# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 1082 |
| # contigs (>= 1000 bp) | 401 |
| Total length (>= 0 bp) | 1083010 |
| Total length (>= 1000 bp) | 598099 |
| # contigs | 1082 |
| Largest contig | 4336 |
| Total length | 1083010 |
| Reference length | 615980 |
| GC (%) | 25.43 |
| Reference GC (%) | 25.34 |
| N50 | 1053 |
| NG50 | 1438 |
| N75 | 760 |
| NG75 | 1162 |
| L50 | 346 |
| LG50 | 155 |
| L75 | 645 |
| LG75 | 274 |
| # misassemblies | 17 |
| # misassembled contigs | 16 |
| Misassembled contigs length | 21539 |
| # local misassemblies | 0 |
| # unaligned contigs | 2 + 1 part |
| Unaligned length | 1386 |
| Genome fraction (%) | 90.495 |
| Duplication ratio | 1.940 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1406.45 |
| # indels per 100 kbp | 0.72 |
| Largest alignment | 4336 |
| NA50 | 1037 |
| NGA50 | 1409 |
| NA75 | 748 |
| NGA75 | 1156 |
| LA50 | 350 |
| LGA50 | 157 |
| LA75 | 652 |
| LGA75 | 277 |

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

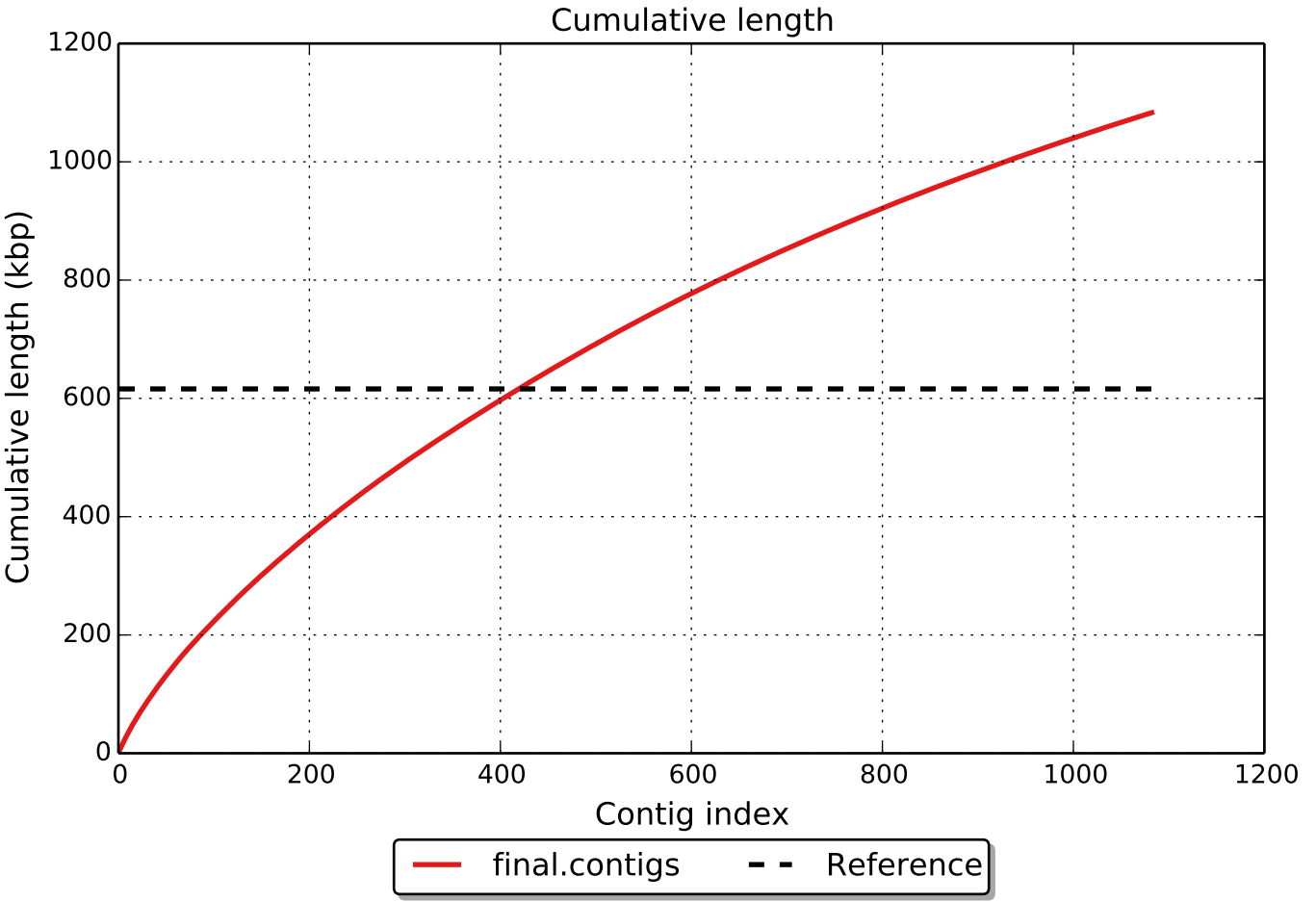
| | final.contigs |
|---|---|
| # misassemblies | 17 |
| # relocations | 17 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 16 |
| Misassembled contigs length | 21539 |
| # local misassemblies | 0 |
| # mismatches | 7840 |
| # indels | 4 |
| # short indels | 4 |
| # long indels | 0 |
| Indels length | 4 |

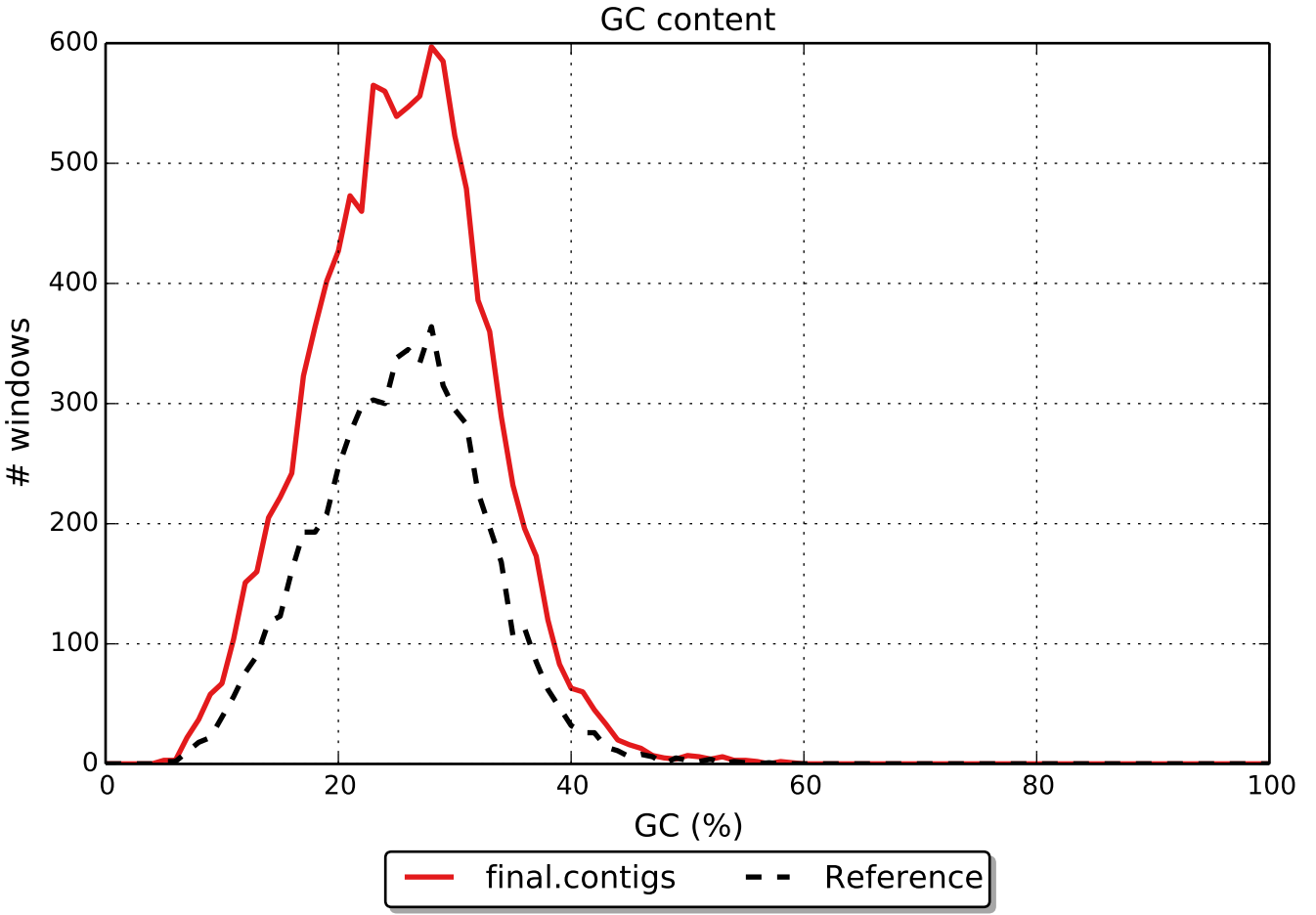
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

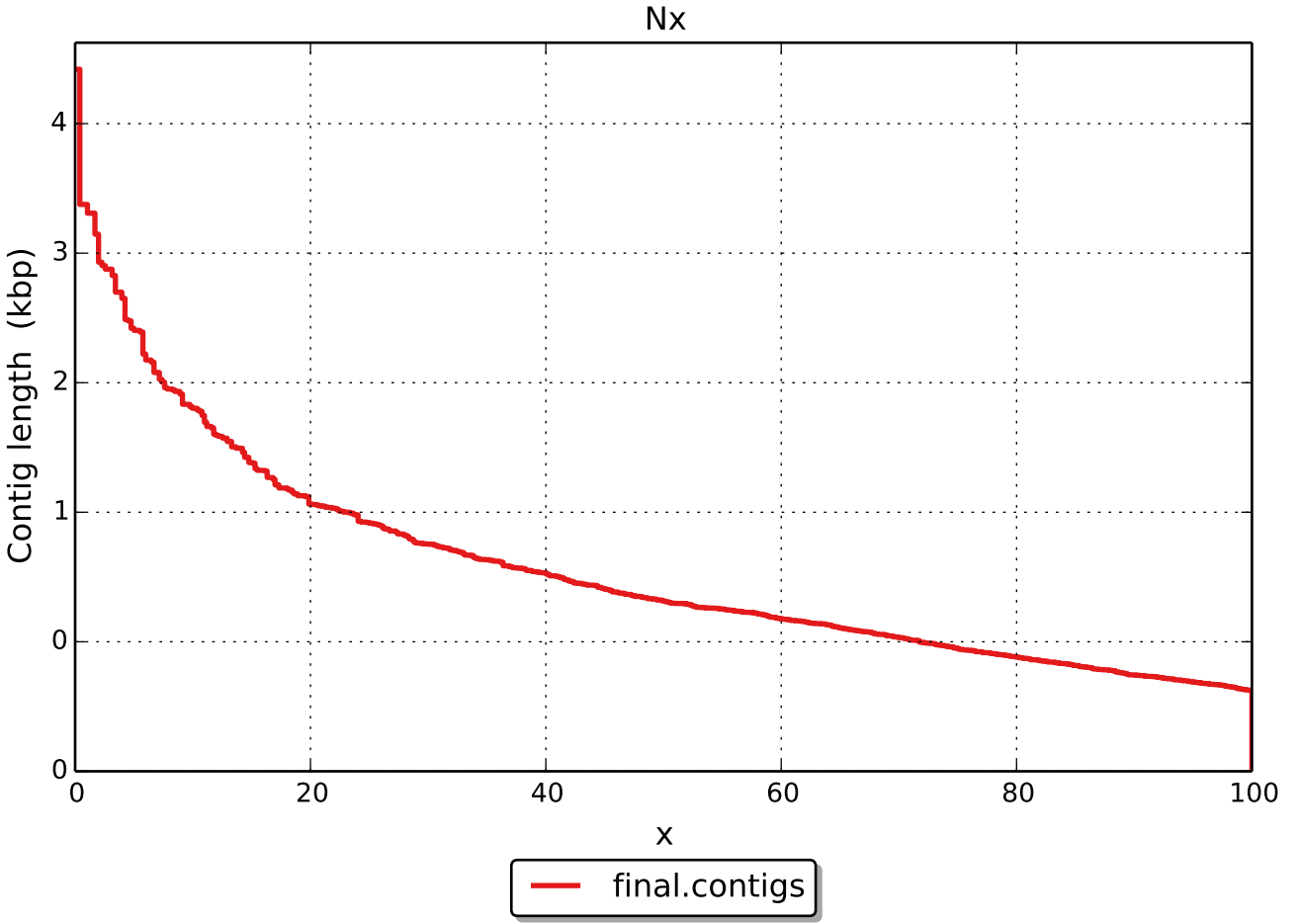
# Unaligned report

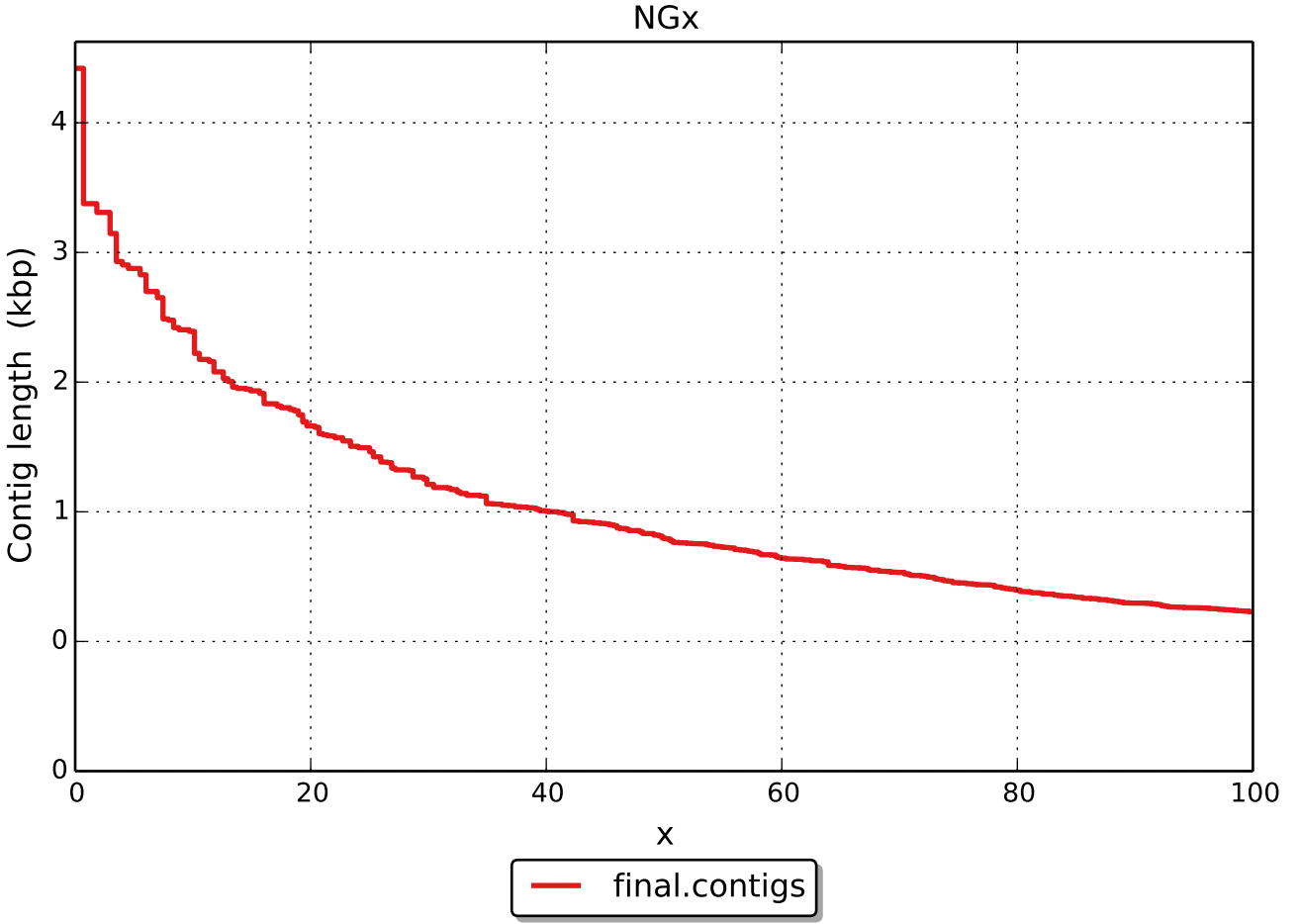
| | final.contigs |
|---|---|
| # fully unaligned contigs | 2 |
| Fully unaligned length | 1205 |
| # partially unaligned contigs | 1 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 181 |
| # N's | 0 |

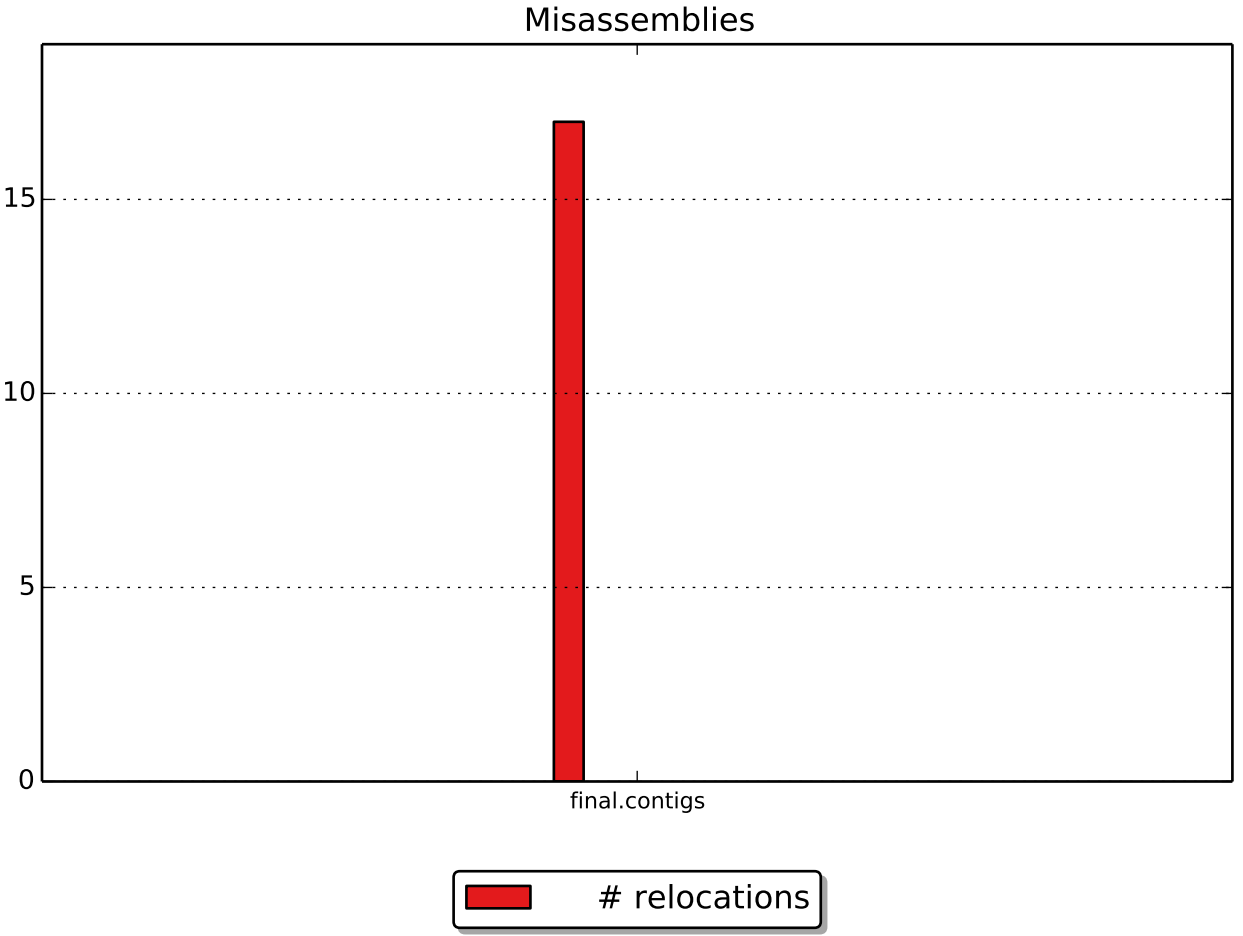
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

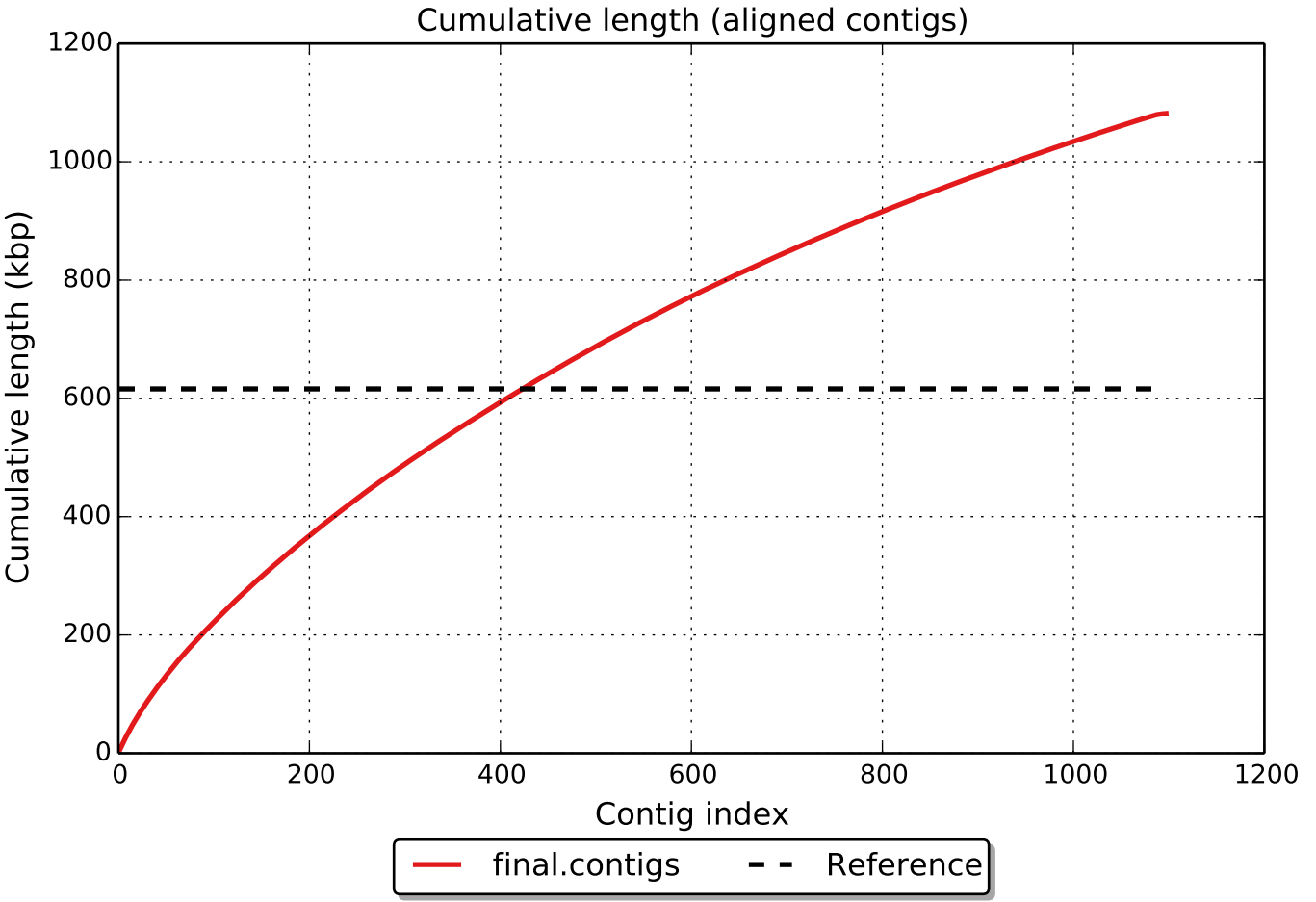

Cumulative length
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference

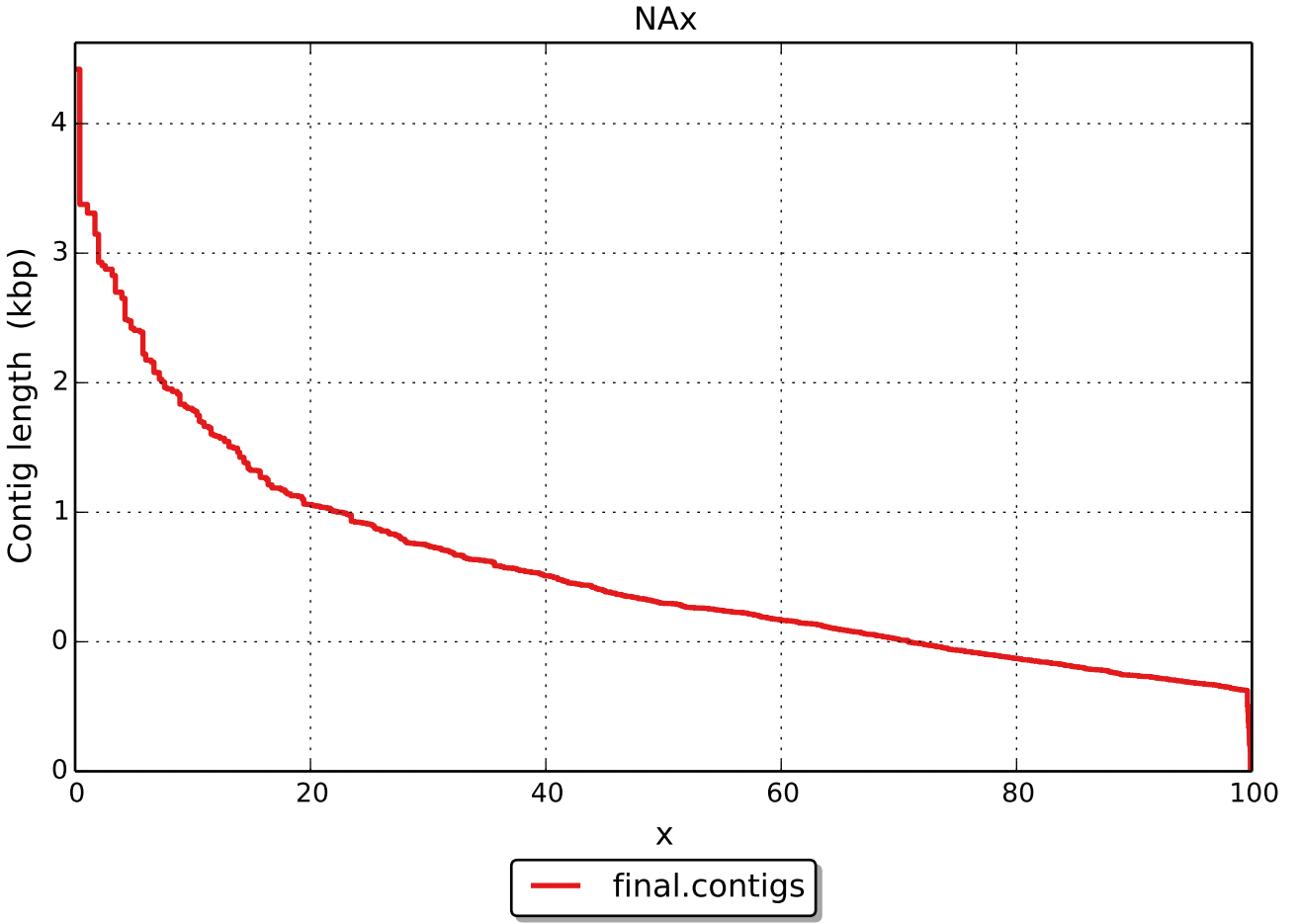

GC content
600
500
400
300
200
100
0
# windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

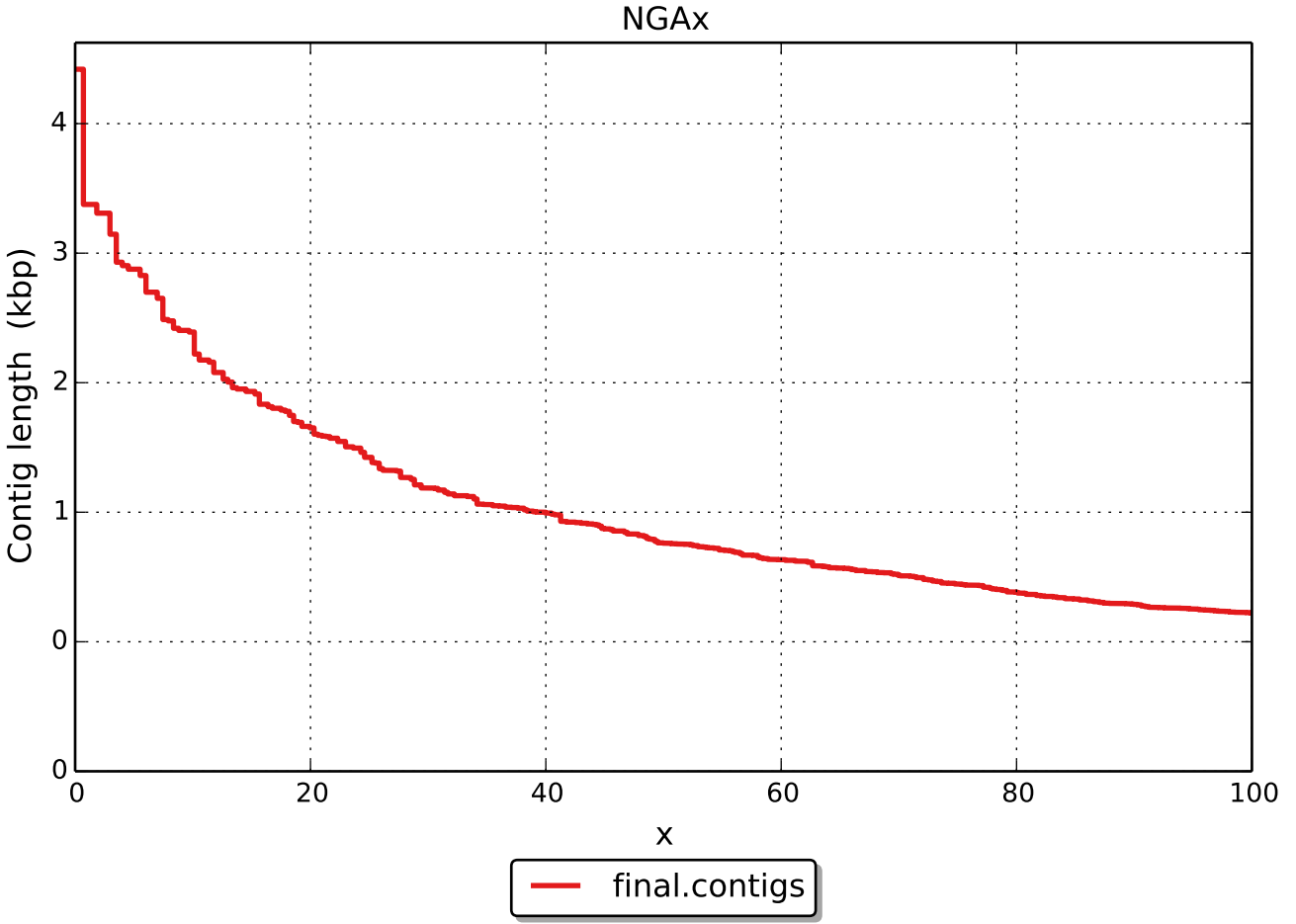

Nx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
15
10
5
0
final.contigs
# relocations


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


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


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