Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 516 |
| # contigs (>= 1000 bp) | 354 |
| Total length (>= 0 bp) | 1261696 |
| Total length (>= 1000 bp) | 1166163 |
| # contigs | 450 |
| Largest contig | 17588 |
| Total length | 1236944 |
| Reference length | 1231960 |
| GC (%) | 25.38 |
| Reference GC (%) | 25.34 |
| N50 | 3892 |
| NG50 | 3892 |
| N75 | 2341 |
| NG75 | 2360 |
| L50 | 99 |
| LG50 | 99 |
| L75 | 202 |
| LG75 | 200 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 97.682 |
| Duplication ratio | 1.028 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 26.84 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 17588 |
| NA50 | 3892 |
| NGA50 | 3892 |
| NA75 | 2341 |
| NGA75 | 2360 |
| LA50 | 99 |
| LGA50 | 99 |
| LA75 | 202 |
| LGA75 | 200 |

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

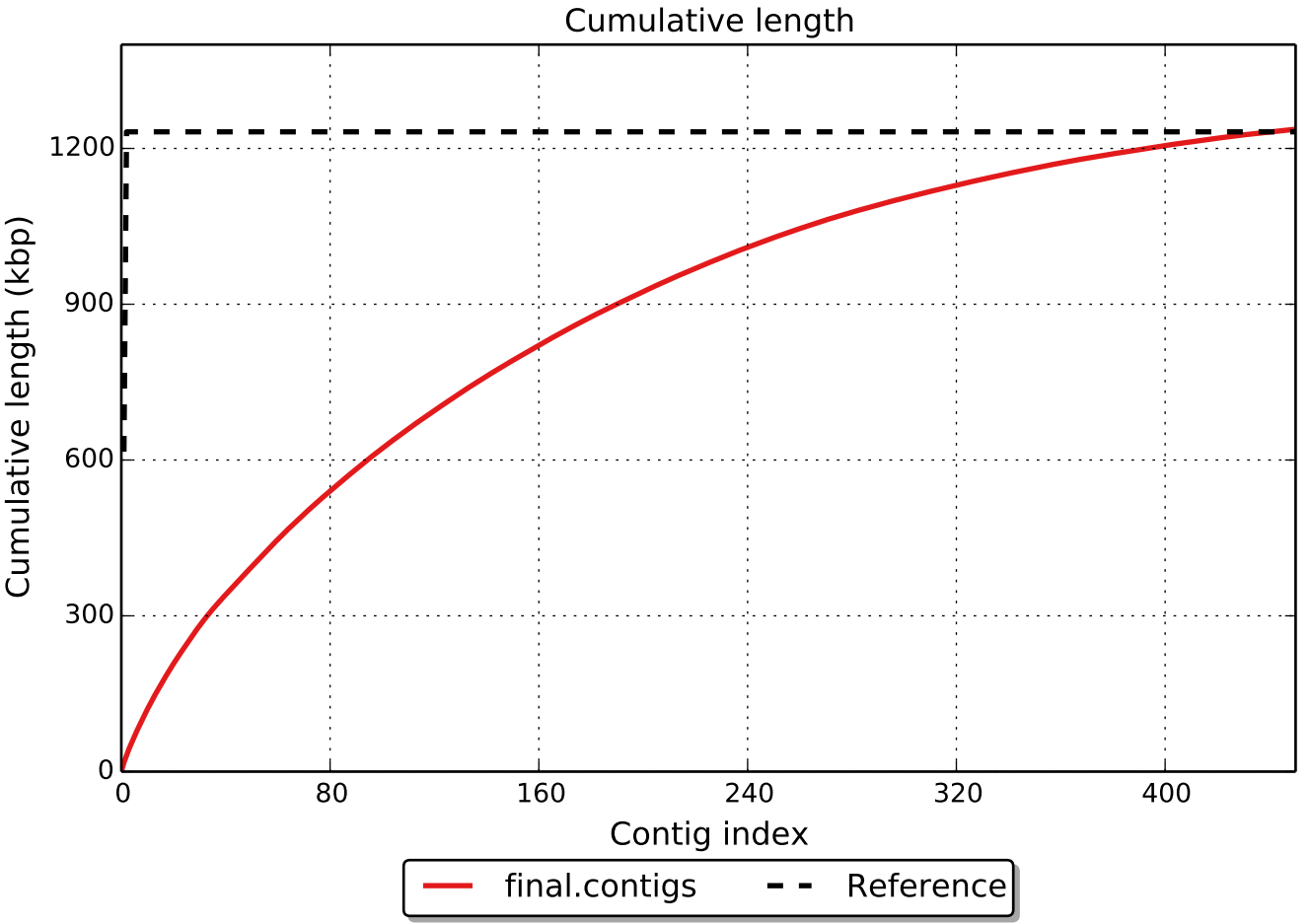
| | final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 323 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

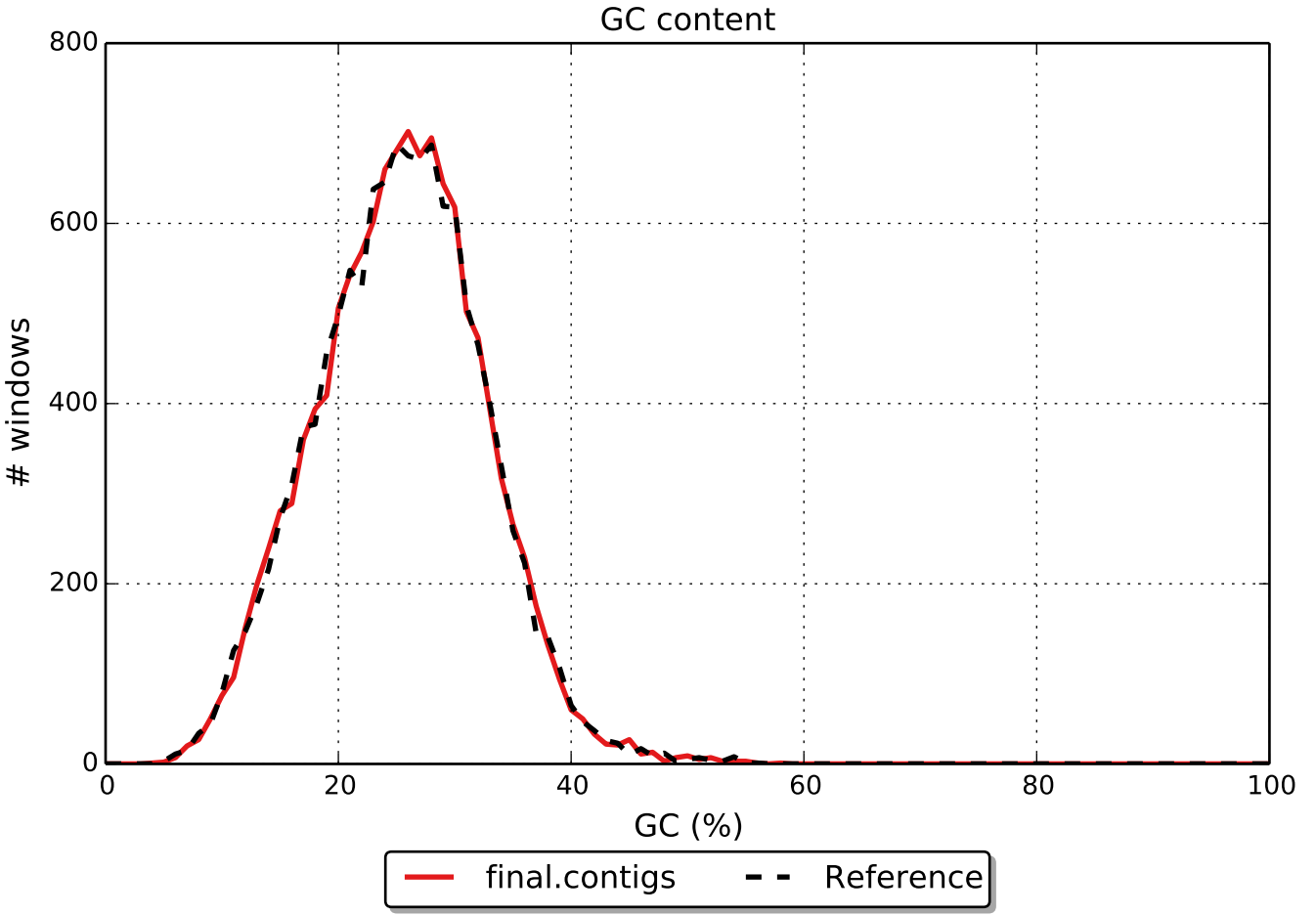
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

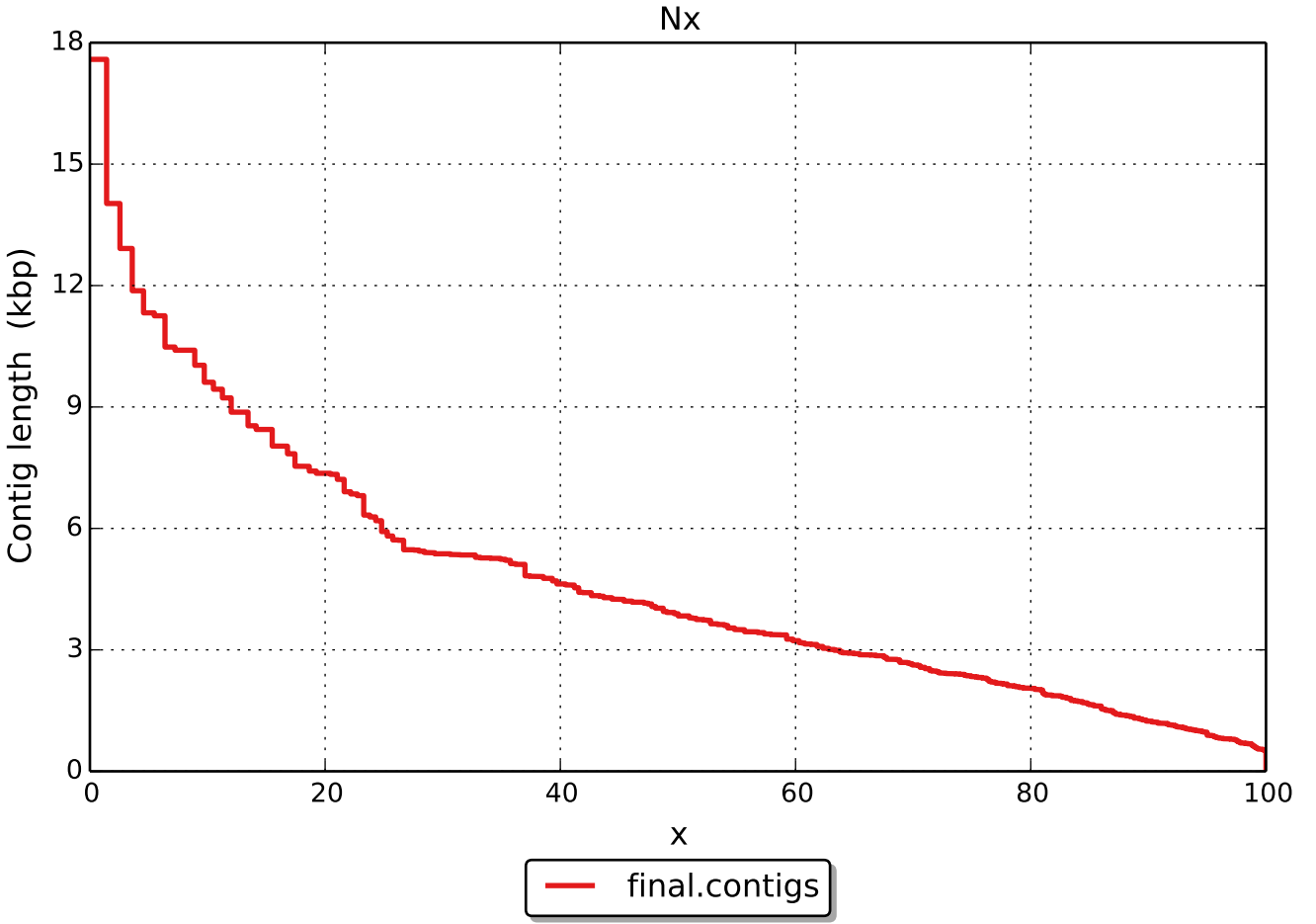
# Unaligned report

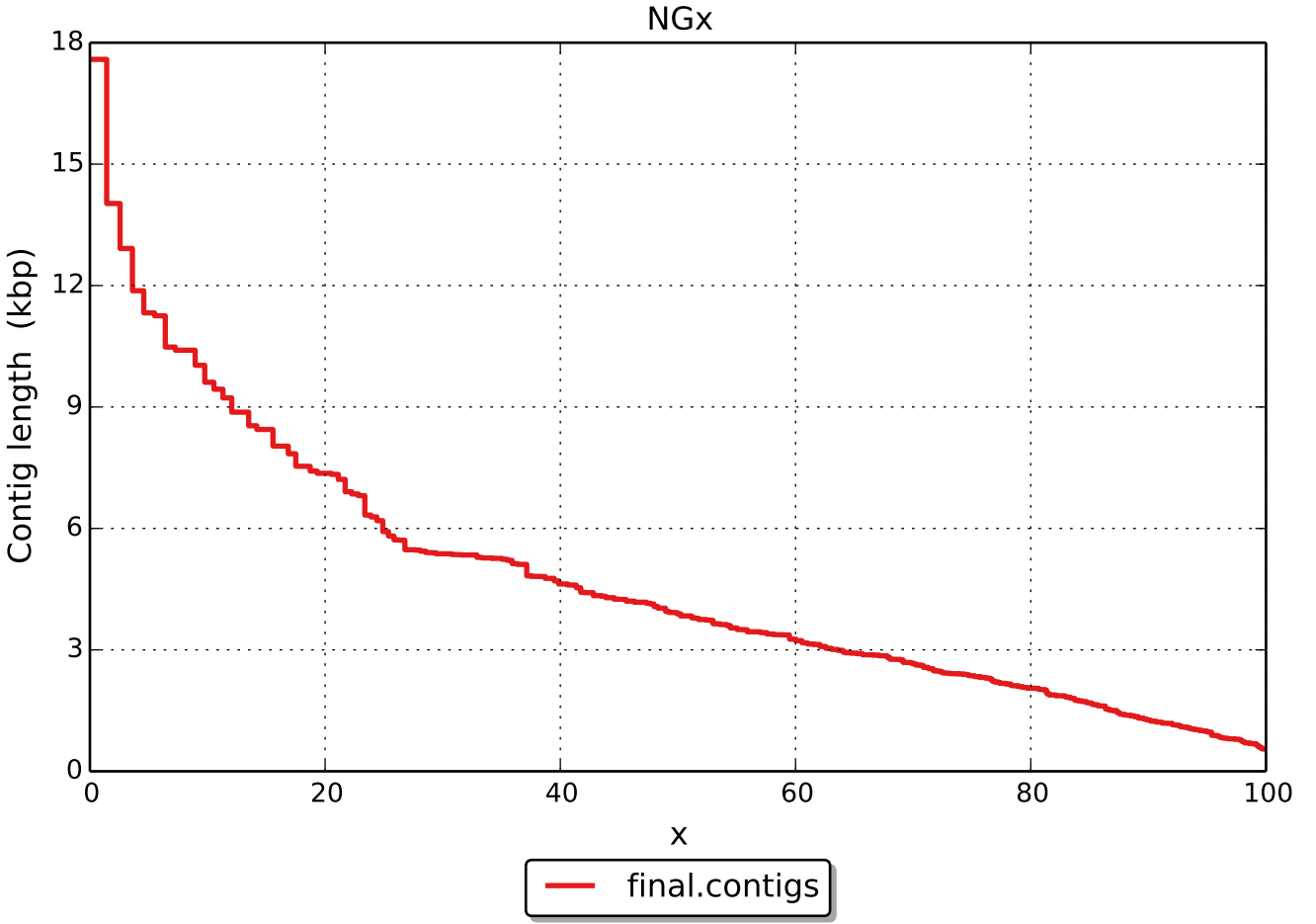
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

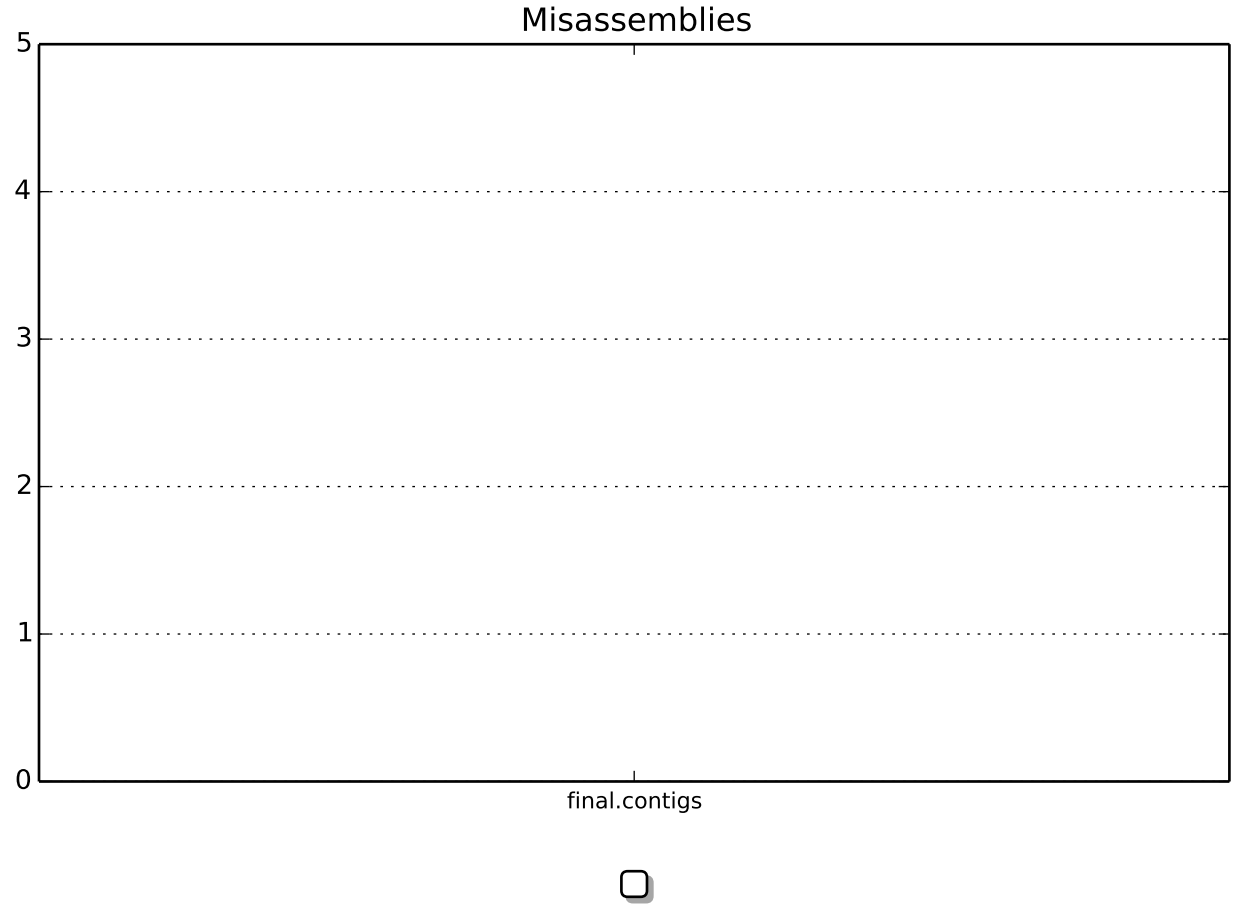
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

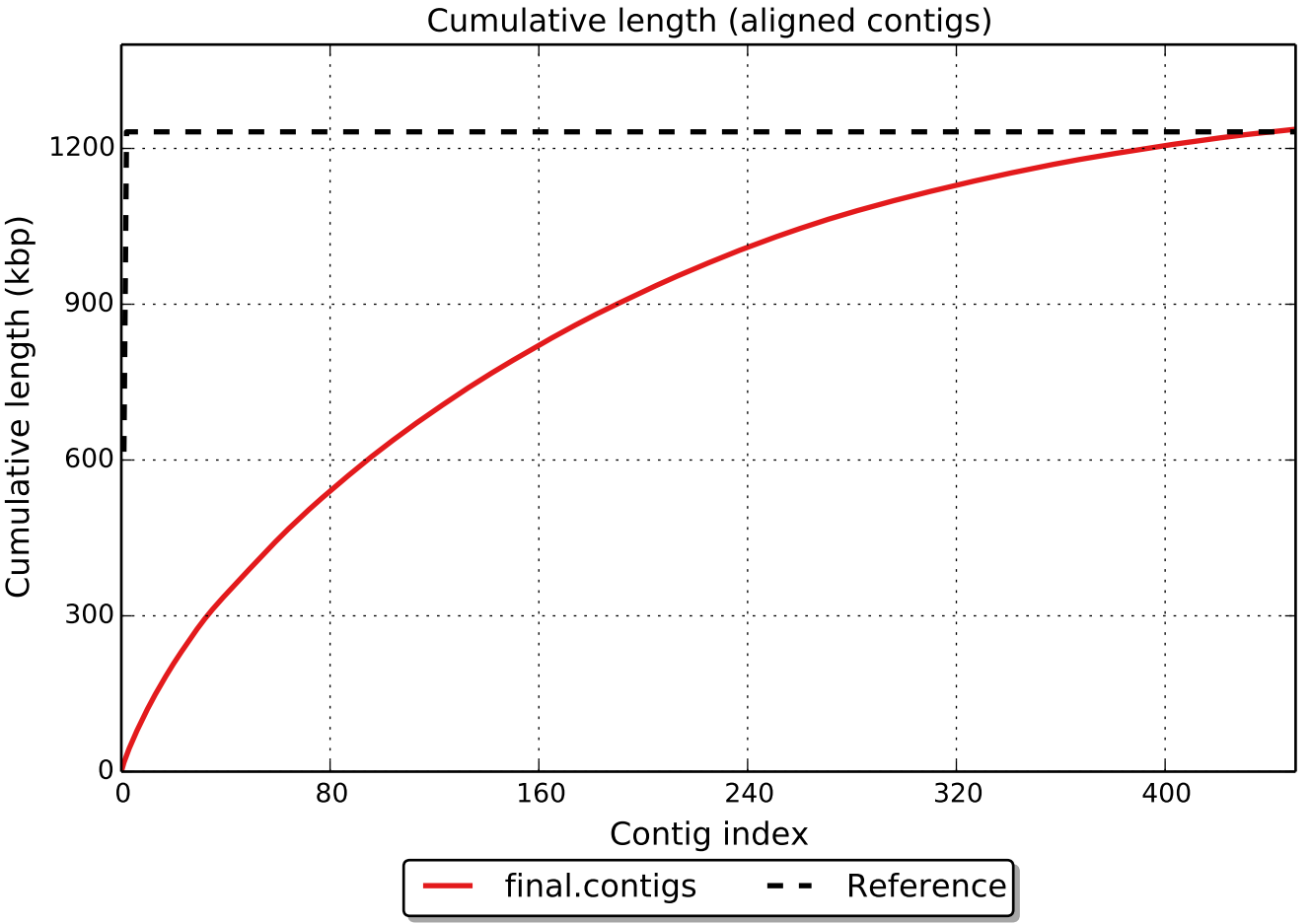

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
80
160
240
320
400
Contig index
final.contigs
Reference

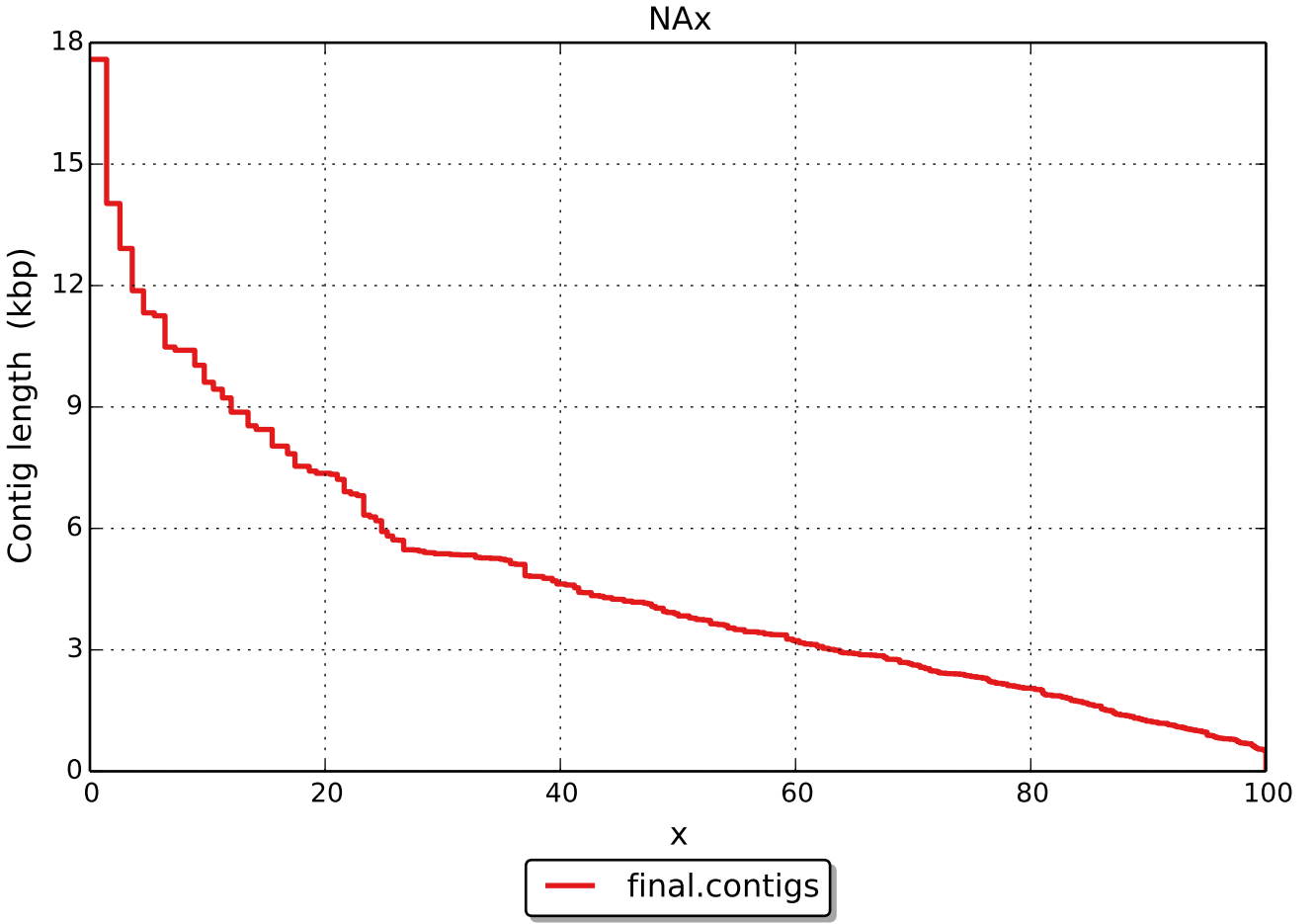

GC content
800
600
400
200
0
# windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

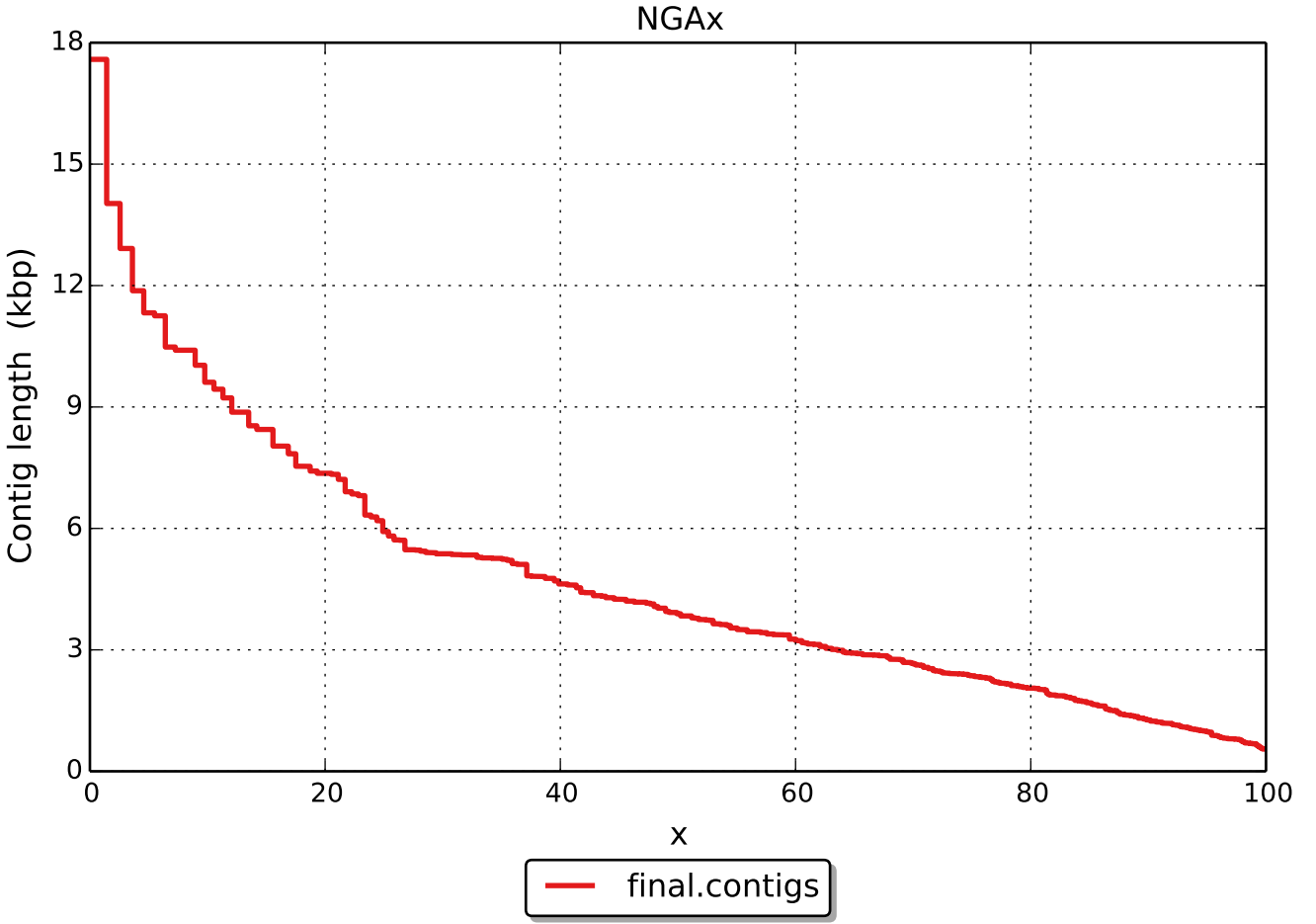

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
300
600
900
1200
0
80
160
240
320
400
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs