# Report

| | contigs |
|---|---|
| # contigs (>= 0 bp) | 9769 |
| # contigs (>= 1000 bp) | 120 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 3699358 |
| Total length (>= 1000 bp) | 148723 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1757 |
| Largest contig | 3569 |
| Total length | 1199393 |
| Reference length | 4641652 |
| GC (%) | 50.80 |
| Reference GC (%) | 50.79 |
| N50 | 663 |
| N75 | 567 |
| L50 | 701 |
| L75 | 1191 |
| # misassemblies | 12 |
| # misassembled contigs | 12 |
| Misassembled contigs length | 19697 |
| # local misassemblies | 3 |
| # unaligned contigs | 1 + 8 part |
| Unaligned length | 1650 |
| Genome fraction (%) | 25.437 |
| Duplication ratio | 1.014 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 937.33 |
| # indels per 100 kbp | 1.61 |
| Largest alignment | 3447 |
| NA50 | 662 |
| NGA50 | - |
| NA75 | 565 |
| LA50 | 707 |
| LA75 | 1198 |

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

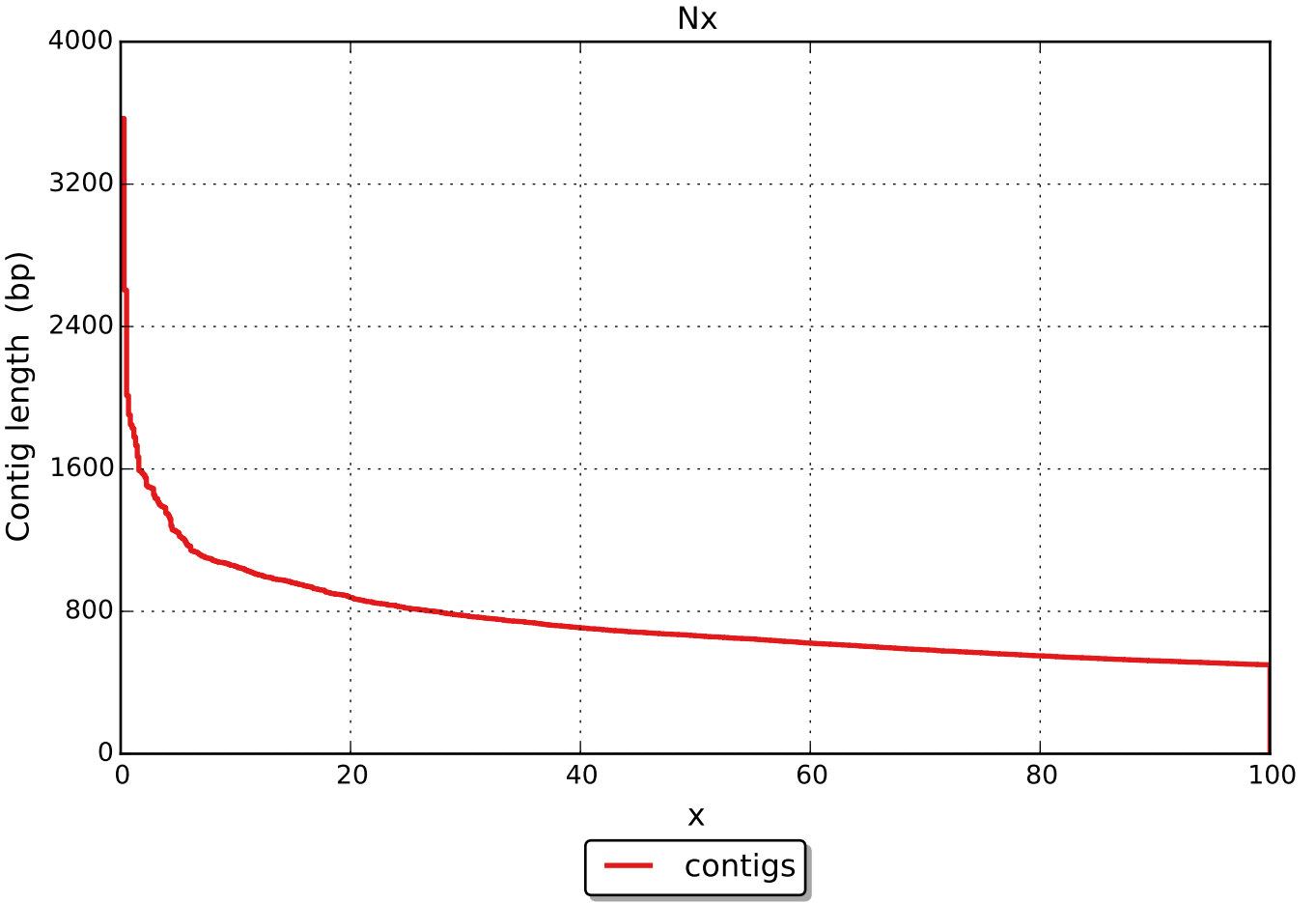
| | contigs |
|---|---|
| # misassemblies | 12 |
| # relocations | 12 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 12 |
| Misassembled contigs length | 19697 |
| # local misassemblies | 3 |
| # mismatches | 11067 |
| # indels | 19 |
| # short indels | 19 |
| # long indels | 0 |
| Indels length | 24 |

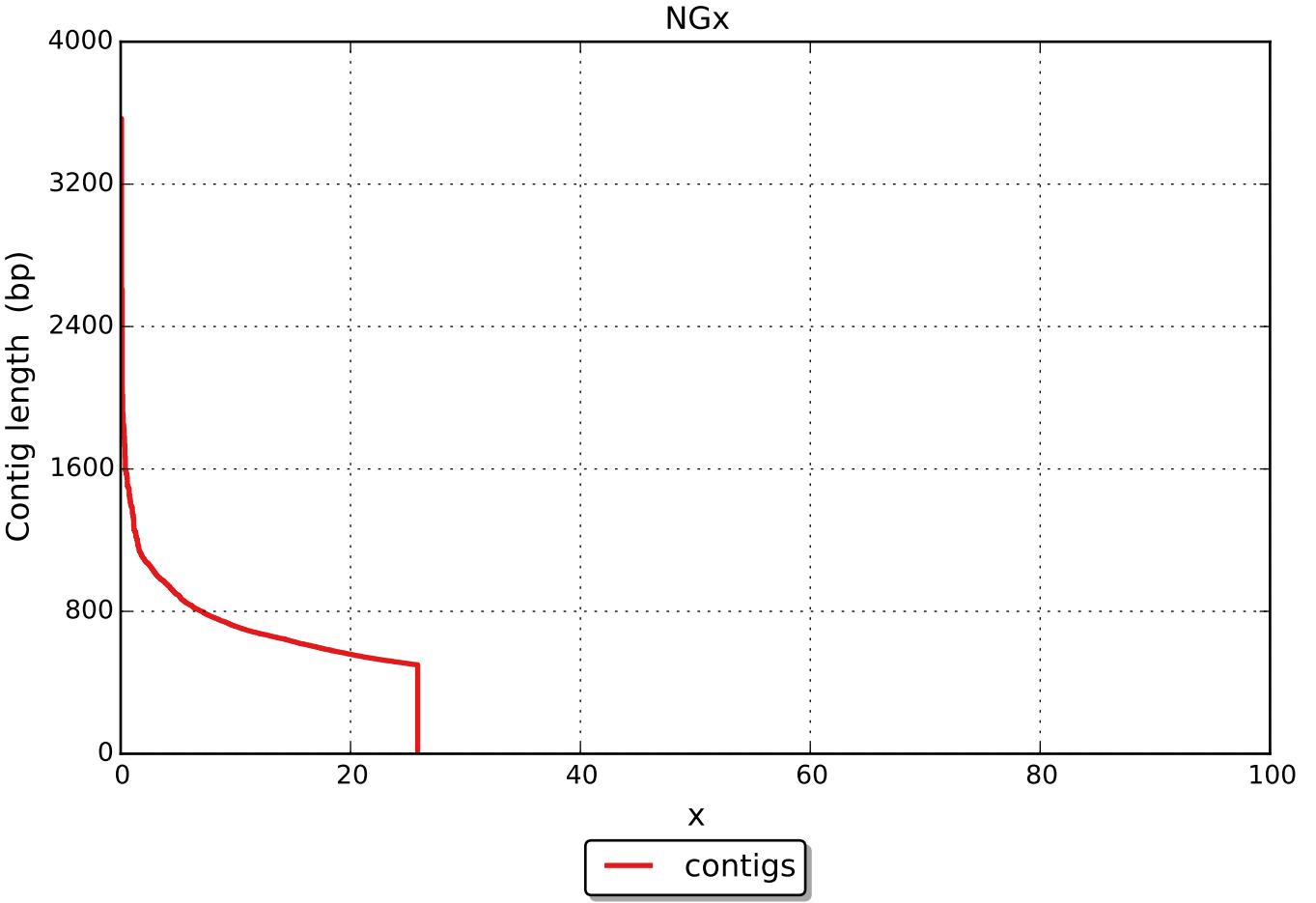
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

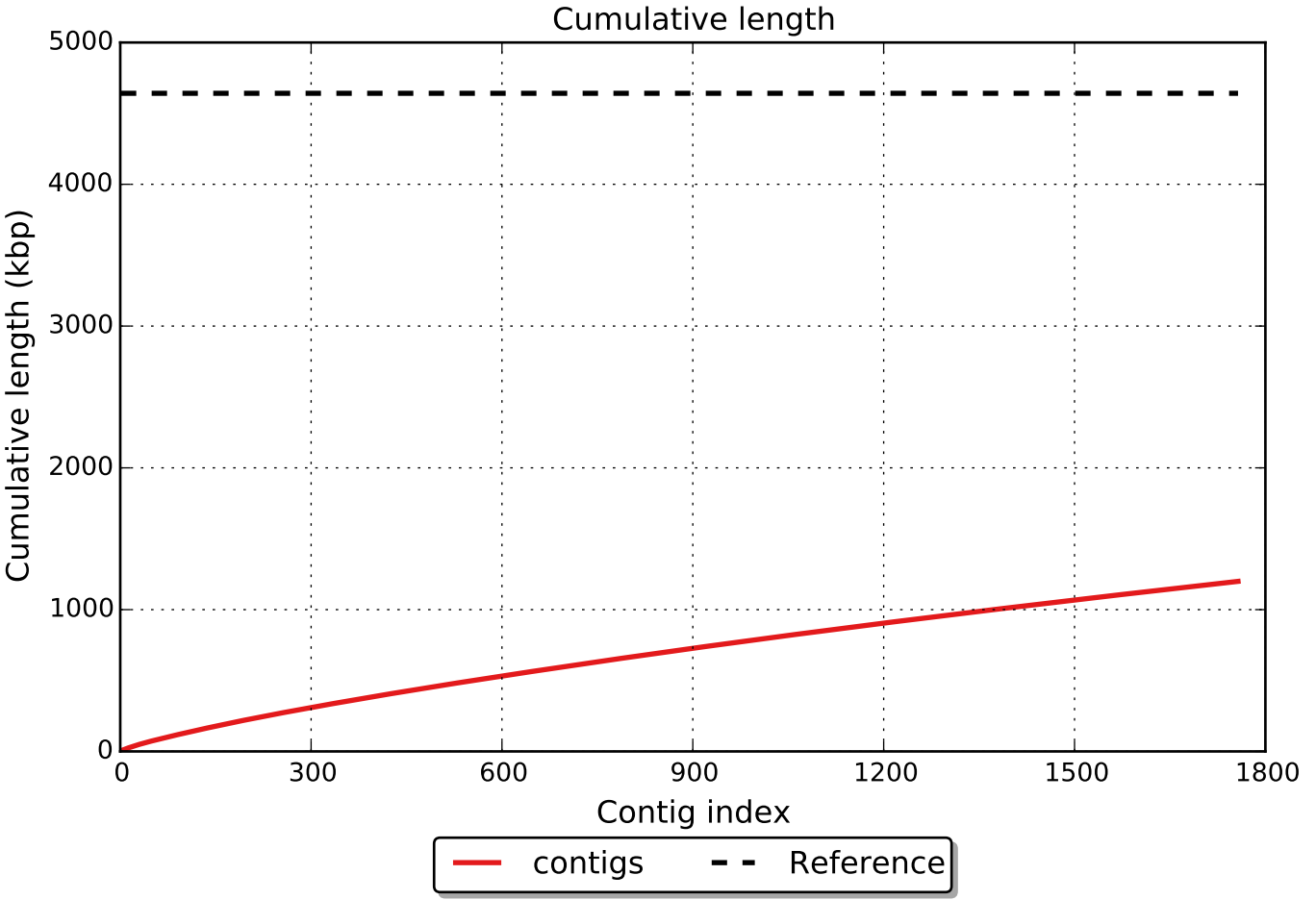
## Unaligned report

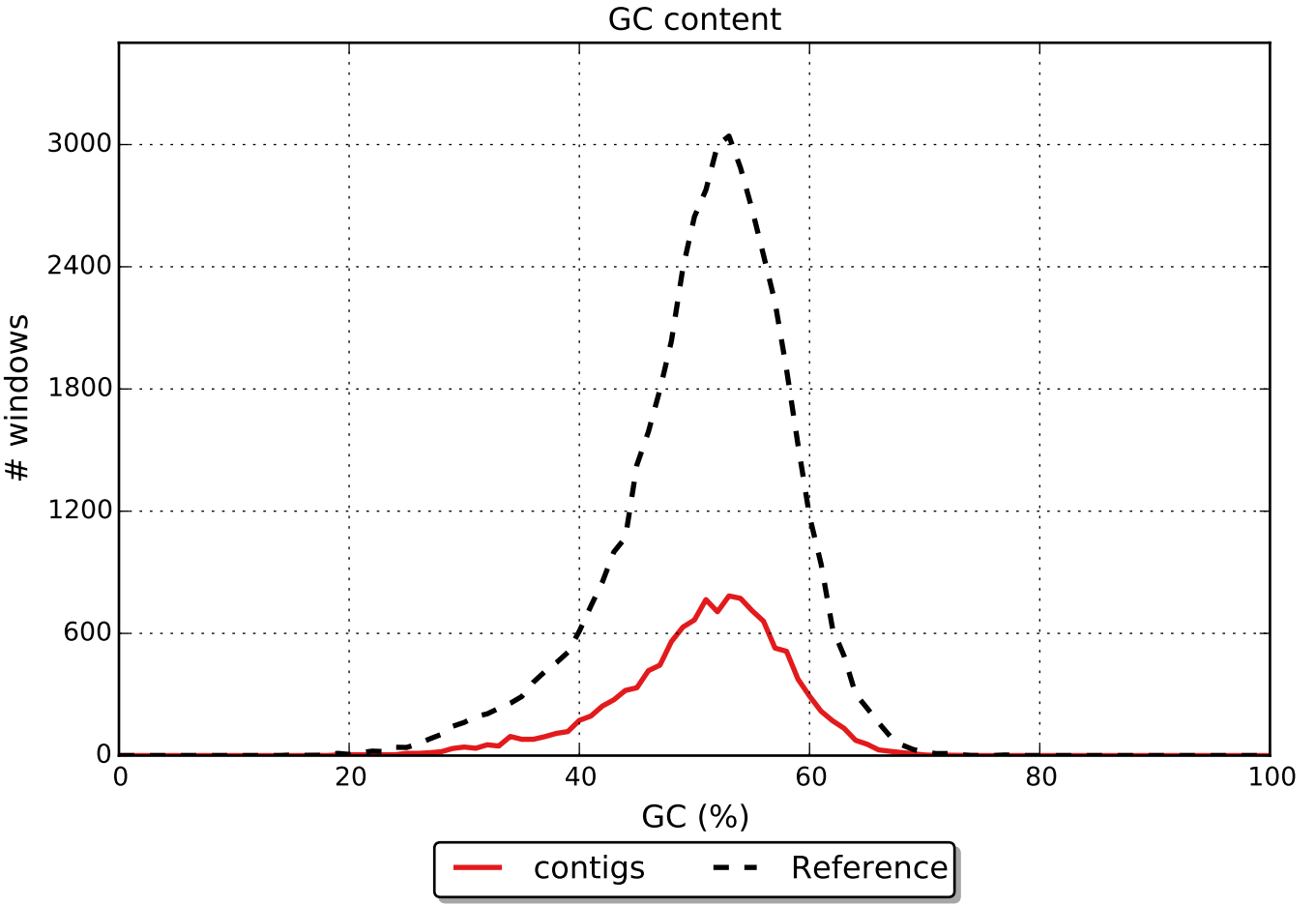
| | contigs |
|---|---|
| # fully unaligned contigs | 1 |
| Fully unaligned length | 551 |
| # partially unaligned contigs | 8 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 1099 |
| # N's | 0 |

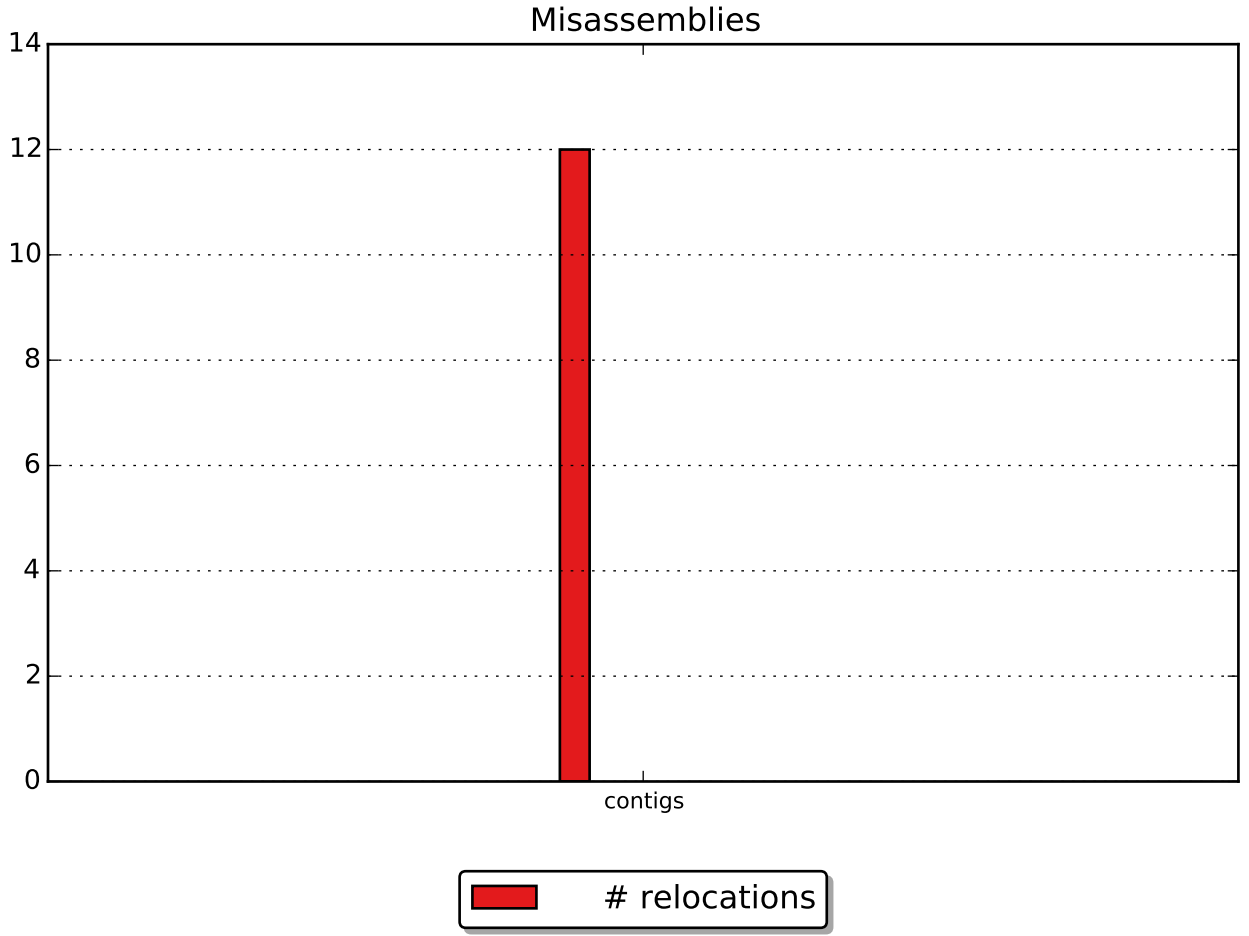
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

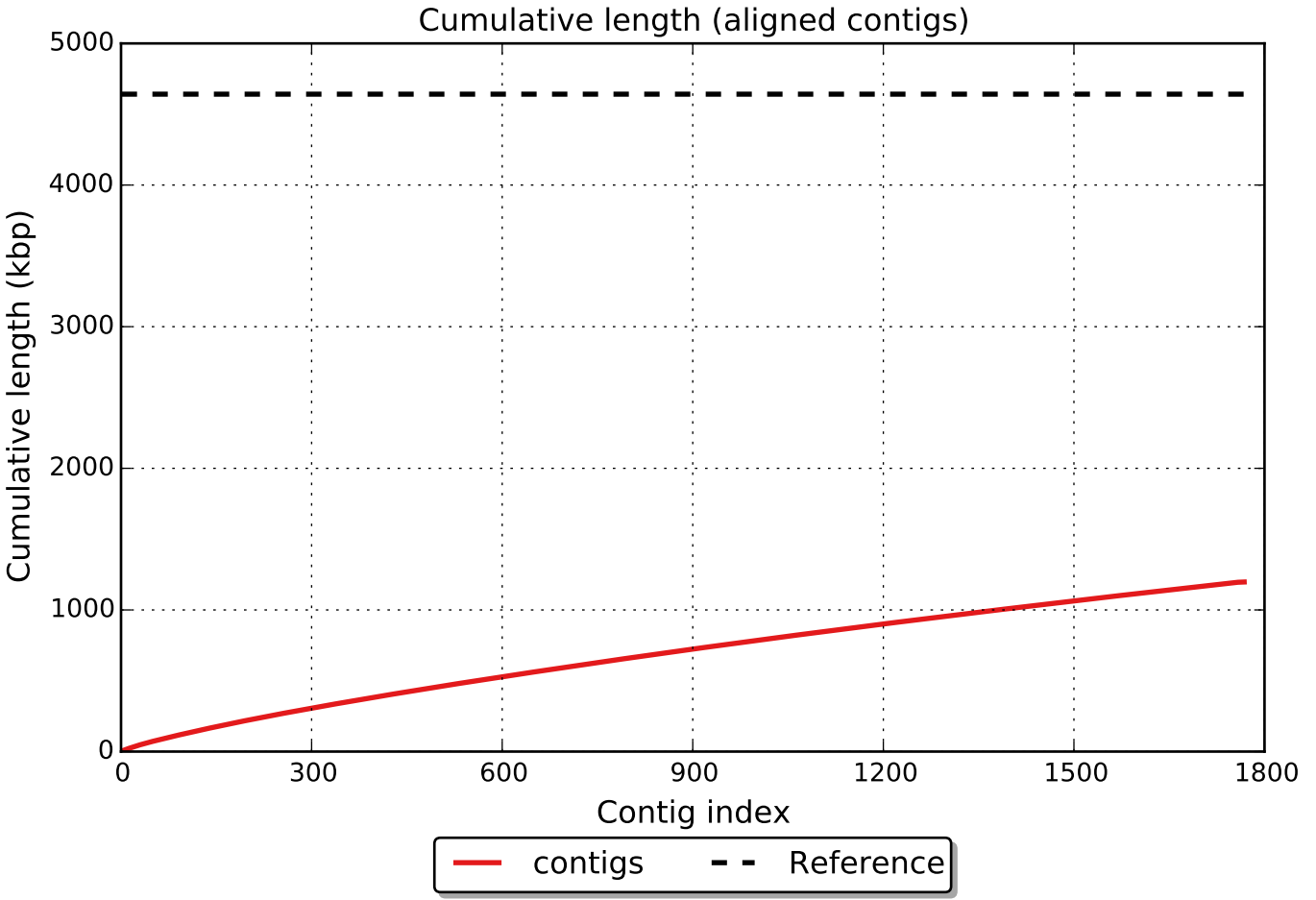

Nx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
contigs

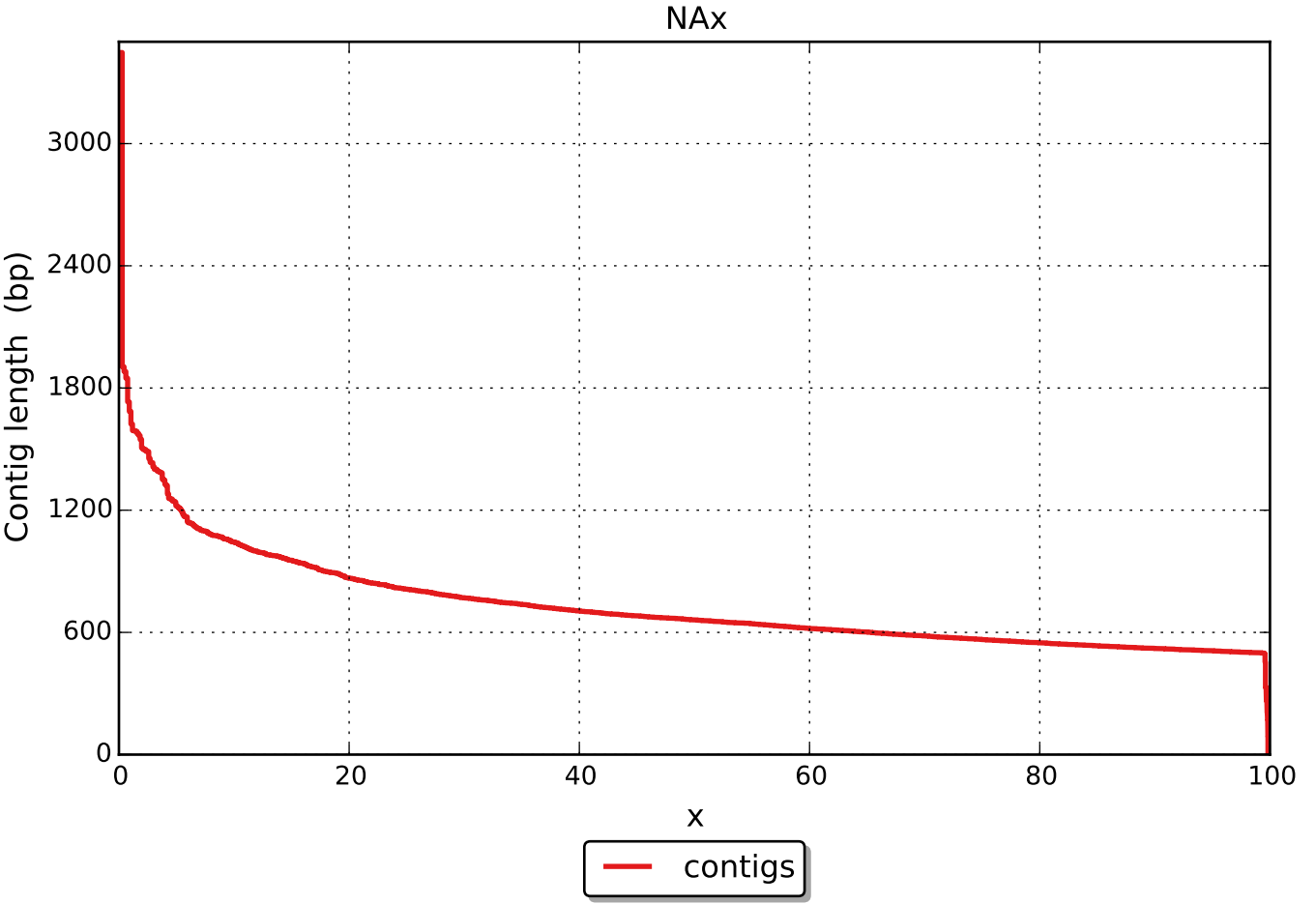

NGx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
contigs

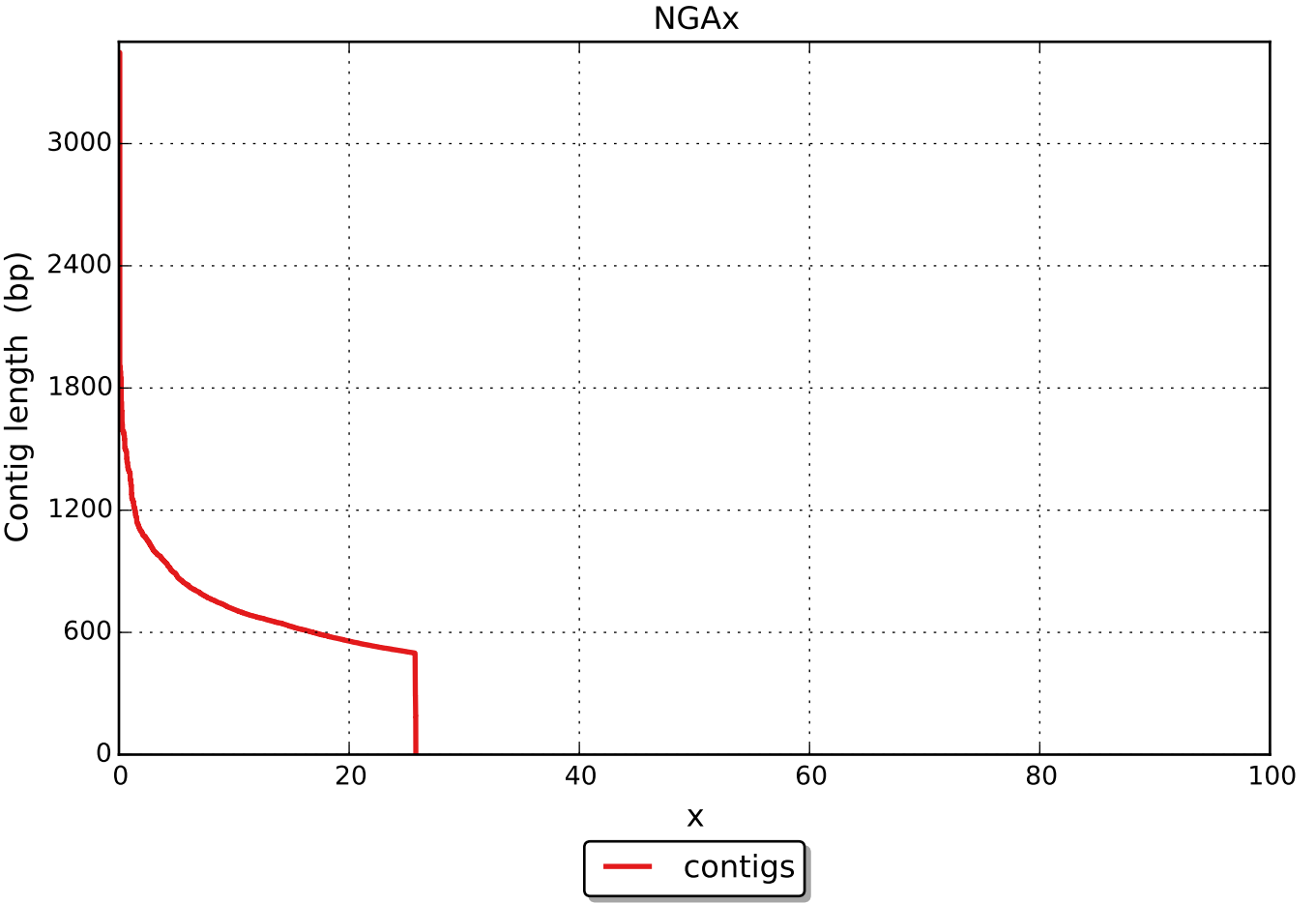

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
1800
Contig index
contigs
Reference


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


Misassemblies
14
12
10
8
6
4
2
0
contigs
# relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
1800
Contig index
contigs
Reference


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs