Report

| | final.contigs |
|---|---|
| # contigs (>= 1000 bp) | 721 |
| # contigs (>= 5000 bp) | 105 |
| # contigs (>= 10000 bp) | 8 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 2177126 |
| Total length (>= 5000 bp) | 723497 |
| Total length (>= 10000 bp) | 92965 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1091 |
| Largest contig | 15182 |
| Total length | 2427600 |
| Reference length | 4857432 |
| GC (%) | 52.25 |
| Reference GC (%) | 52.22 |
| N50 | 3383 |
| N75 | 1842 |
| L50 | 226 |
| L75 | 468 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 7463 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 49.077 |
| Duplication ratio | 1.018 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 374.89 |
| # indels per 100 kbp | 0.21 |
| Largest alignment | 15182 |
| NA50 | 3383 |
| NGA50 | - |
| NA75 | 1842 |
| LA50 | 226 |
| LA75 | 468 |

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

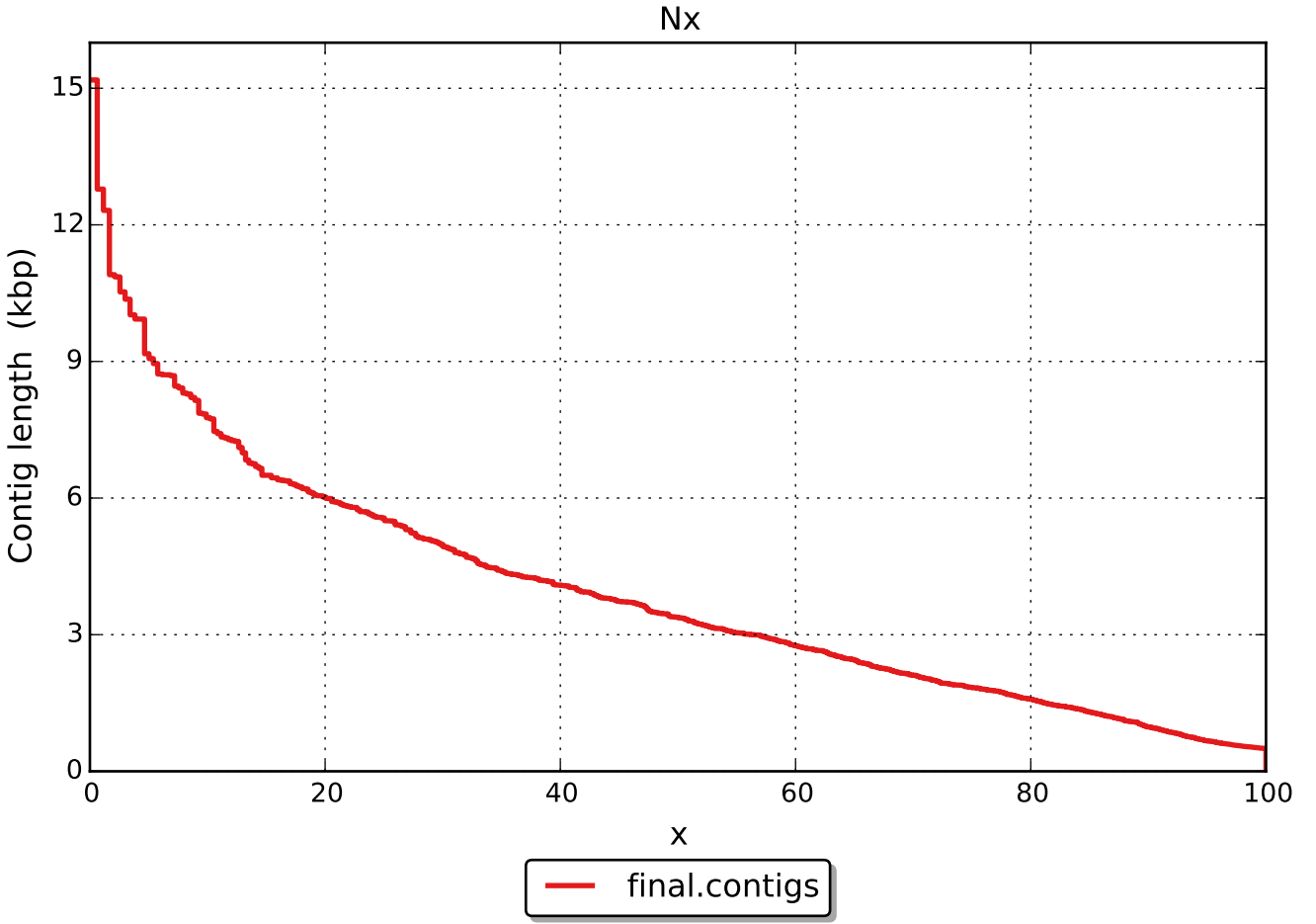
| | final.contigs |
|---|---|
| # misassemblies | 1 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 7463 |
| # local misassemblies | 0 |
| # mismatches | 8937 |
| # indels | 5 |
| # short indels | 5 |
| # long indels | 0 |
| Indels length | 8 |

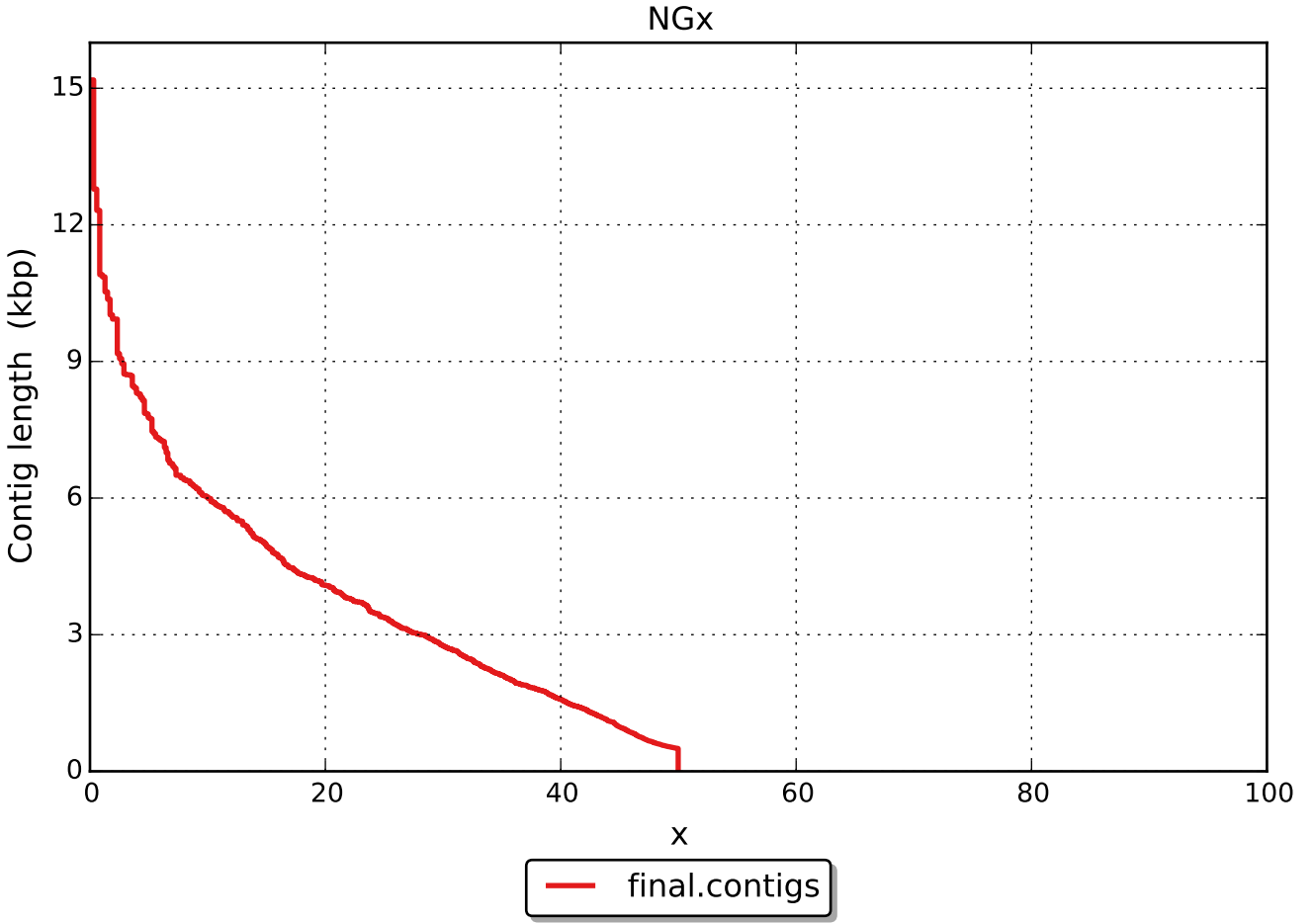
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

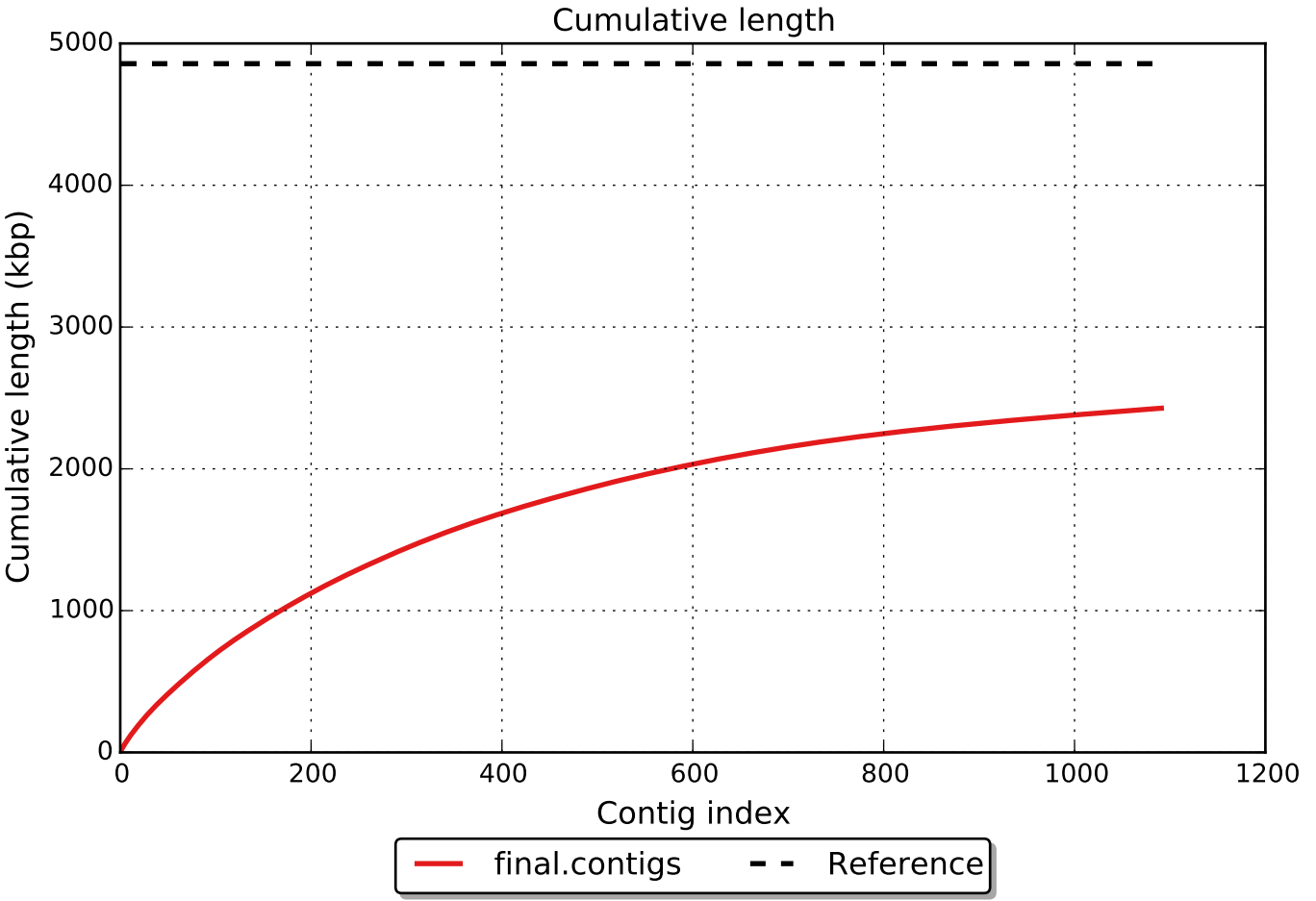
# Unaligned report

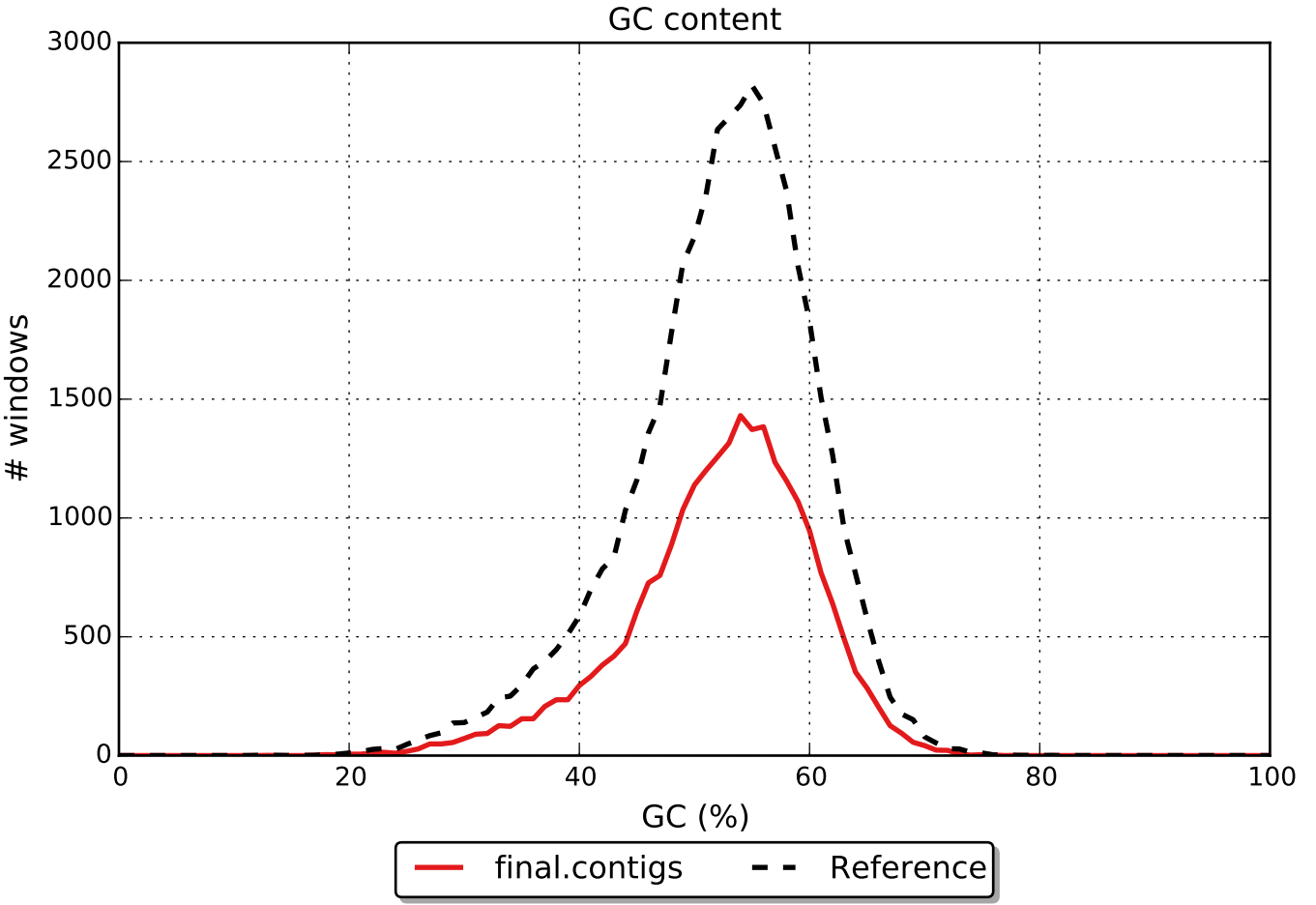
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

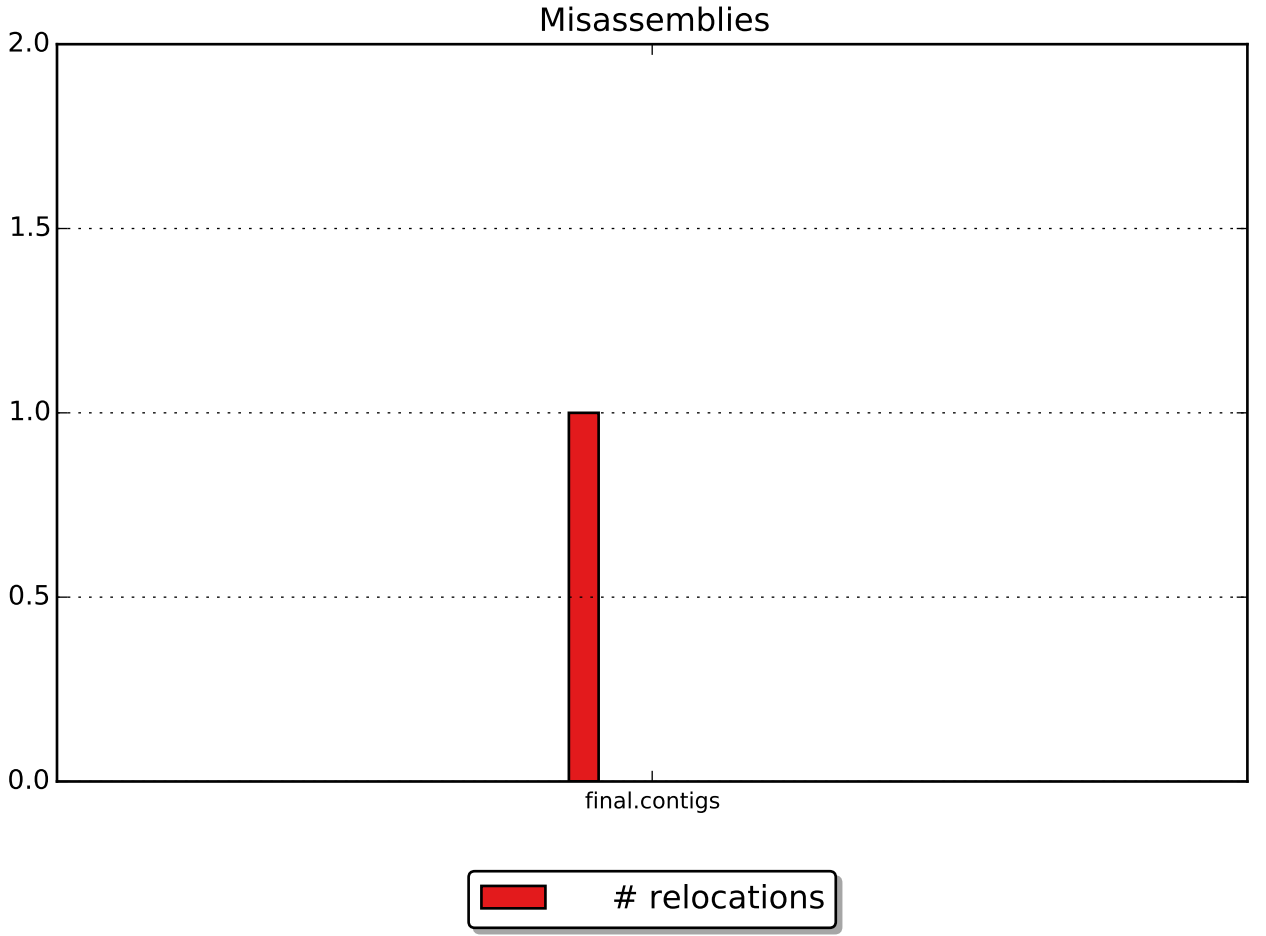
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

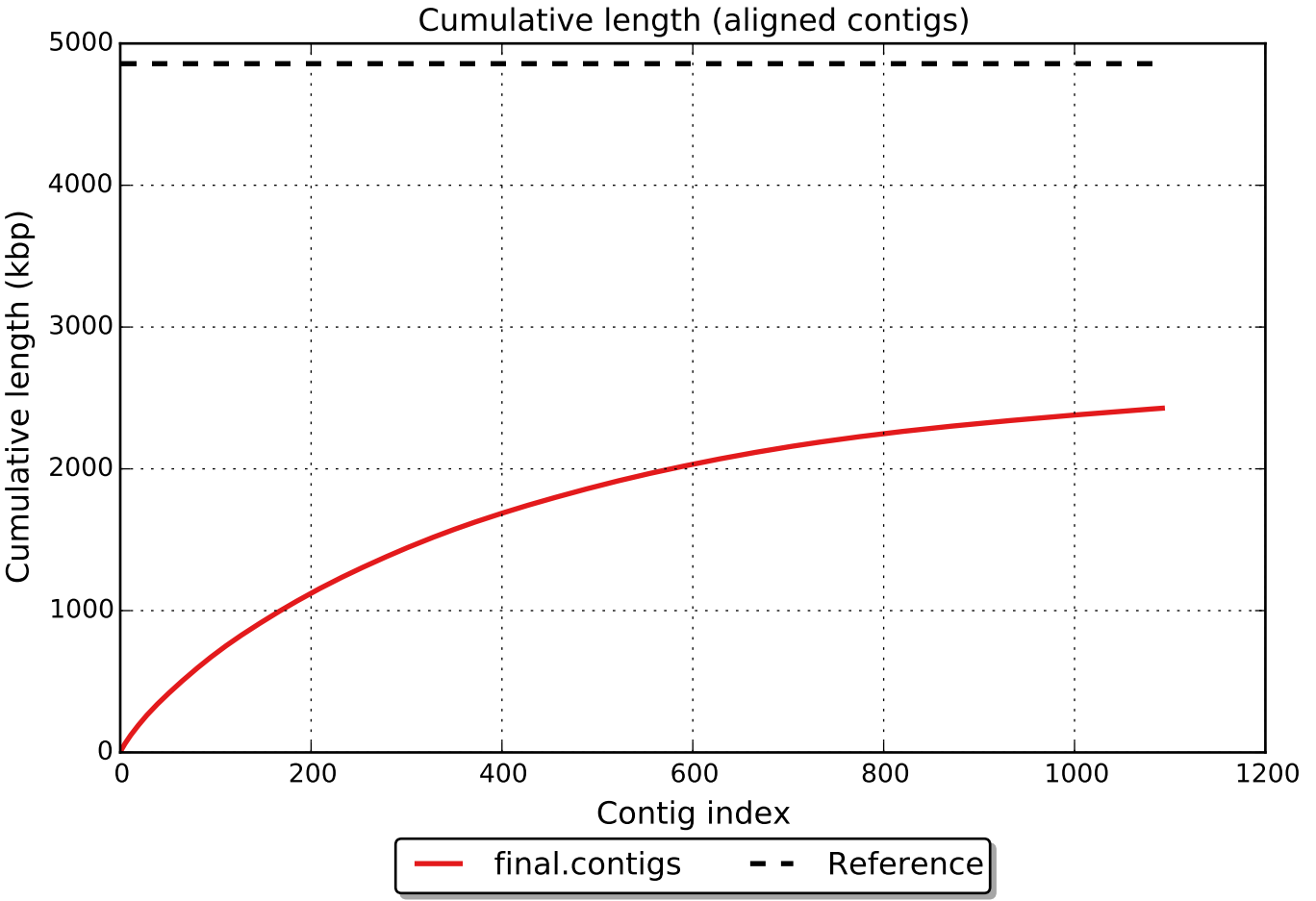

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

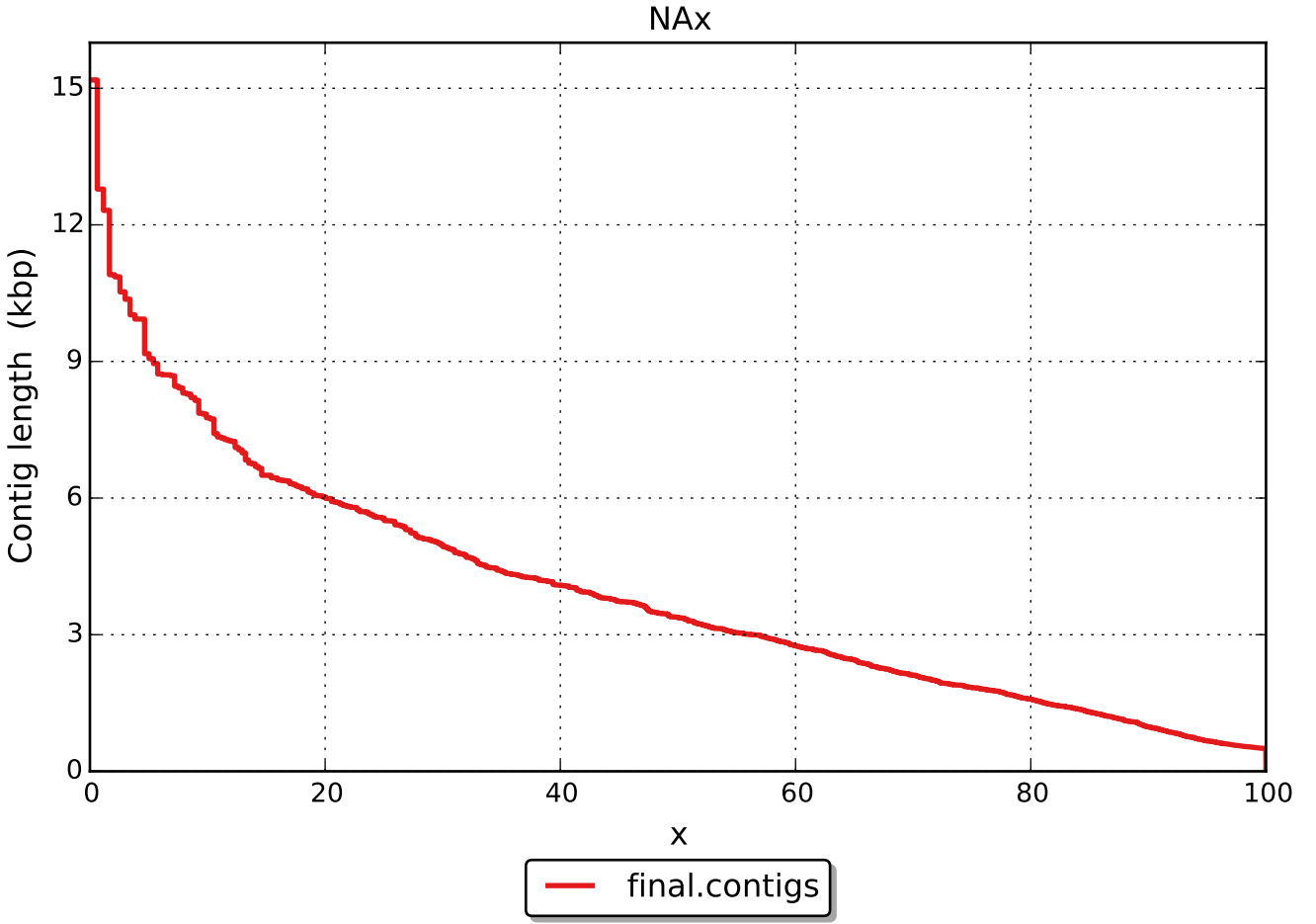

NGx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

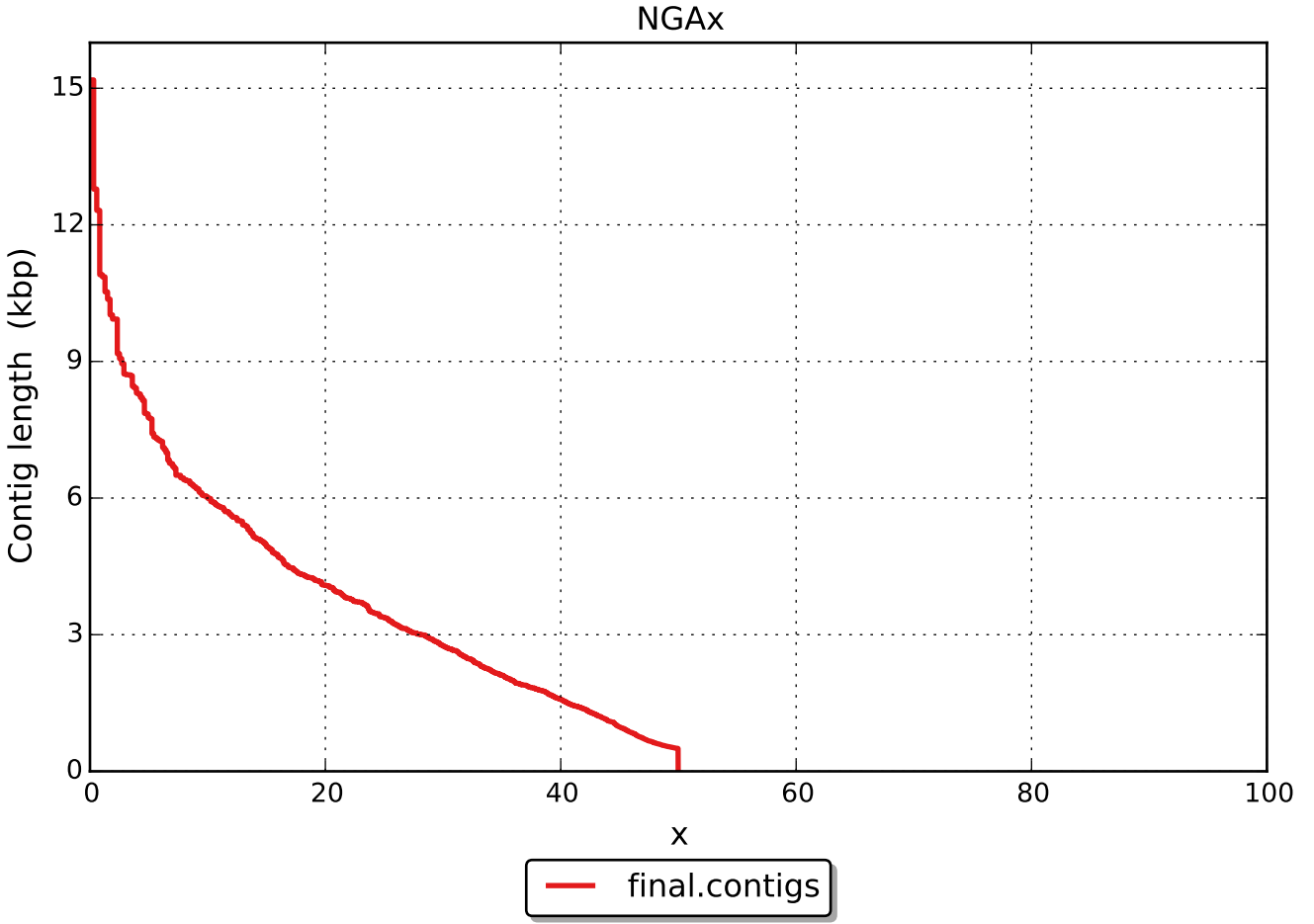

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
# windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
# relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs