# Report

| | contigs |
|---|---|
| # contigs (>= 0 bp) | 5874 |
| # contigs (>= 1000 bp) | 1728 |
| # contigs (>= 5000 bp) | 8 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 5013280 |
| Total length (>= 1000 bp) | 2956576 |
| Total length (>= 5000 bp) | 44583 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 3578 |
| Largest contig | 5860 |
| Total length | 4291000 |
| Reference length | 4641652 |
| GC (%) | 50.75 |
| Reference GC (%) | 50.79 |
| N50 | 1374 |
| NG50 | 1284 |
| N75 | 900 |
| NG75 | 801 |
| L50 | 1032 |
| LG50 | 1163 |
| L75 | 2005 |
| LG75 | 2314 |
| # misassemblies | 20 |
| # misassembled contigs | 20 |
| Misassembled contigs length | 48720 |
| # local misassemblies | 9 |
| # unaligned contigs | 2 + 13 part |
| Unaligned length | 4591 |
| Genome fraction (%) | 87.921 |
| Duplication ratio | 1.050 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 470.16 |
| # indels per 100 kbp | 1.03 |
| Largest alignment | 5860 |
| NA50 | 1366 |
| NGA50 | 1275 |
| NA75 | 895 |
| NGA75 | 796 |
| LA50 | 1040 |
| LGA50 | 1173 |
| LA75 | 2019 |
| LGA75 | 2330 |

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

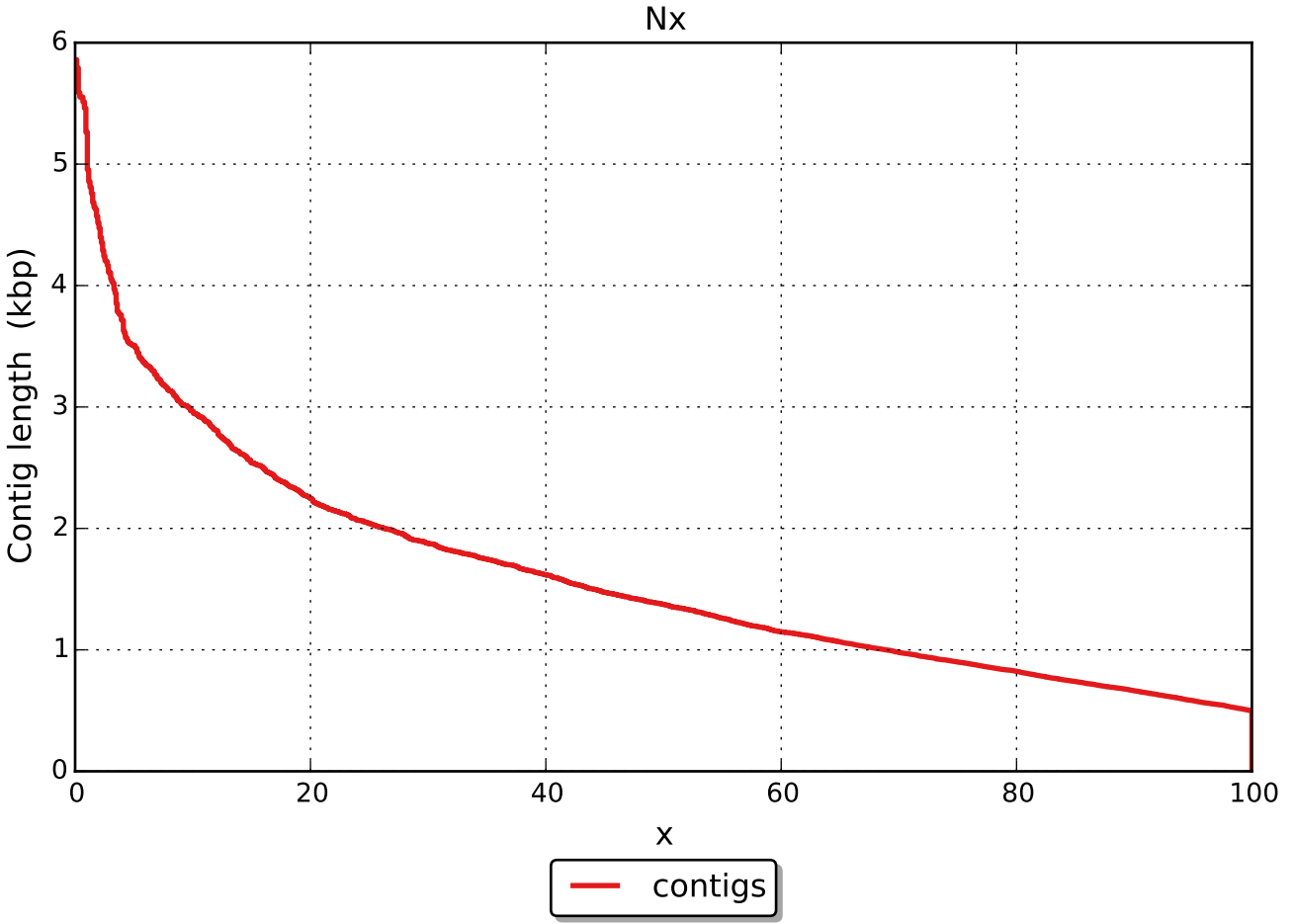
| | contigs |
|---|---|
| # misassemblies | 20 |
| # relocations | 20 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 20 |
| Misassembled contigs length | 48720 |
| # local misassemblies | 9 |
| # mismatches | 19187 |
| # indels | 42 |
| # short indels | 41 |
| # long indels | 1 |
| Indels length | 124 |

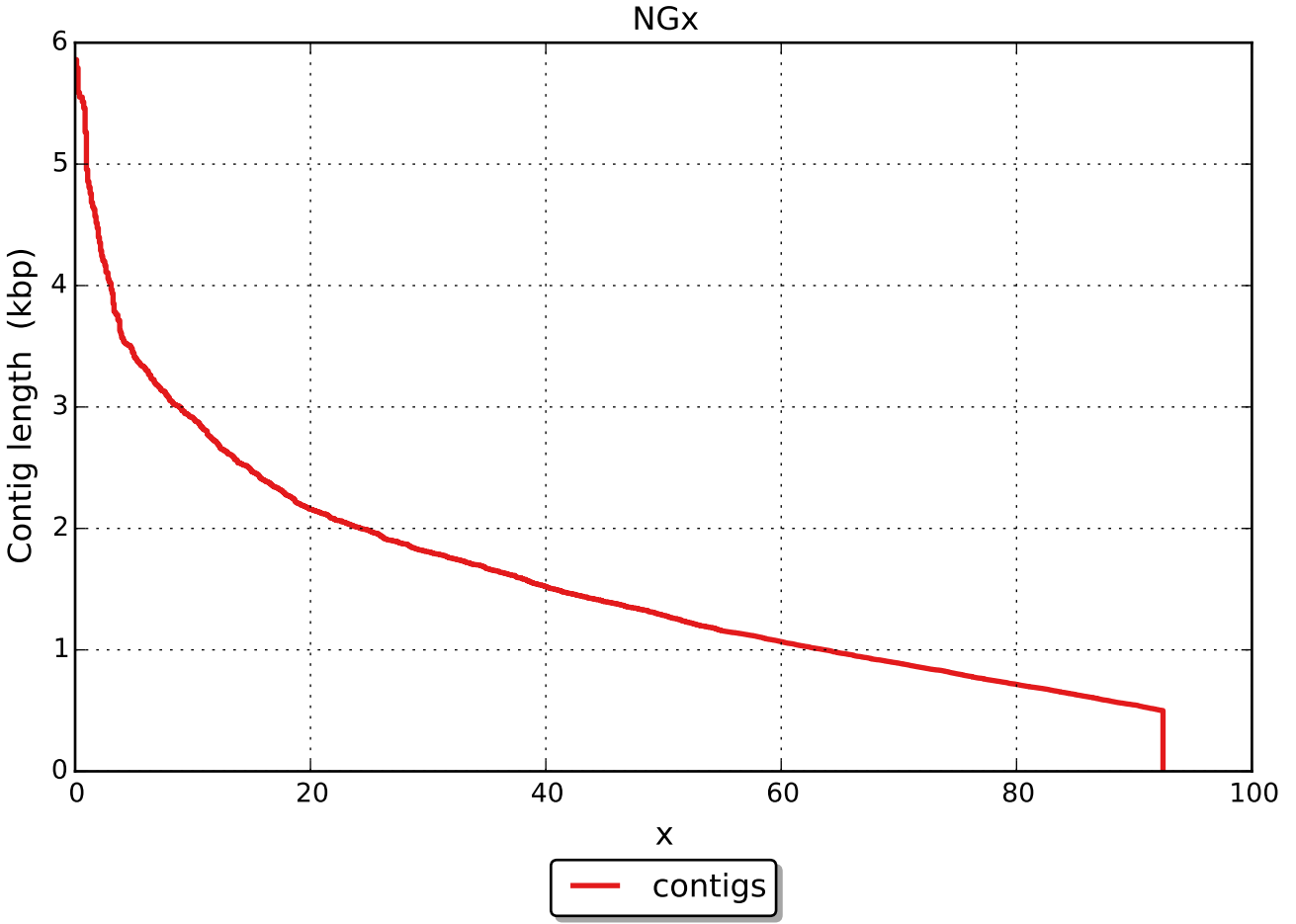
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

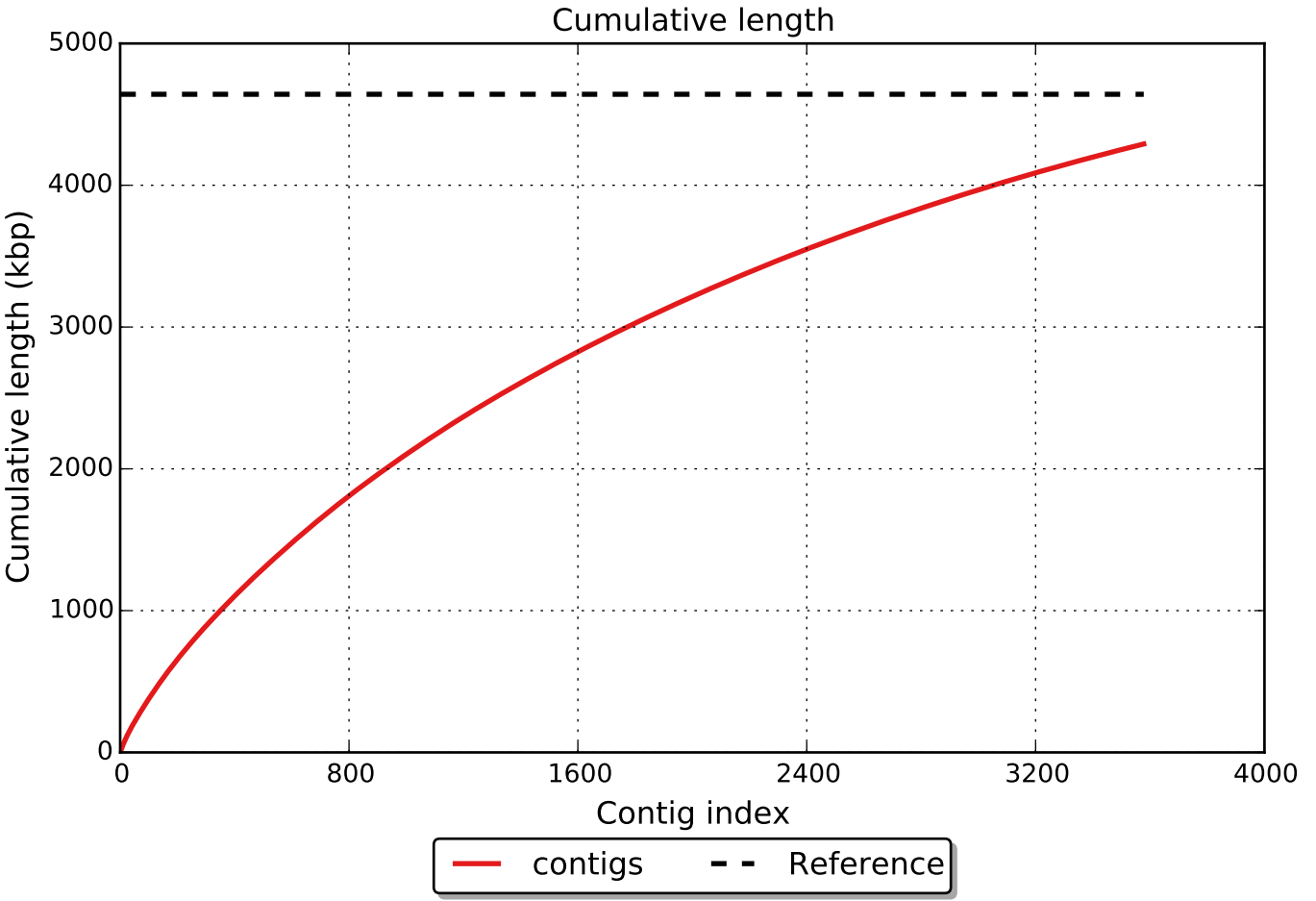
## Unaligned report

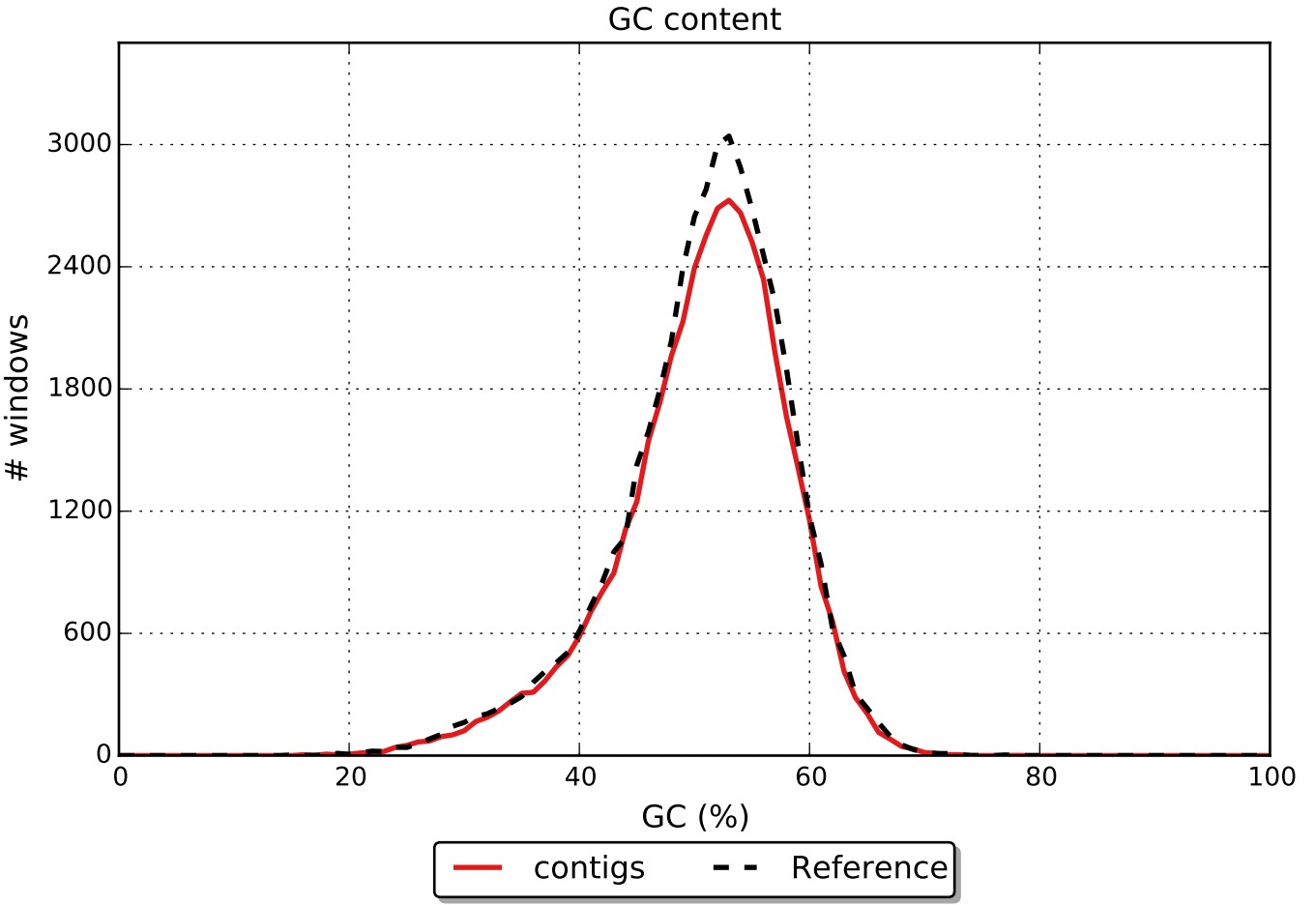
| | contigs |
|---|---|
| # fully unaligned contigs | 2 |
| Fully unaligned length | 1766 |
| # partially unaligned contigs | 13 |
| # with misassembly | 0 |
| # both parts are significant | 1 |
| Partially unaligned length | 2825 |
| # N's | 0 |

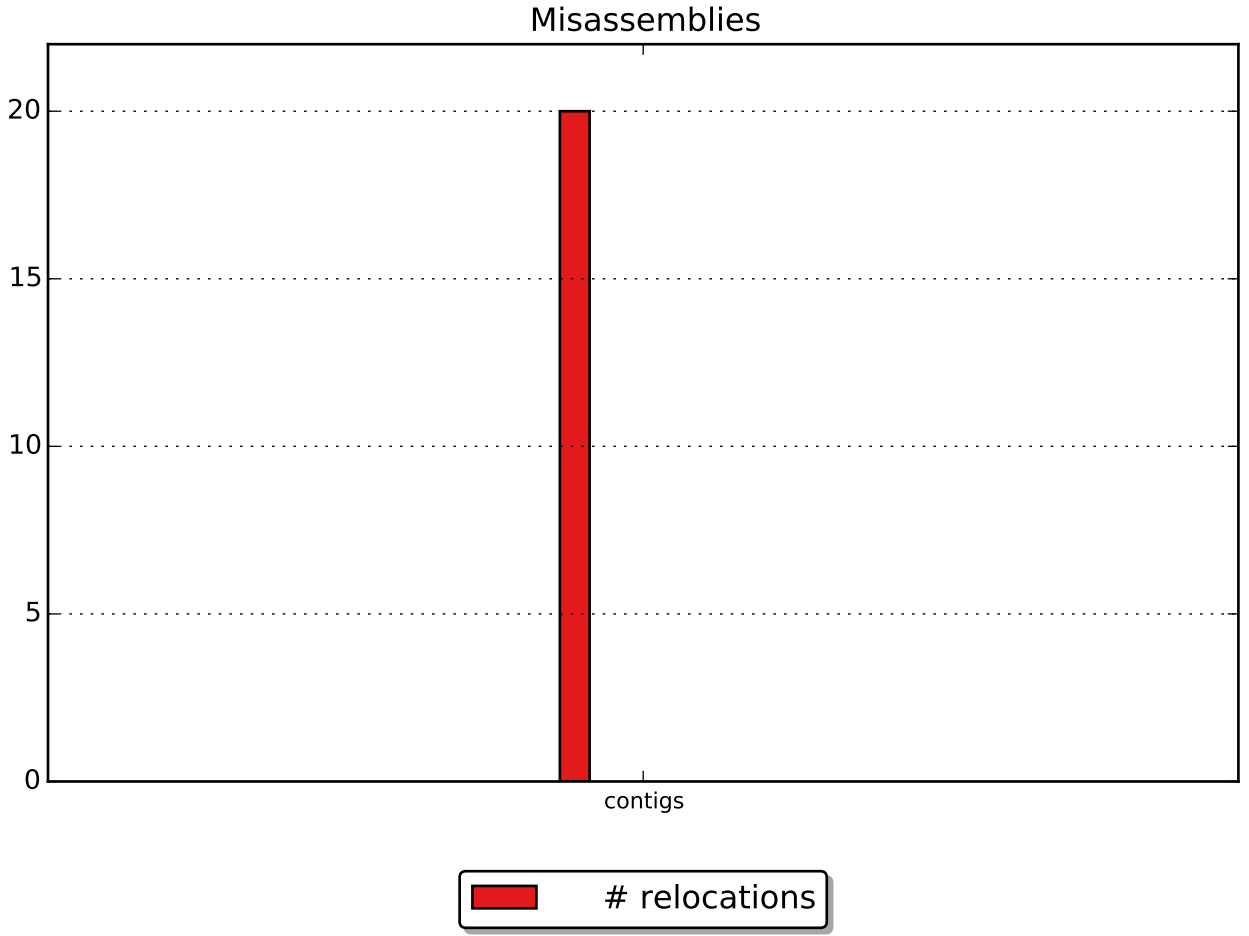
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

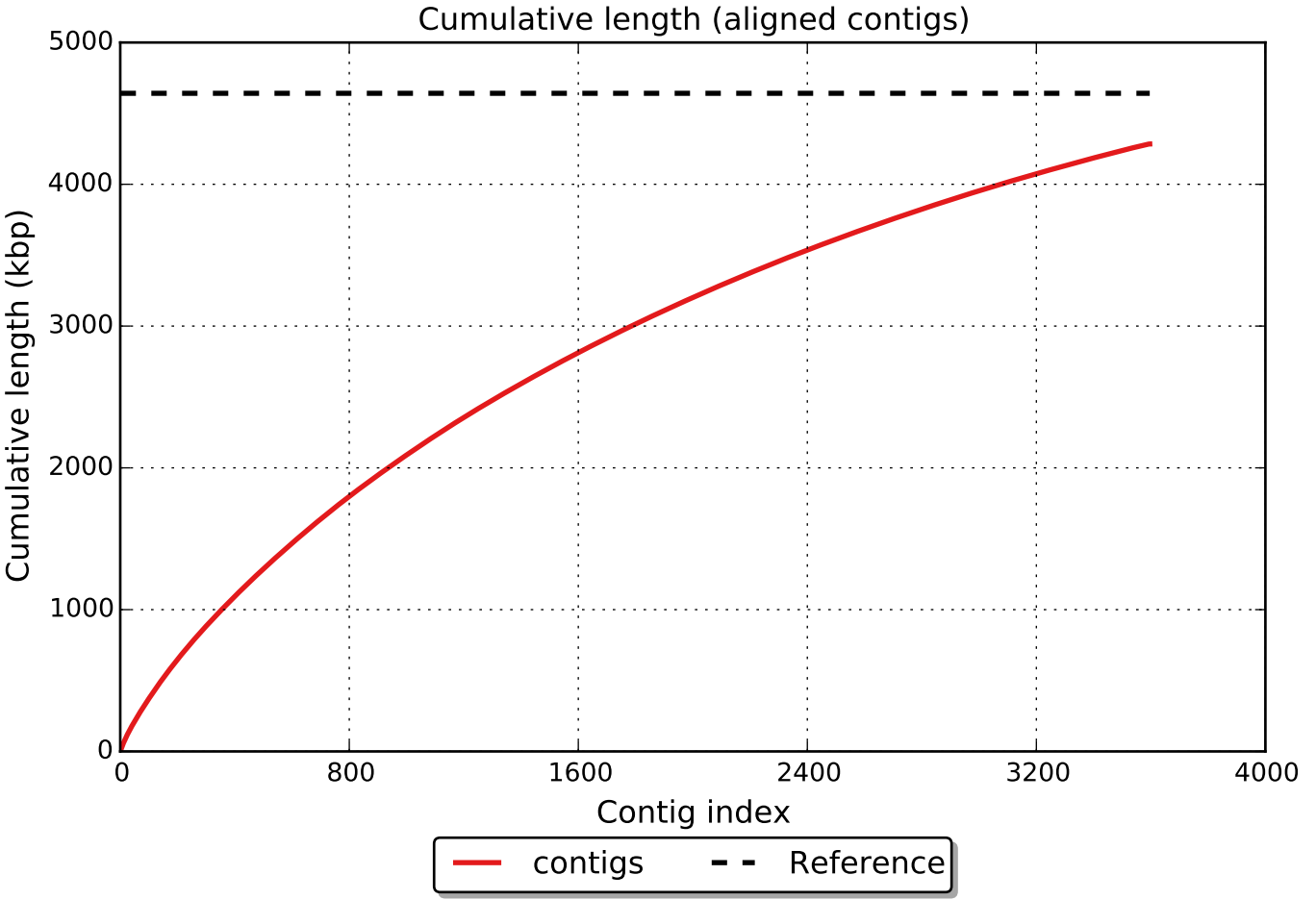

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs

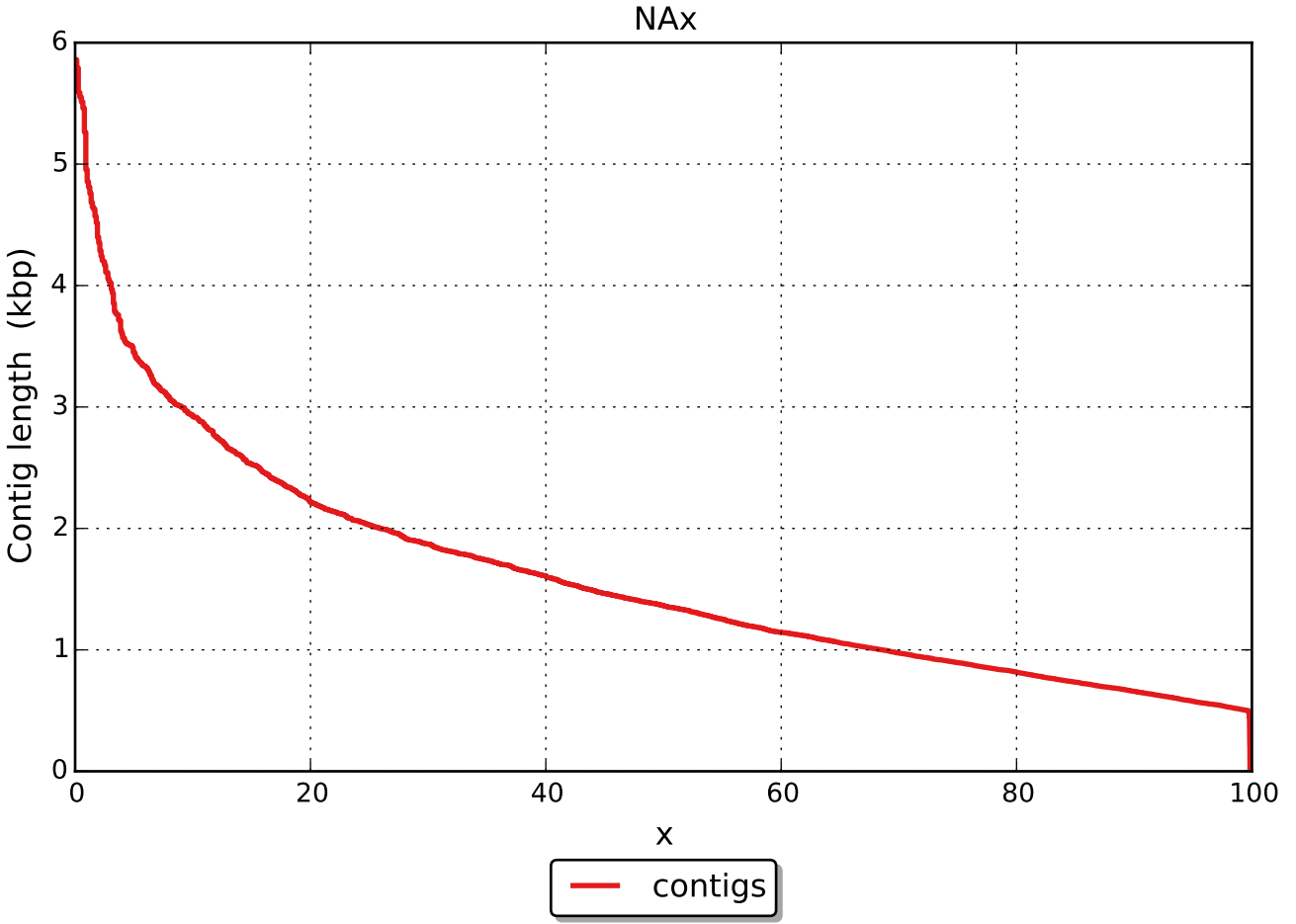

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs

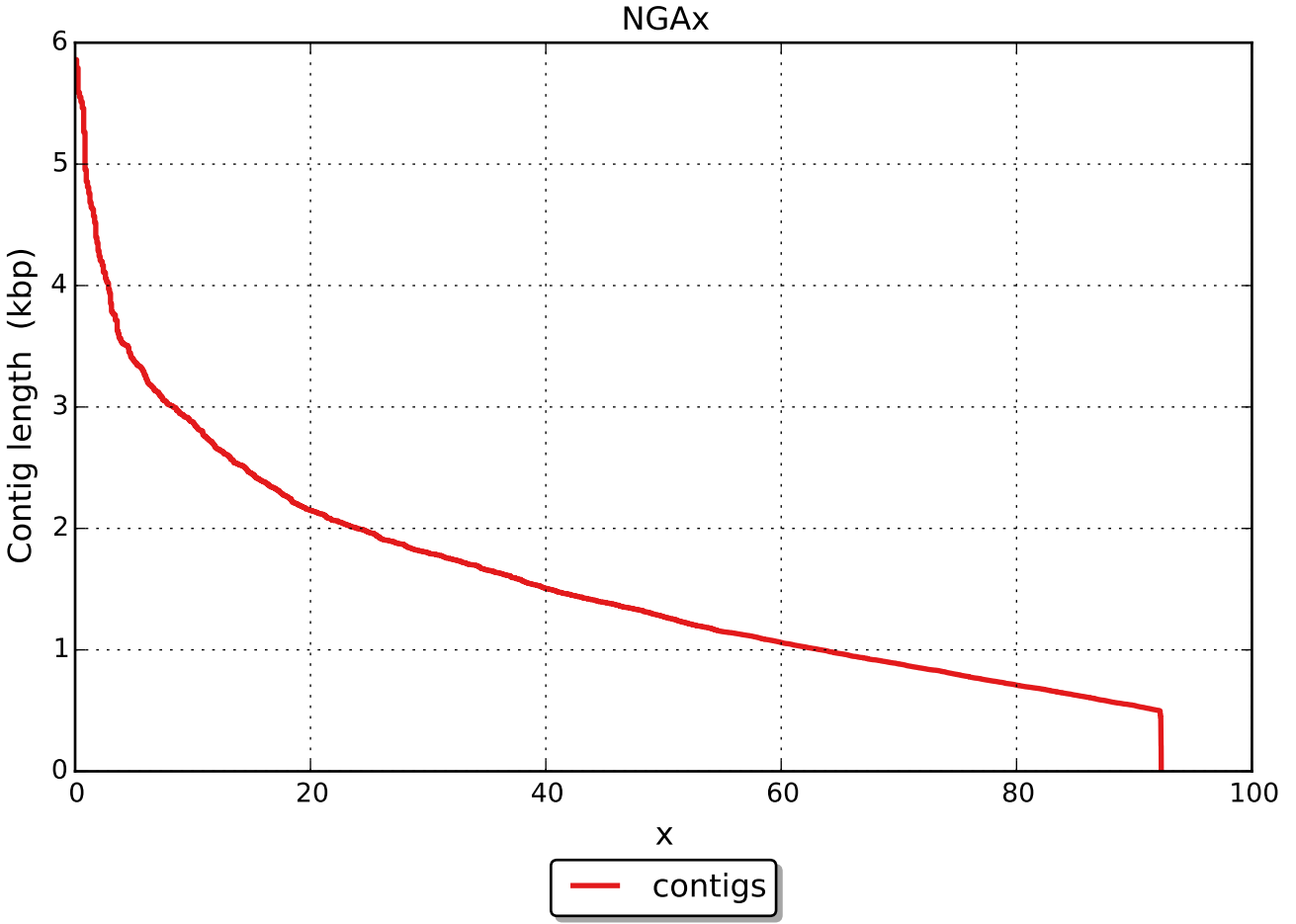

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
contigs
Reference


GC content
# windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contigs
Reference


Misassemblies
20
15
10
5
0
contigs
# relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
contigs
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs