Report

	sim5M.Colormap
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	9
Total length (>= 0 bp)	5025782
Total length (>= 1000 bp)	5025782
Total length (>= 5000 bp)	5025782
Total length (>= 10000 bp)	5018224
Total length (>= 25000 bp)	4977711
Total length (>= 50000 bp)	4977711
# contigs	13
Largest contig	1779657
Total length	5025782
Reference length	5000040
GC (%)	35.84
Reference GC (%)	35.84
N50	1259797
NG50	1259797
N75	368449
NG75	368449
L50	2
LG50	2
L75	4
LG75	4
# 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 (%)	99.453
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	30.06
# indels per 100 kbp	1.31
Largest alignment	1779657
Total aligned length	5025780
NA50	1259795
NGA50	1259795
NA75	368449
NGA75	368449
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

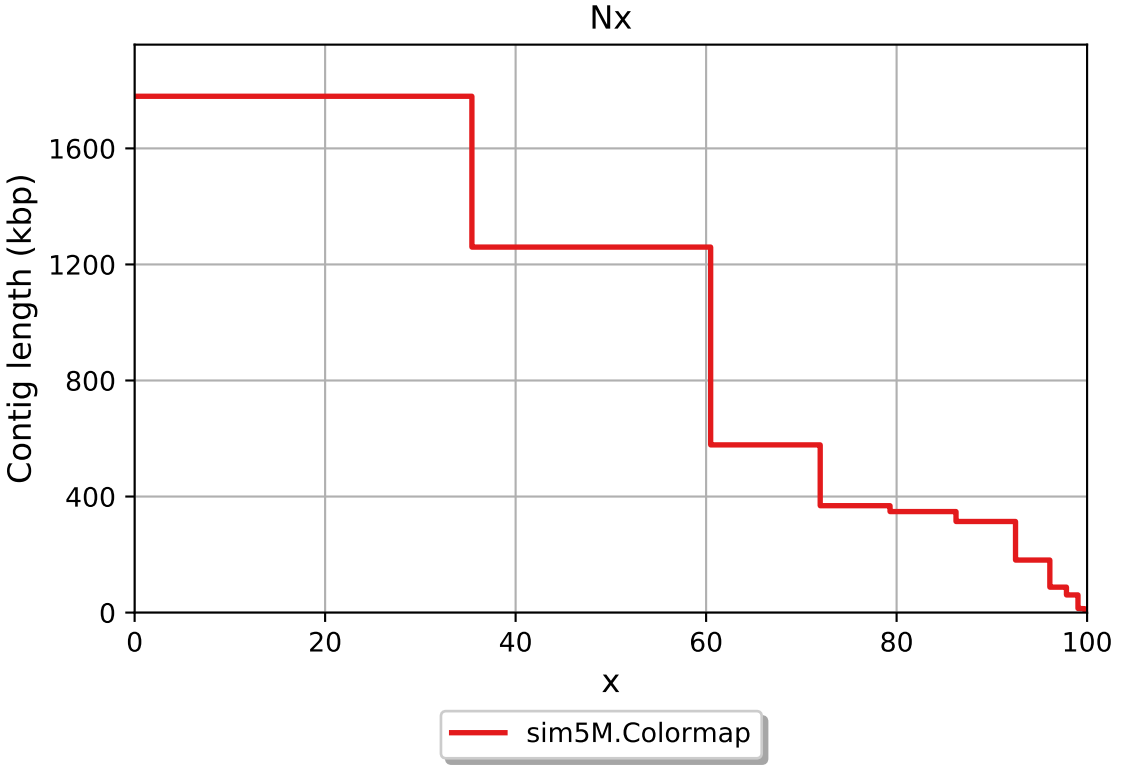
	sim5M.Colormap
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	1495
# indels	65
# indels (<= 5 bp)	64
# indels (> 5 bp)	1
Indels length	77

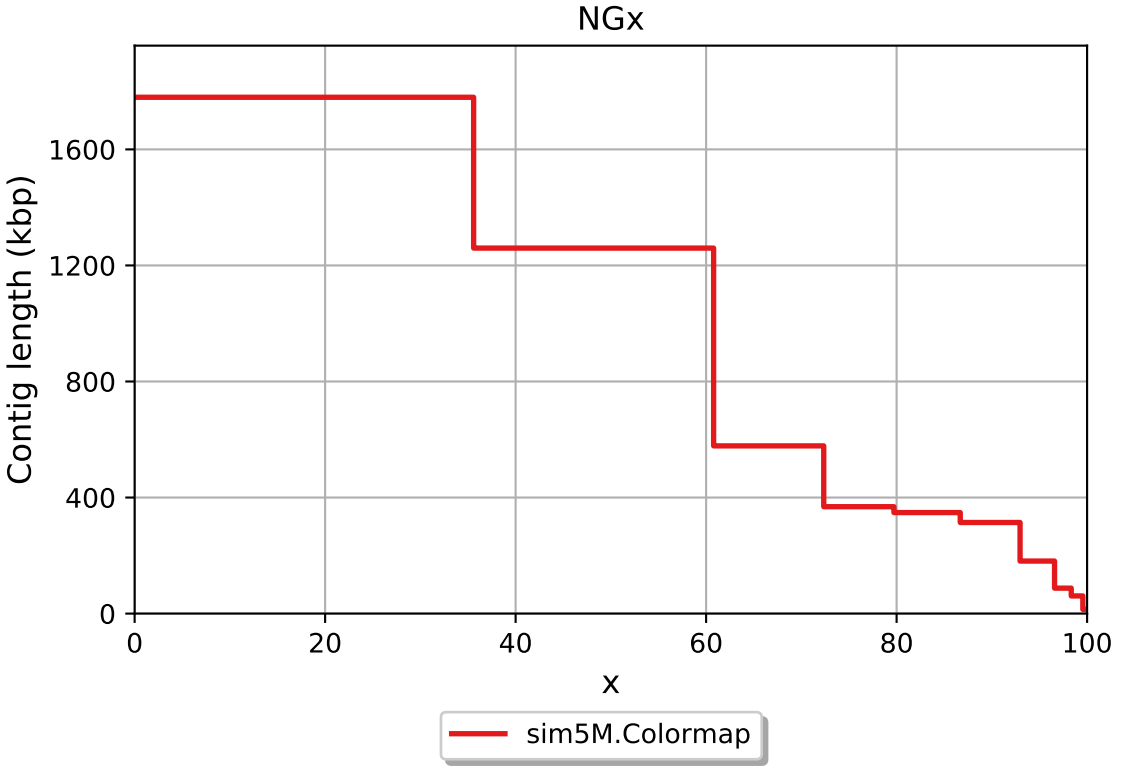
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

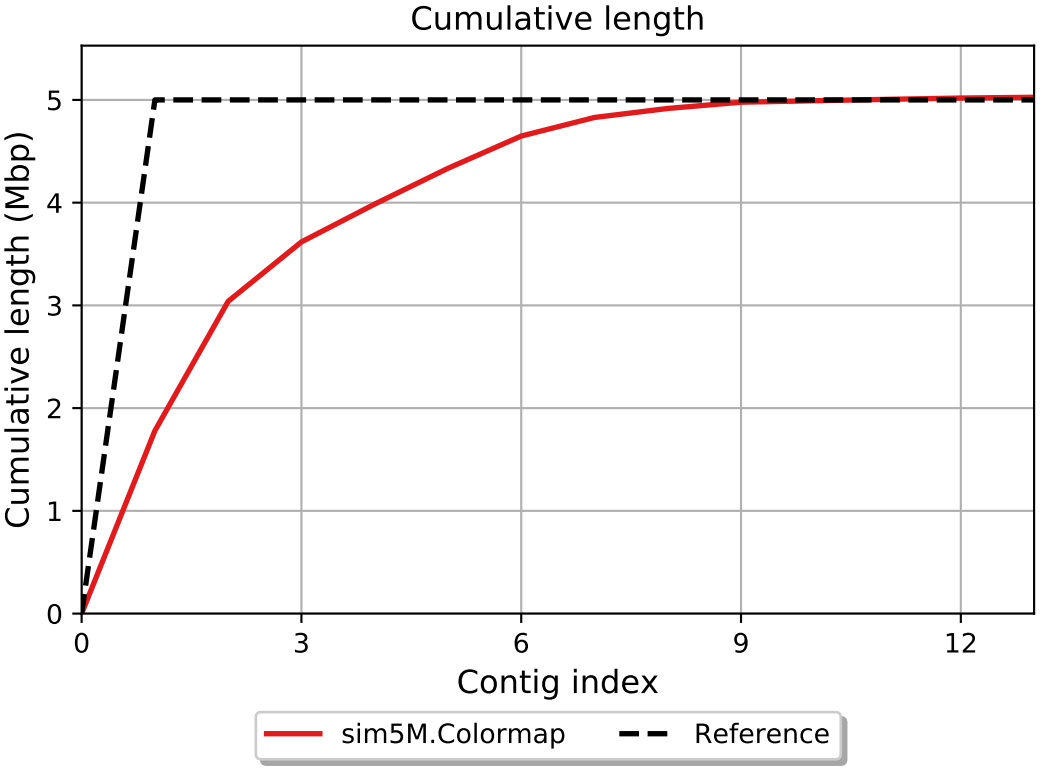
Unaligned report

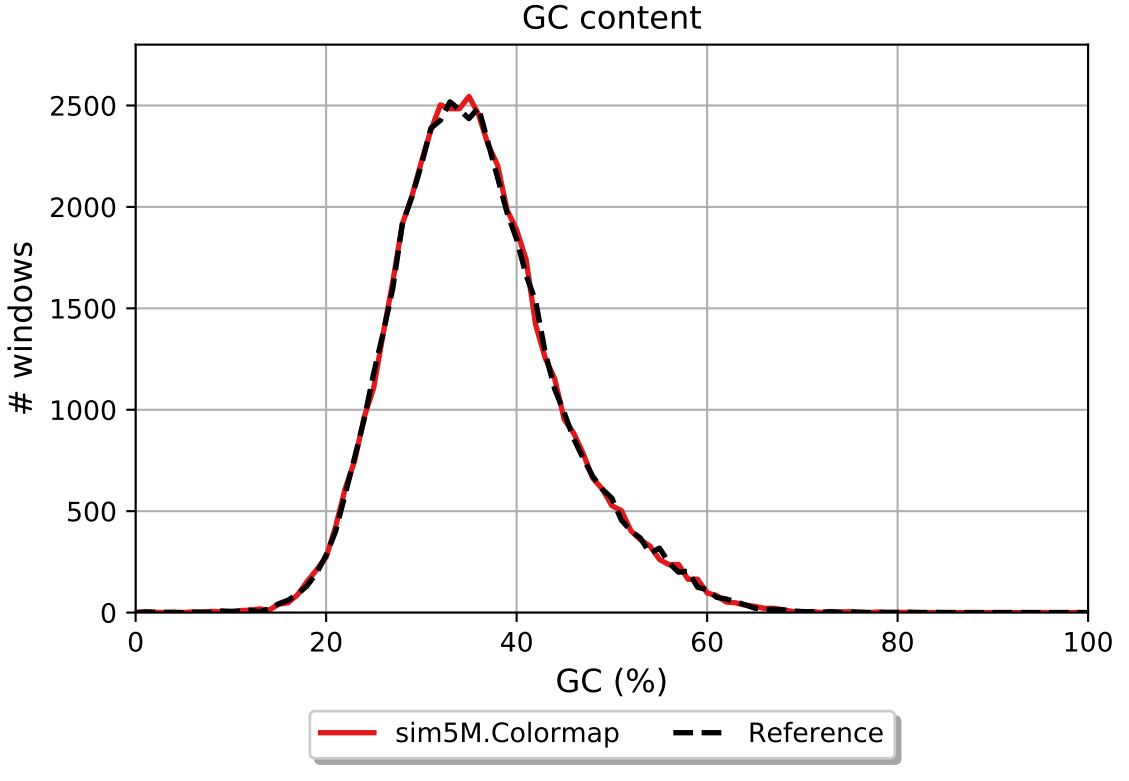
	sim5M.Colormap
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

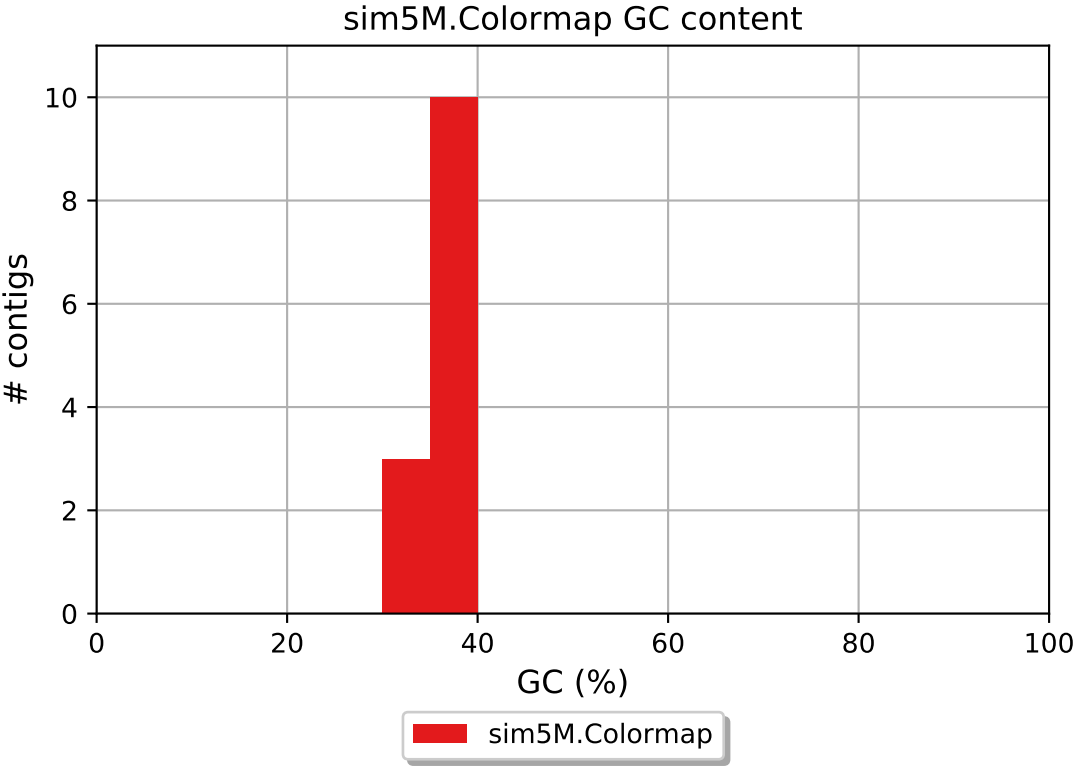
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

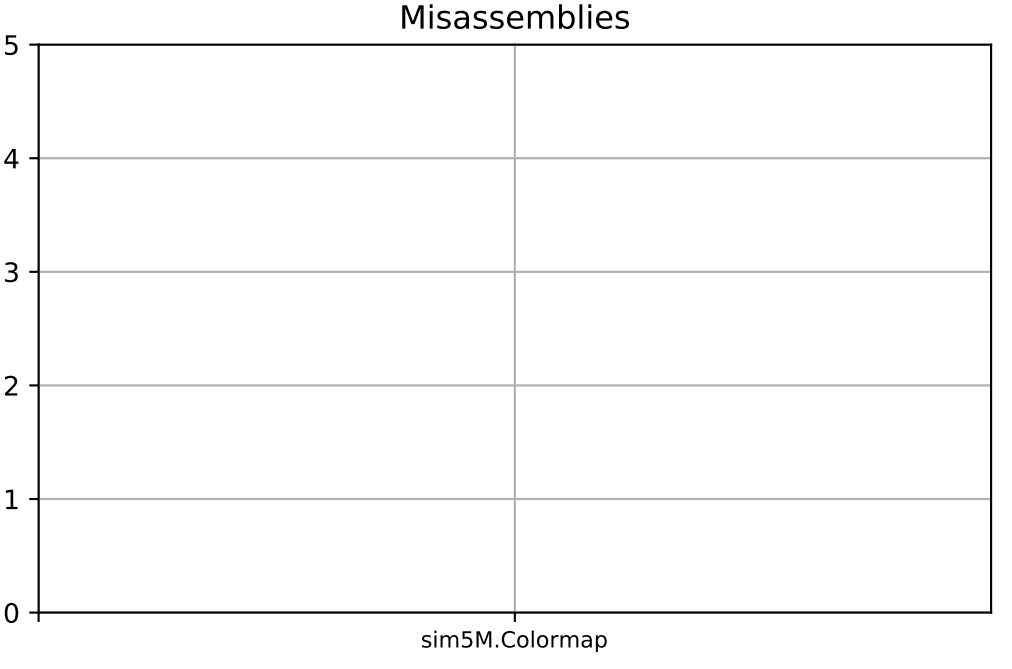

Nx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
sim5M.Colormap

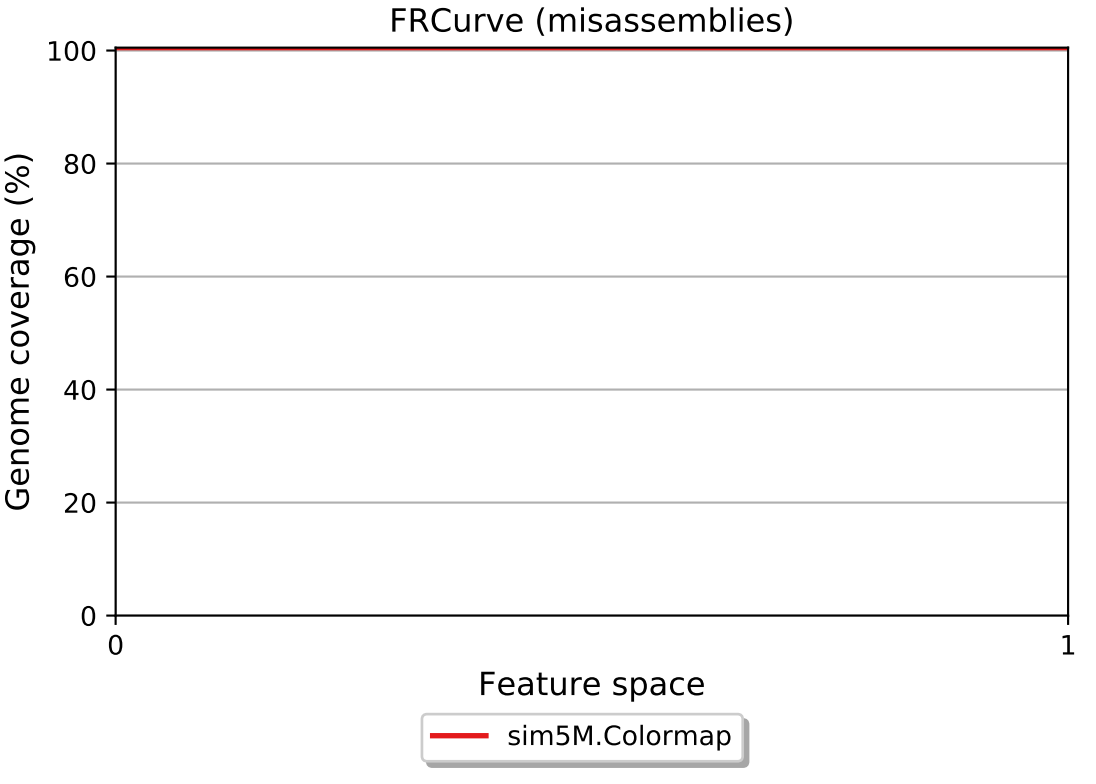

NGx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
sim5M.Colormap

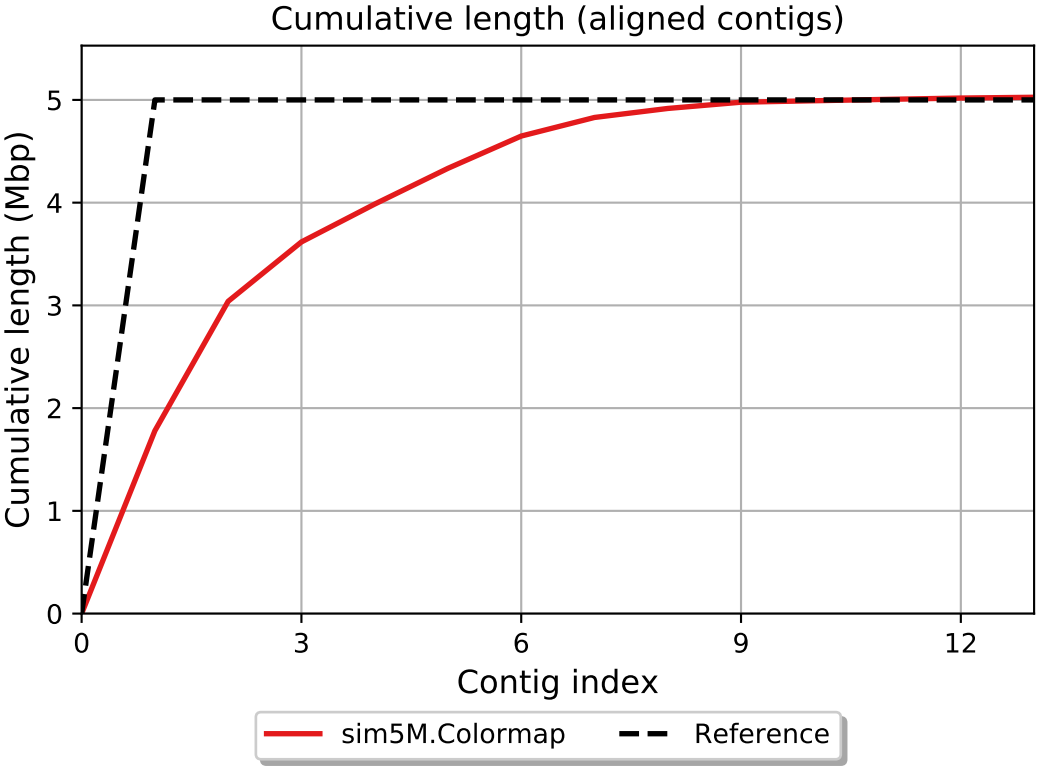

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
3
6
9
12
Contig index
sim5M.Colormap
Reference

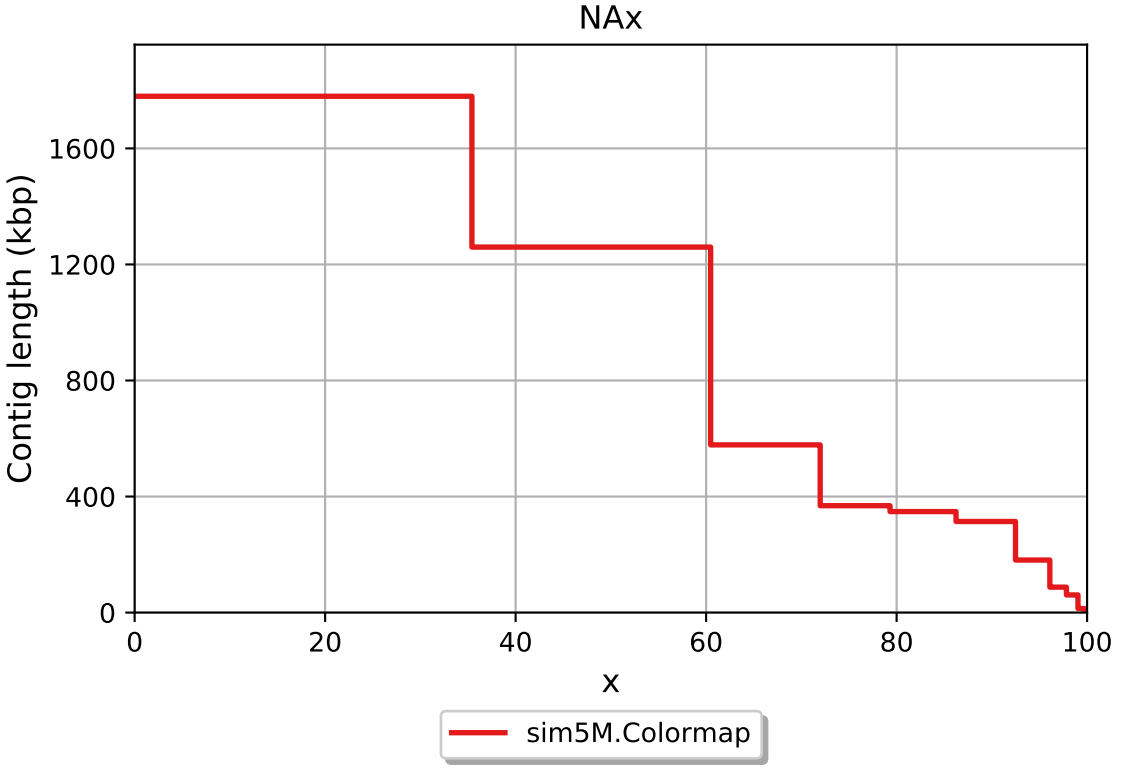

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
sim5M.Colormap
Reference

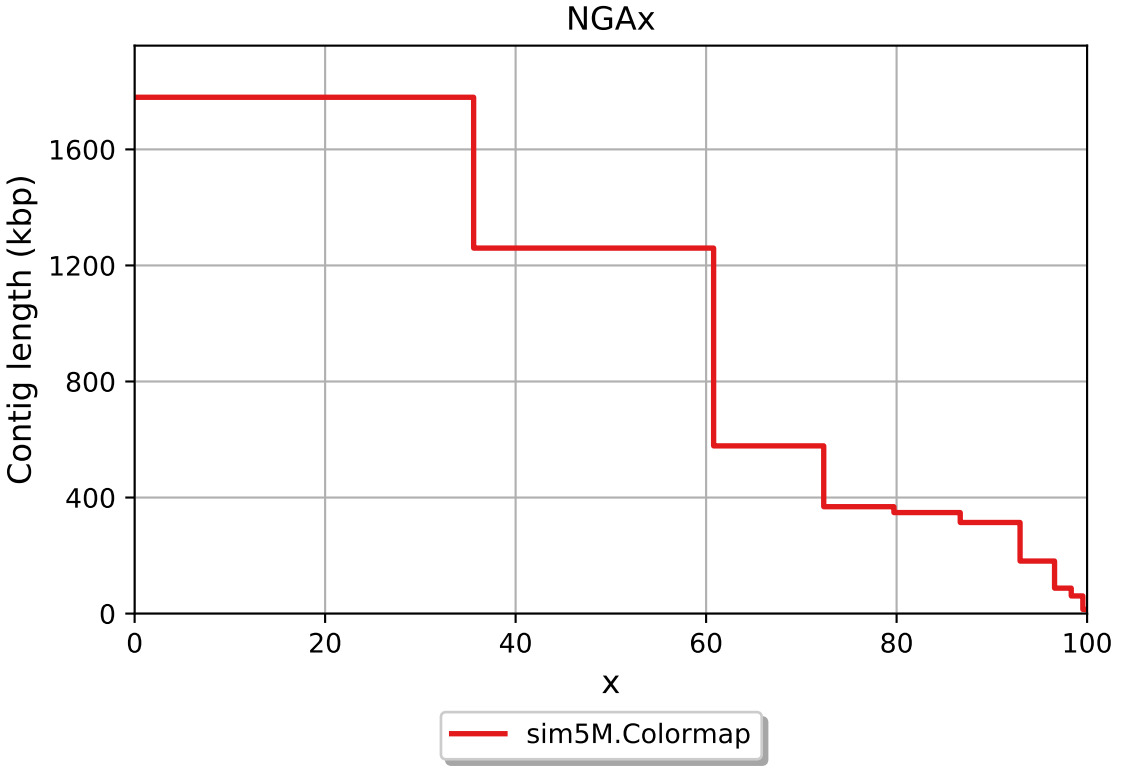

sim5M.Colormap GC content
contigs
0
2
4
6
8
10
0
20
40
60
80
100
GC (%)
sim5M.Colormap


Misassemblies
5
4
3
2
1
0
sim5M.Colormap


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
3
6
9
12
Contig index
sim5M.Colormap
Reference


NAx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
sim5M.Colormap


NGAx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
sim5M.Colormap