# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 8511 |
| # contigs (>= 1000 bp) | 4094 |
| Total length (>= 0 bp) | 11195088 |
| Total length (>= 1000 bp) | 8731046 |
| # contigs | 6541 |
| Largest contig | 10098 |
| Total length | 10518594 |
| Reference length | 10957366 |
| GC (%) | 50.38 |
| Reference GC (%) | 50.49 |
| N50 | 2007 |
| NG50 | 1939 |
| N75 | 1241 |
| NG75 | 1143 |
| L50 | 1681 |
| LG50 | 1792 |
| L75 | 3338 |
| LG75 | 3615 |
| # misassemblies | 2 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 3732 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 92.327 |
| Duplication ratio | 1.040 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 30.87 |
| # indels per 100 kbp | 0.11 |
| Largest alignment | 10098 |
| NA50 | 2007 |
| NGA50 | 1939 |
| NA75 | 1241 |
| NGA75 | 1142 |
| LA50 | 1681 |
| LGA50 | 1792 |
| LA75 | 3338 |
| LGA75 | 3615 |

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

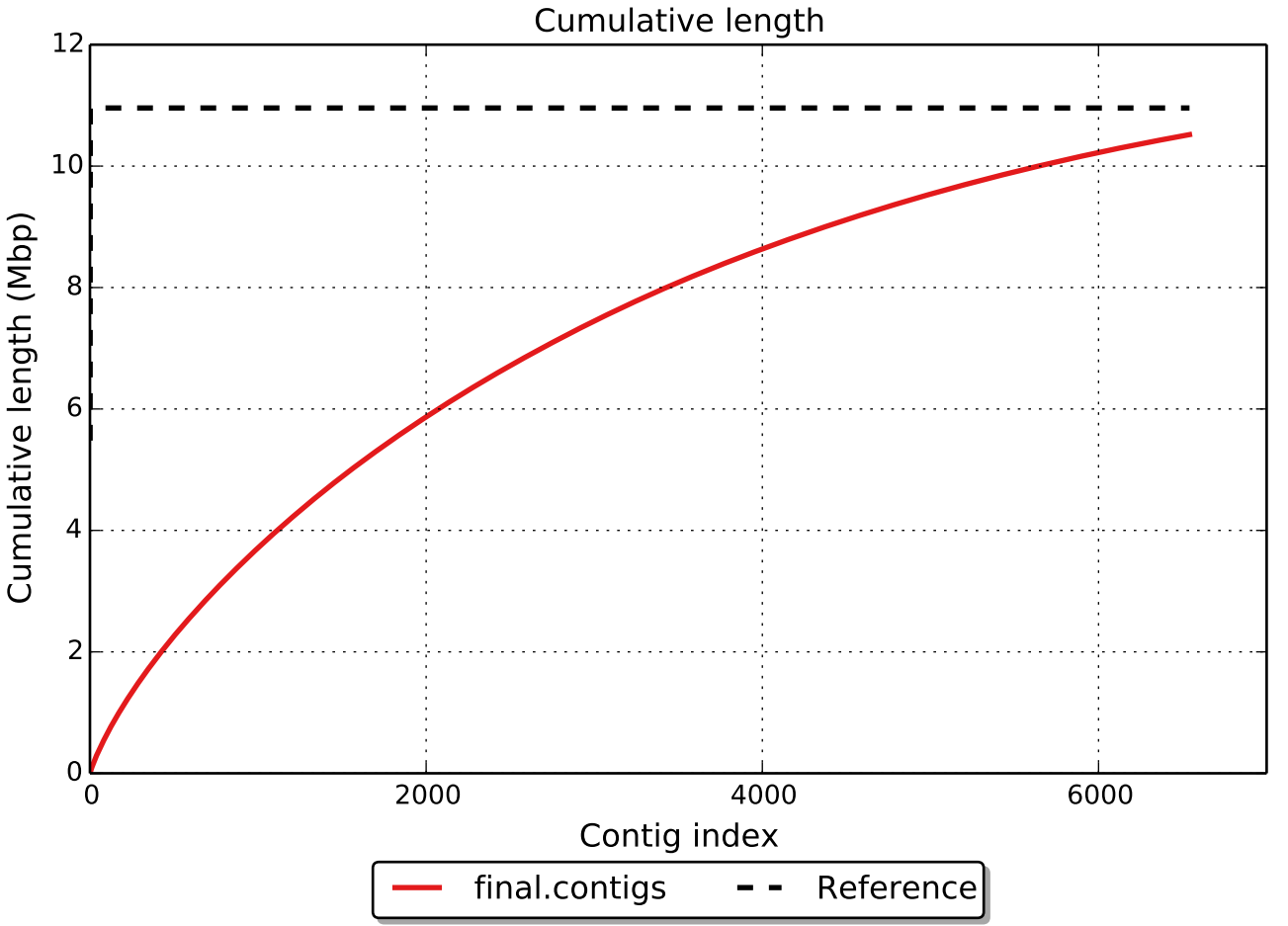
| | final.contigs |
|---|---|
| # misassemblies | 2 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 2 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 3732 |
| # local misassemblies | 2 |
| # mismatches | 3123 |
| # indels | 11 |
| # short indels | 11 |
| # long indels | 0 |
| Indels length | 17 |

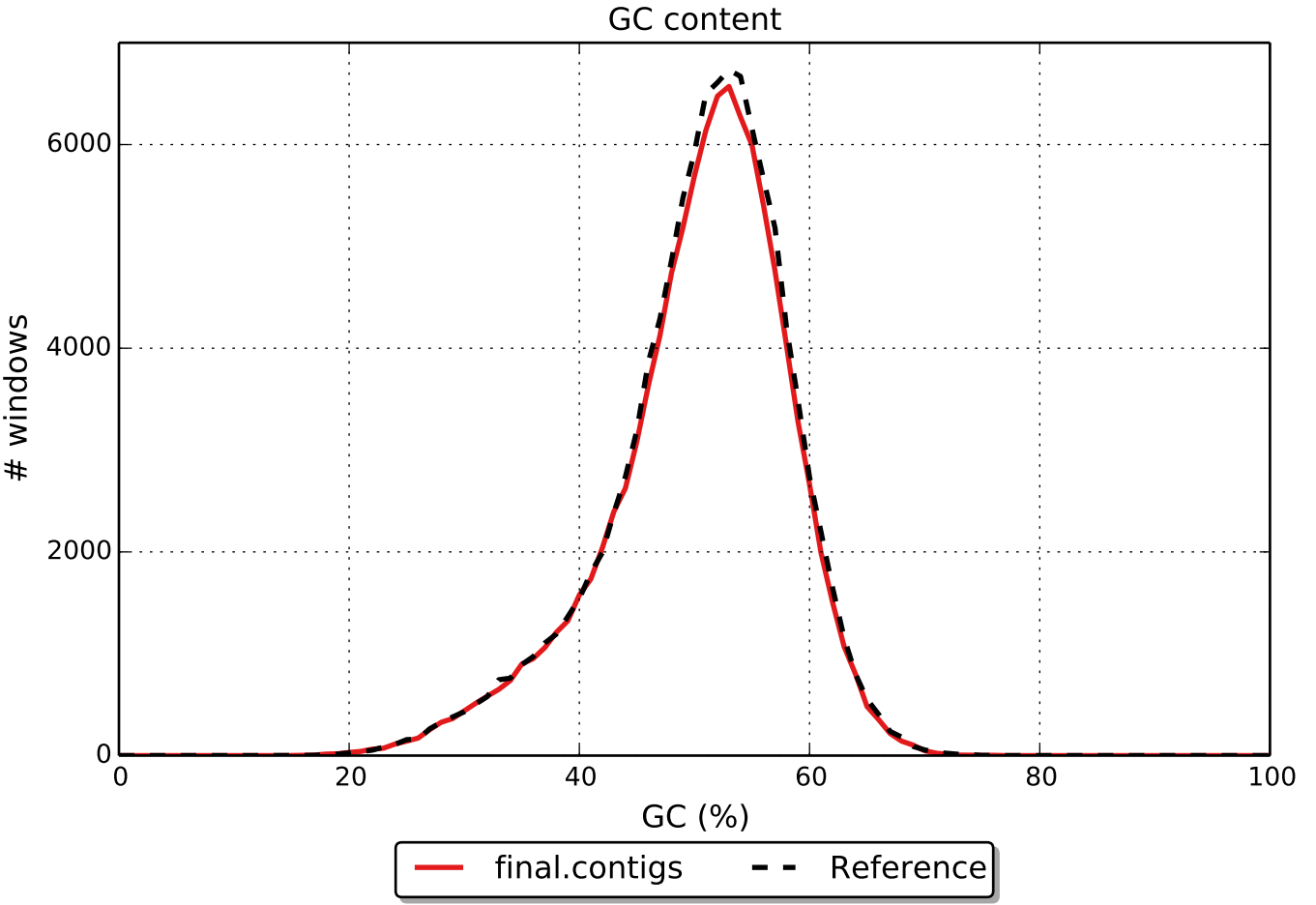
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

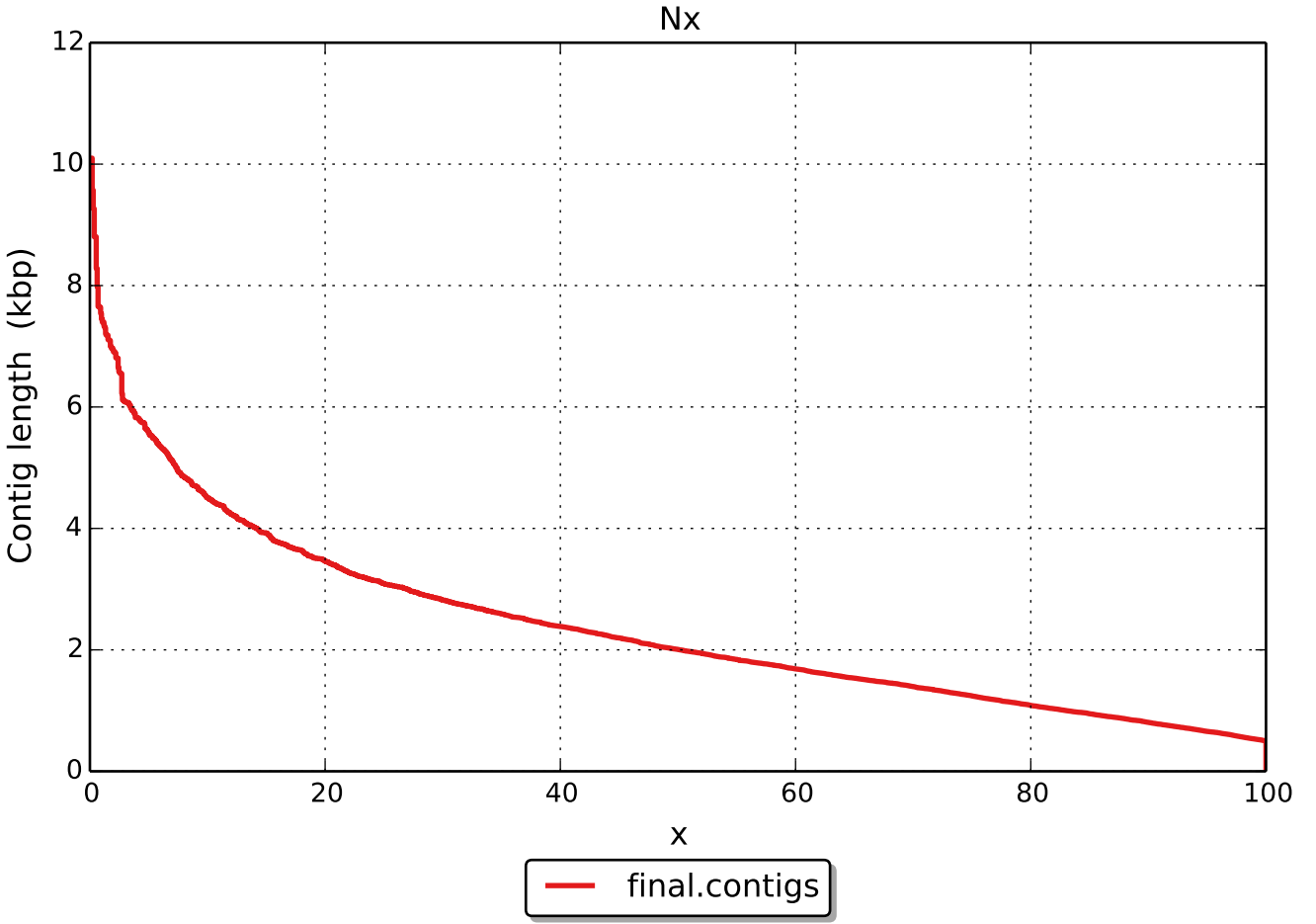
# Unaligned report

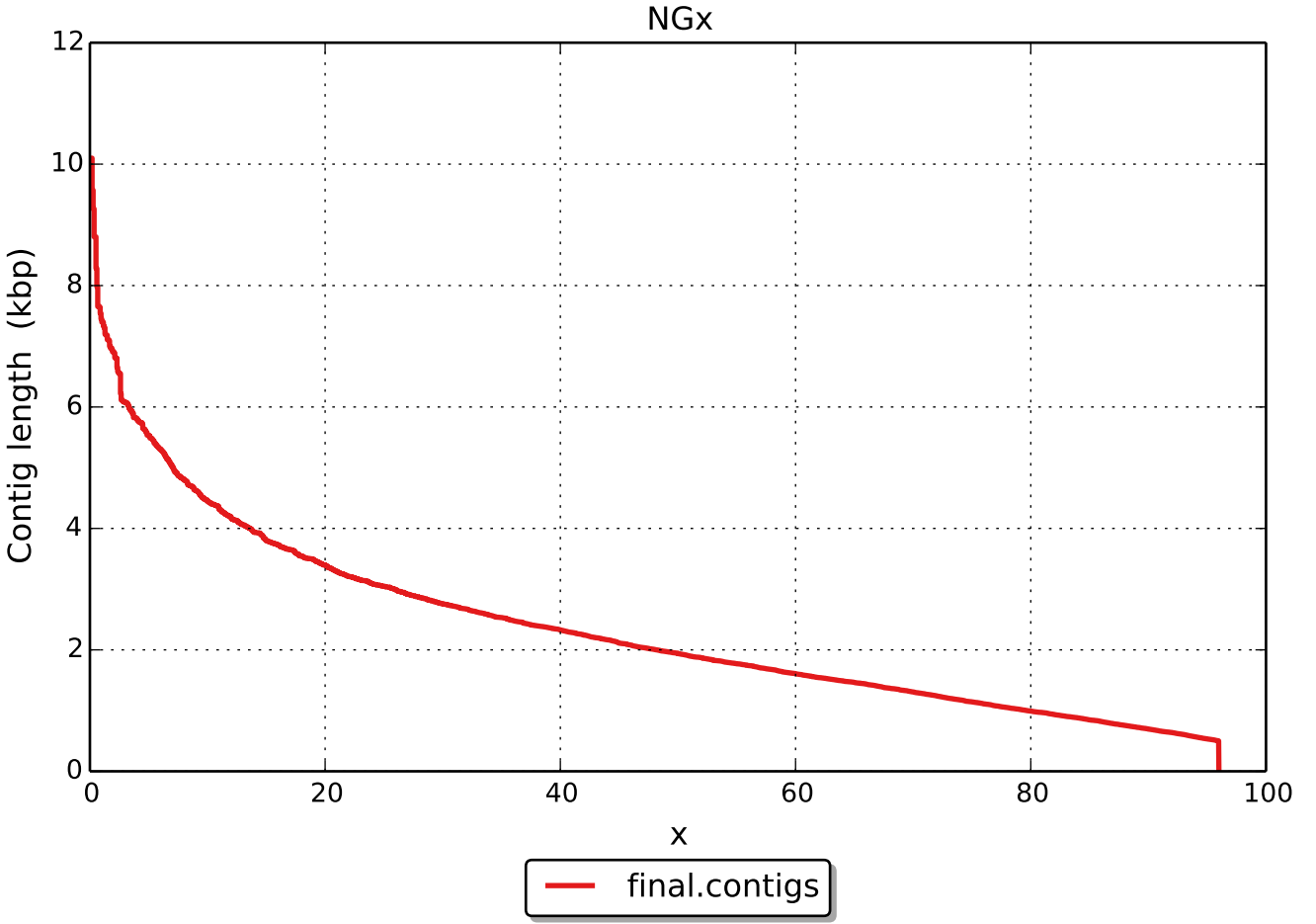
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

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).

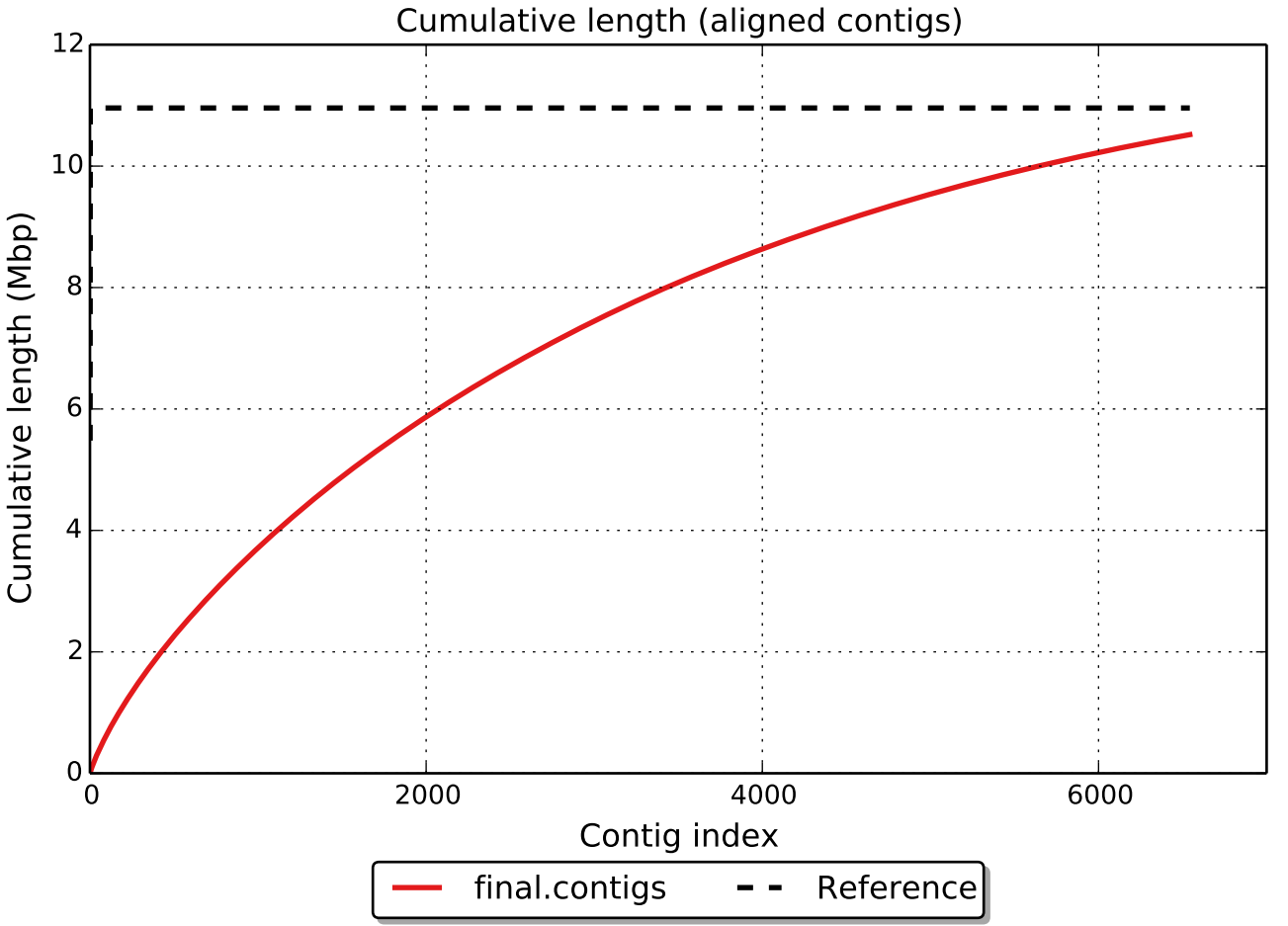

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
2000
4000
6000
Contig index
final.contigs
Reference

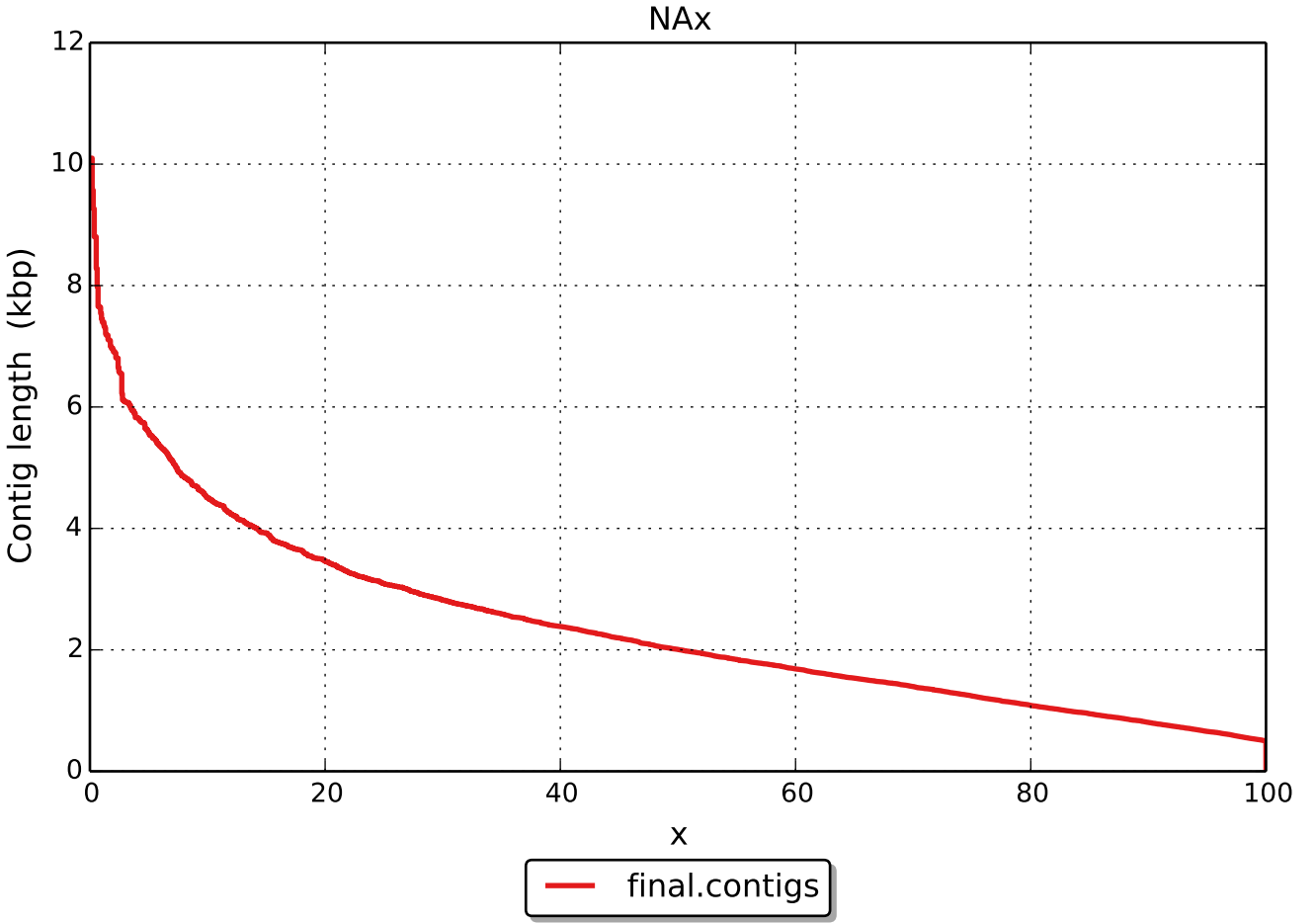

GC content
# windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

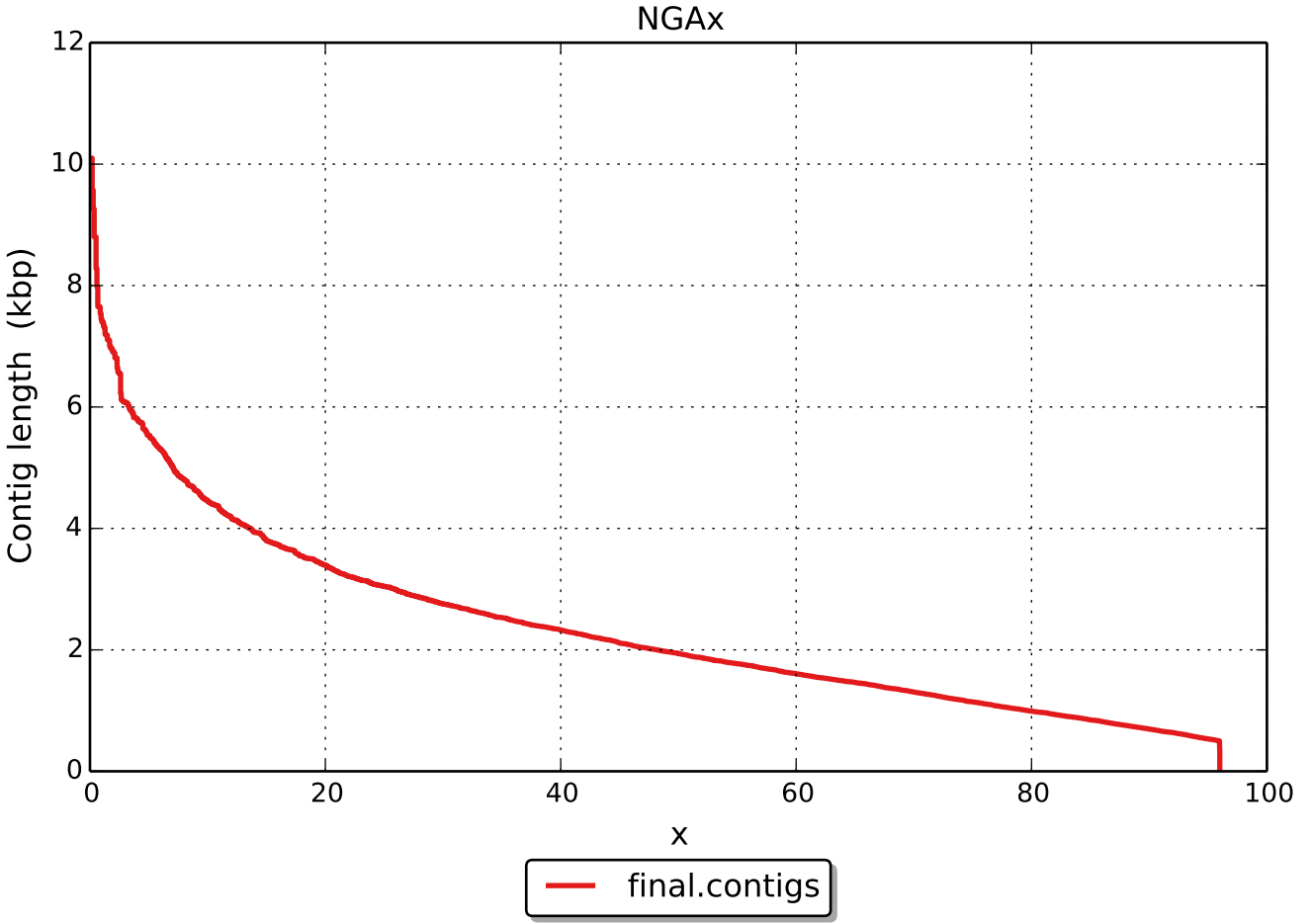

Nx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs

Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
# interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
2000
4000
6000
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs