# Report

| | combined.final.contigs |
|---|---|
| # contigs (>= 1000 bp) | 9 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 14082 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 20 |
| Largest contig | 2884 |
| Total length | 21086 |
| Reference length | 4555826 |
| GC (%) | 49.54 |
| Reference GC (%) | 57.02 |
| N50 | 1440 |
| N75 | 655 |
| L50 | 6 |
| L75 | 12 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 11 part |
| Unaligned length | 14088 |
| Genome fraction (%) | 0.057 |
| Duplication ratio | 2.691 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2268.36 |
| # indels per 100 kbp | 269.13 |
| Largest alignment | 642 |
| Total aligned length | 3195 |
| 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

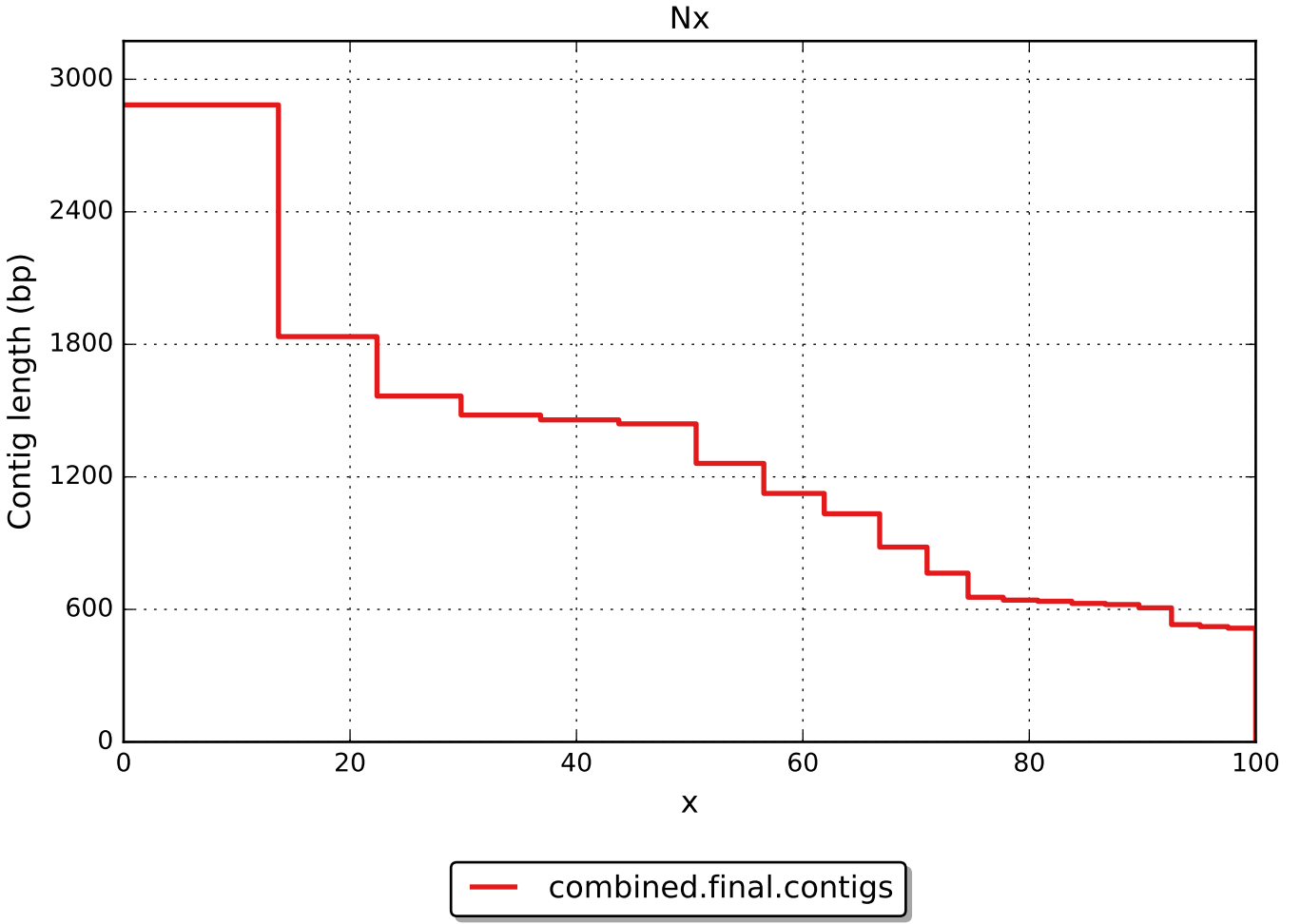
| | combined.final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 0 |
| # possible misassemblies | 0 |
| # local misassemblies | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 59 |
| # indels | 7 |
| # indels (<= 5 bp) | 7 |
| # indels (> 5 bp) | 0 |
| Indels length | 7 |

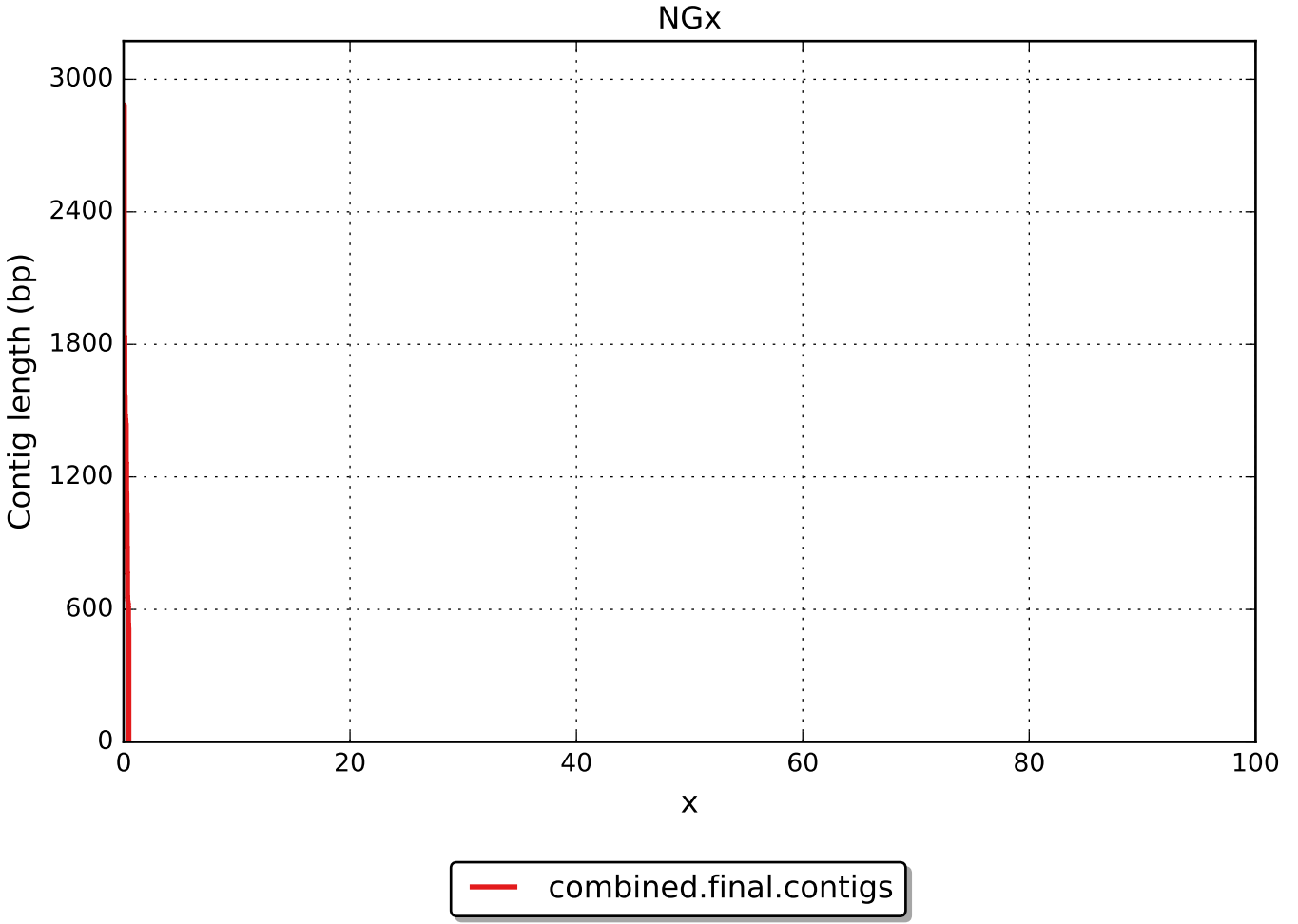
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

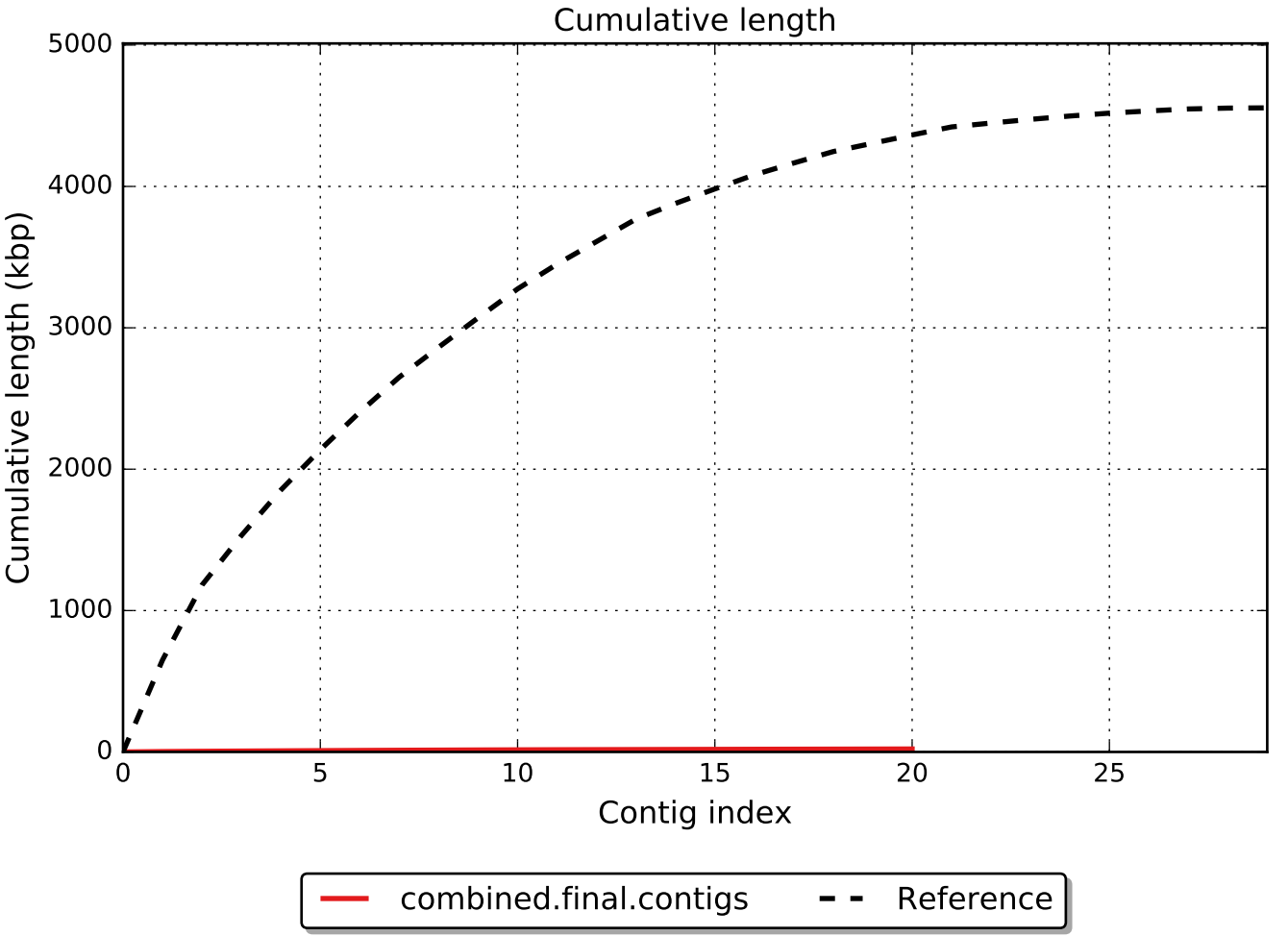
# Unaligned report

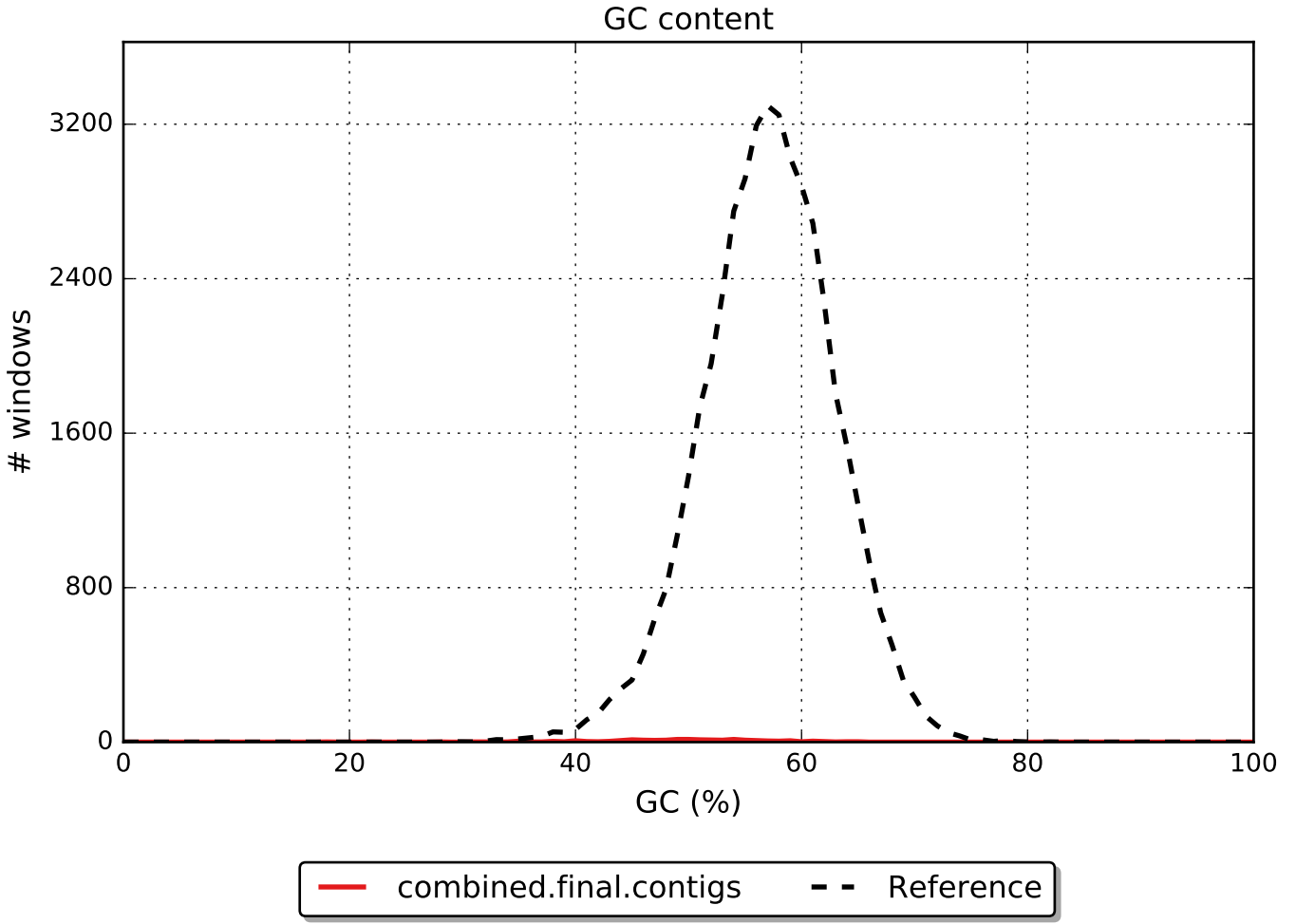
| | combined.final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 11 |
| Partially unaligned length | 14088 |
| # N's | 0 |

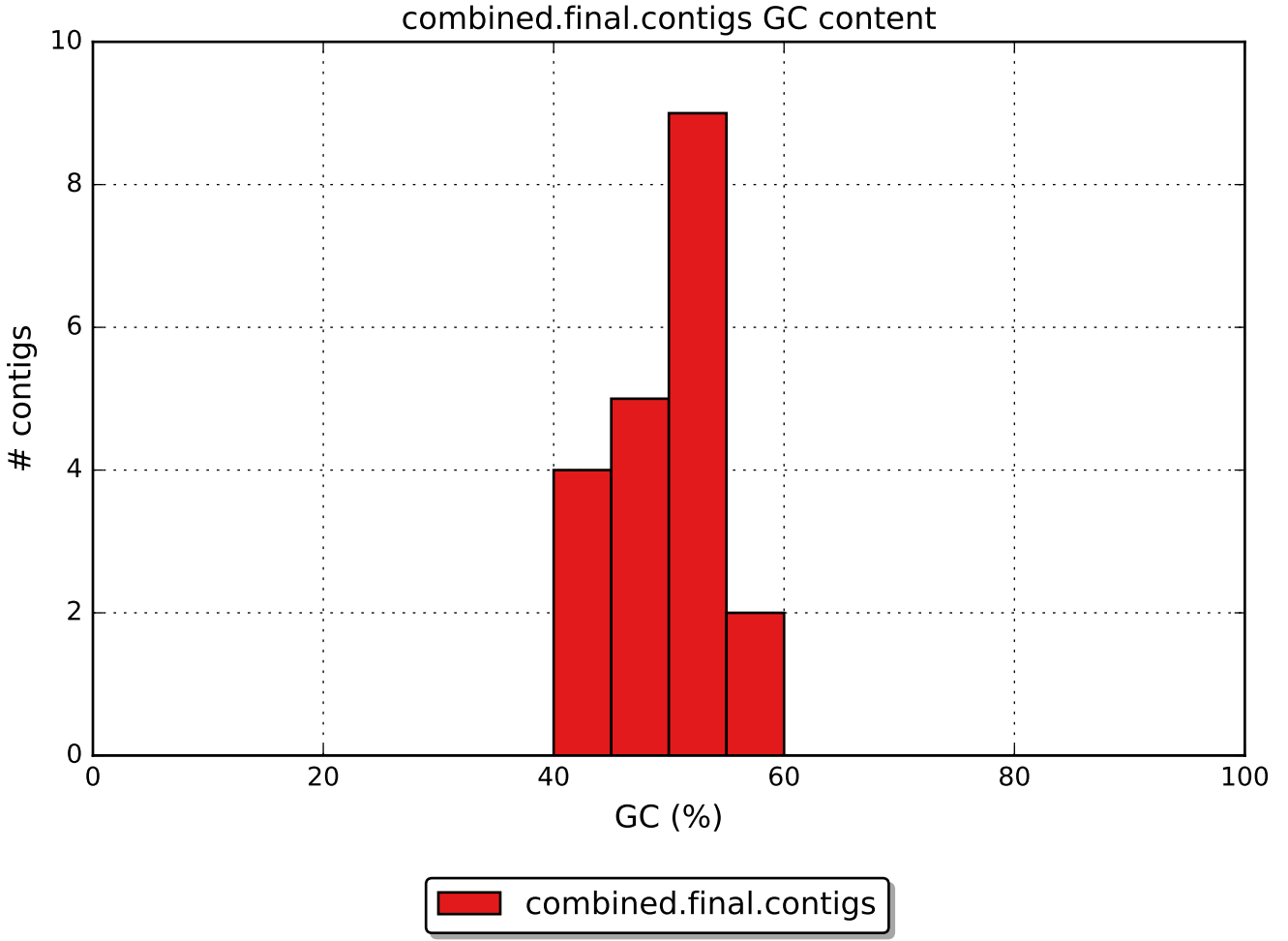
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

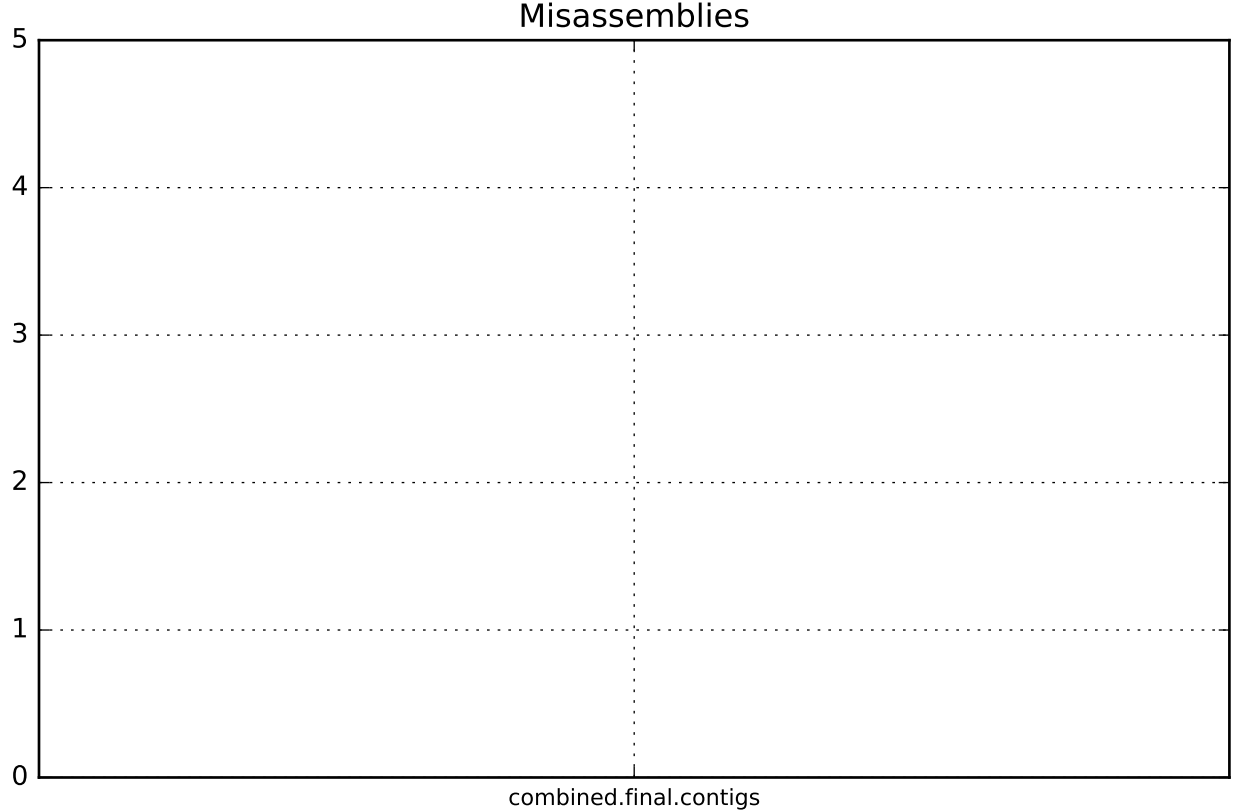

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
combined.final.contigs

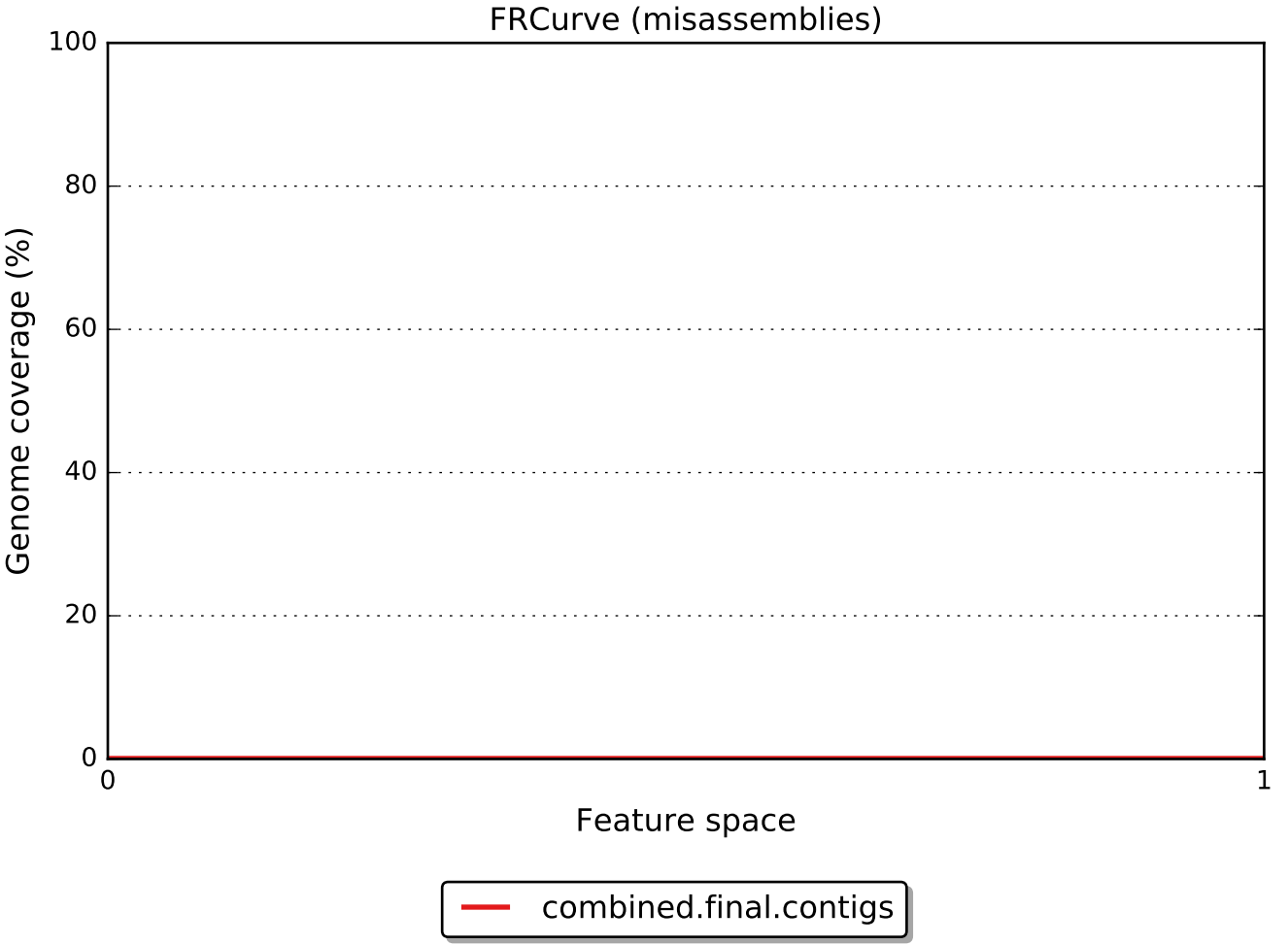

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
combined.final.contigs

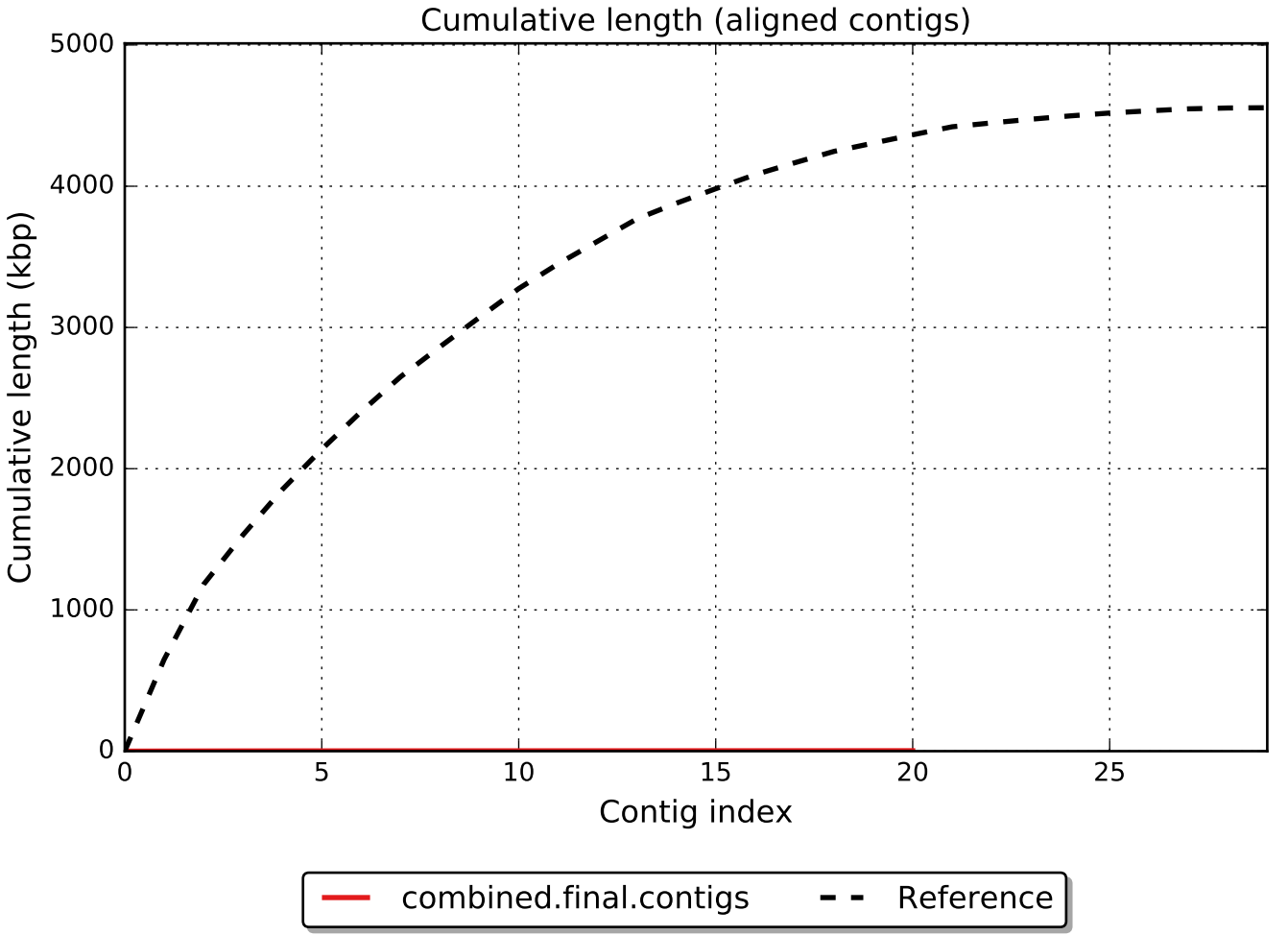

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
combined.final.contigs
Reference

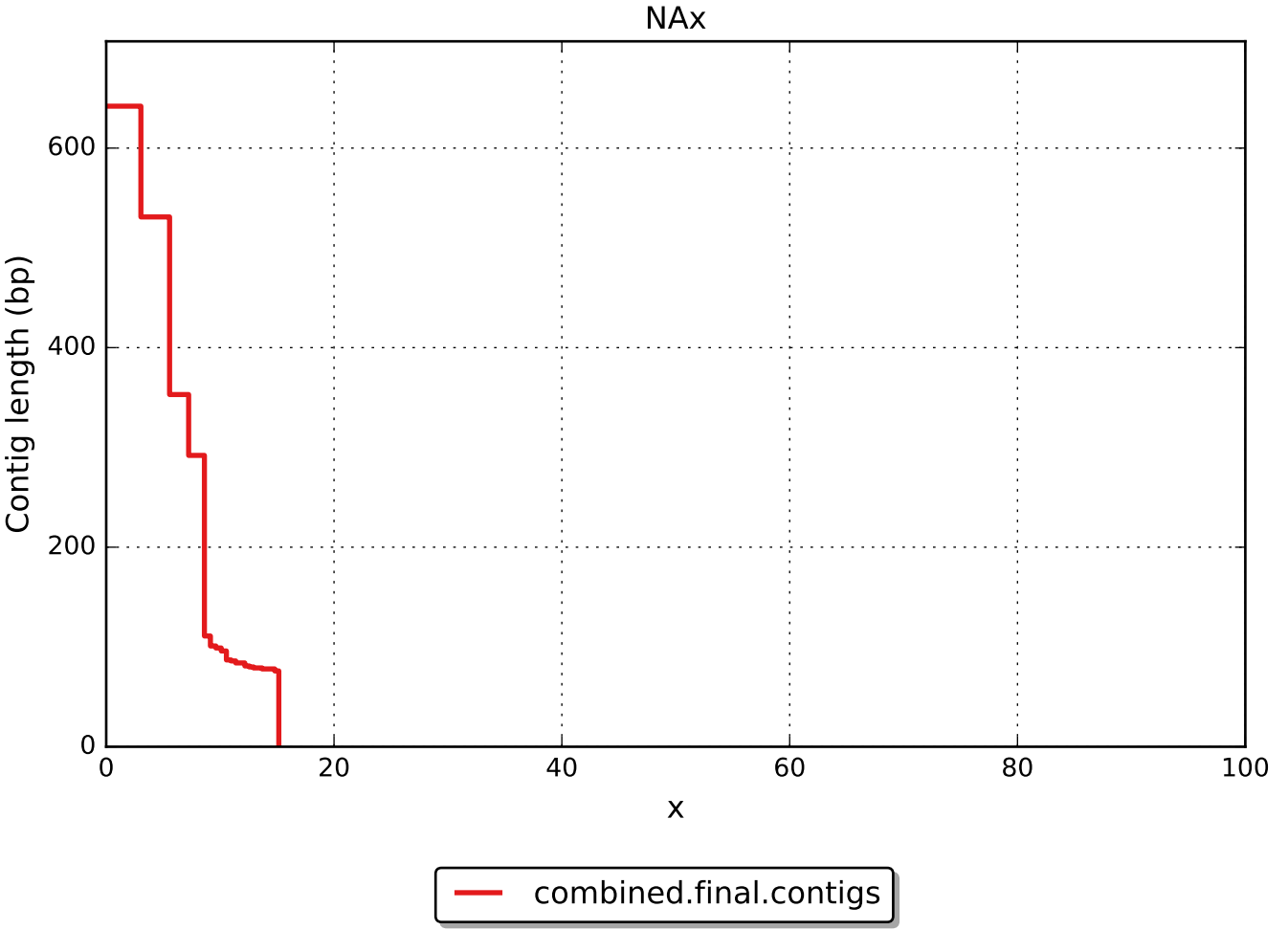

GC content
3200
2400
1600
800
0
# windows
0
20
40
60
80
100
GC (%)
combined.final.contigs
Reference

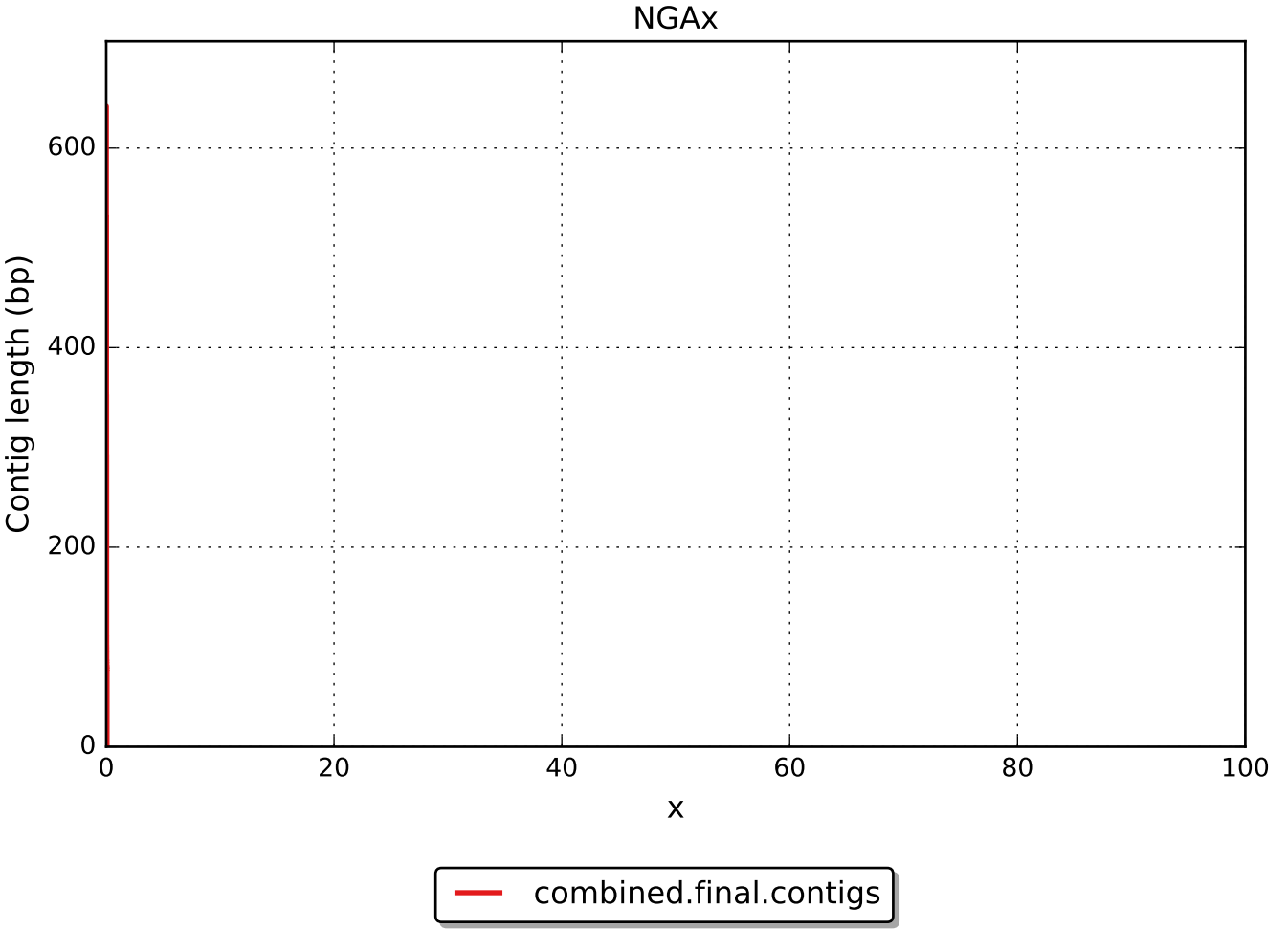

combined.final.contigs GC content
# contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
combined.final.contigs


Misassemblies
5
4
3
2
1
0
combined.final.contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
combined.final.contigs
Reference


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


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