# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 3263 |
| # contigs (>= 1000 bp) | 2173 |
| Total length (>= 0 bp) | 11052617 |
| Total length (>= 1000 bp) | 10545119 |
| # contigs | 2571 |
| Largest contig | 30455 |
| Total length | 10834958 |
| Reference length | 11094646 |
| GC (%) | 50.39 |
| Reference GC (%) | 50.48 |
| N50 | 6653 |
| NG50 | 6530 |
| N75 | 3624 |
| NG75 | 3494 |
| L50 | 508 |
| LG50 | 527 |
| L75 | 1061 |
| LG75 | 1116 |
| # misassemblies | 3 |
| # misassembled contigs | 3 |
| Misassembled contigs length | 33243 |
| # local misassemblies | 4 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 96.994 |
| Duplication ratio | 1.021 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 28.08 |
| # indels per 100 kbp | 0.38 |
| Largest alignment | 30455 |
| NA50 | 6653 |
| NGA50 | 6515 |
| NA75 | 3616 |
| NGA75 | 3489 |
| LA50 | 509 |
| LGA50 | 529 |
| LA75 | 1064 |
| LGA75 | 1118 |

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

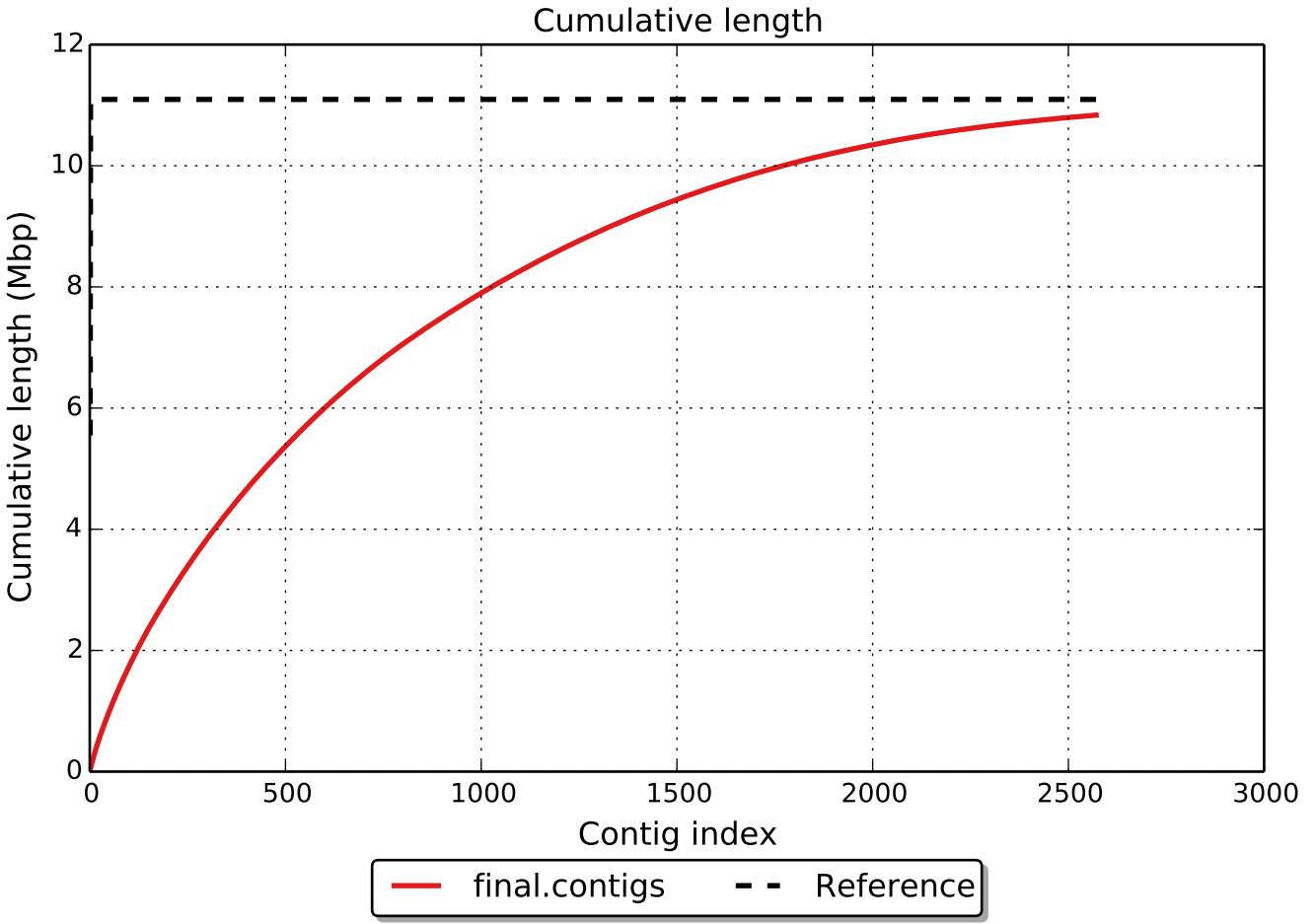
| | final.contigs |
|---|---|
| # misassemblies | 3 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 3 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 3 |
| Misassembled contigs length | 33243 |
| # local misassemblies | 4 |
| # mismatches | 3022 |
| # indels | 41 |
| # short indels | 37 |
| # long indels | 4 |
| Indels length | 162 |

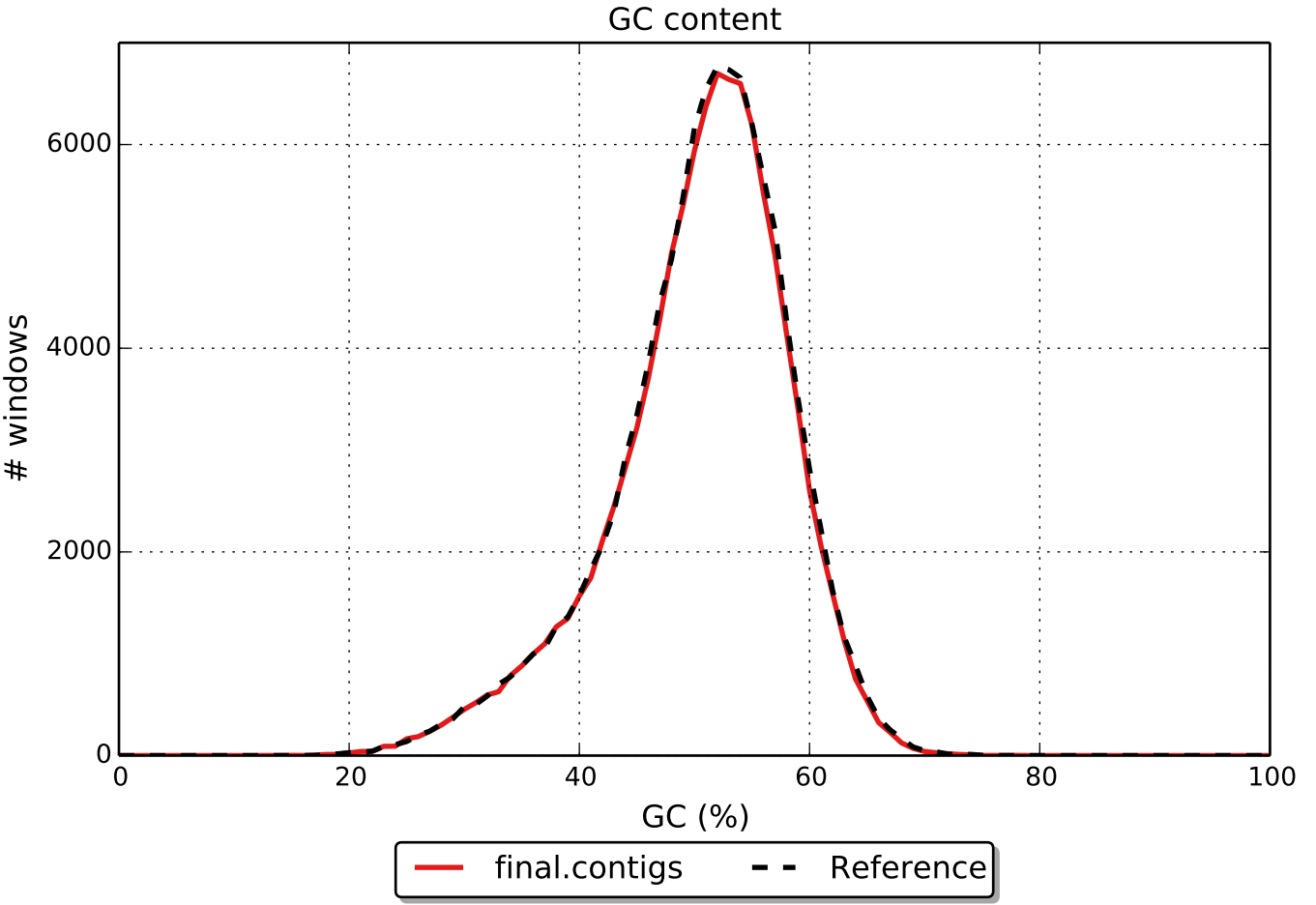
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

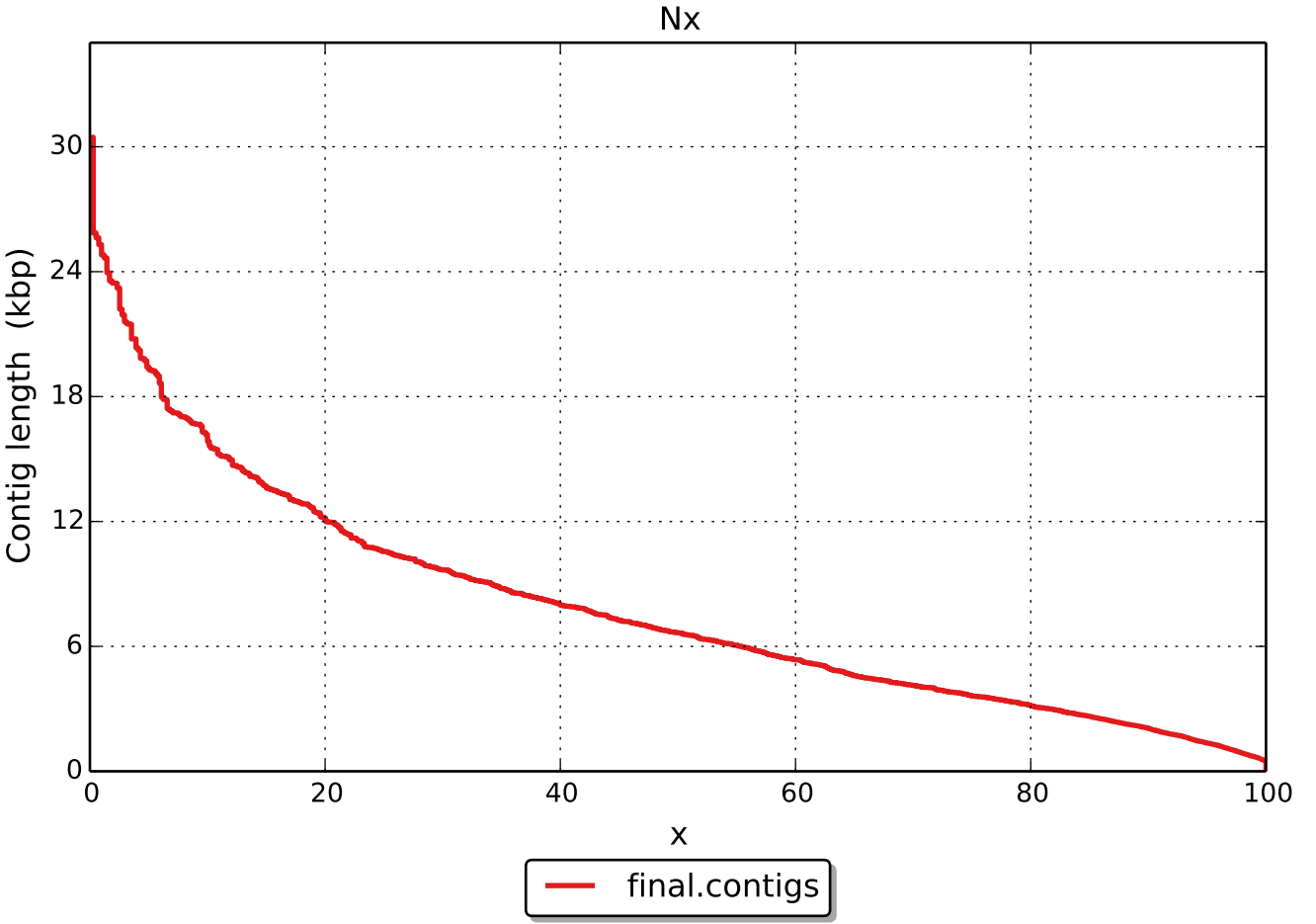
# Unaligned report

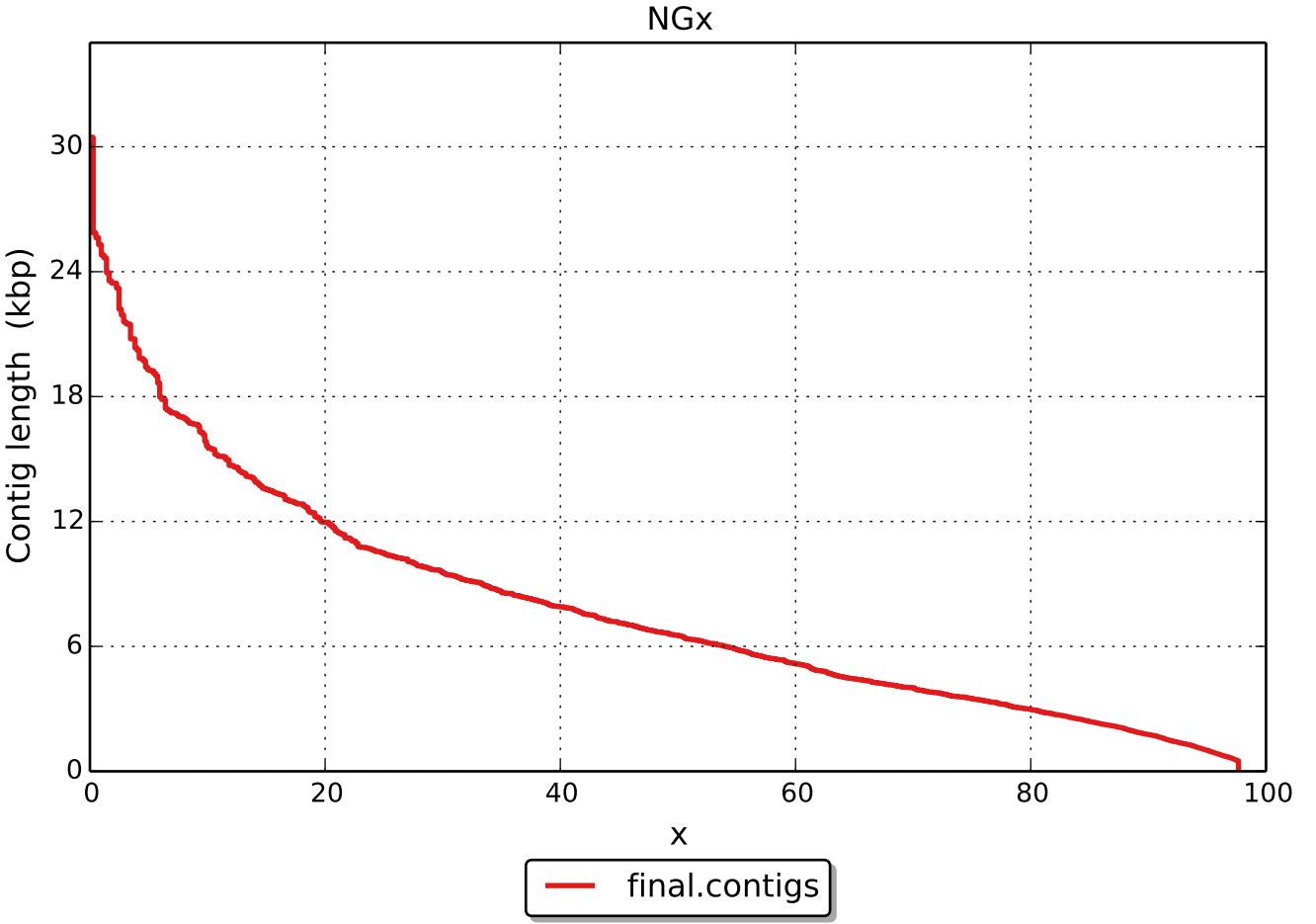
| | final.contigs |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

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).

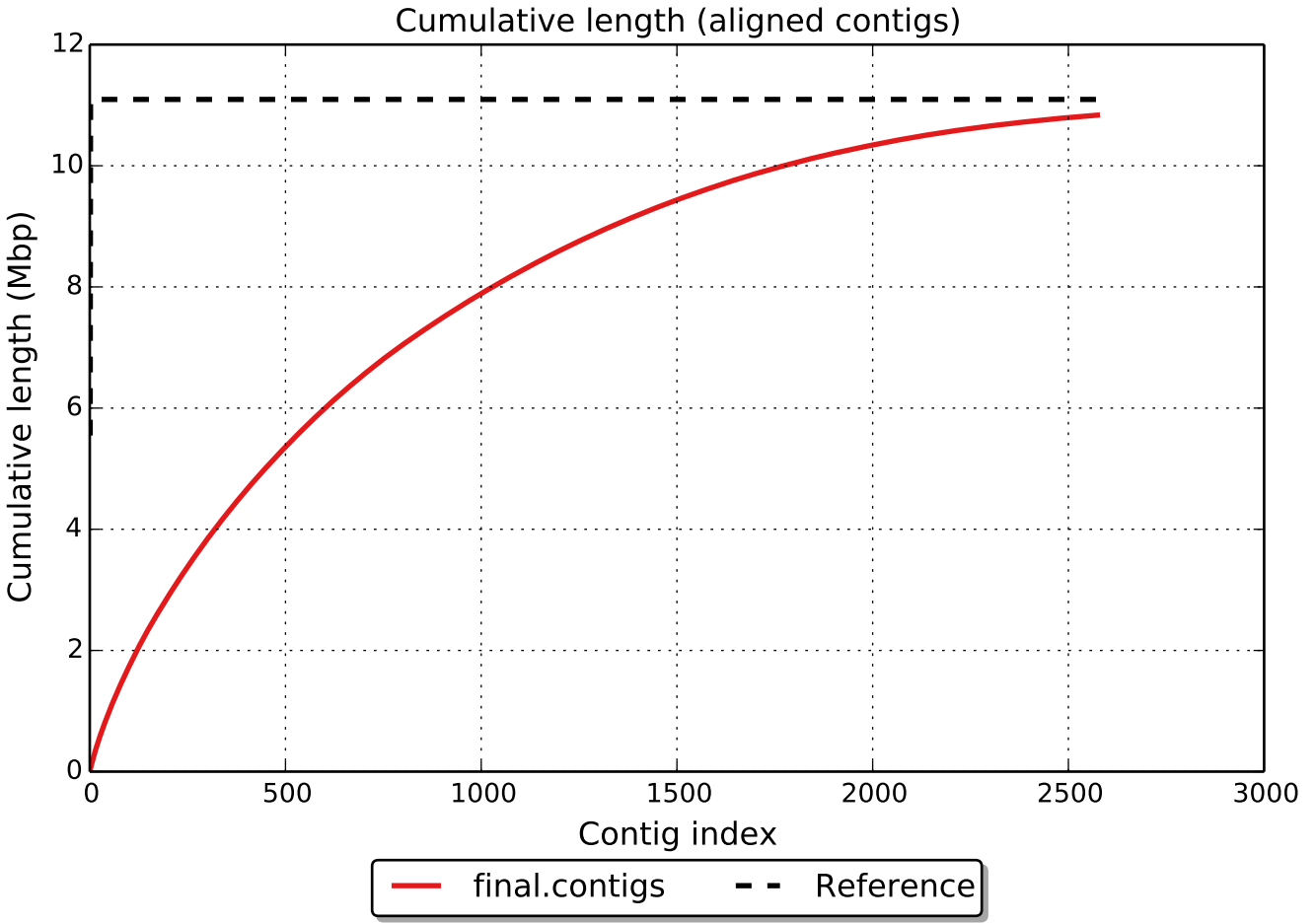

Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
500
1000
1500
2000
2500
3000
final.contigs
Reference

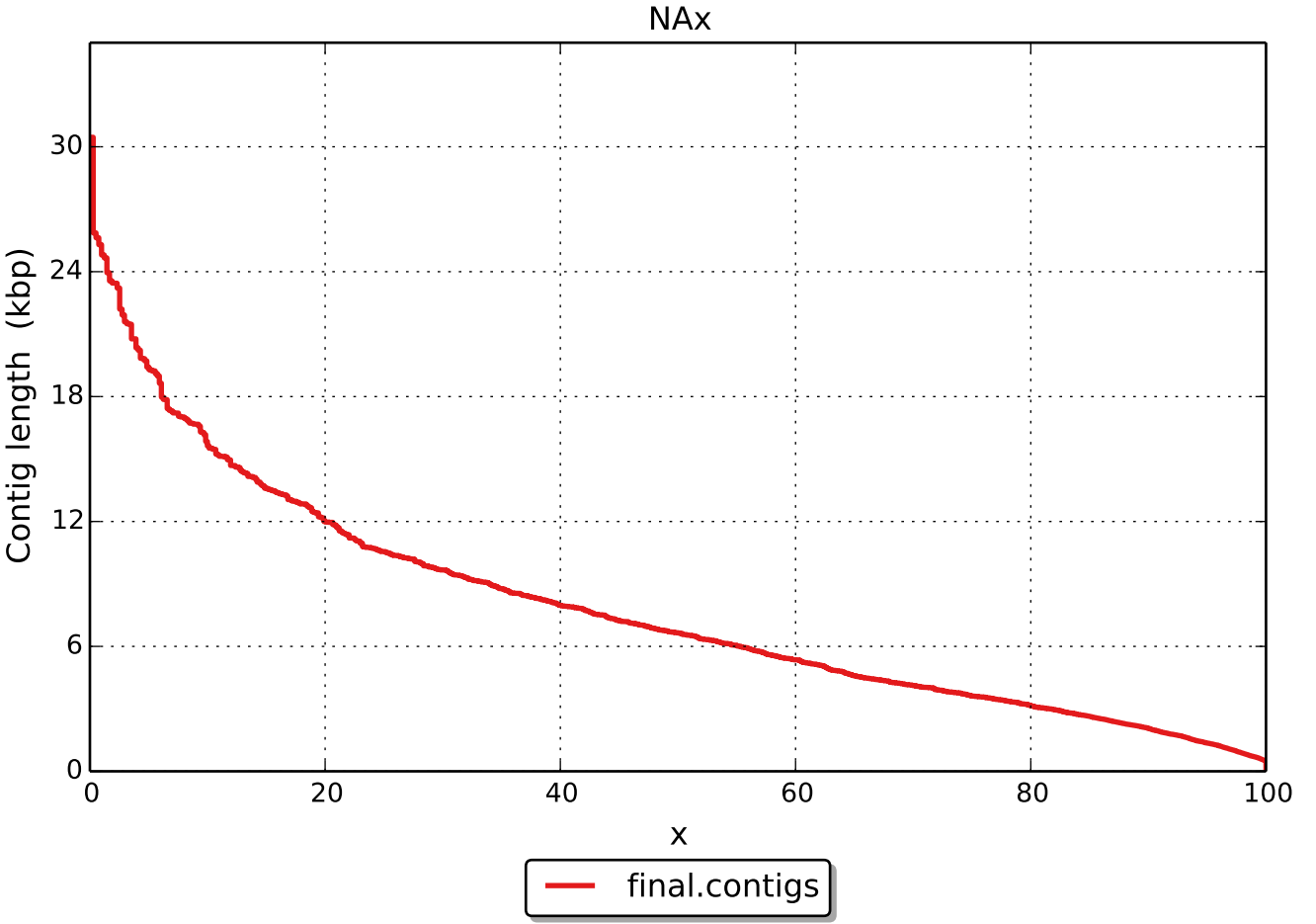

GC content
# windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

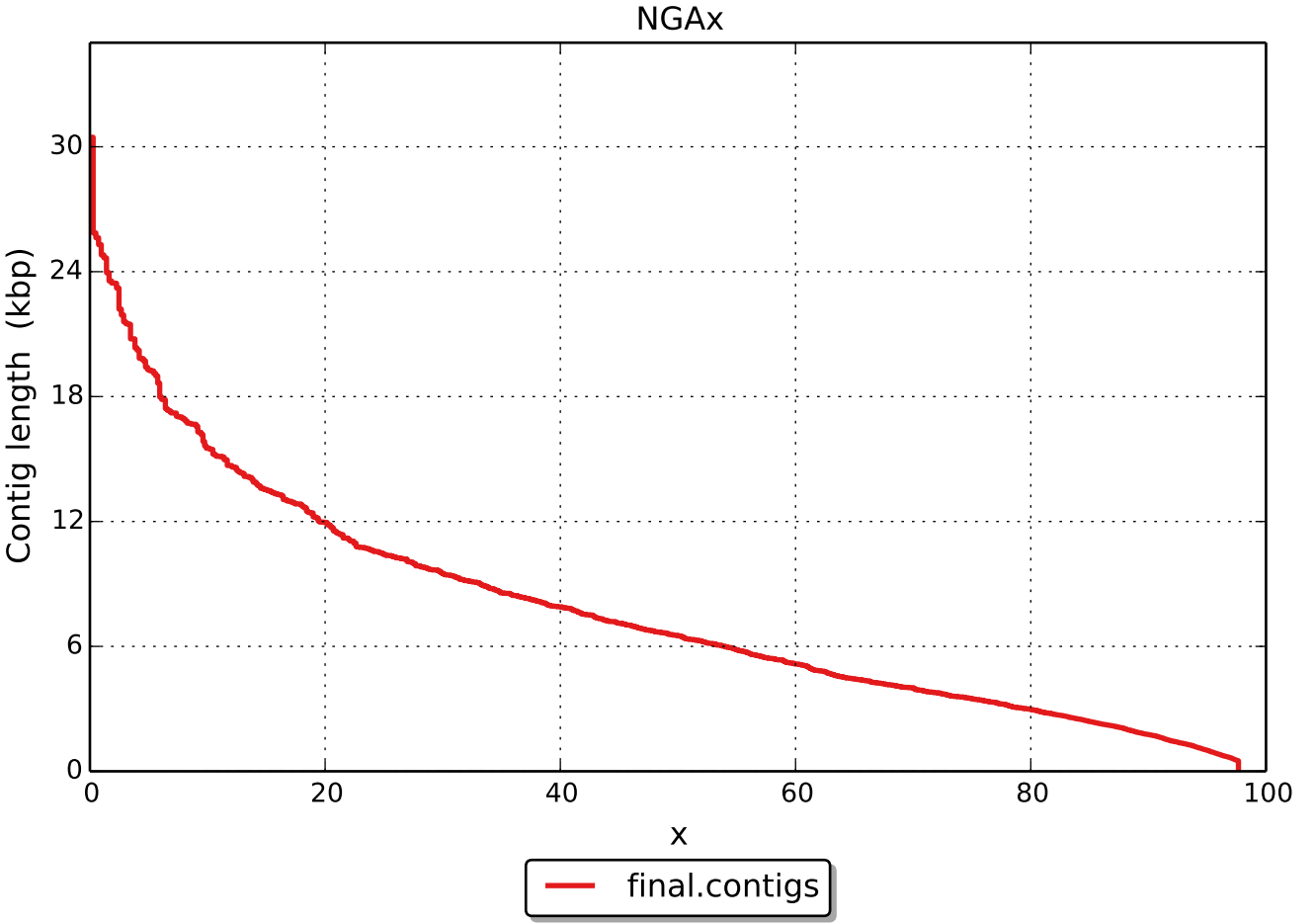

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

Misassemblies
4.0
3.5
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
500
1000
1500
2000
2500
3000
final.contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs