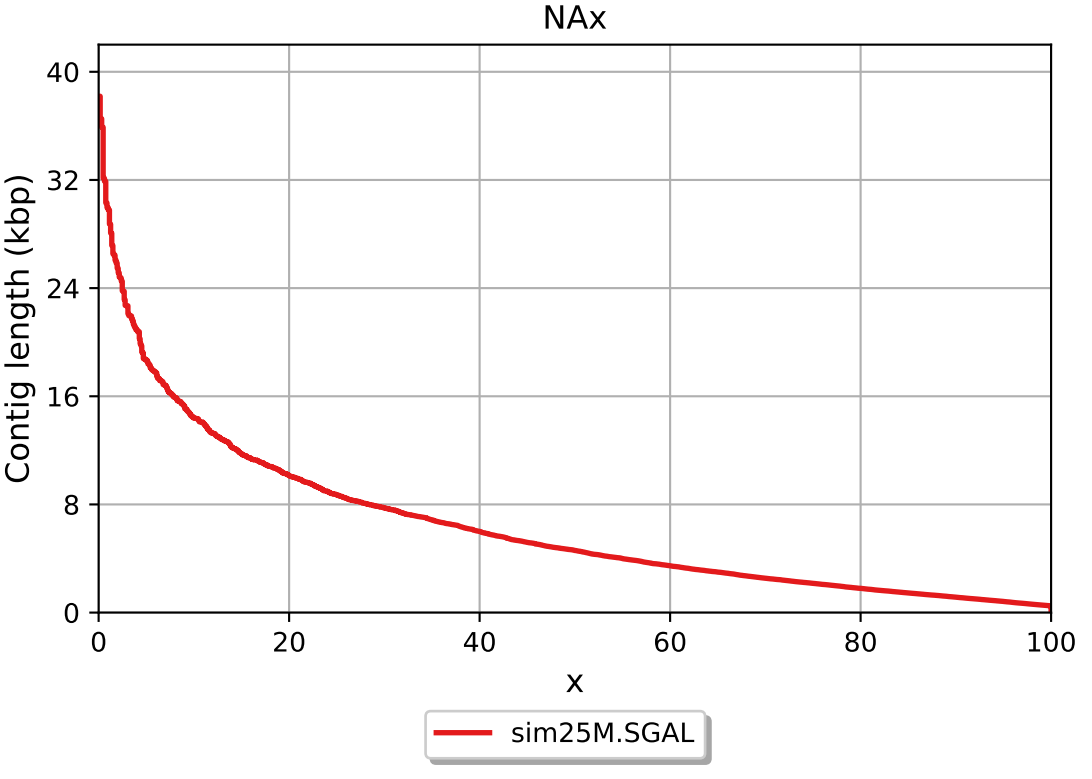

GC content
8000
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
sim25M.SGAL
Reference

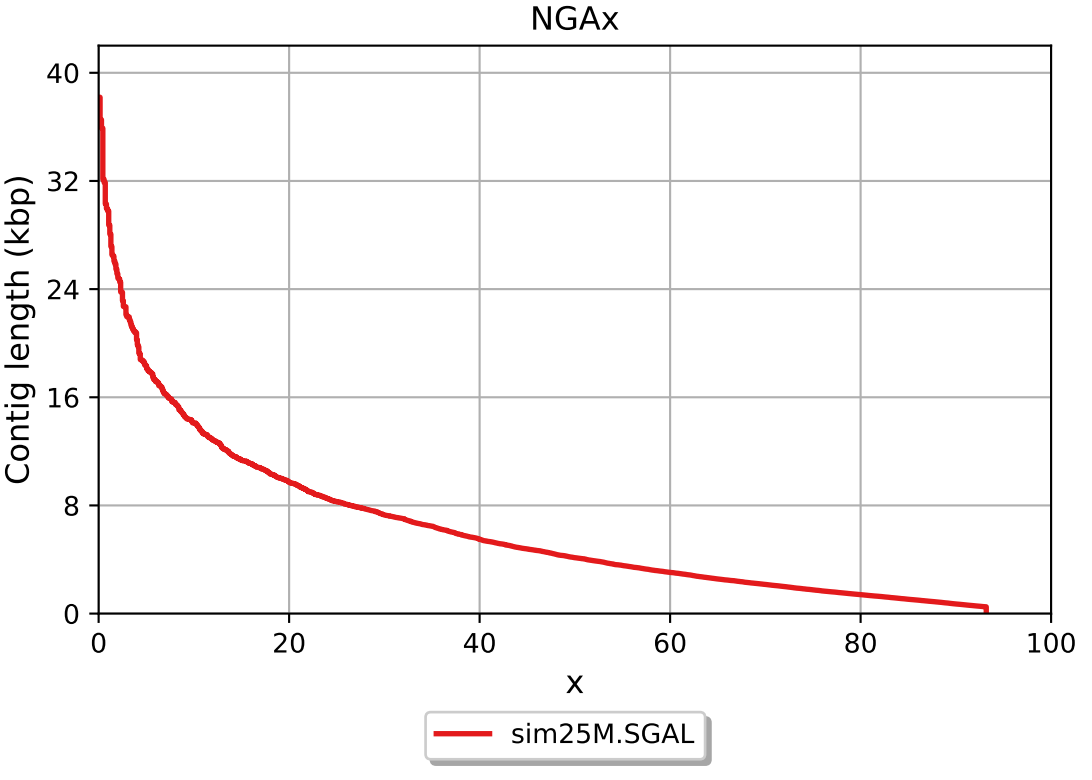

sim25M.SGAL GC content
3000
2400
1800
1200
600
0
contigs
0
20
40
60
80
100
GC (%)
sim25M.SGAL


Misassemblies
5
4
3
2
1
0
sim25M.SGAL


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


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


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


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