# Report

| | sim5M.Colormap.cr |
|---|---|
| # contigs (>= 0 bp) | 2000 |
| # contigs (>= 1000 bp) | 1994 |
| # contigs (>= 5000 bp) | 1643 |
| # contigs (>= 10000 bp) | 514 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 16218163 |
| Total length (>= 1000 bp) | 16215442 |
| Total length (>= 5000 bp) | 14933469 |
| Total length (>= 10000 bp) | 6430571 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1997 |
| Largest contig | 23973 |
| Total length | 16217989 |
| Reference length | 5000040 |
| GC (%) | 35.94 |
| Reference GC (%) | 35.84 |
| N50 | 9158 |
| NG50 | 12883 |
| N75 | 7063 |
| NG75 | 11759 |
| L50 | 690 |
| LG50 | 166 |
| L75 | 1190 |
| LG75 | 268 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned mis. contigs | 1 |
| # unaligned contigs | 28 + 4 part |
| Unaligned length | 357699 |
| Genome fraction (%) | 95.975 |
| Duplication ratio | 3.305 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 234.14 |
| # indels per 100 kbp | 146.06 |
| Largest alignment | 23973 |
| Total aligned length | 15858437 |
| NA50 | 9015 |
| NGA50 | 12774 |
| NA75 | 6863 |
| NGA75 | 11589 |
| LA50 | 700 |
| LGA50 | 168 |
| LA75 | 1210 |
| LGA75 | 271 |

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

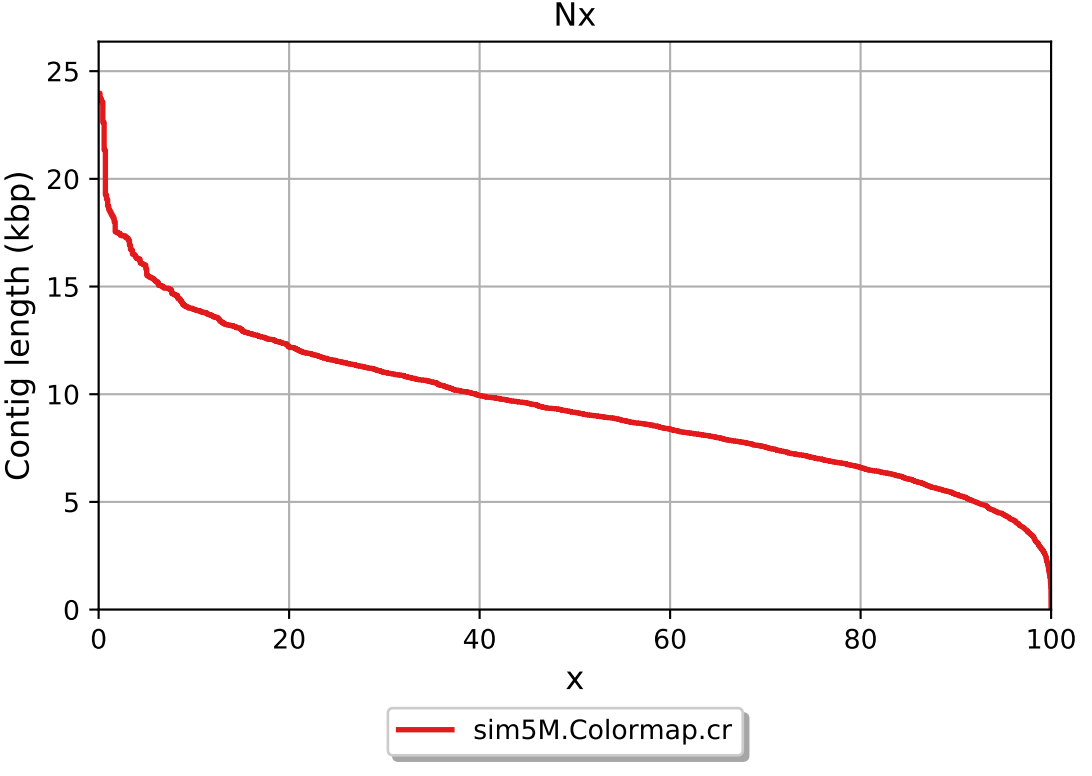
| | sim5M.Colormap.cr |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned mis. contigs | 1 |
| # mismatches | 11236 |
| # indels | 7009 |
| # indels (<= 5 bp) | 6997 |
| # indels (> 5 bp) | 12 |
| Indels length | 8134 |

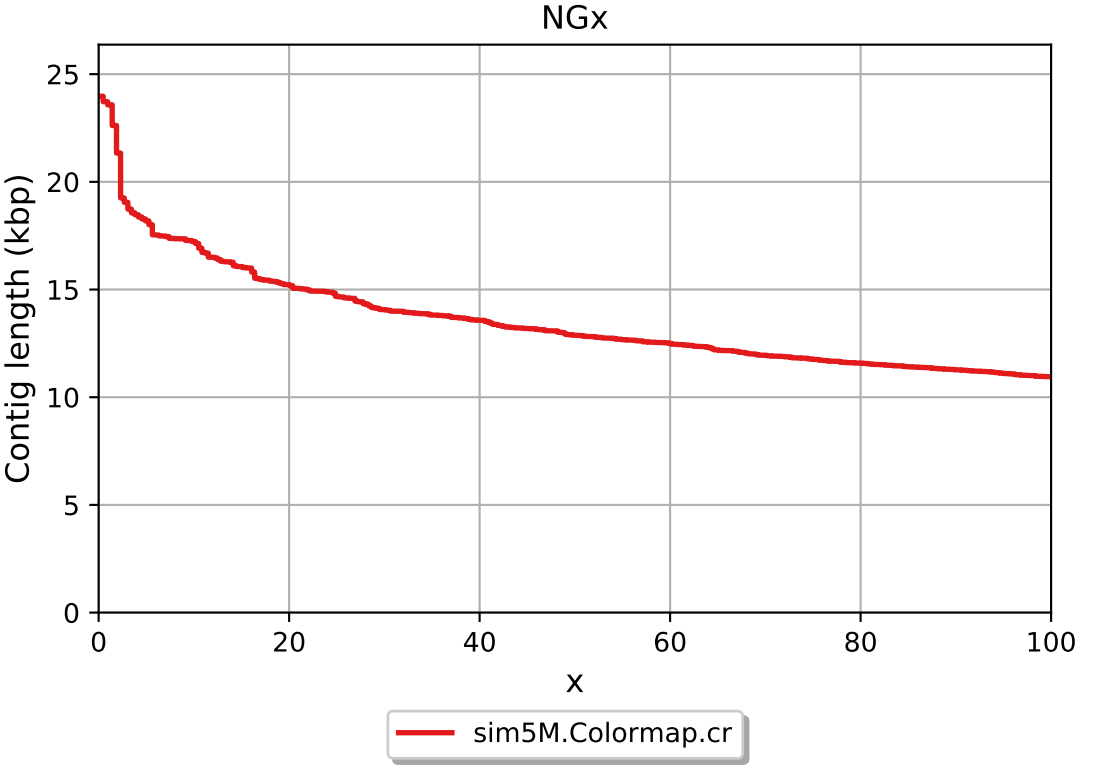
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

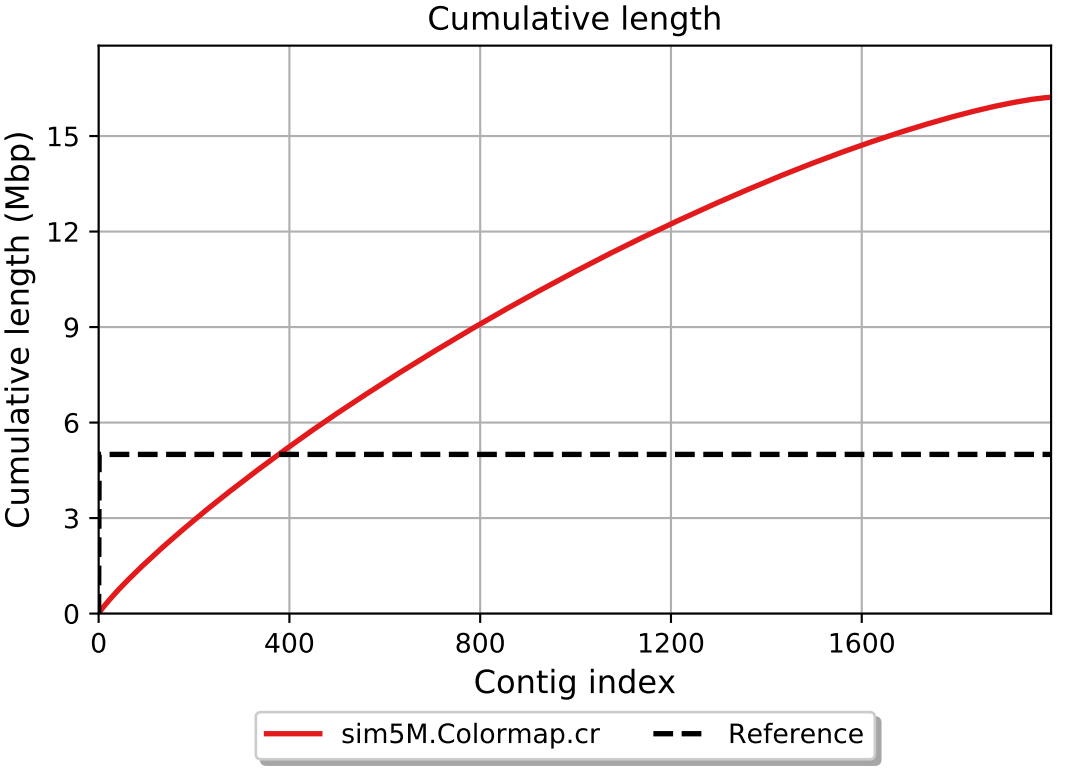
# Unaligned report

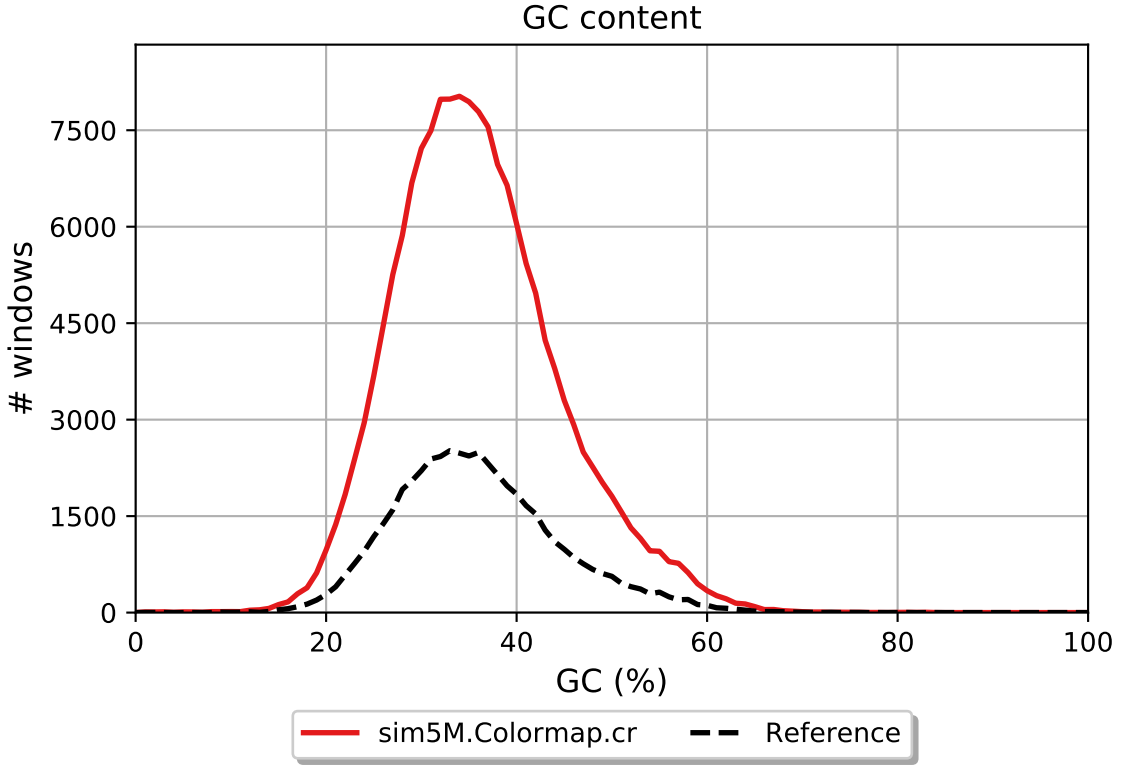
| | sim5M.Colormap.cr |
|---|---|
| # fully unaligned contigs | 28 |
| Fully unaligned length | 297925 |
| # partially unaligned contigs | 4 |
| Partially unaligned length | 59774 |
| # N's | 0 |

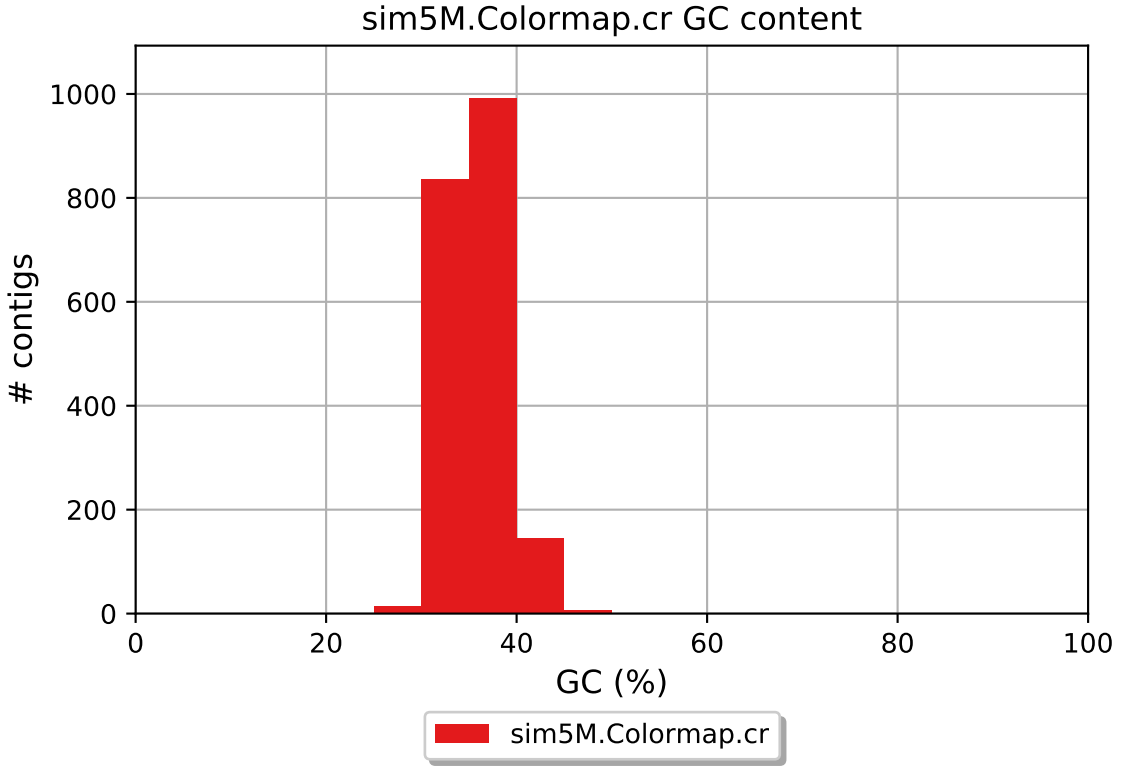
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.Colormap.cr

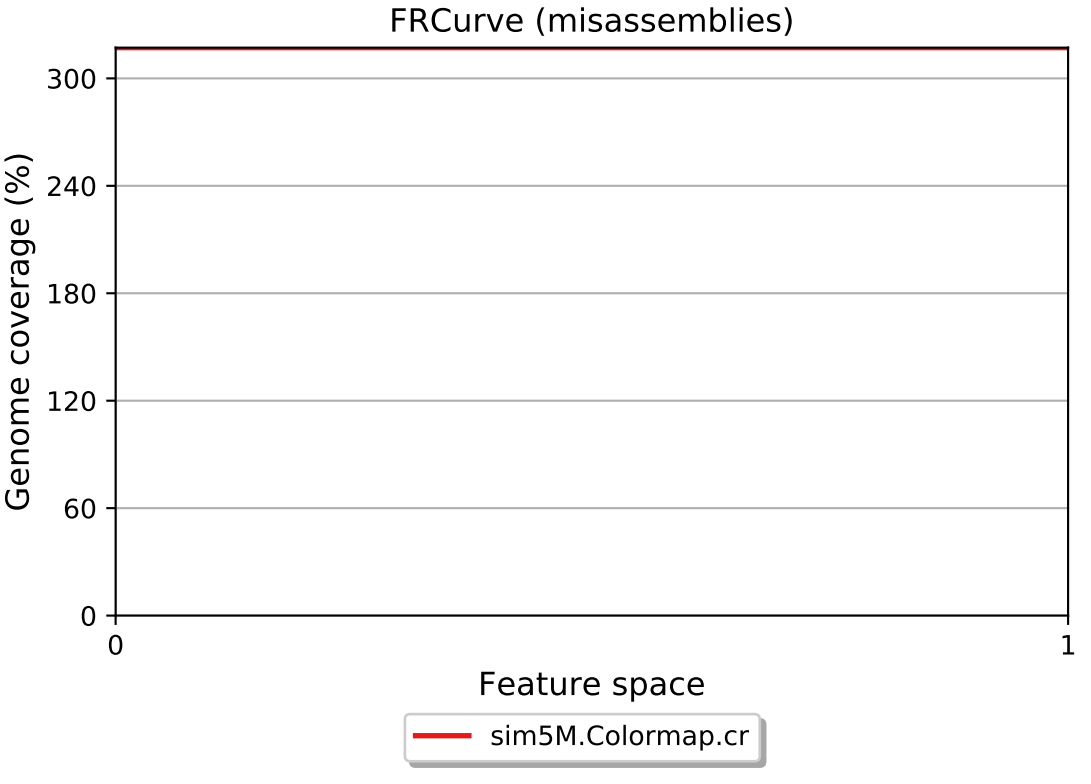

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.Colormap.cr

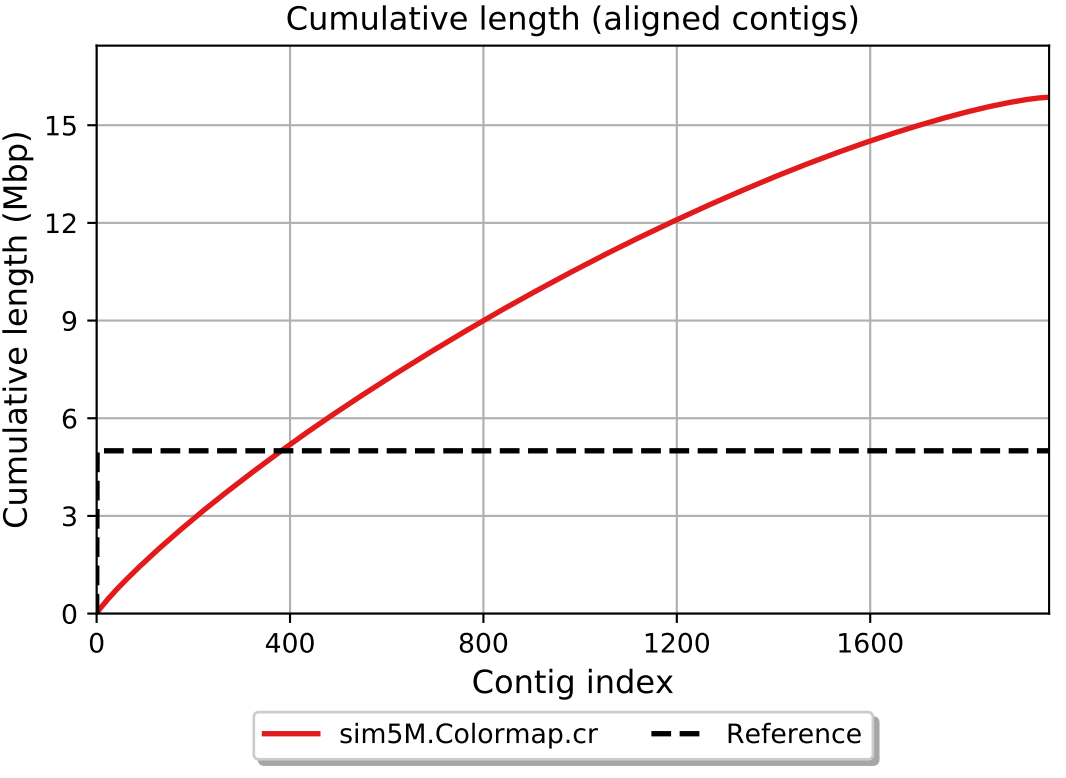

Cumulative length
Cumulative length (Mbp)
0
3
6
9
12
15
0
400
800
1200
1600
Contig index
sim5M.Colormap.cr
Reference

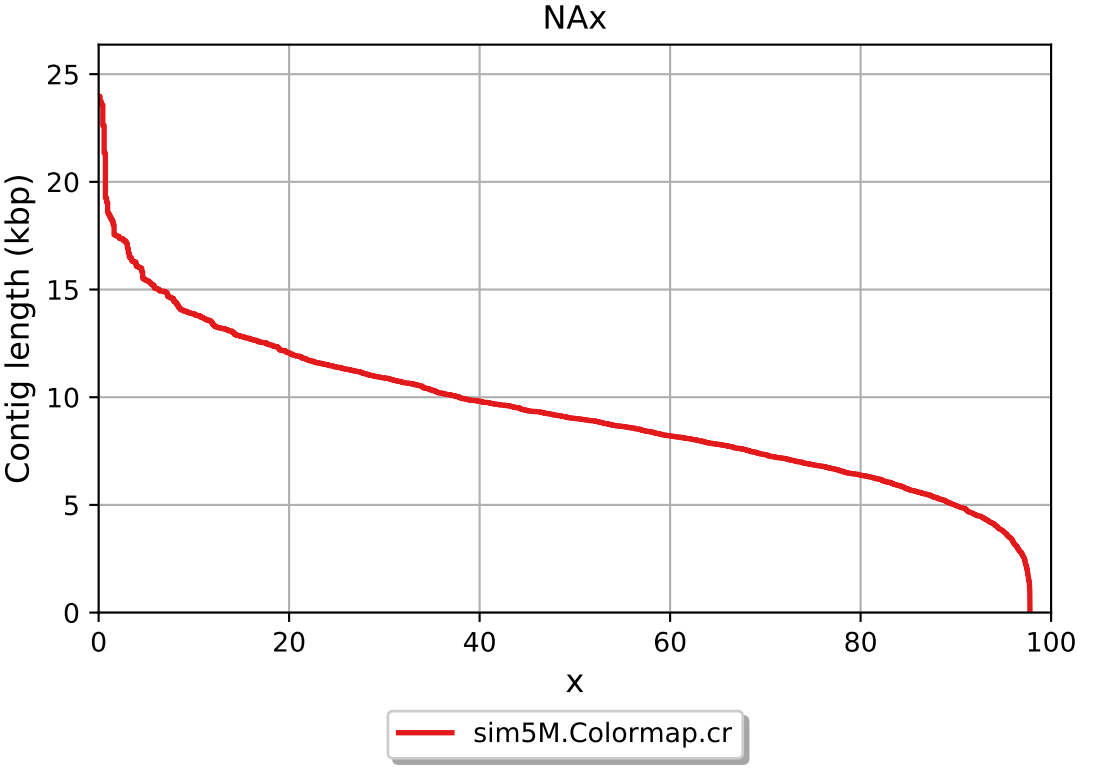

GC content
# windows
7500
6000
4500
3000
1500
0
0
20
40
60
80
100
GC (%)
sim5M.Colormap.cr
Reference

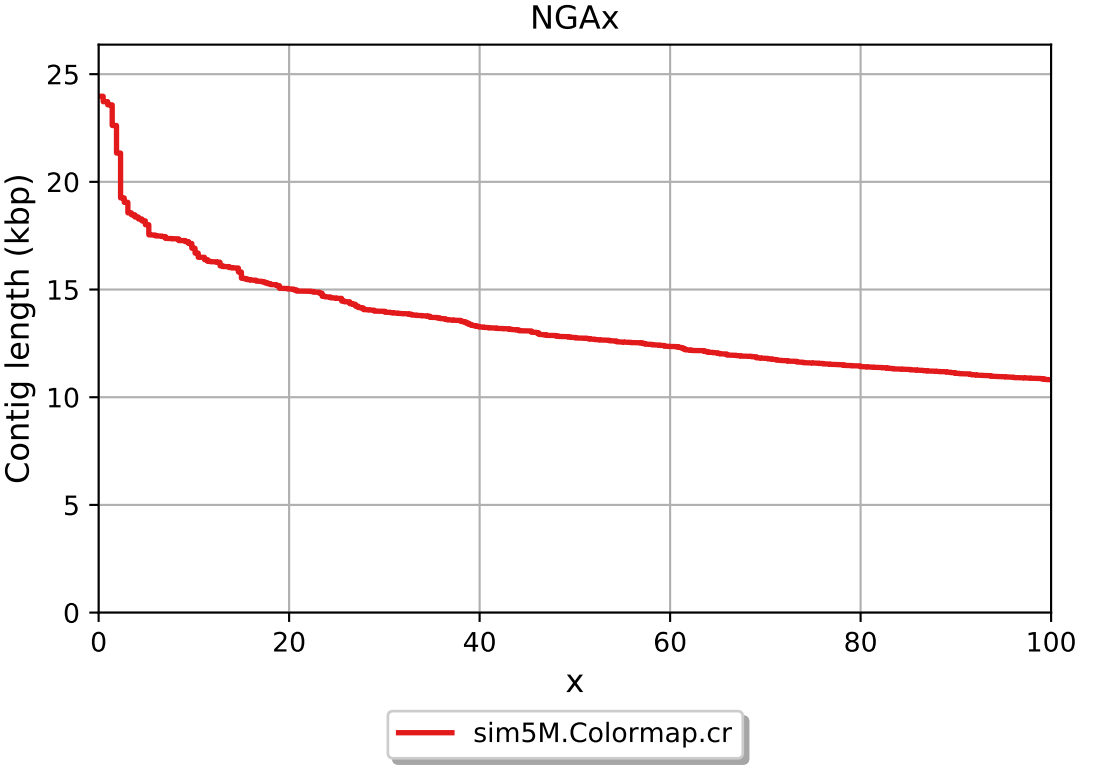

sim5M.Colormap.cr GC content
# contigs
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
sim5M.Colormap.cr

Misassemblies
5
4
3
2
1
0
sim5M.Colormap.cr


FRCurve (misassemblies)
Genome coverage (%)
300
240
180
120
60
0
0
1
Feature space
sim5M.Colormap.cr


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
3
6
9
12
15
0
400
800
1200
1600
Contig index
sim5M.Colormap.cr
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.Colormap.cr


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
sim5M.Colormap.cr