# Report

| | final.contigs |
|---|---|
| # contigs (>= 1000 bp) | 10 |
| # contigs (>= 5000 bp) | 5 |
| # contigs (>= 10000 bp) | 1 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 59423 |
| Total length (>= 5000 bp) | 45657 |
| Total length (>= 10000 bp) | 17225 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 17 |
| Largest contig | 17225 |
| Total length | 64464 |
| Reference length | 4775416 |
| GC (%) | 60.74 |
| Reference GC (%) | 68.59 |
| N50 | 6873 |
| N75 | 3725 |
| L50 | 4 |
| L75 | 6 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 12 part |
| Unaligned length | 60023 |
| Genome fraction (%) | 0.037 |
| Duplication ratio | 2.506 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2200.90 |
| # indels per 100 kbp | 338.60 |
| Largest alignment | 577 |
| Total aligned length | 2446 |
| NGA50 | - |

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

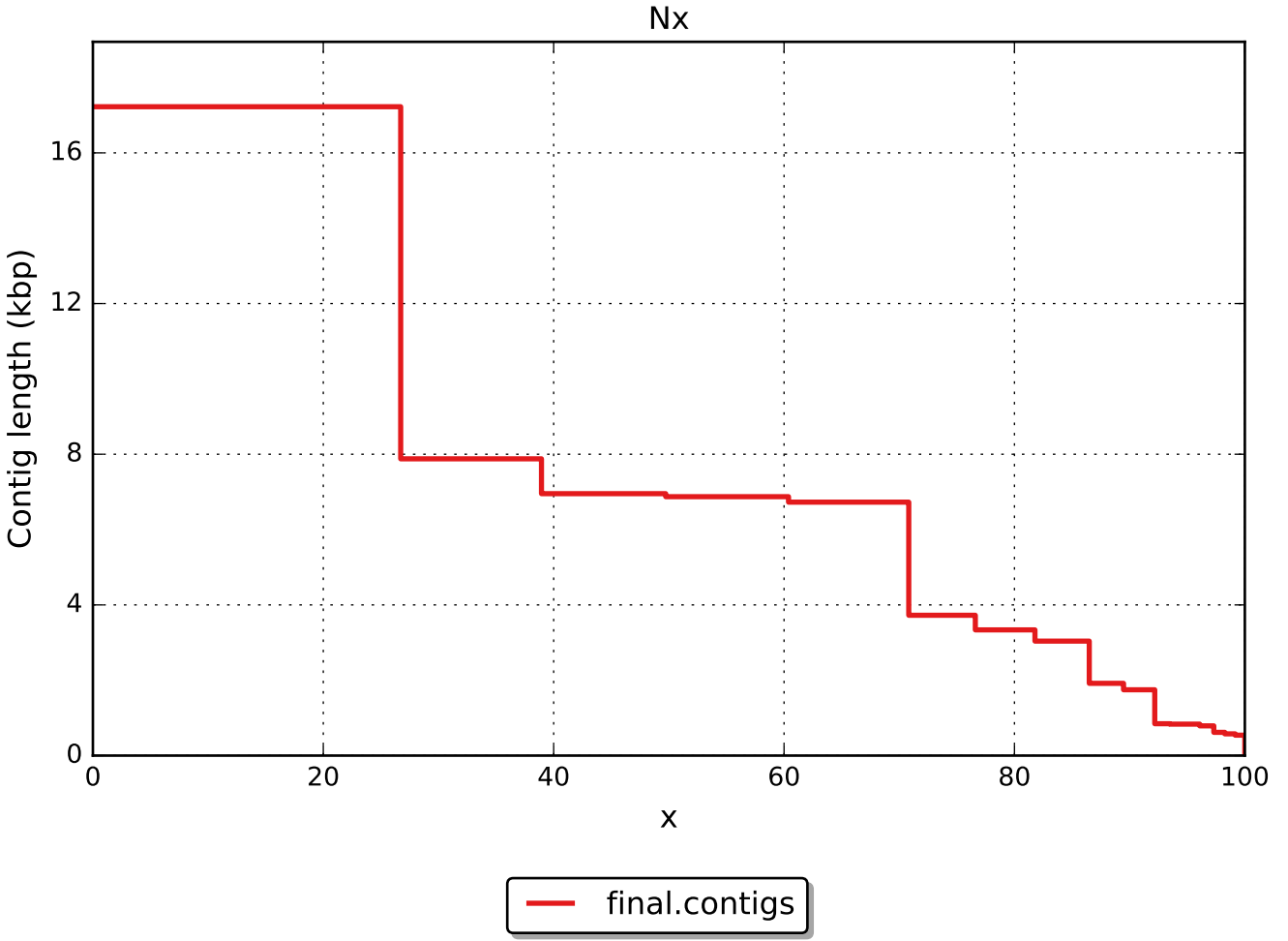
| | final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 0 |
| # possible misassemblies | 0 |
| # local misassemblies | 1 |
| # unaligned mis. contigs | 0 |
| # mismatches | 39 |
| # indels | 6 |
| # indels (<= 5 bp) | 6 |
| # indels (> 5 bp) | 0 |
| Indels length | 7 |

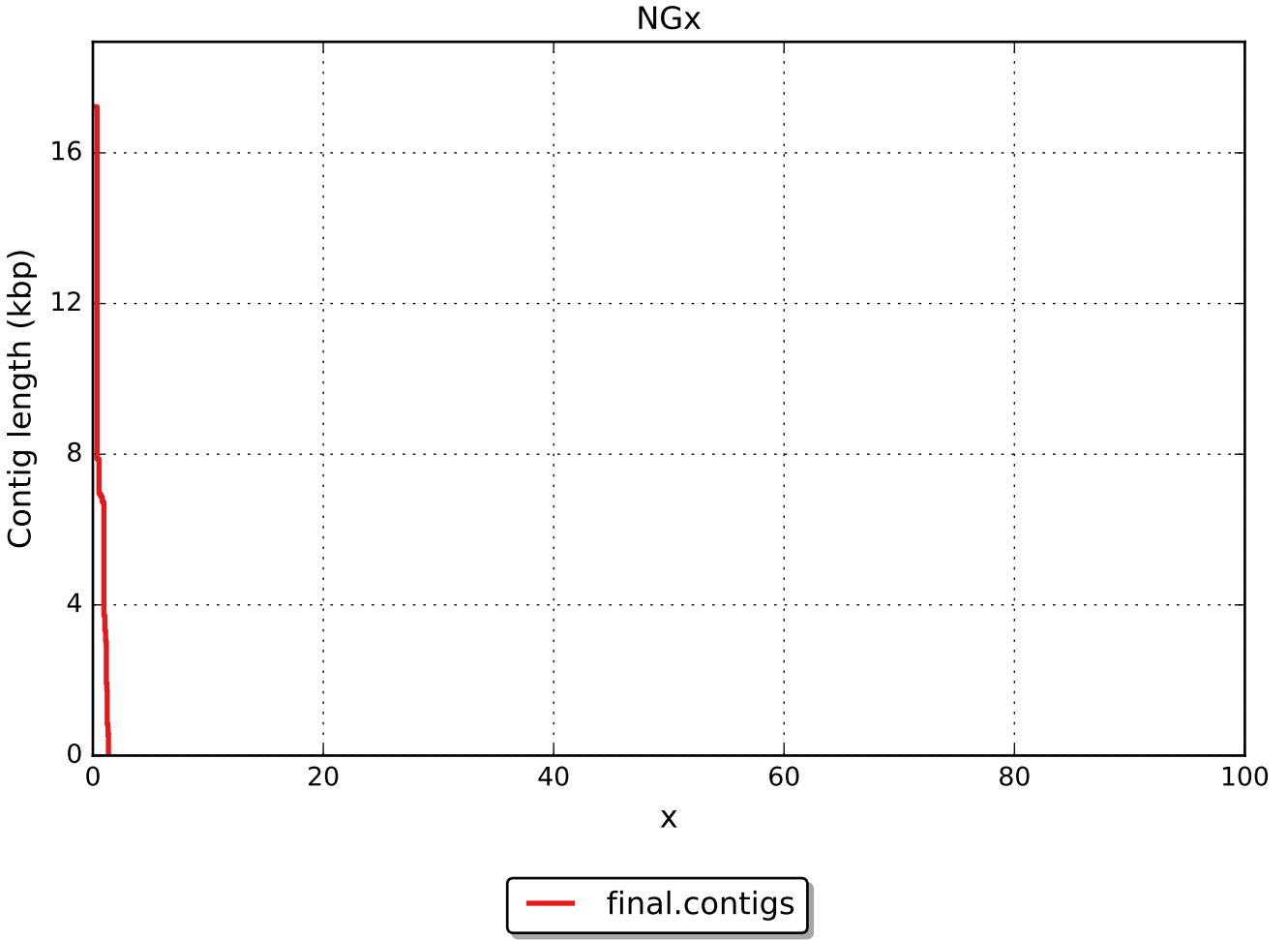
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

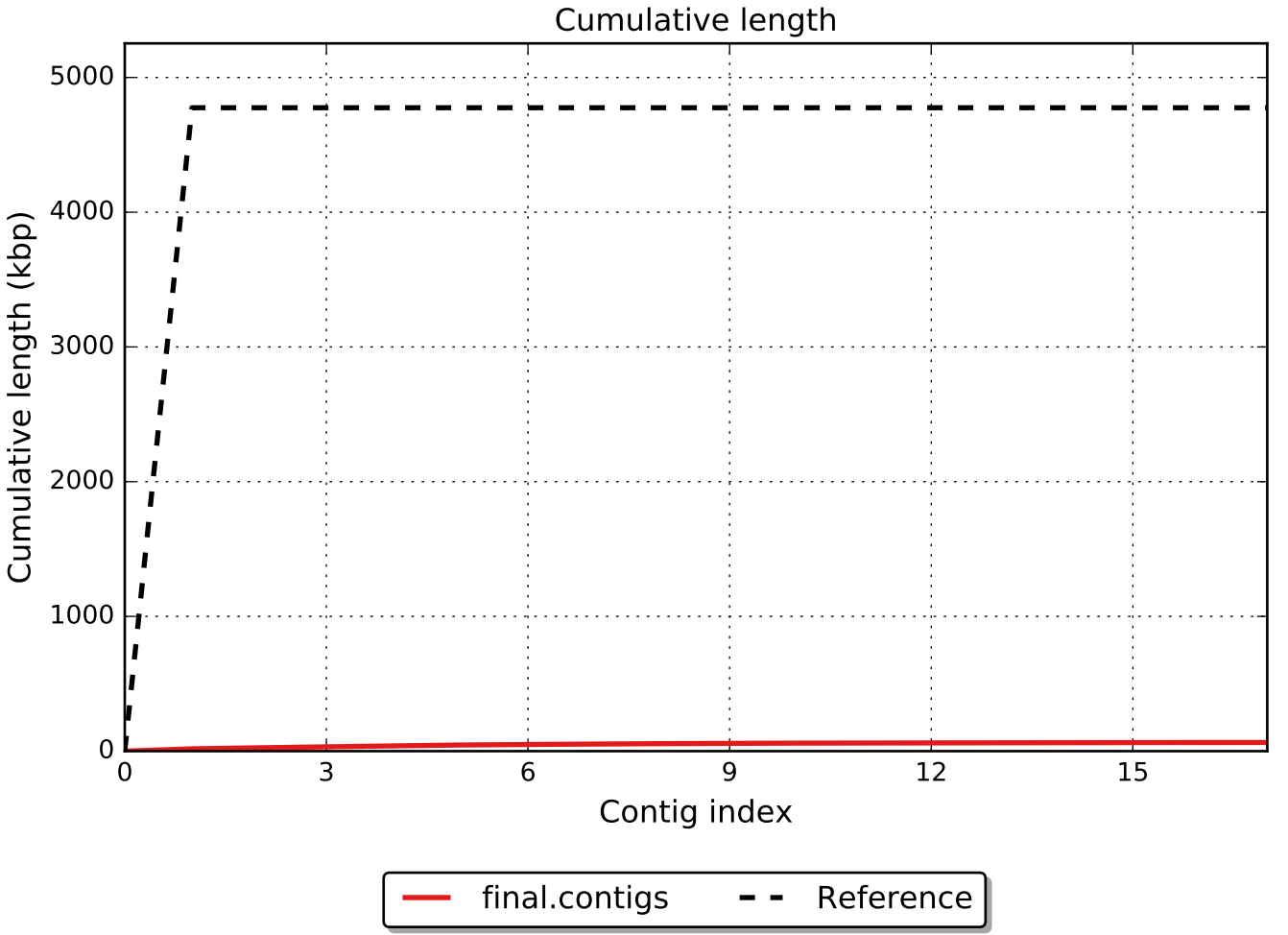
# Unaligned report

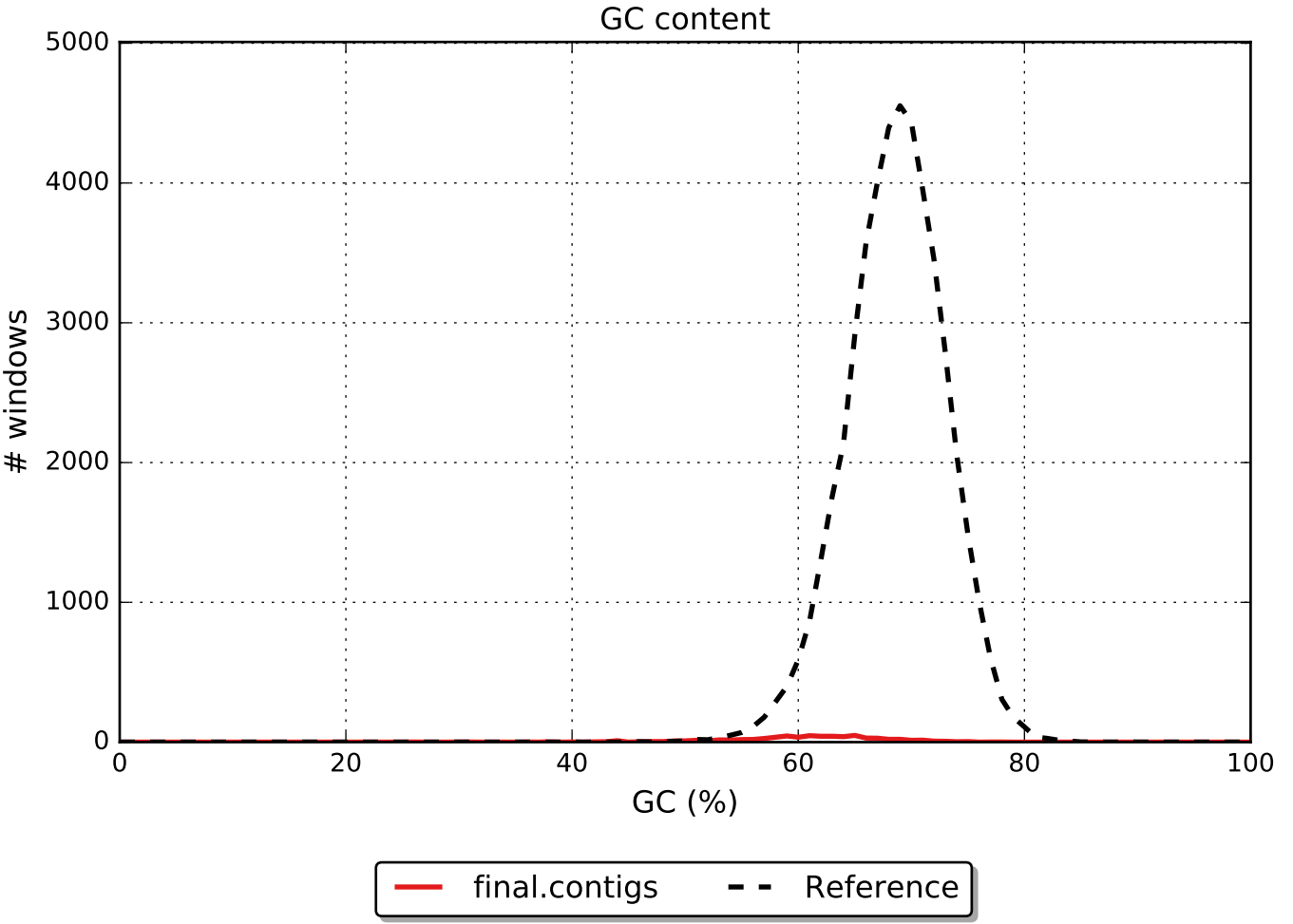
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 12 |
| Partially unaligned length | 60023 |
| # N's | 0 |

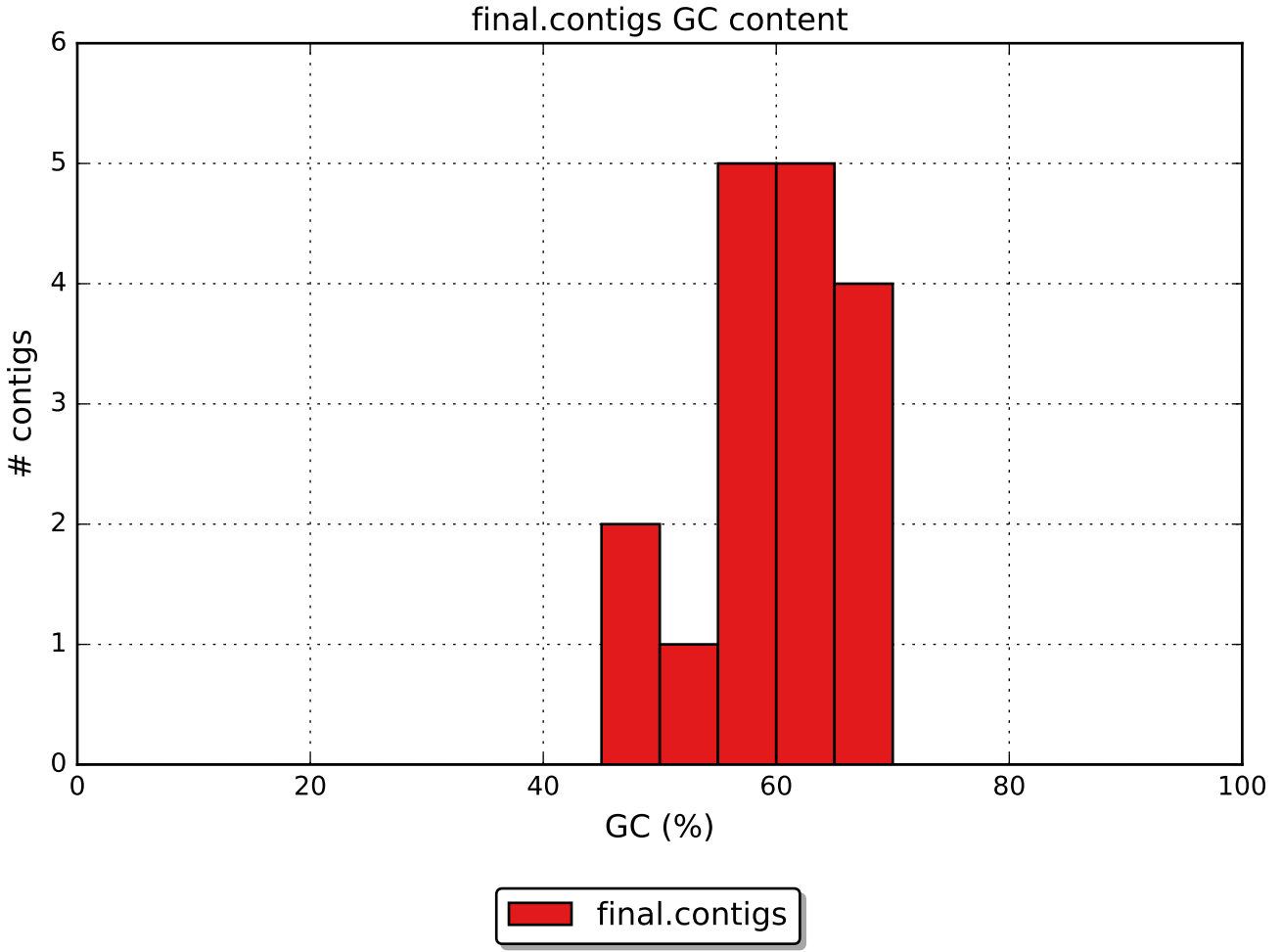
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

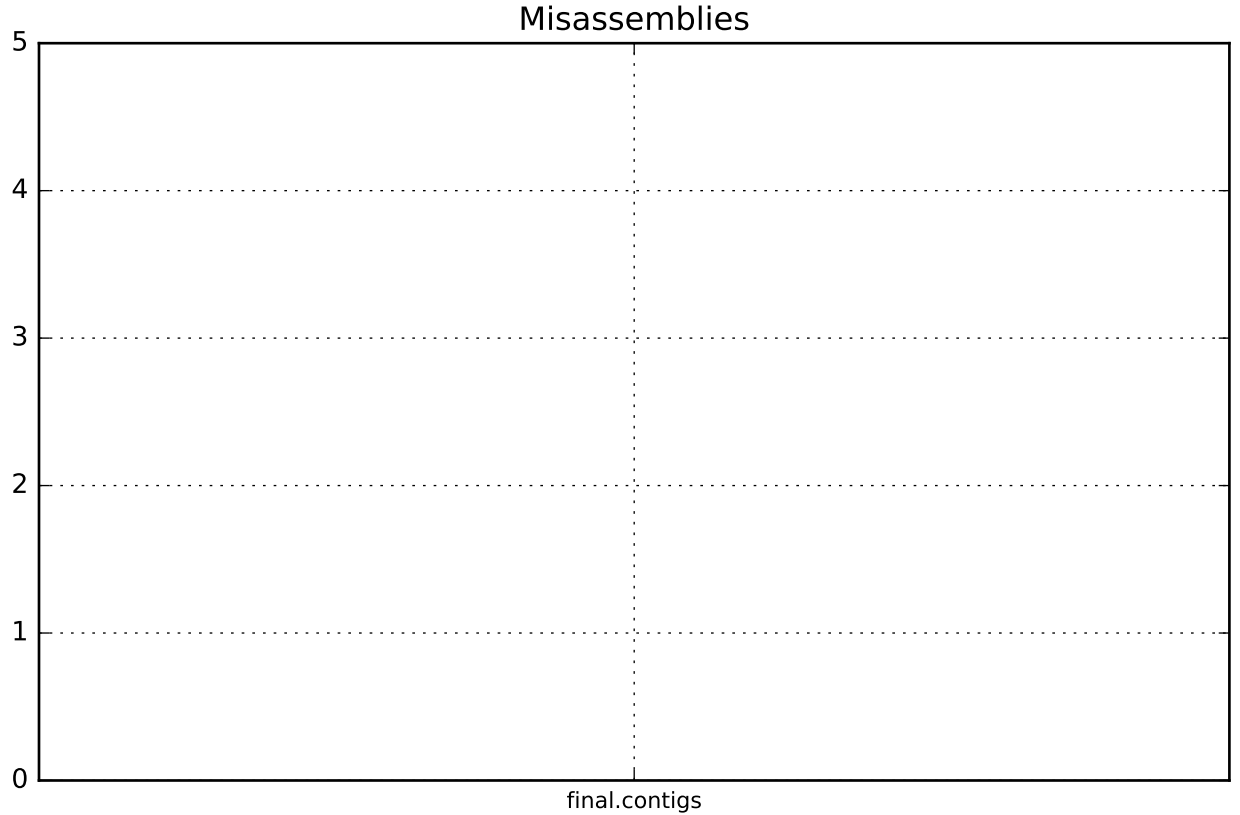

Nx
Contig length (kbp)
0
4
8
12
16
0
20
40
60
80
100
x
final.contigs

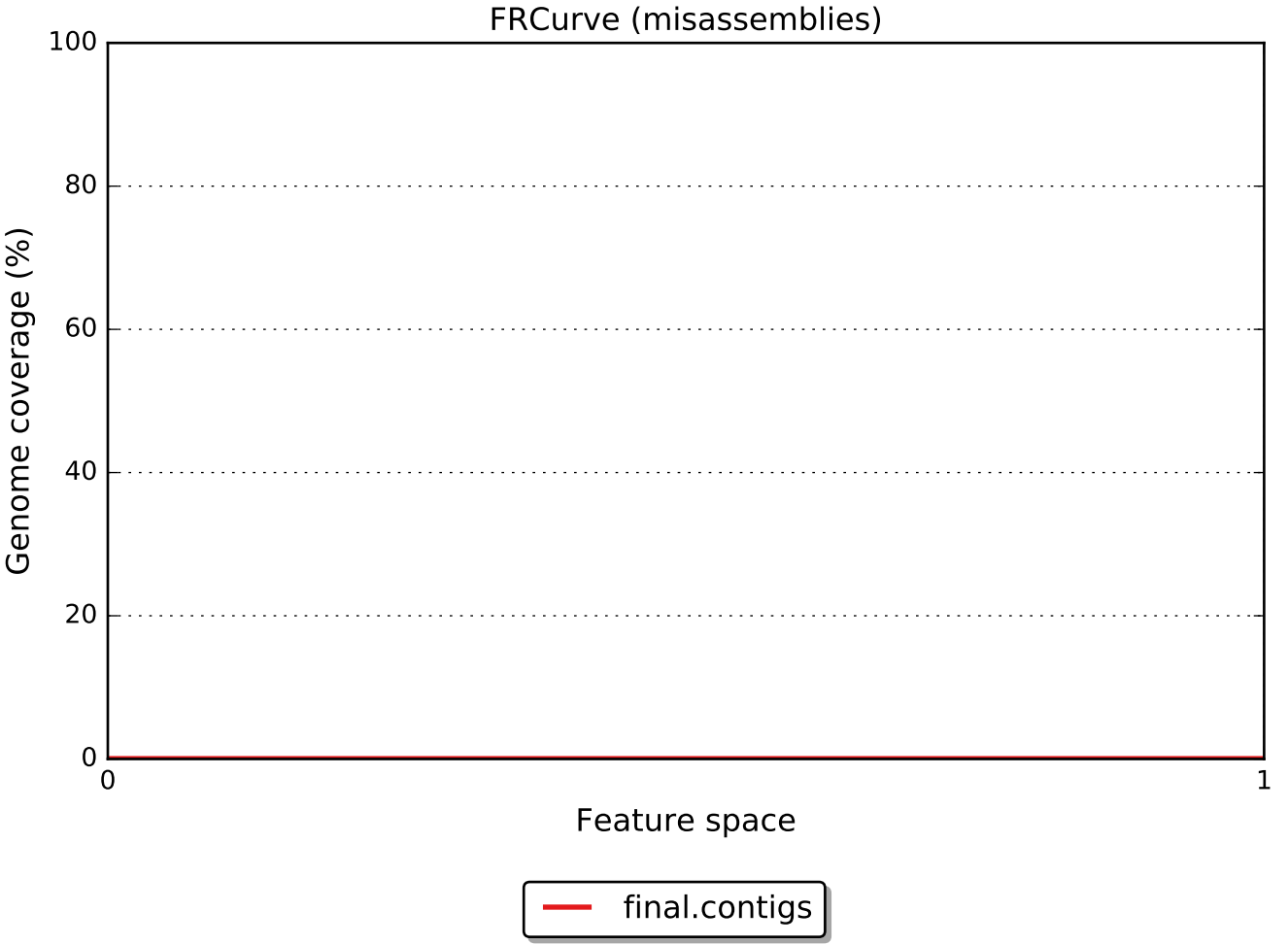

NGx
Contig length (kbp)
0
4
8
12
16
0
20
40
60
80
100
x
final.contigs

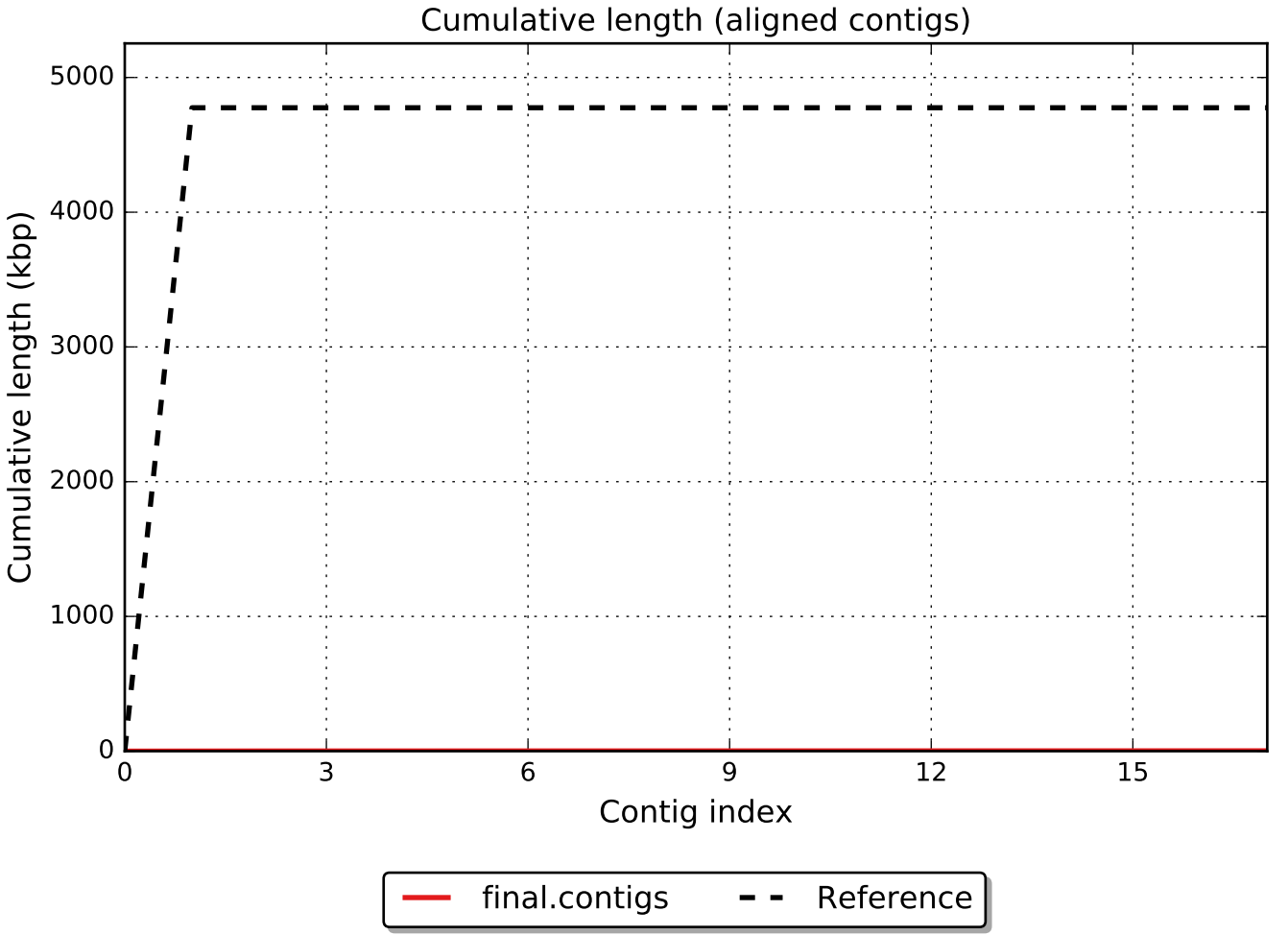

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
final.contigs
Reference

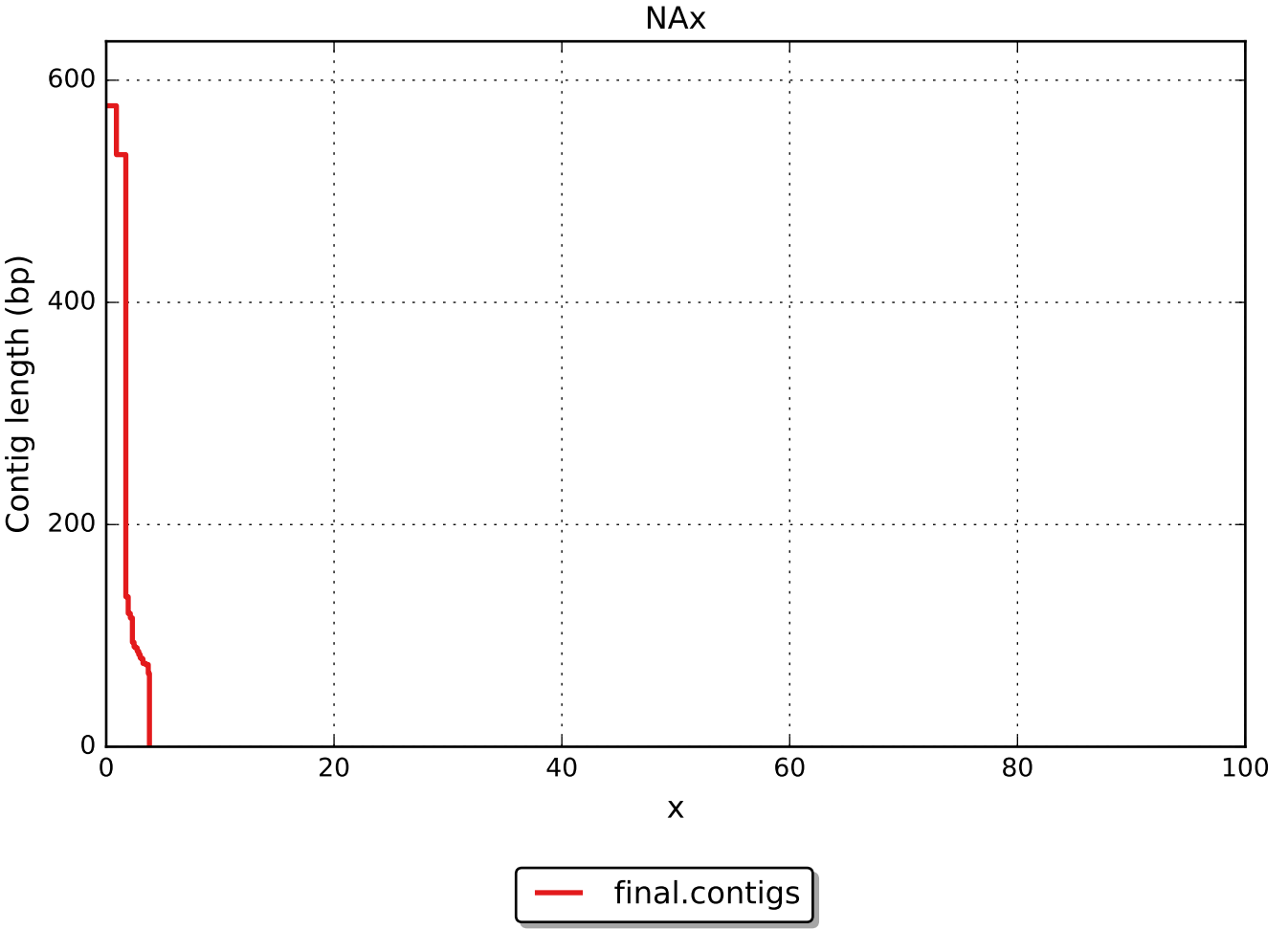

GC content
5000
4000
3000
2000
1000
0
# windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

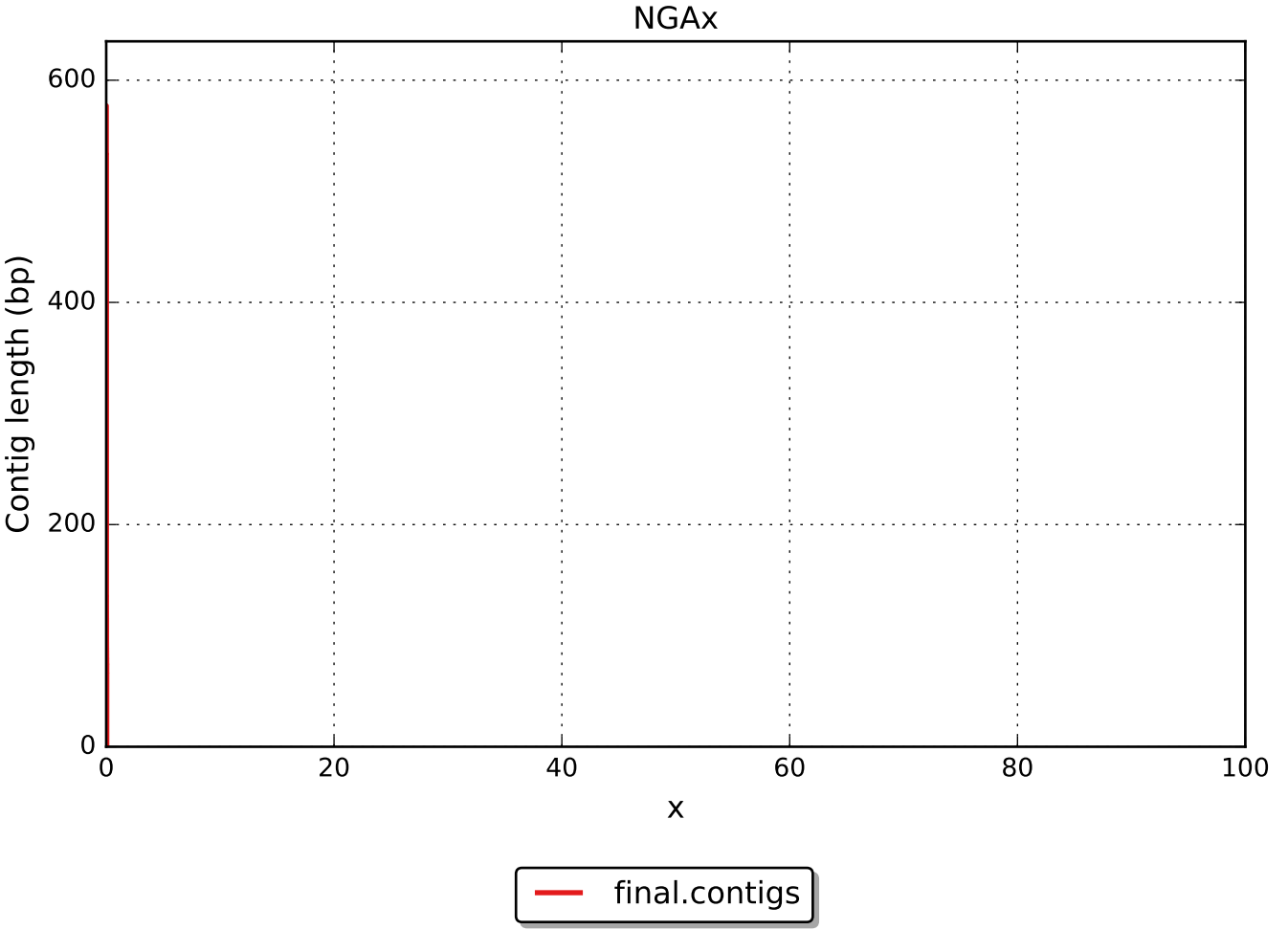

final.contigs GC content
# contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
final.contigs
Reference


NAx
600
400
200
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
600
400
200
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs