# Report

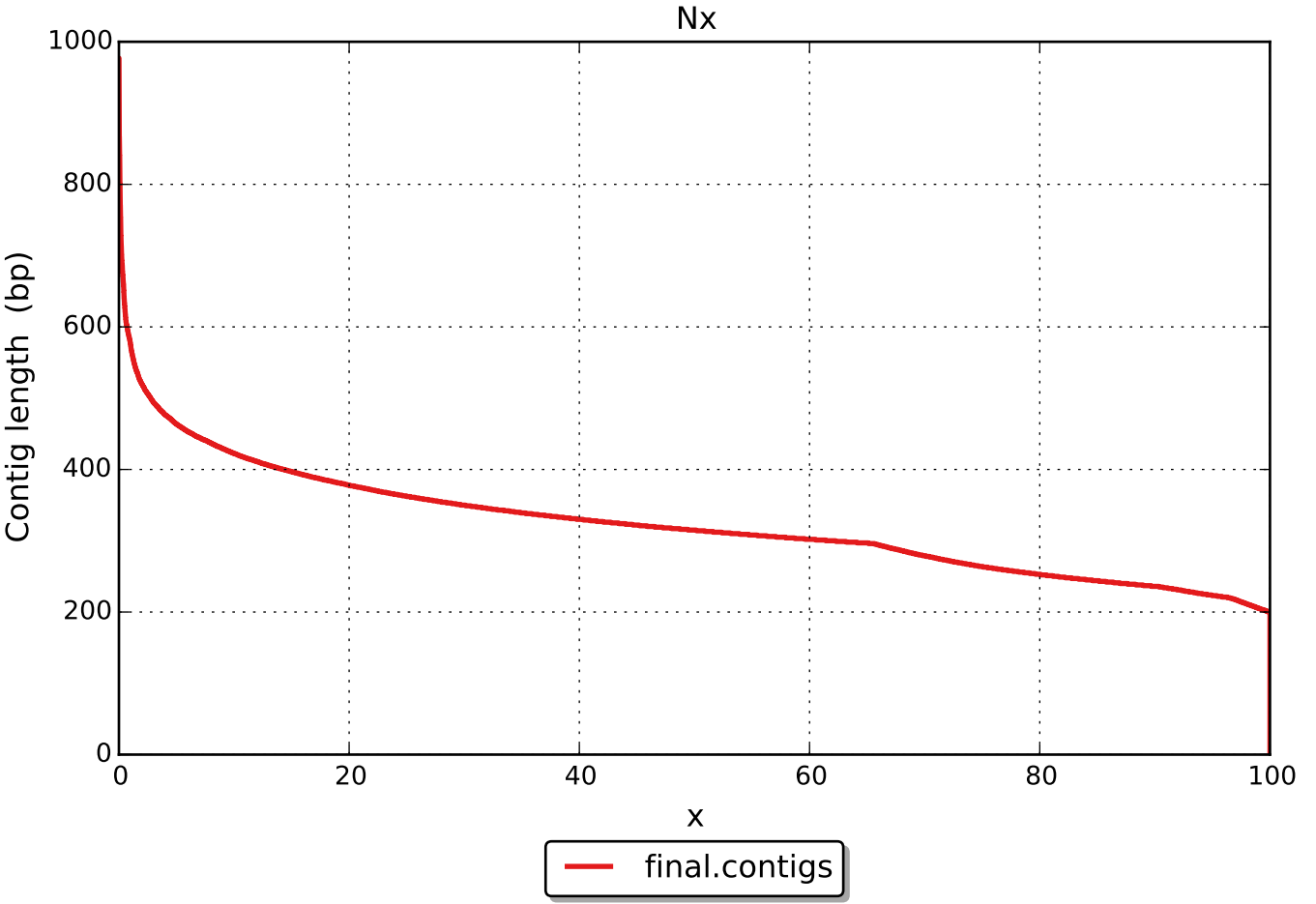
| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 48356 |
| # contigs (>= 1000 bp) | 0 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 14889940 |
| Total length (>= 1000 bp) | 0 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 48356 |
| Largest contig | 977 |
| Total length | 14889940 |
| Reference length | 4641652 |
| GC (%) | 50.78 |
| Reference GC (%) | 50.79 |
| N50 | 315 |
| NG50 | 394 |
| N75 | 264 |
| NG75 | 367 |
| L50 | 19974 |
| LG50 | 5153 |
| L75 | 32628 |
| LG75 | 8208 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # unaligned contigs | 28015 + 90 part |
| Unaligned length | 9543151 |
| Genome fraction (%) | 75.992 |
| Duplication ratio | 1.516 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 551.98 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 977 |
| NGA50 | 258 |
| NGA75 | 241 |
| LGA50 | 7341 |
| LGA75 | 12009 |

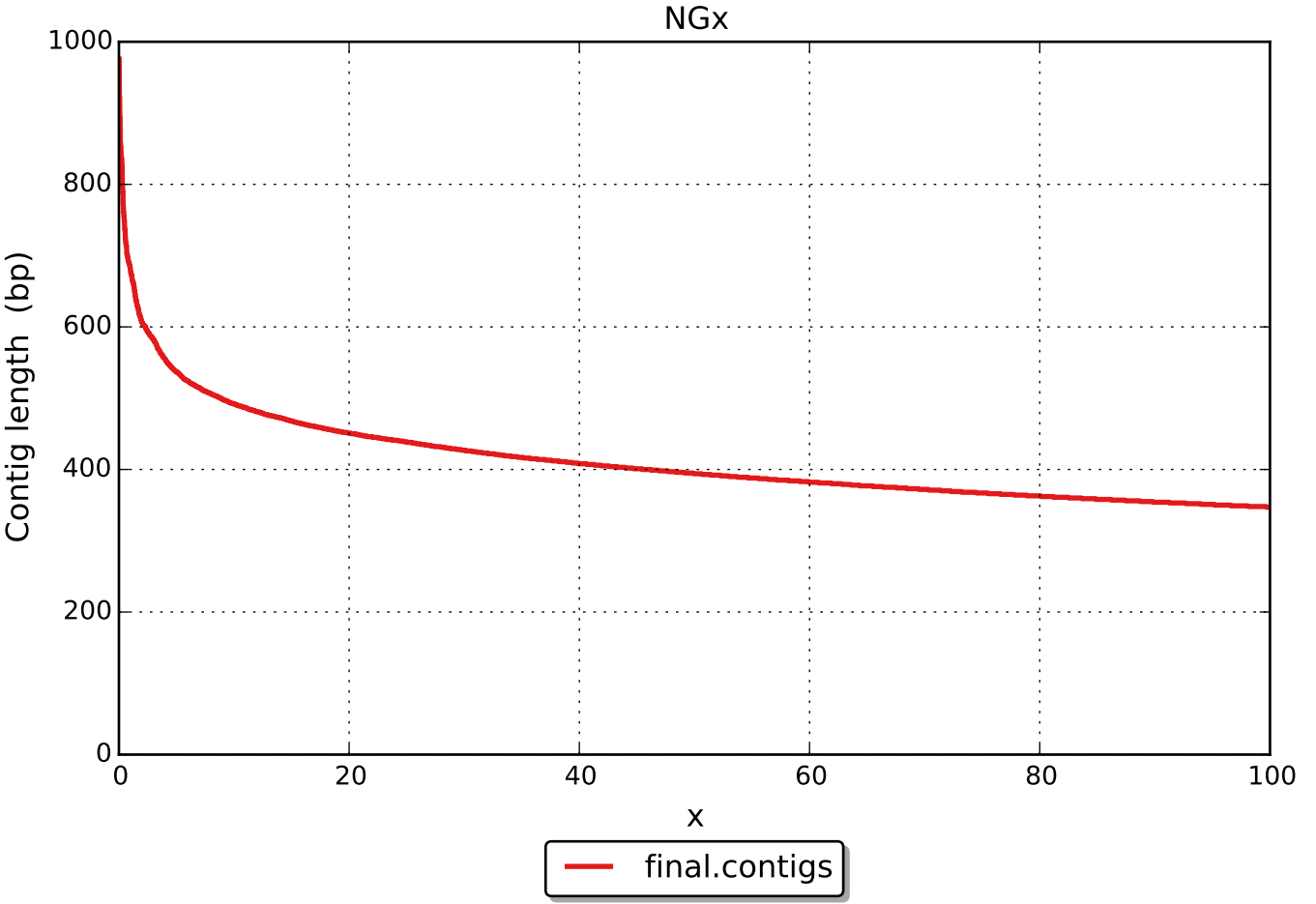
# Misassemblies report

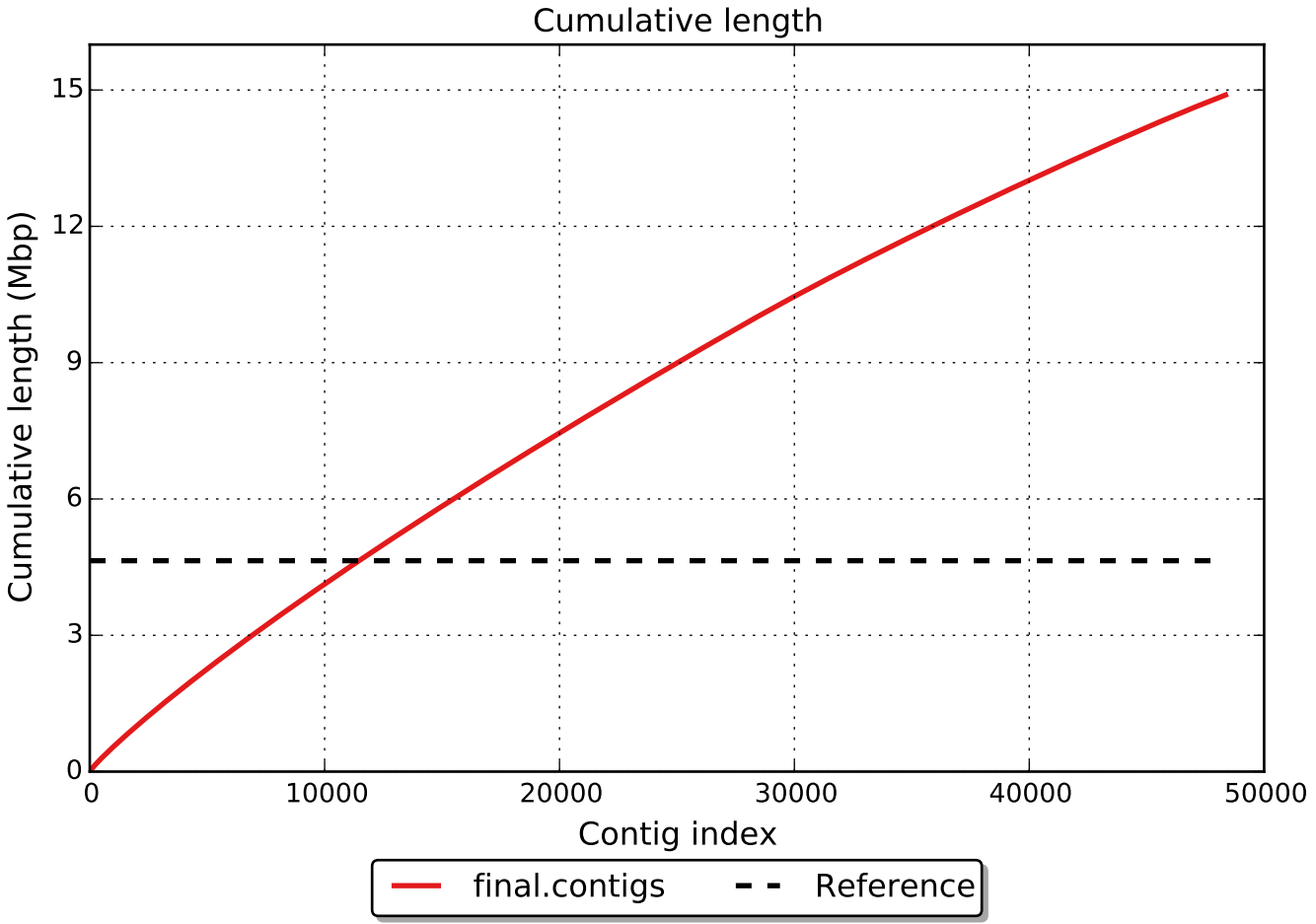
| | final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # mismatches | 19470 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

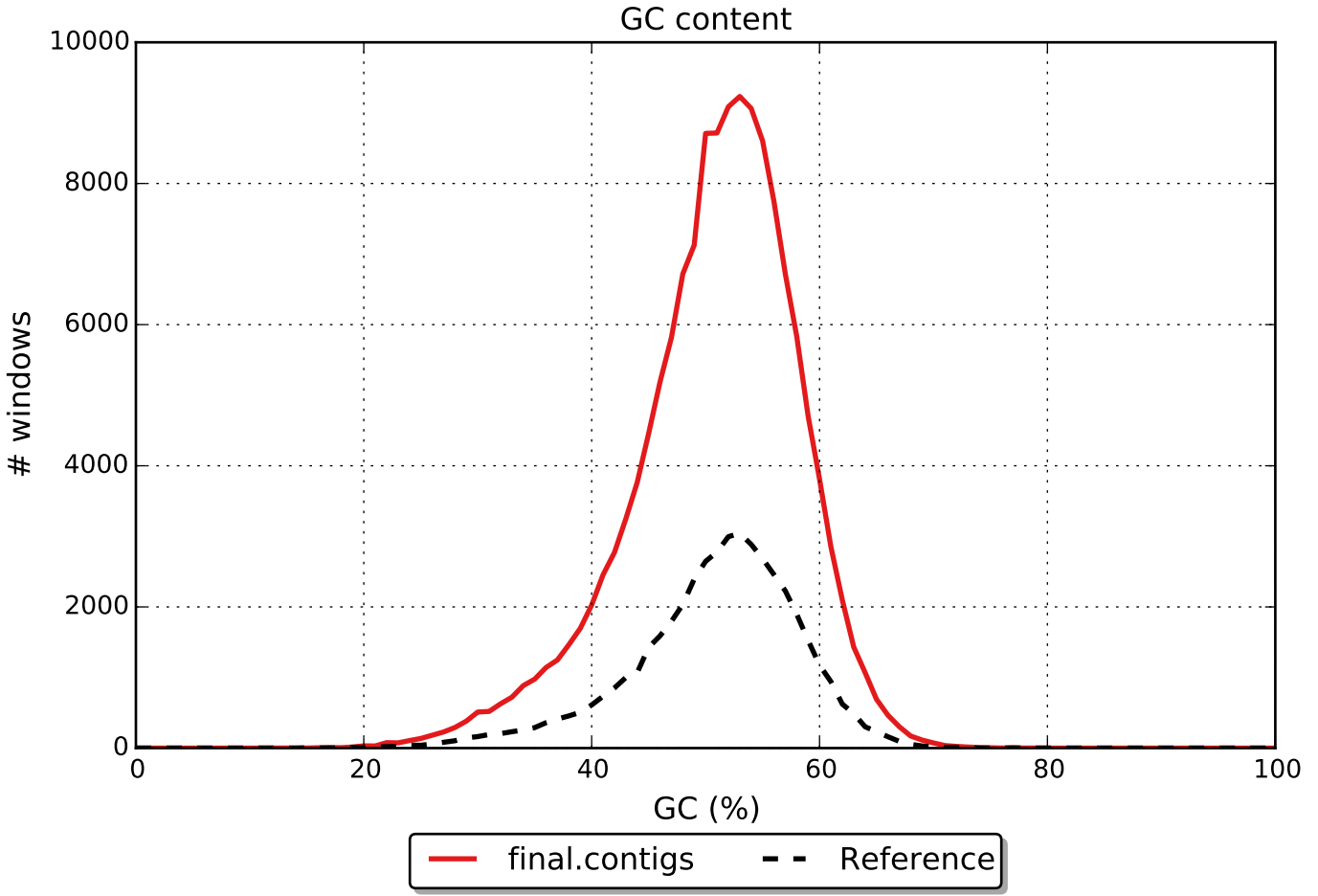
# Unaligned report

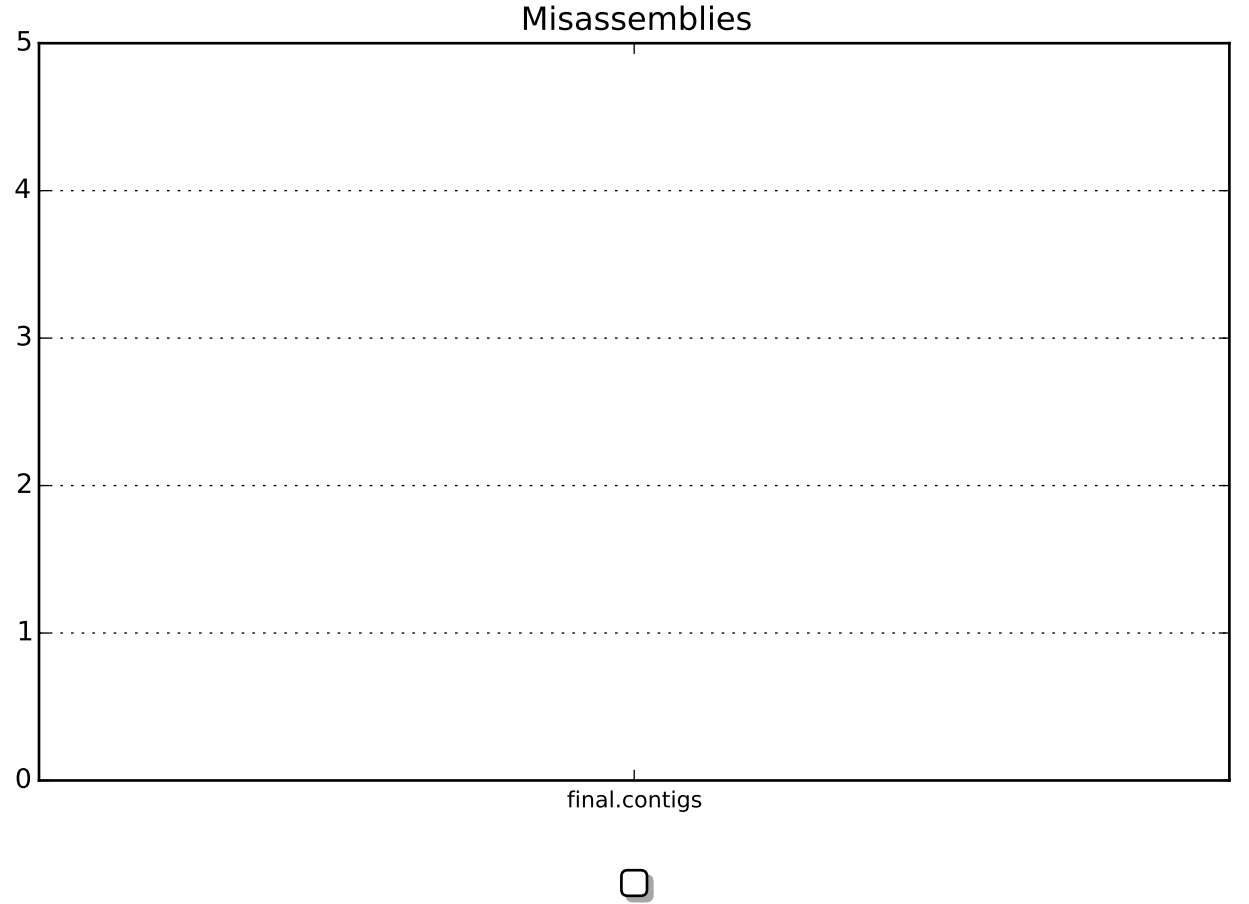
| | final.contigs |
|---|---|
| # fully unaligned contigs | 28015 |
| Fully unaligned length | 9525385 |
| # partially unaligned contigs | 90 |
| # with misassembly | 0 |
| # both parts are significant | 90 |
| Partially unaligned length | 17766 |
| # N's | 0 |

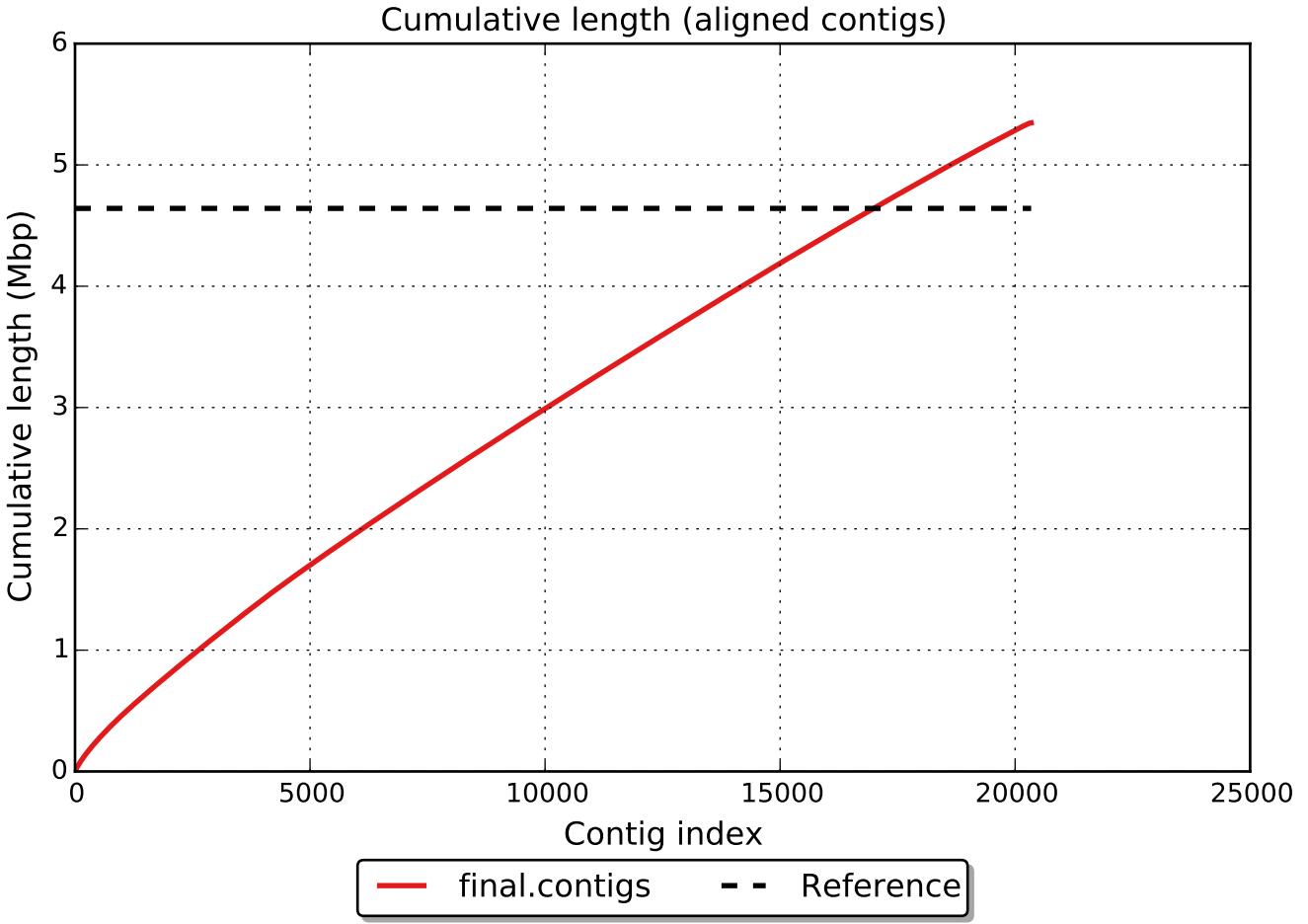

Nx
1000
800
600
400
200
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

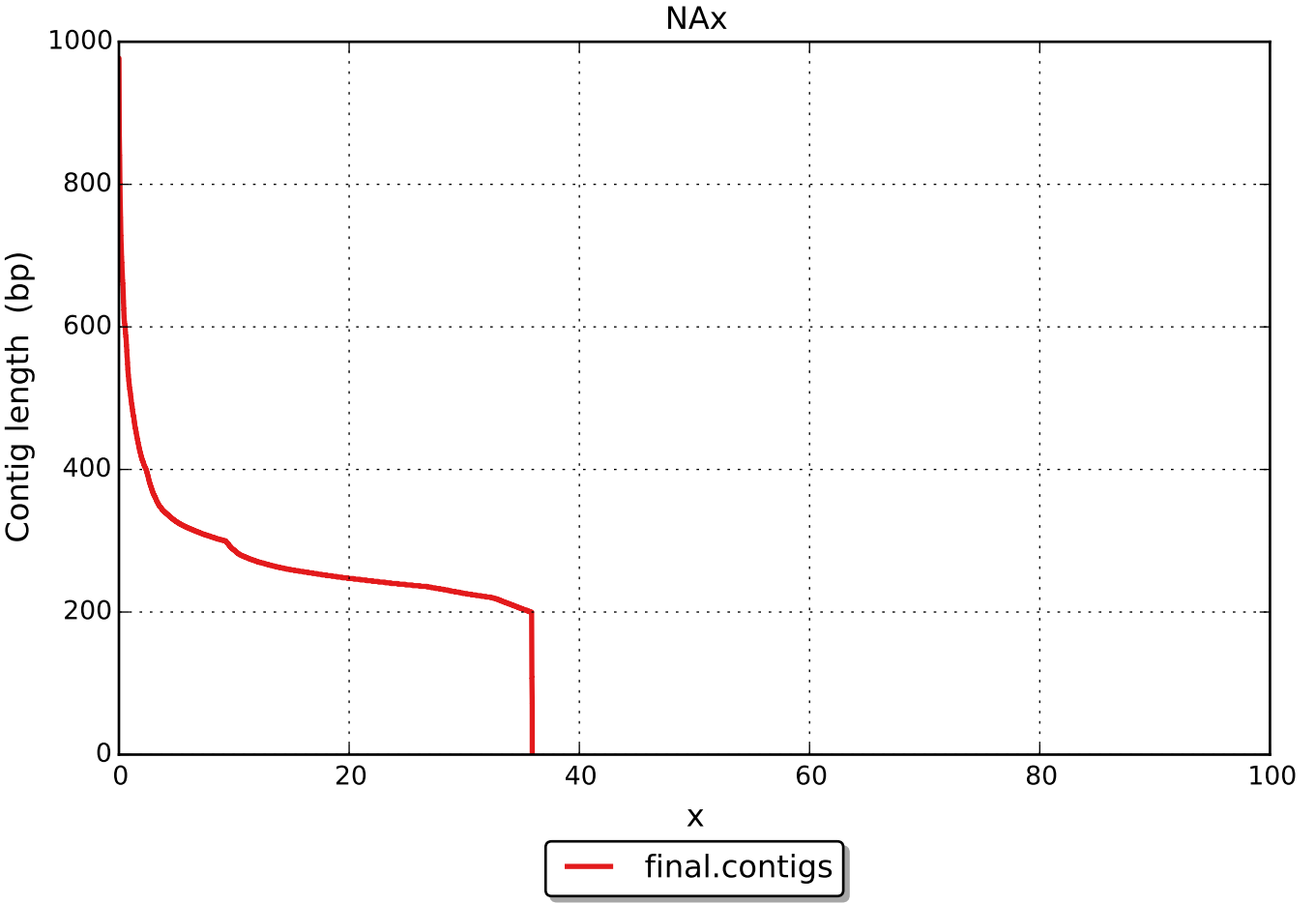

NGx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
final.contigs

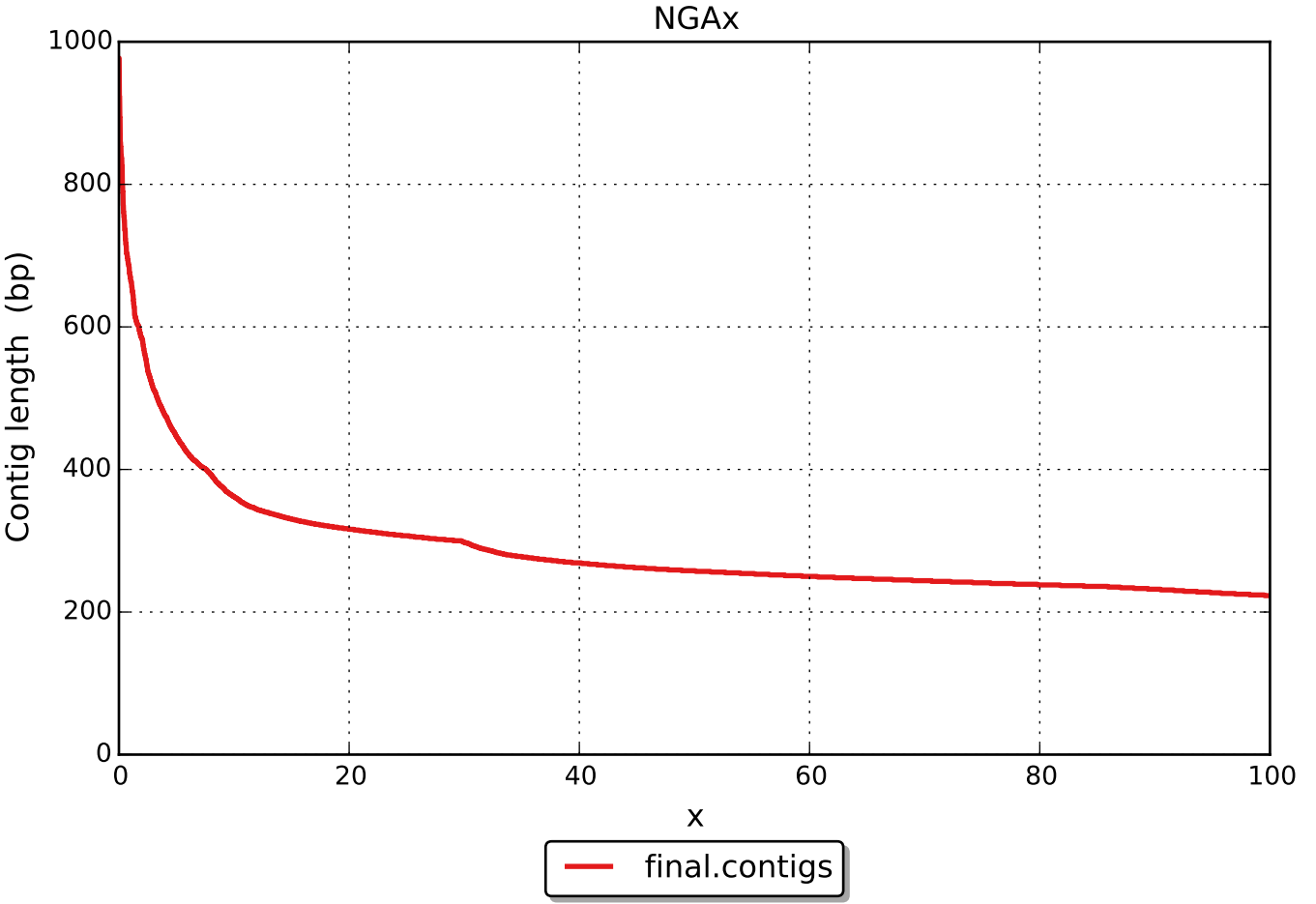

Cumulative length
Cumulative length (Mbp)
0
3
6
9
12
15
0
10000
20000
30000
40000
50000
Contig index
final.contigs
Reference


GC content
10000
8000
6000
4000
2000
0
# windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
5000
10000
15000
20000
25000
Contig index
final.contigs
Reference


NAx
1000
800
600
400
200
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
final.contigs