# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 1087 |
| # contigs (>= 1000 bp) | 349 |
| Total length (>= 0 bp) | 1000855 |
| Total length (>= 1000 bp) | 478013 |
| # contigs | 1087 |
| Largest contig | 3516 |
| Total length | 1000855 |
| Reference length | 615980 |
| GC (%) | 25.37 |
| Reference GC (%) | 25.35 |
| N50 | 972 |
| NG50 | 1202 |
| N75 | 727 |
| NG75 | 1010 |
| L50 | 372 |
| LG50 | 192 |
| L75 | 672 |
| LG75 | 334 |
| # misassemblies | 20 |
| # misassembled contigs | 20 |
| Misassembled contigs length | 21819 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 90.169 |
| Duplication ratio | 1.802 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1293.61 |
| # indels per 100 kbp | 0.72 |
| Largest alignment | 3360 |
| NA50 | 963 |
| NGA50 | 1195 |
| NA75 | 716 |
| NGA75 | 1008 |
| LA50 | 375 |
| LGA50 | 194 |
| LA75 | 677 |
| LGA75 | 336 |

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

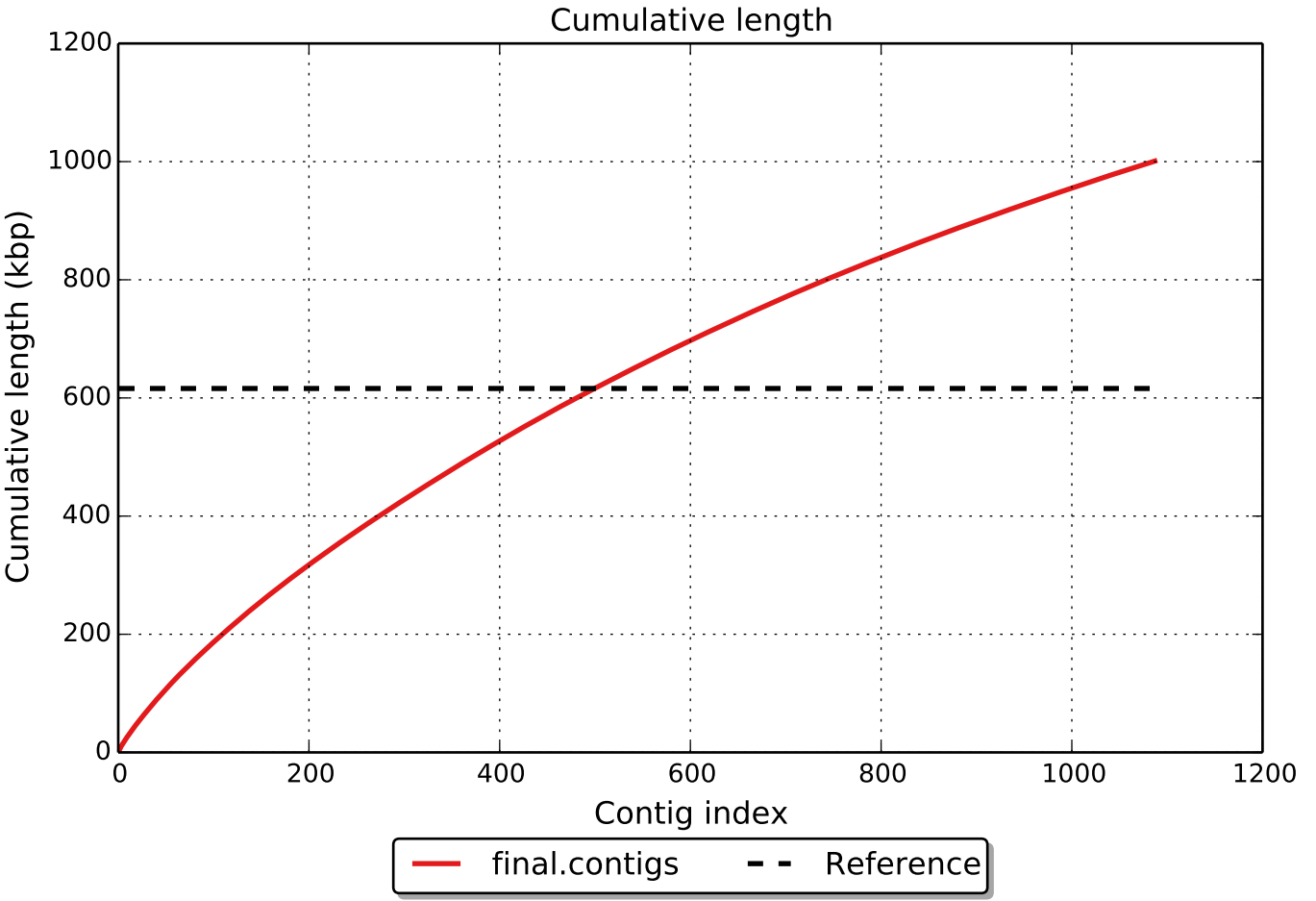
| | final.contigs |
|---|---|
| # misassemblies | 20 |
| # relocations | 20 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 20 |
| Misassembled contigs length | 21819 |
| # local misassemblies | 0 |
| # mismatches | 7185 |
| # indels | 4 |
| # short indels | 4 |
| # long indels | 0 |
| Indels length | 4 |

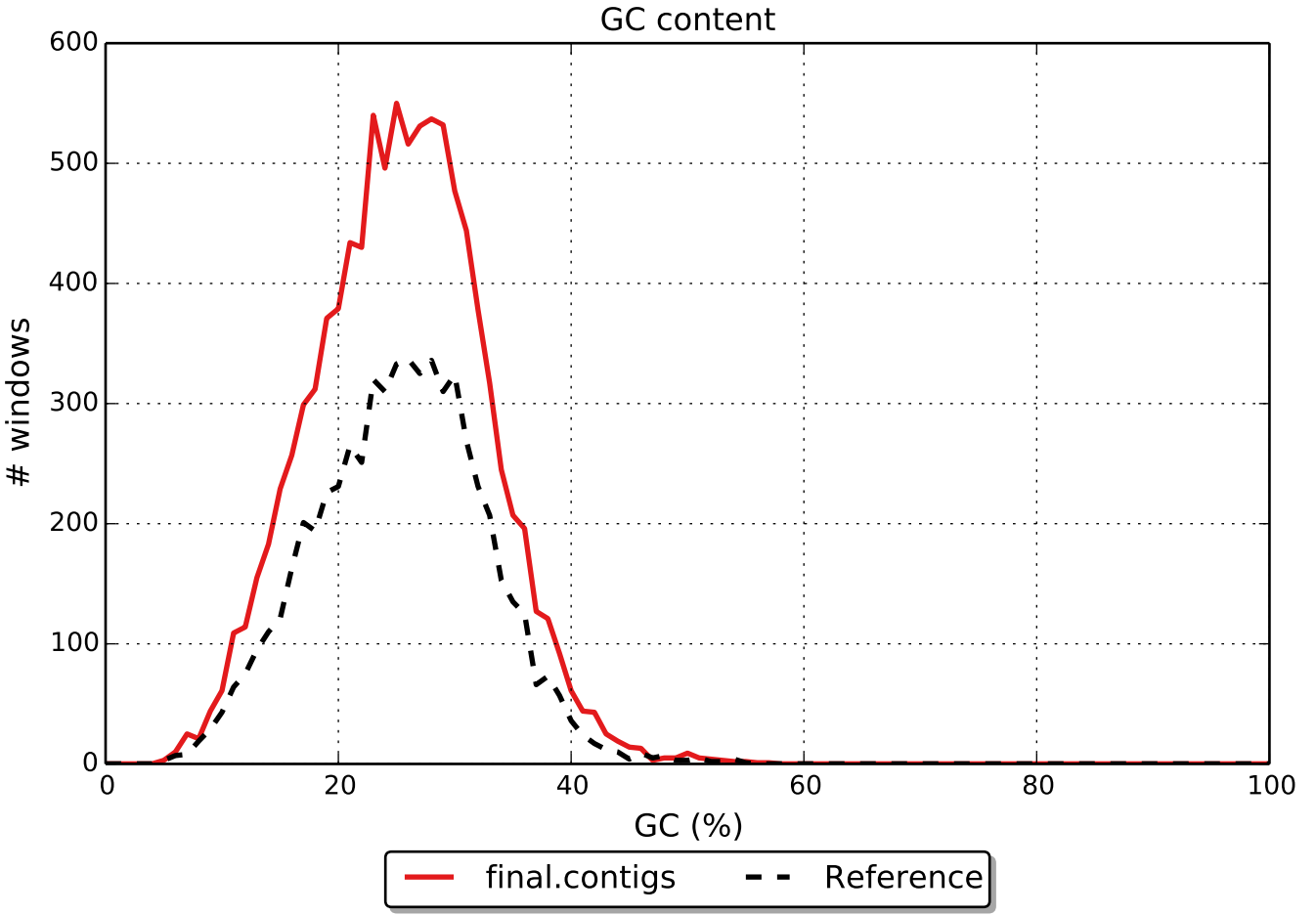
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

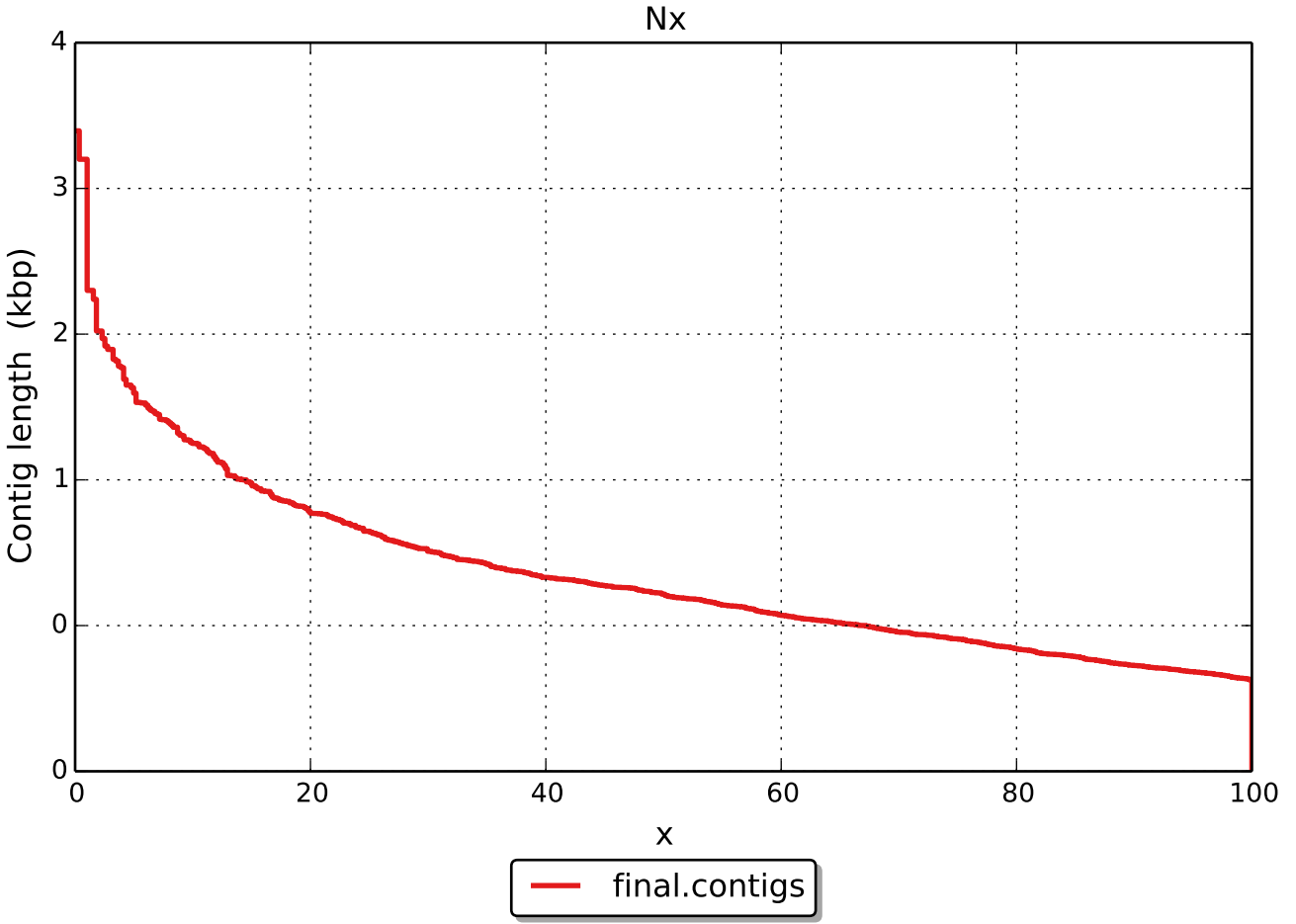
# Unaligned report

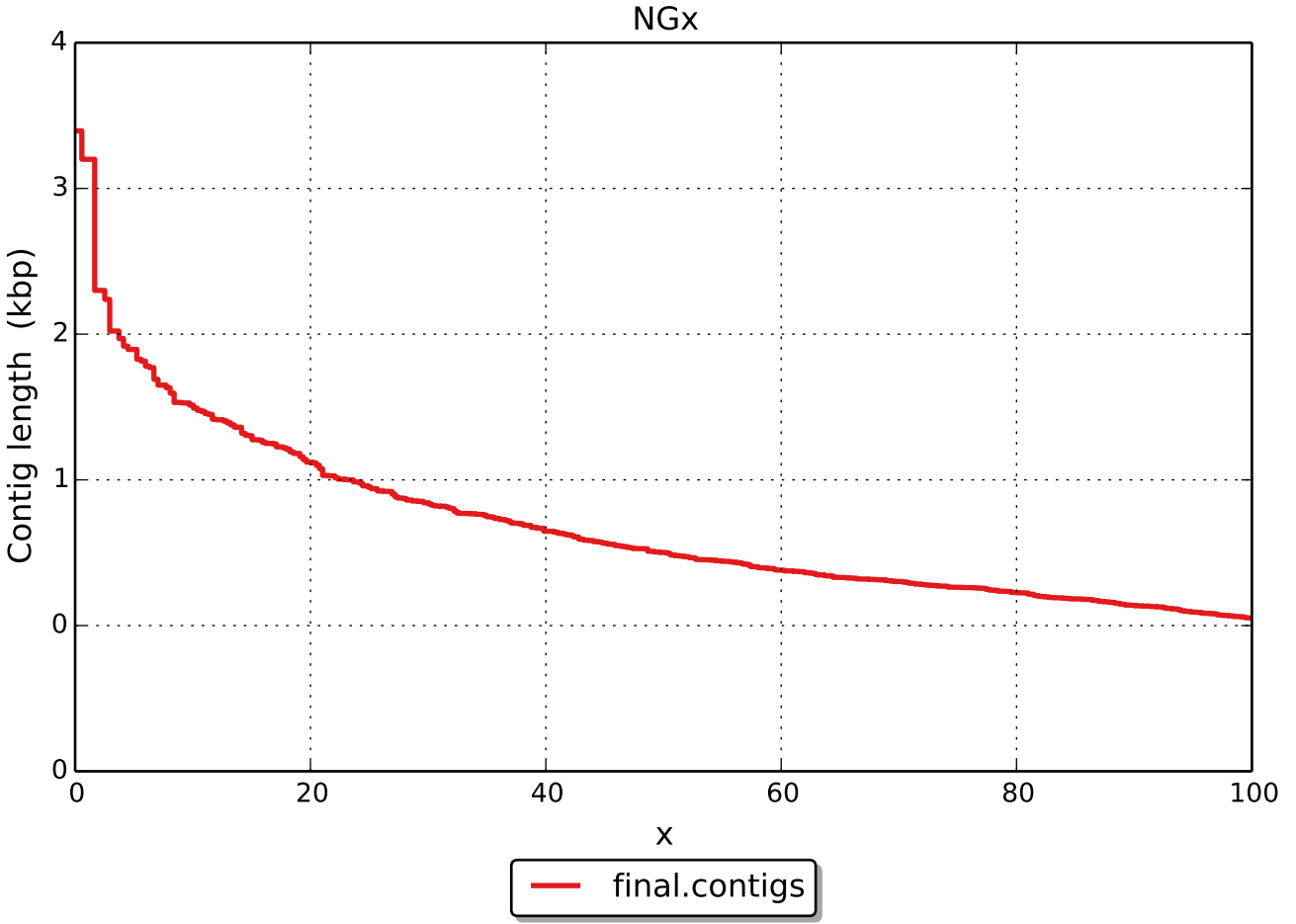
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

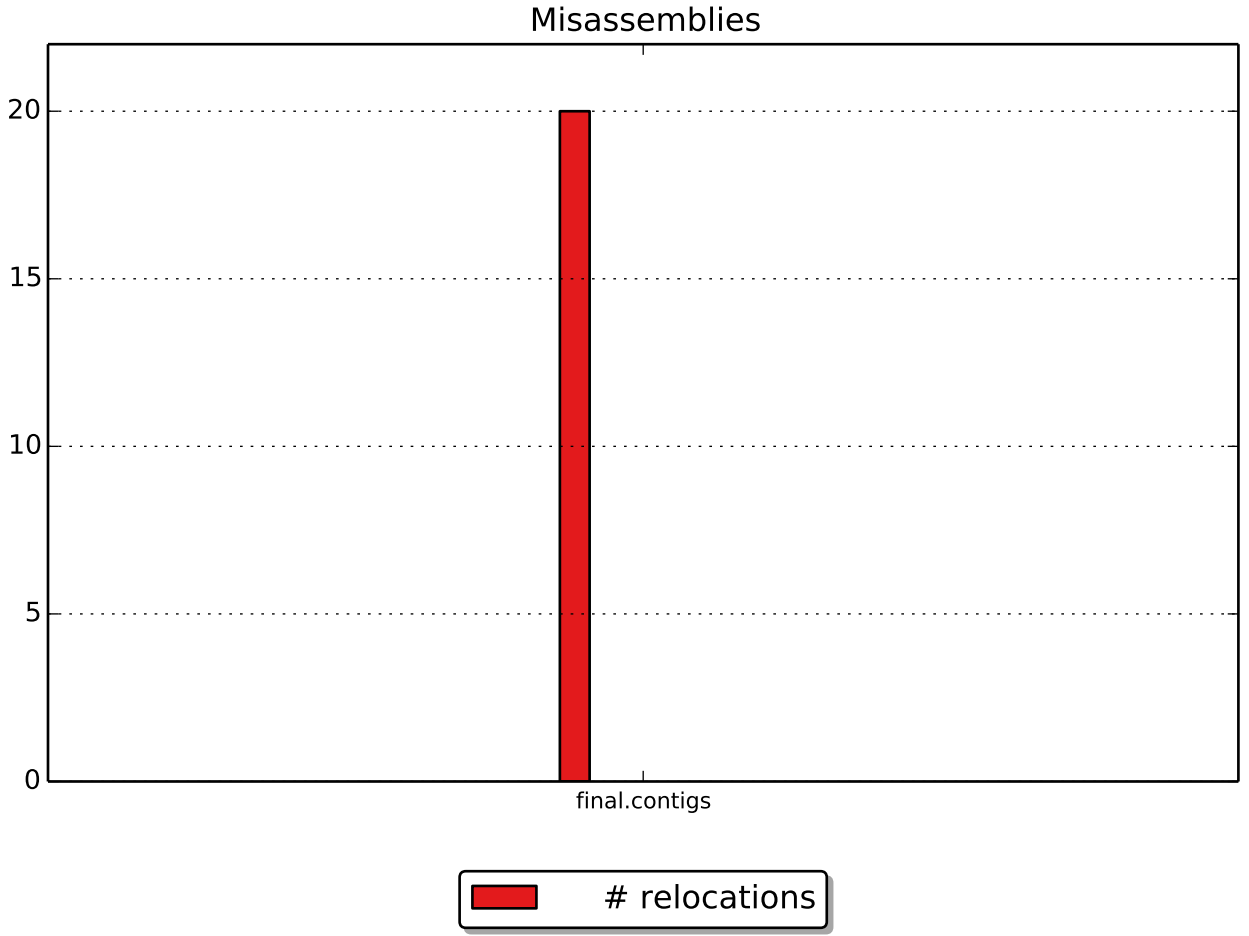
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

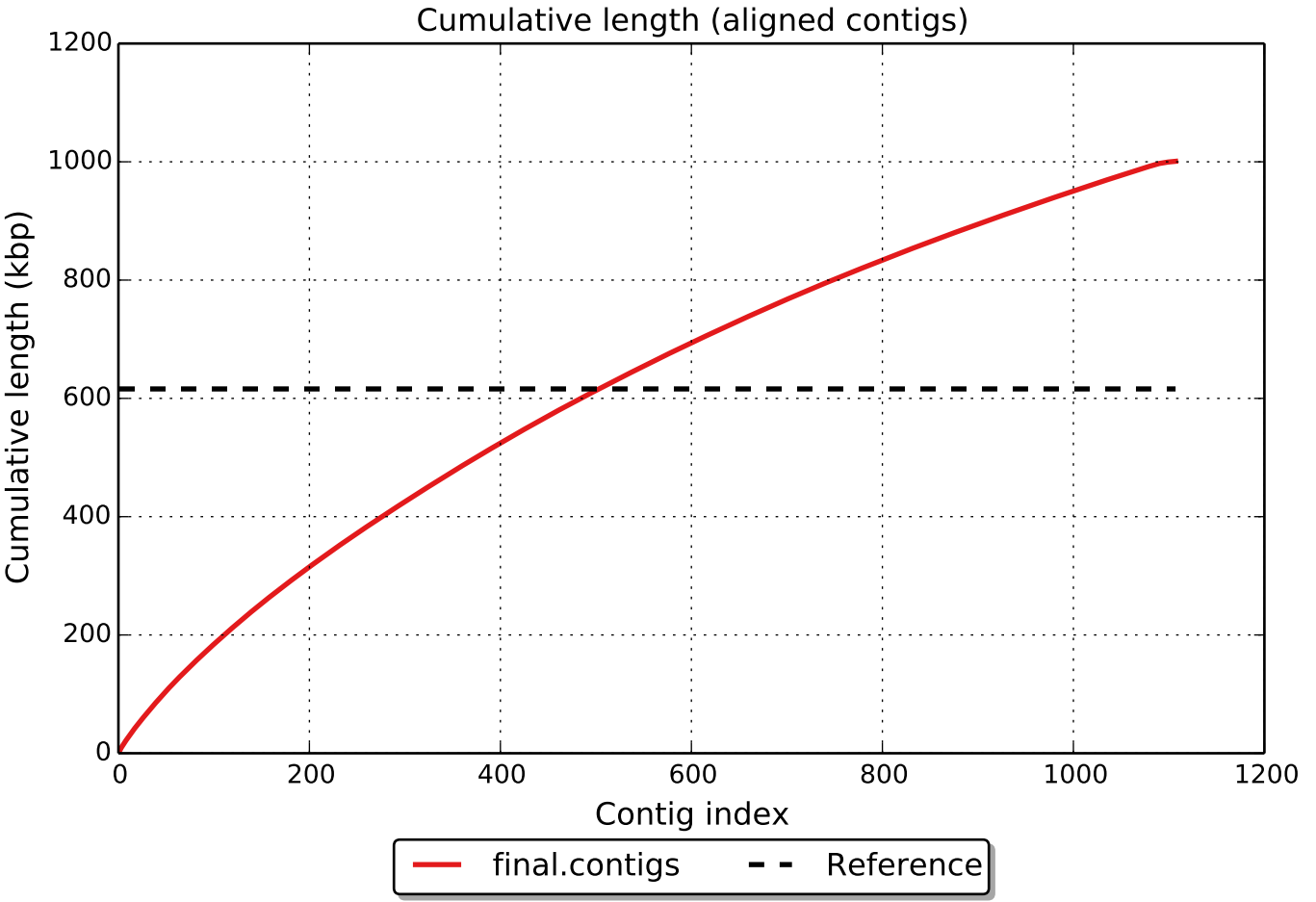

Cumulative length
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference

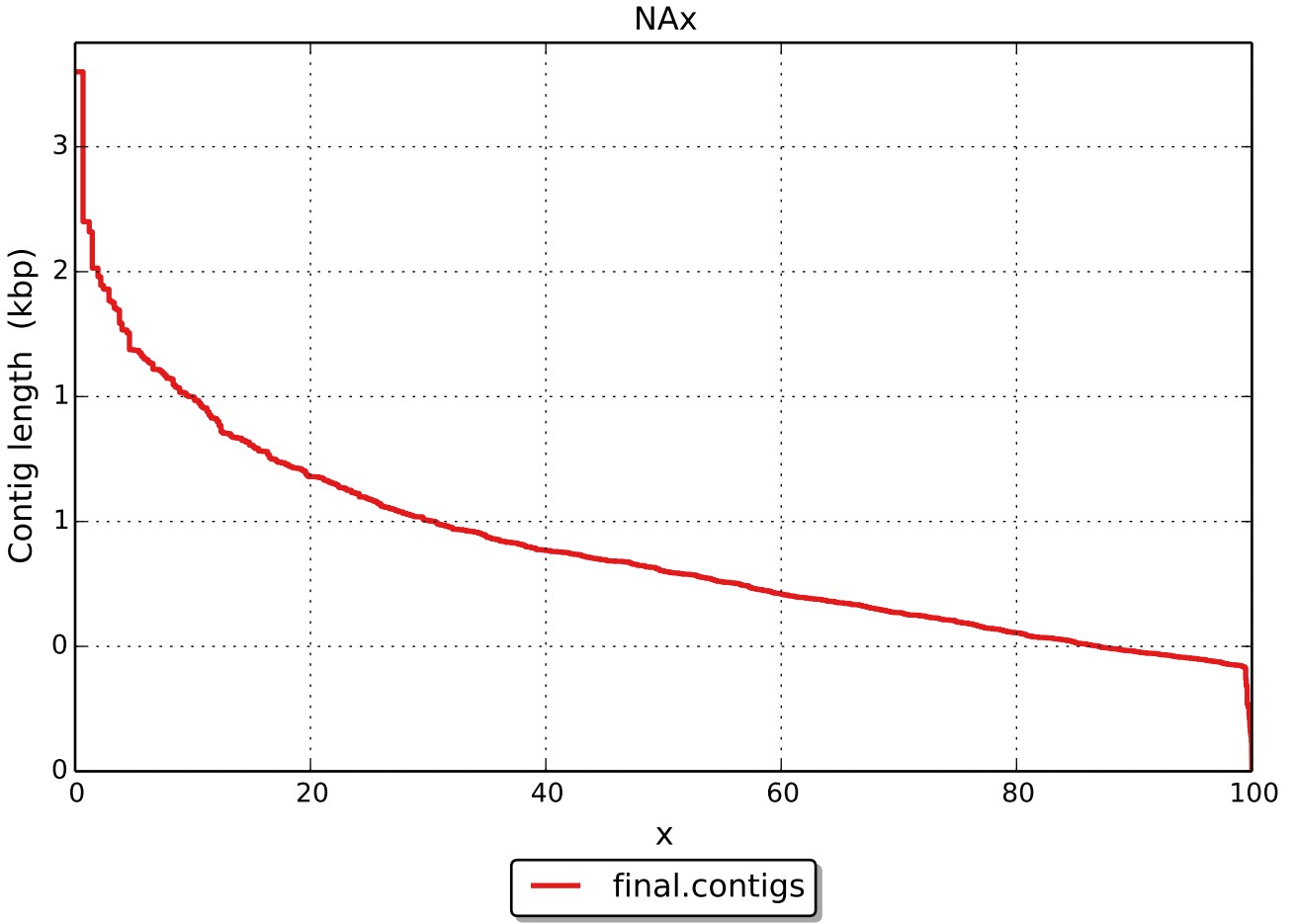

GC content
600
500
400
300
200
100
0
# windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

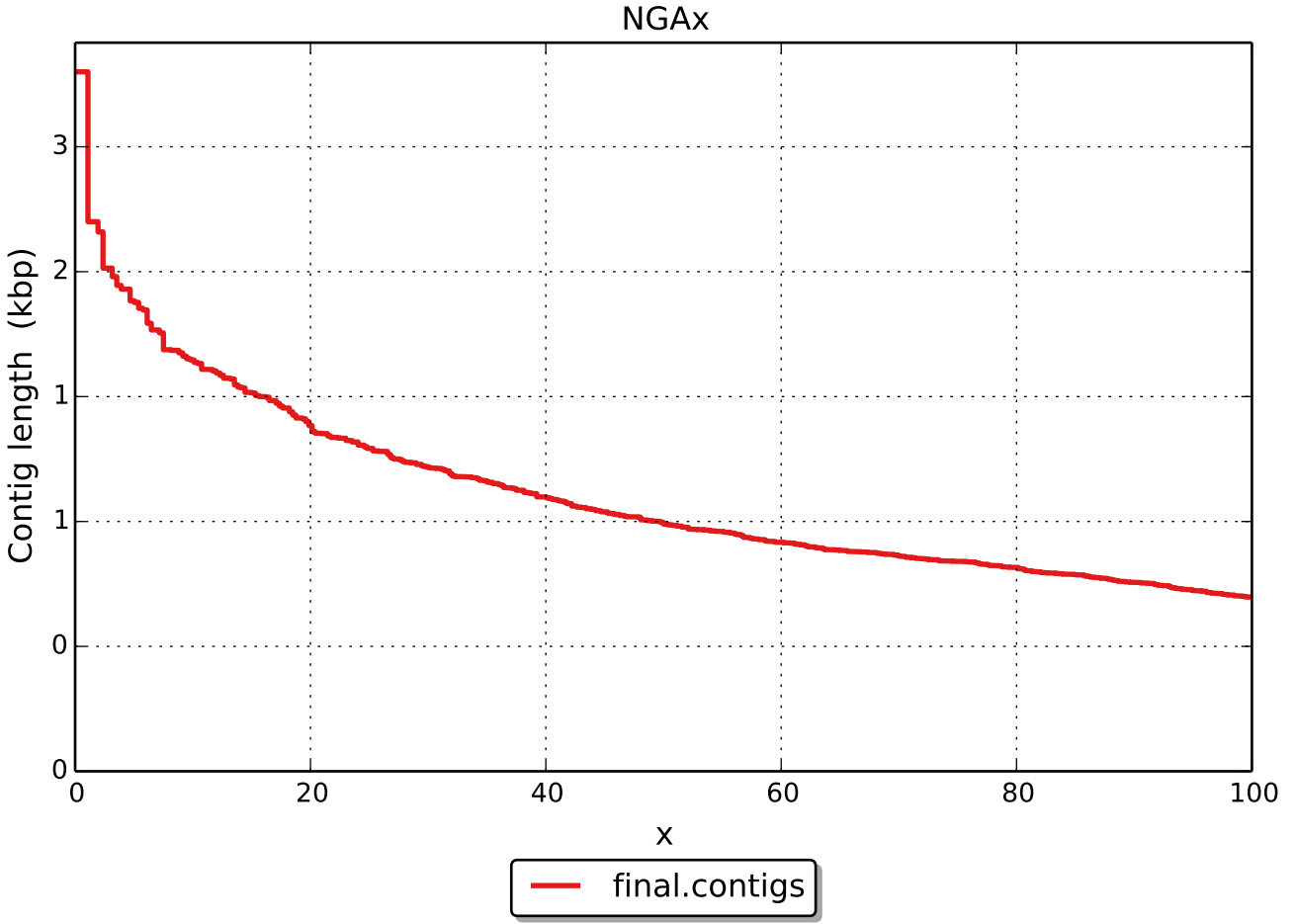

Nx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
20
15
10
5
0
final.contigs
# relocations


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


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


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