Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 851 |
| # contigs (>= 1000 bp) | 480 |
| Total length (>= 0 bp) | 1228283 |
| Total length (>= 1000 bp) | 958247 |
| # contigs | 851 |
| Largest contig | 8613 |
| Total length | 1228283 |
| Reference length | 641799 |
| GC (%) | 26.32 |
| Reference GC (%) | 26.30 |
| N50 | 1743 |
| NG50 | 2771 |
| N75 | 1060 |
| NG75 | 2149 |
| L50 | 215 |
| LG50 | 81 |
| L75 | 444 |
| LG75 | 147 |
| # misassemblies | 33 |
| # misassembled contigs | 32 |
| Misassembled contigs length | 76798 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 1 part |
| Unaligned length | 589 |
| Genome fraction (%) | 94.983 |
| Duplication ratio | 2.014 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1727.20 |
| # indels per 100 kbp | 2.30 |
| Largest alignment | 7611 |
| NA50 | 1684 |
| NGA50 | 2624 |
| NA75 | 1032 |
| NGA75 | 2098 |
| LA50 | 223 |
| LGA50 | 84 |
| LA75 | 459 |
| LGA75 | 152 |

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

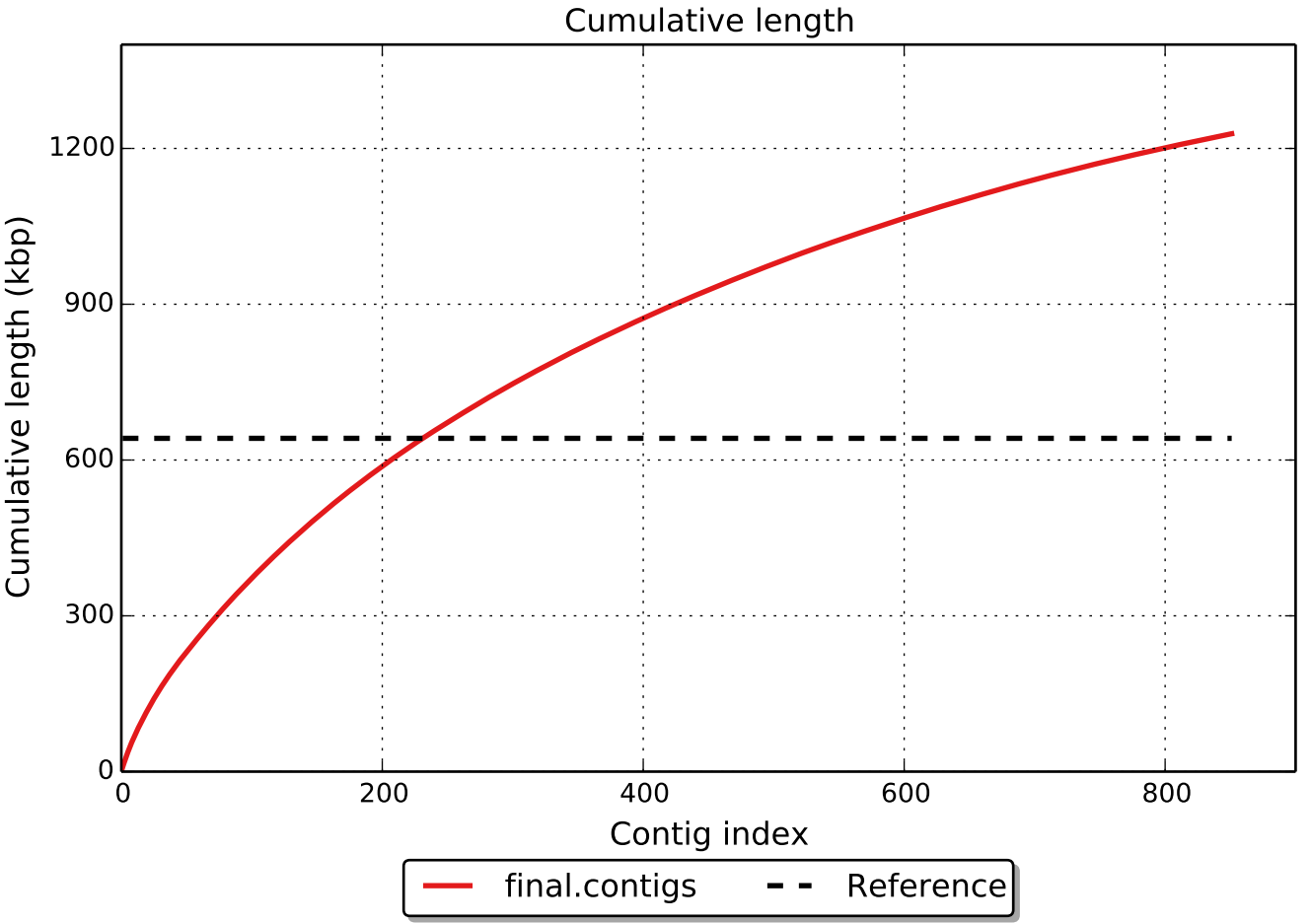
| | final.contigs |
|---|---|
| # misassemblies | 33 |
| # relocations | 33 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 1 |
| # misassembled contigs | 32 |
| Misassembled contigs length | 76798 |
| # local misassemblies | 0 |
| # mismatches | 10529 |
| # indels | 14 |
| # short indels | 14 |
| # long indels | 0 |
| Indels length | 14 |

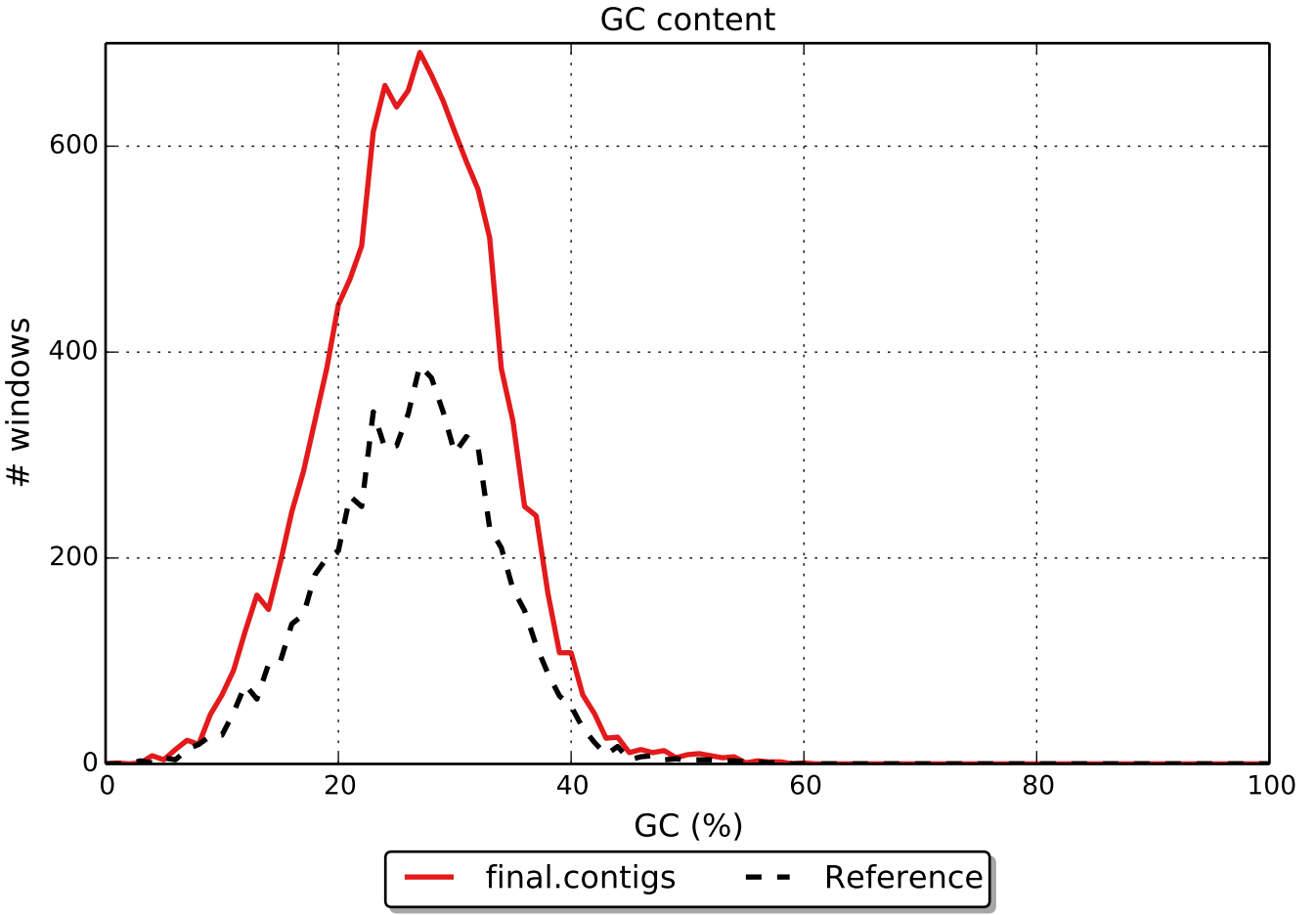
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

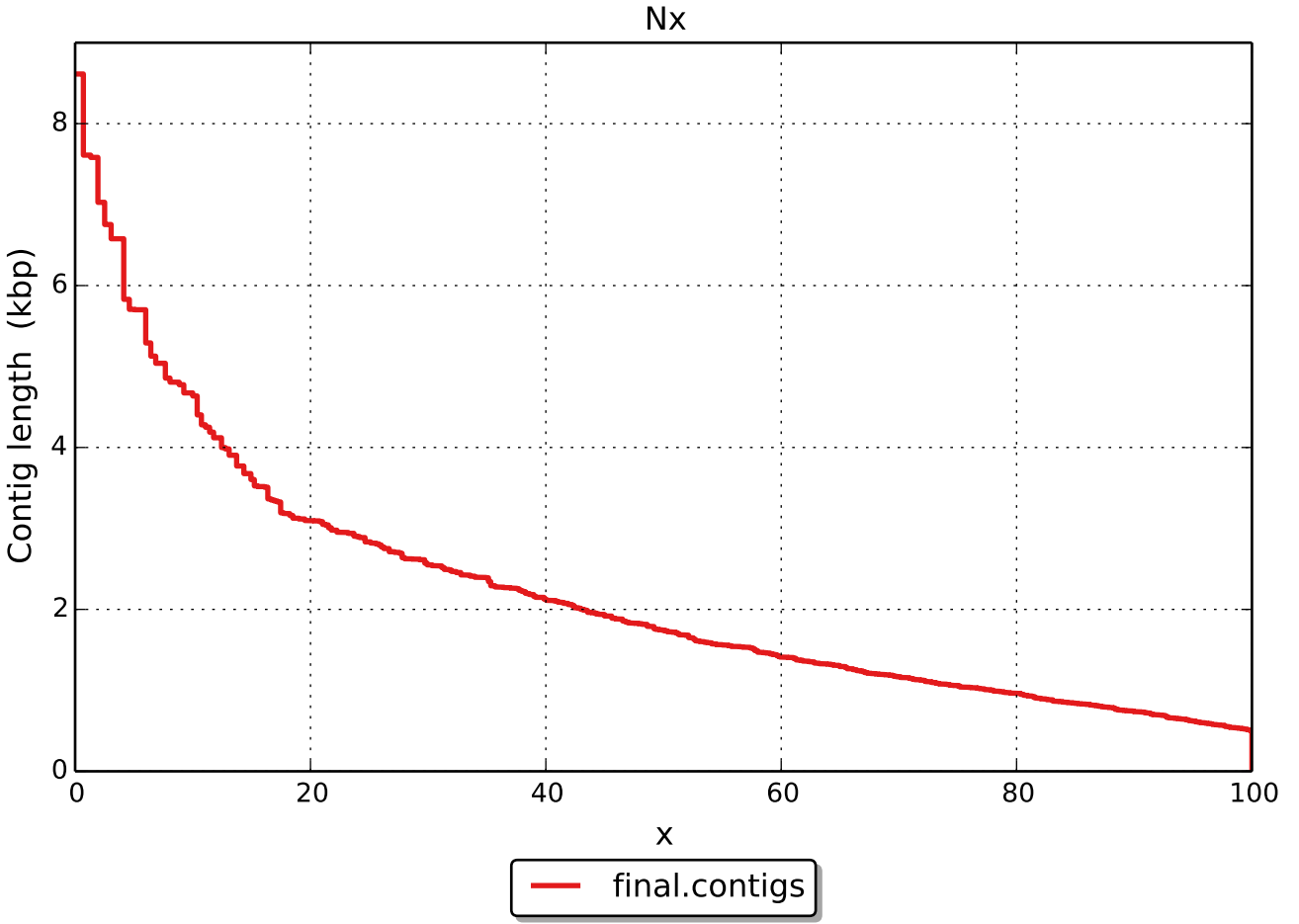
# Unaligned report

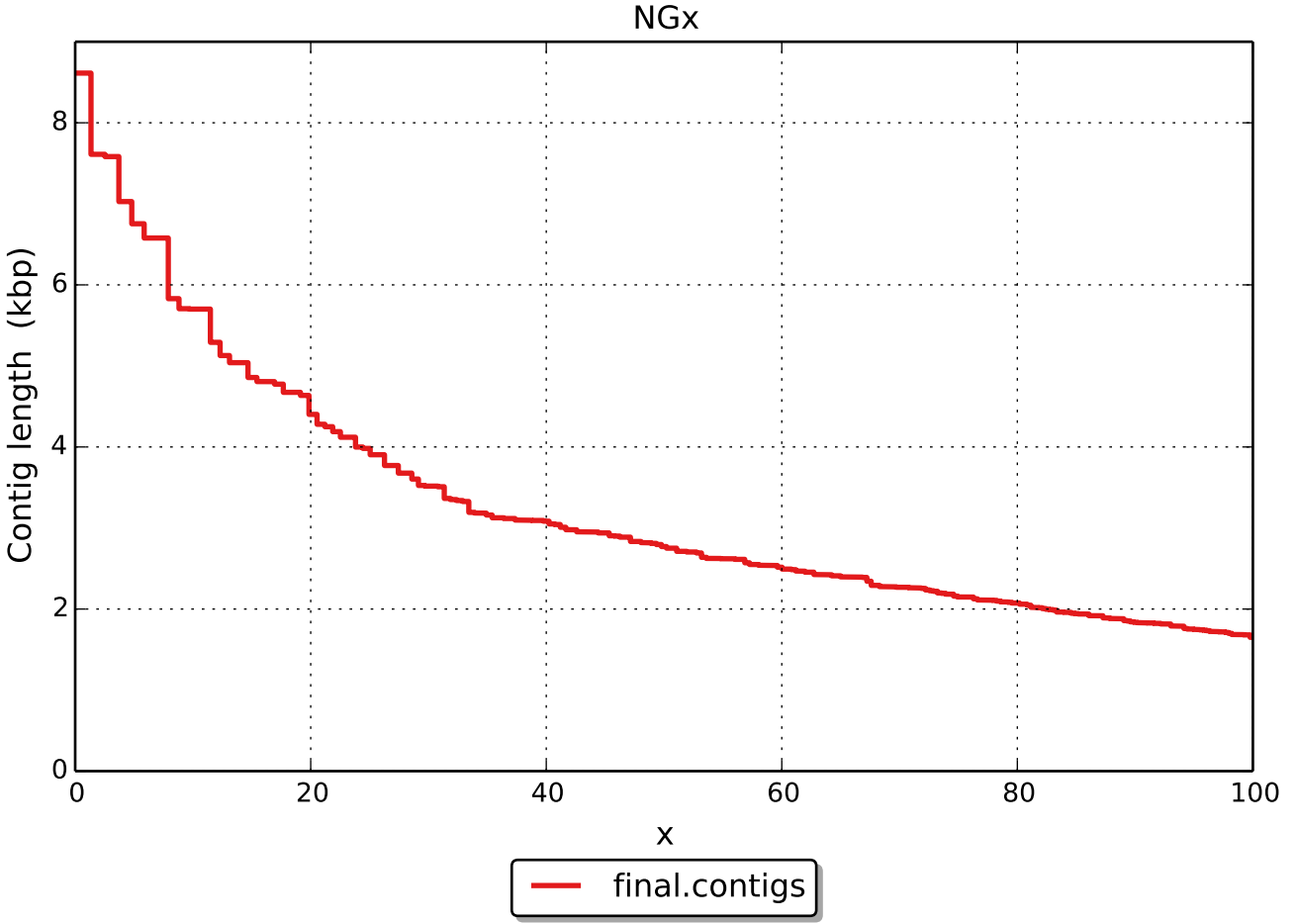
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 1 |
| Partially unaligned length | 589 |
| # N's | 0 |

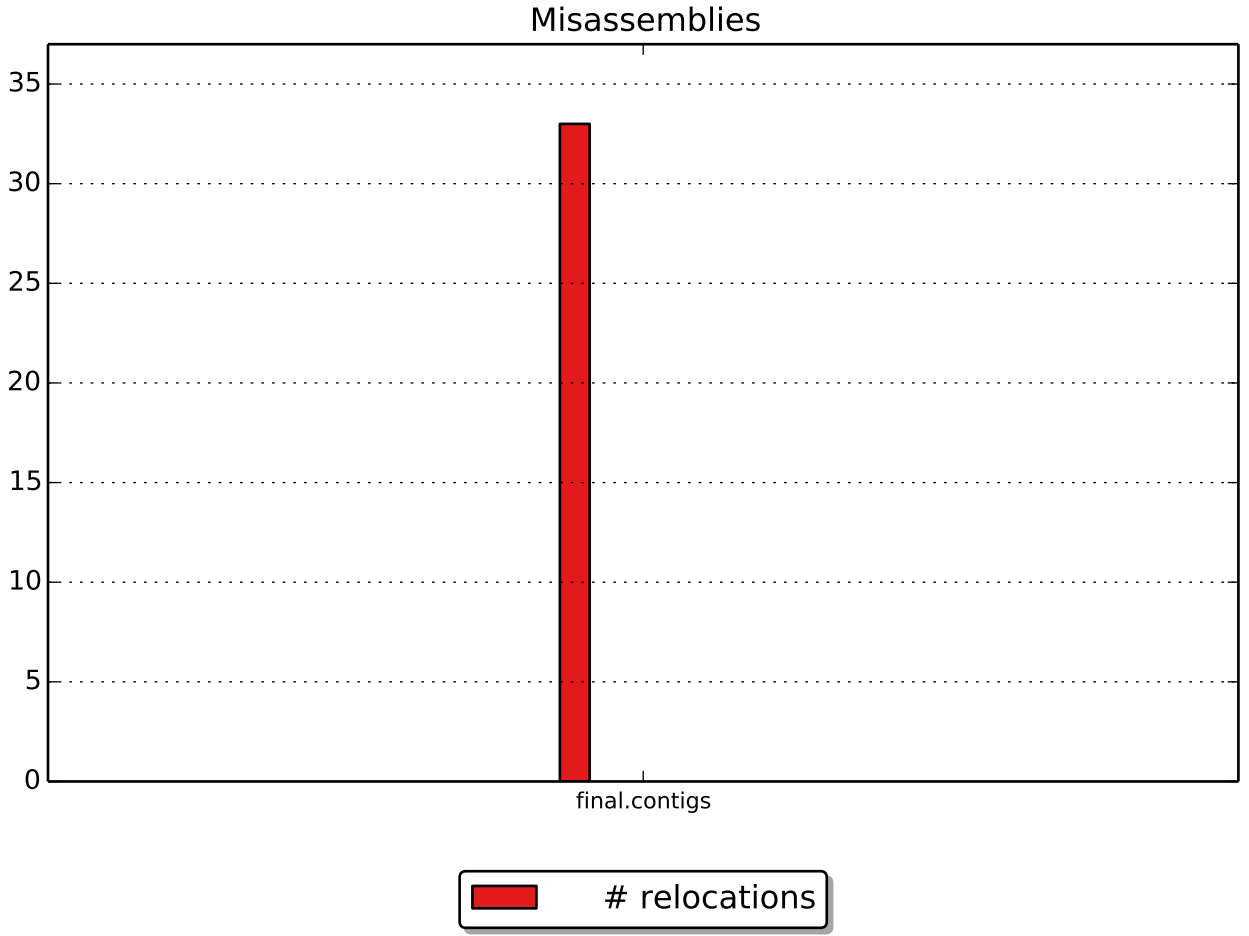
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

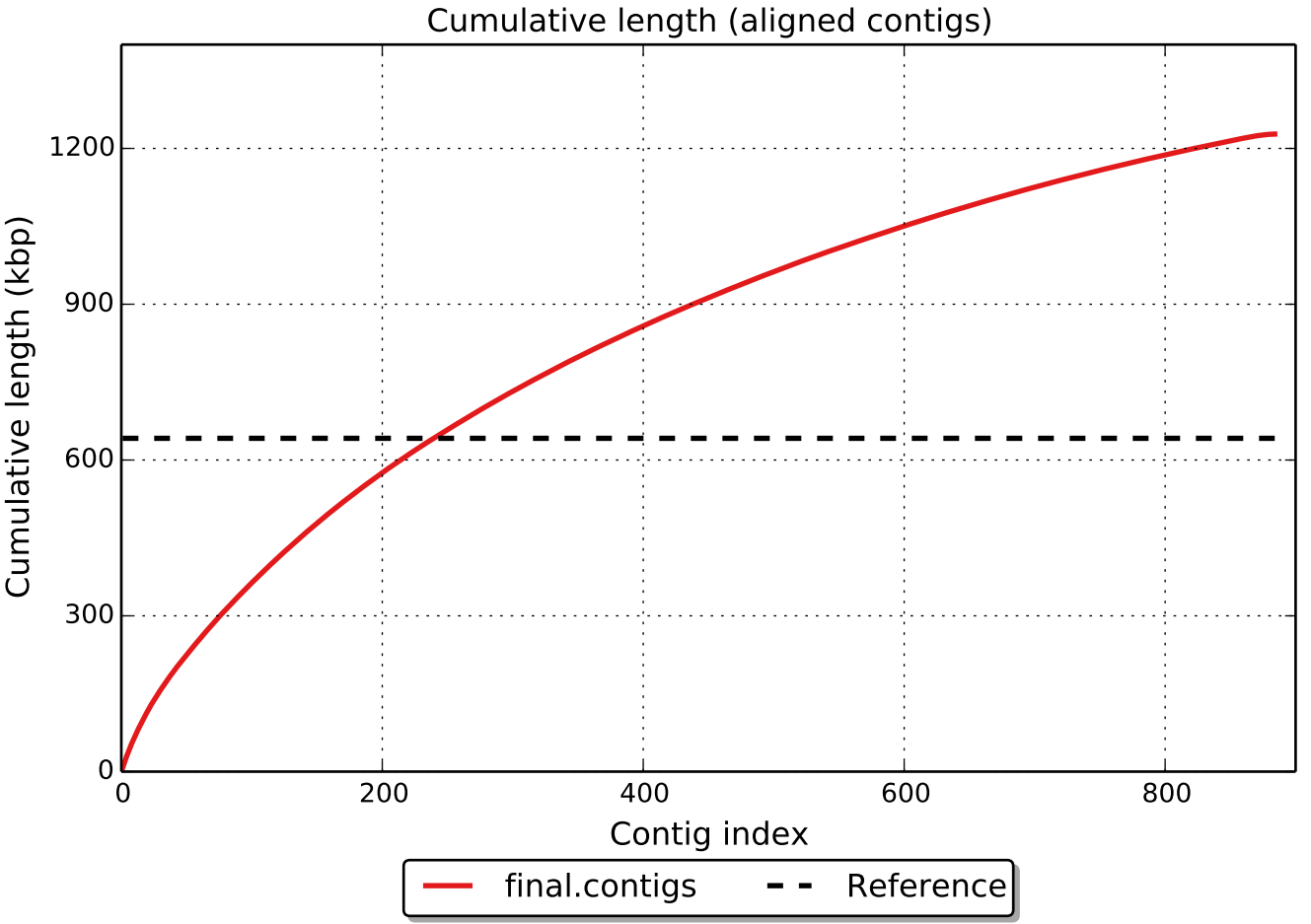

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
200
400
600
800
Contig index
final.contigs
Reference

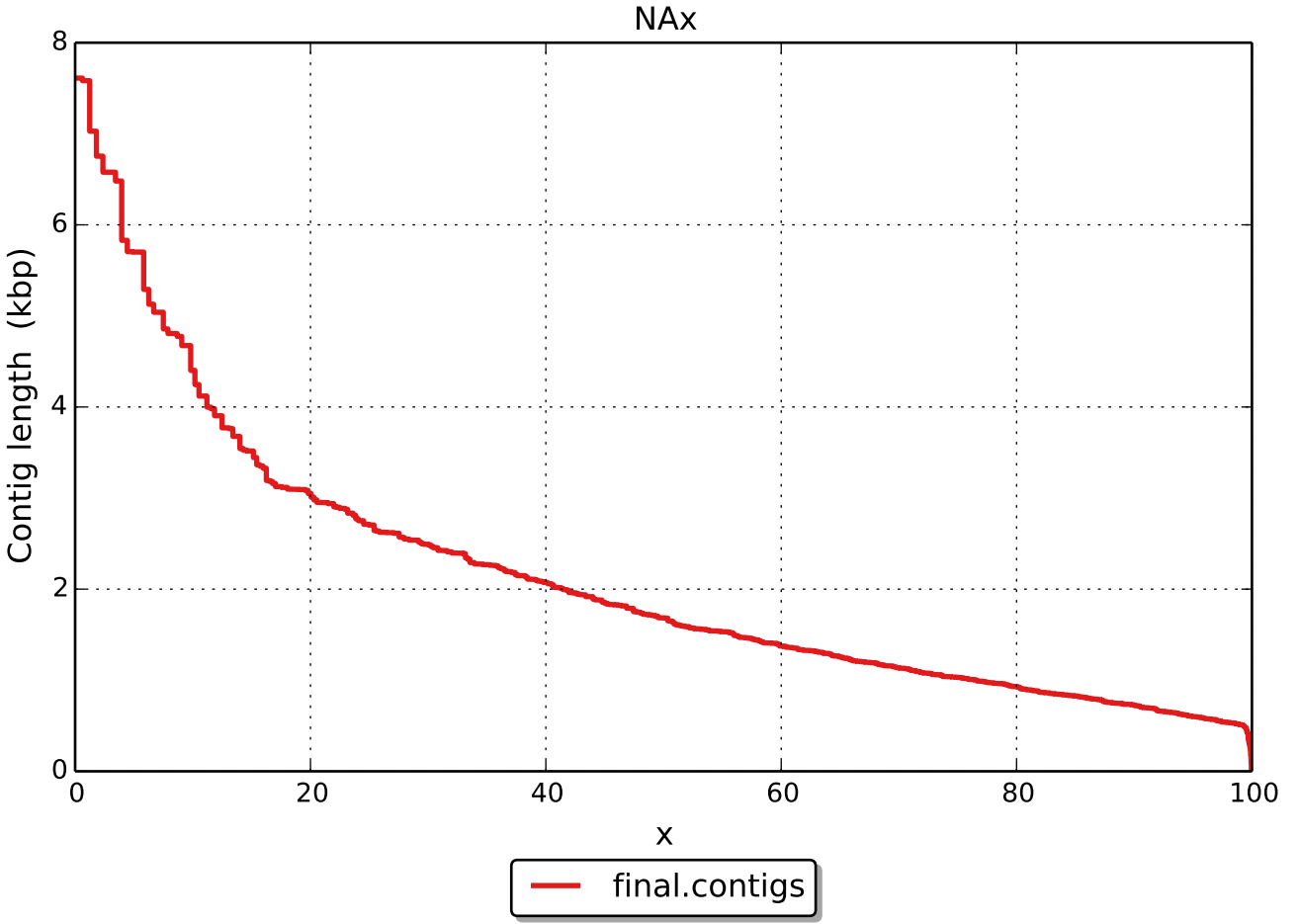

GC content
# windows
GC (%)
0
200
400
600
0
20
40
60
80
100
final.contigs
Reference

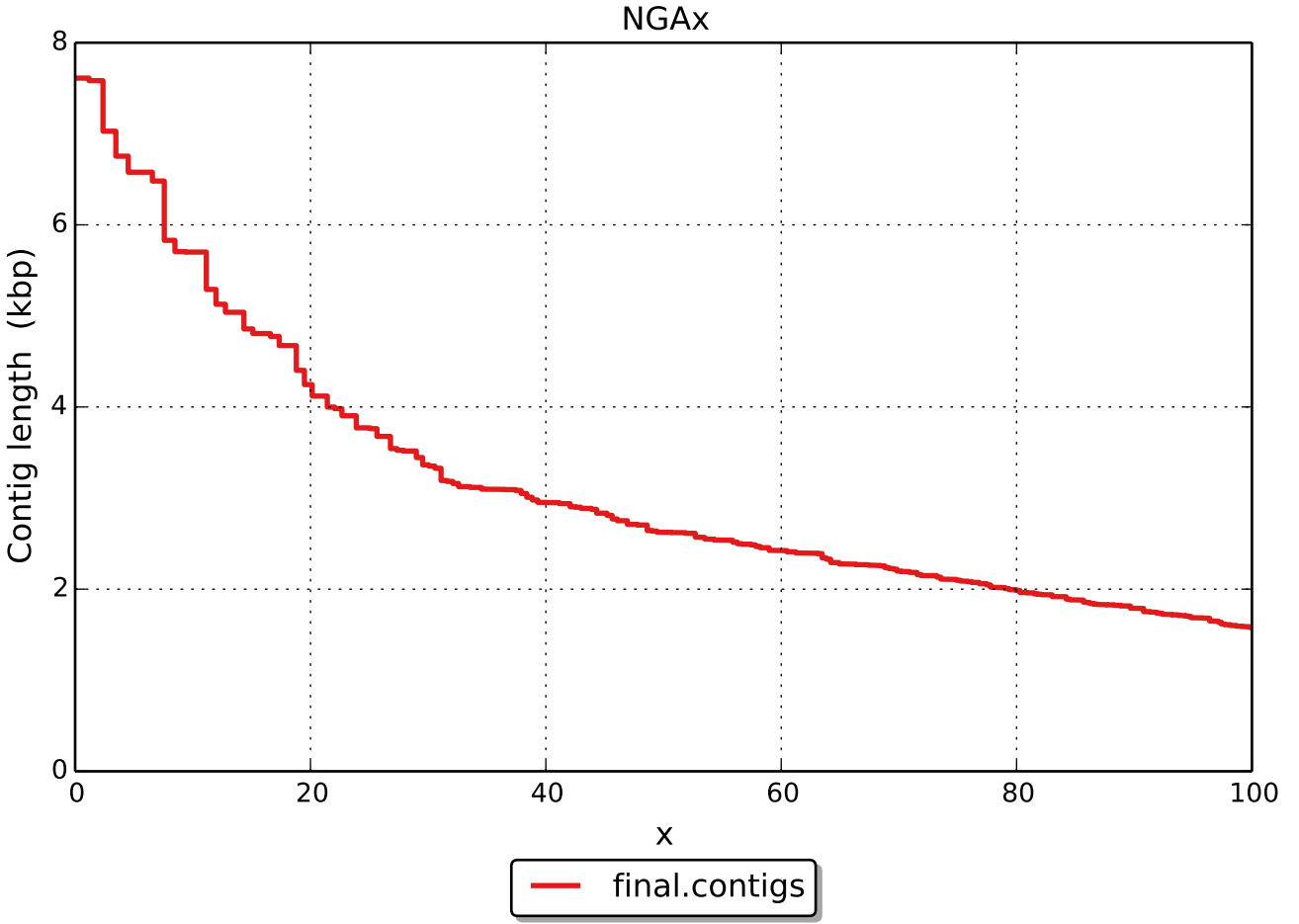

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


Misassemblies
35
30
25
20
15
10
5
0
final.contigs
# relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs