Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 440 |
| # contigs (>= 1000 bp) | 146 |
| # contigs (>= 5000 bp) | 122 |
| # contigs (>= 10000 bp) | 103 |
| # contigs (>= 25000 bp) | 66 |
| # contigs (>= 50000 bp) | 28 |
| Total length (>= 0 bp) | 4638877 |
| Total length (>= 1000 bp) | 4540987 |
| Total length (>= 5000 bp) | 4477714 |
| Total length (>= 10000 bp) | 4338012 |
| Total length (>= 25000 bp) | 3772958 |
| Total length (>= 50000 bp) | 2406475 |
| # contigs | 166 |
| Largest contig | 169087 |
| Total length | 4554962 |
| Reference length | 4641652 |
| GC (%) | 50.74 |
| Reference GC (%) | 50.79 |
| N50 | 53827 |
| NG50 | 53801 |
| N75 | 31696 |
| NG75 | 31480 |
| L50 | 26 |
| LG50 | 27 |
| L75 | 54 |
| LG75 | 56 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 2 + 0 part |
| Unaligned length | 1090 |
| Genome fraction (%) | 97.993 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1.85 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 169087 |
| NA50 | 53827 |
| NGA50 | 53801 |
| NA75 | 31696 |
| NGA75 | 31480 |
| LA50 | 26 |
| LGA50 | 27 |
| LA75 | 54 |
| LGA75 | 56 |

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

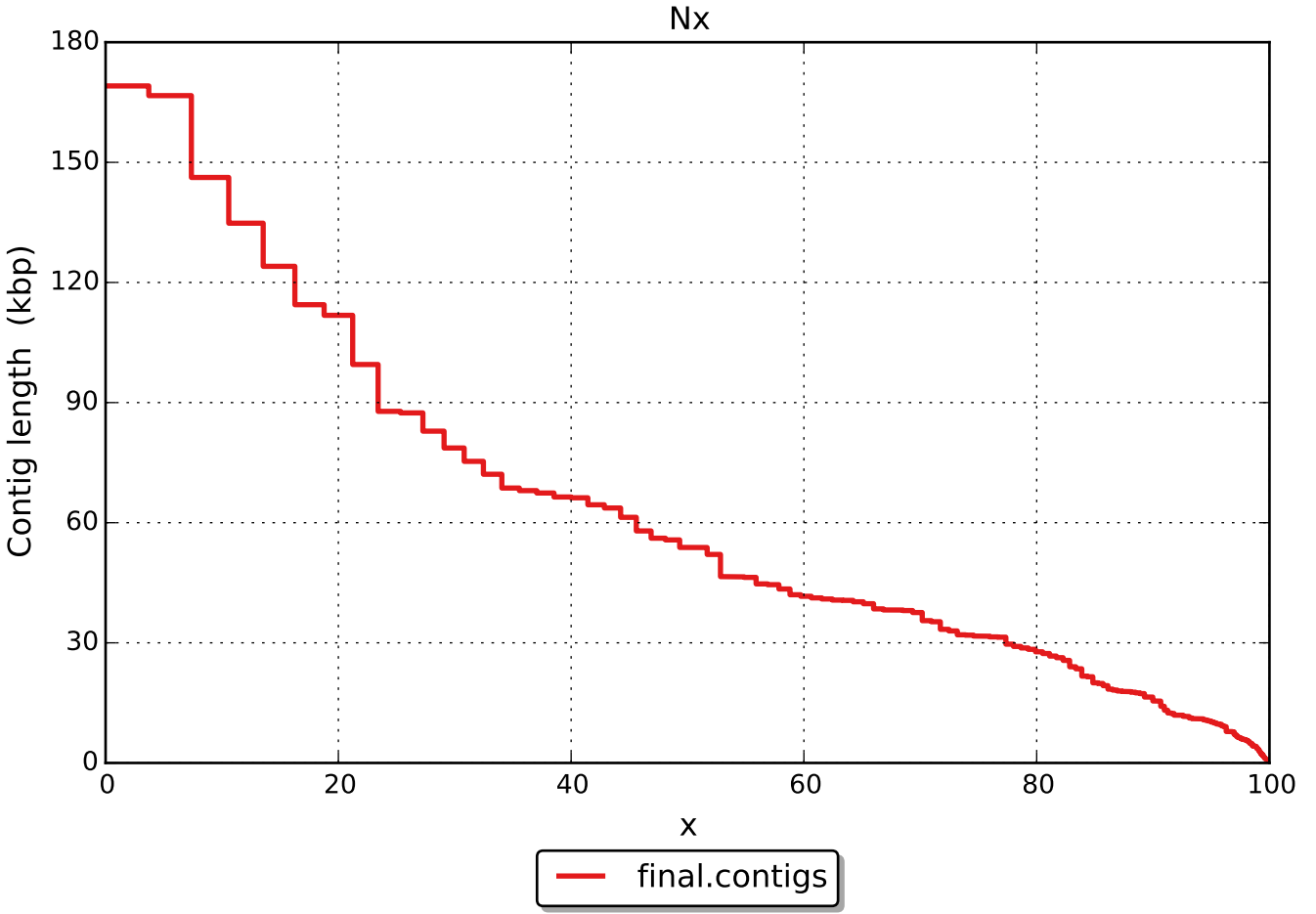
| | final.contigs |
|---|---|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 84 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 0 |

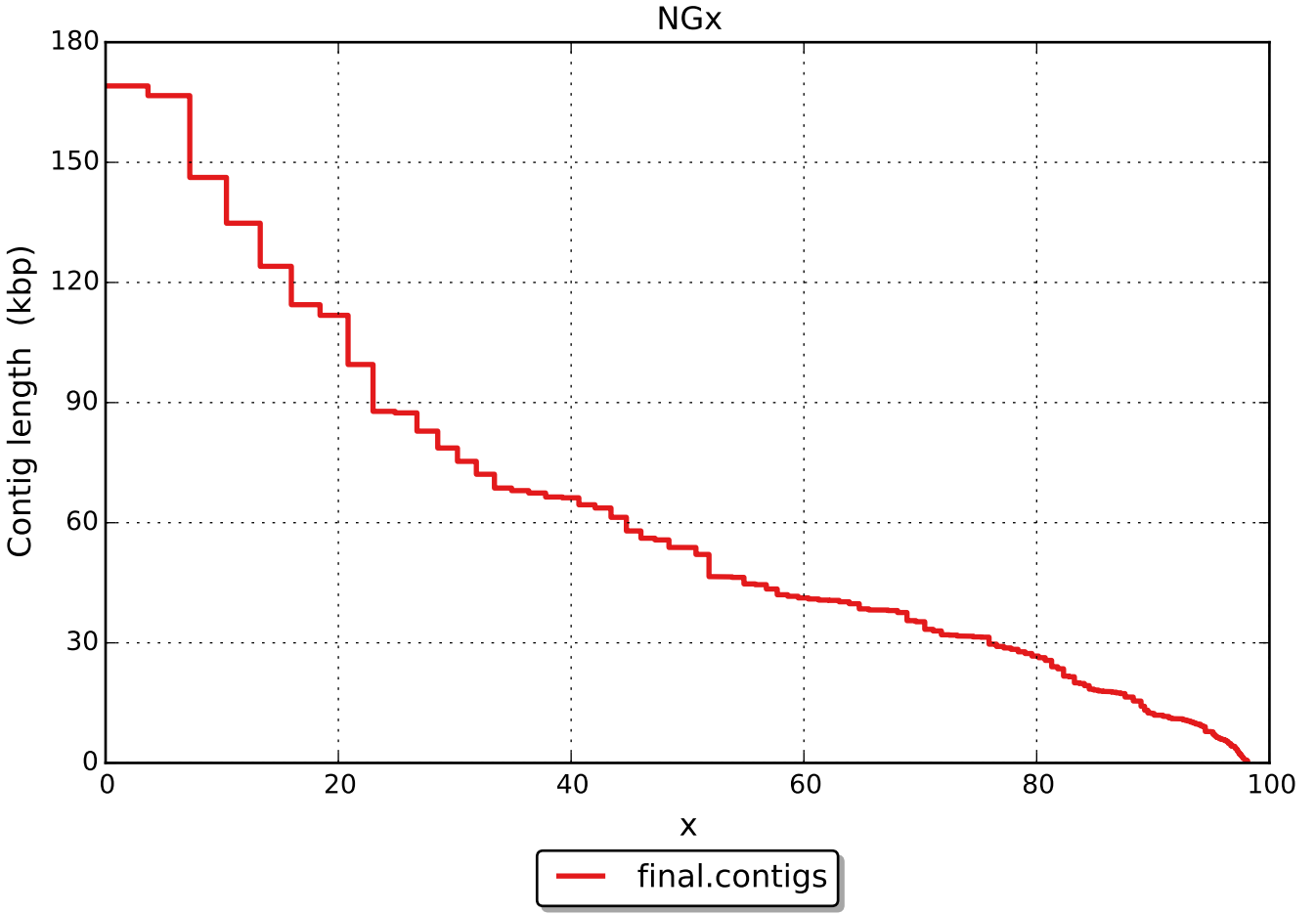
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

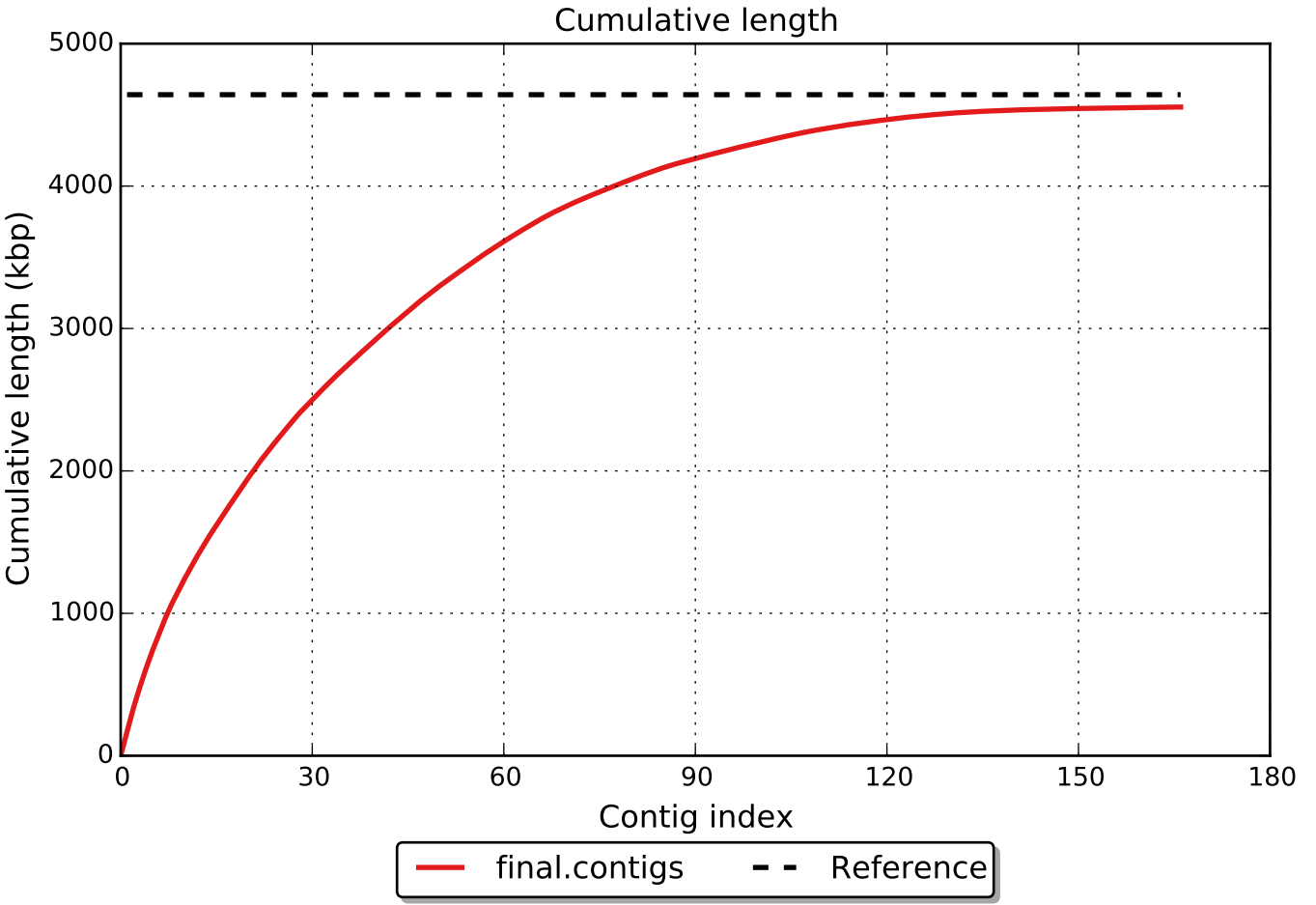
# Unaligned report

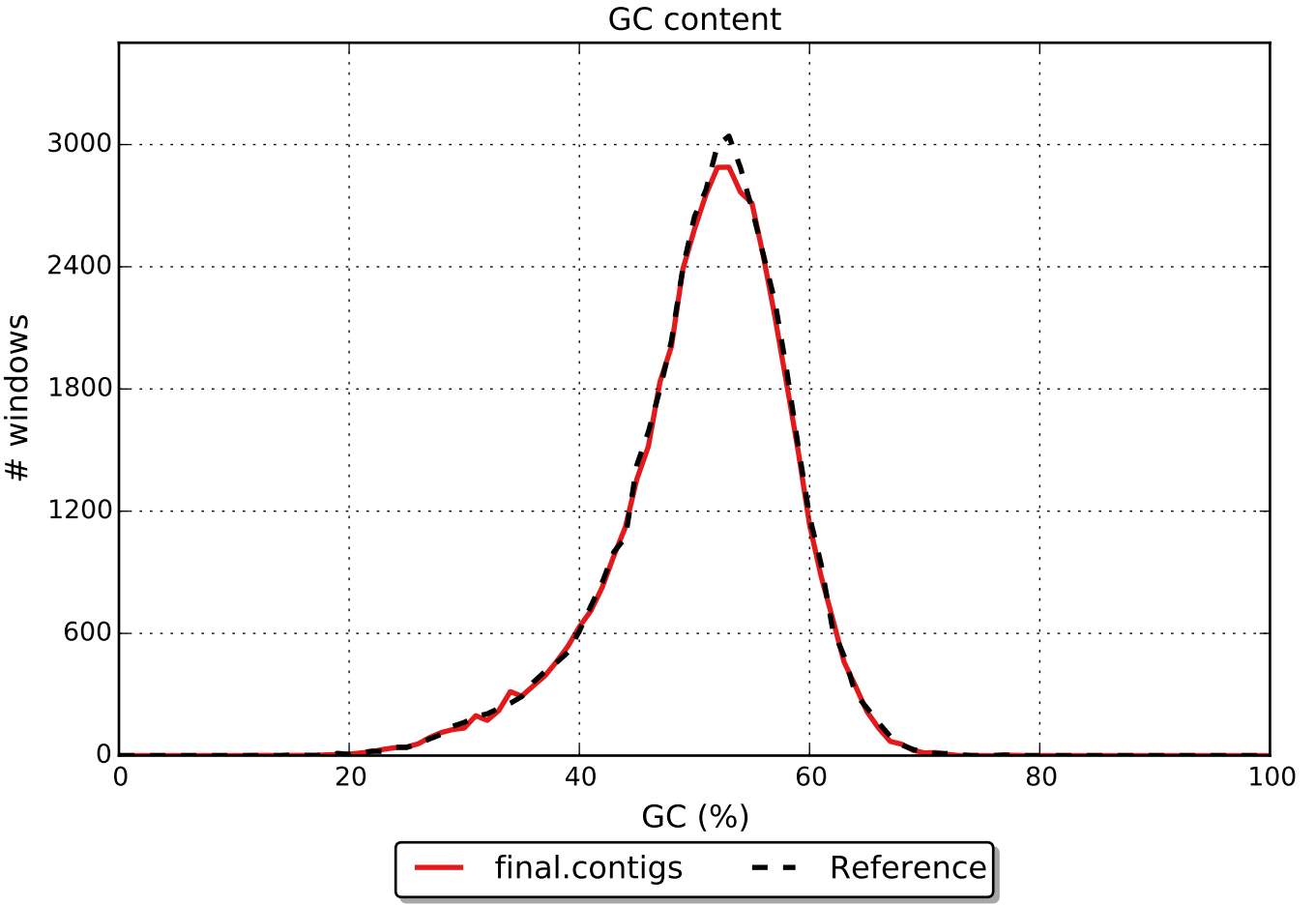
| | final.contigs |
|---|---|
| # fully unaligned contigs | 2 |
| Fully unaligned length | 1090 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

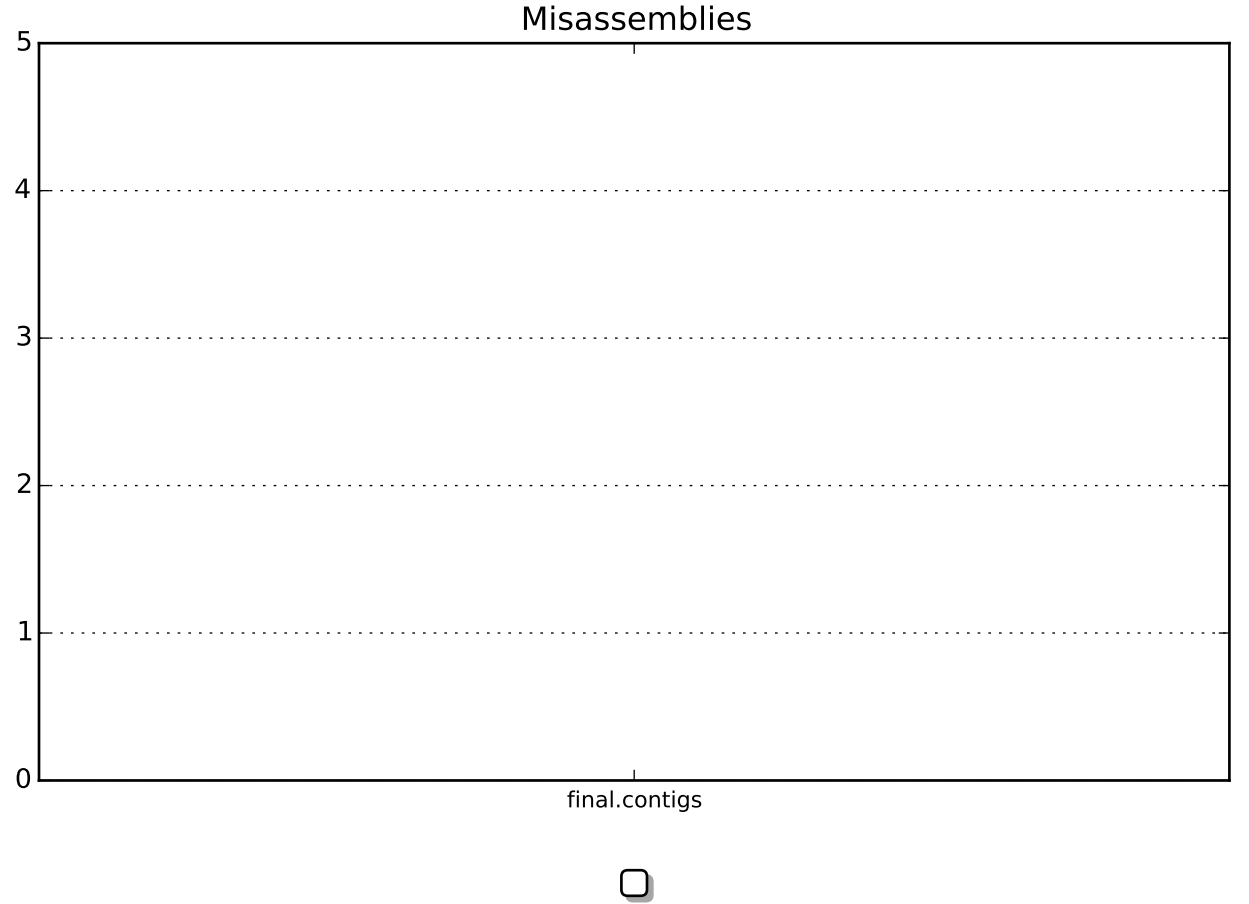
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

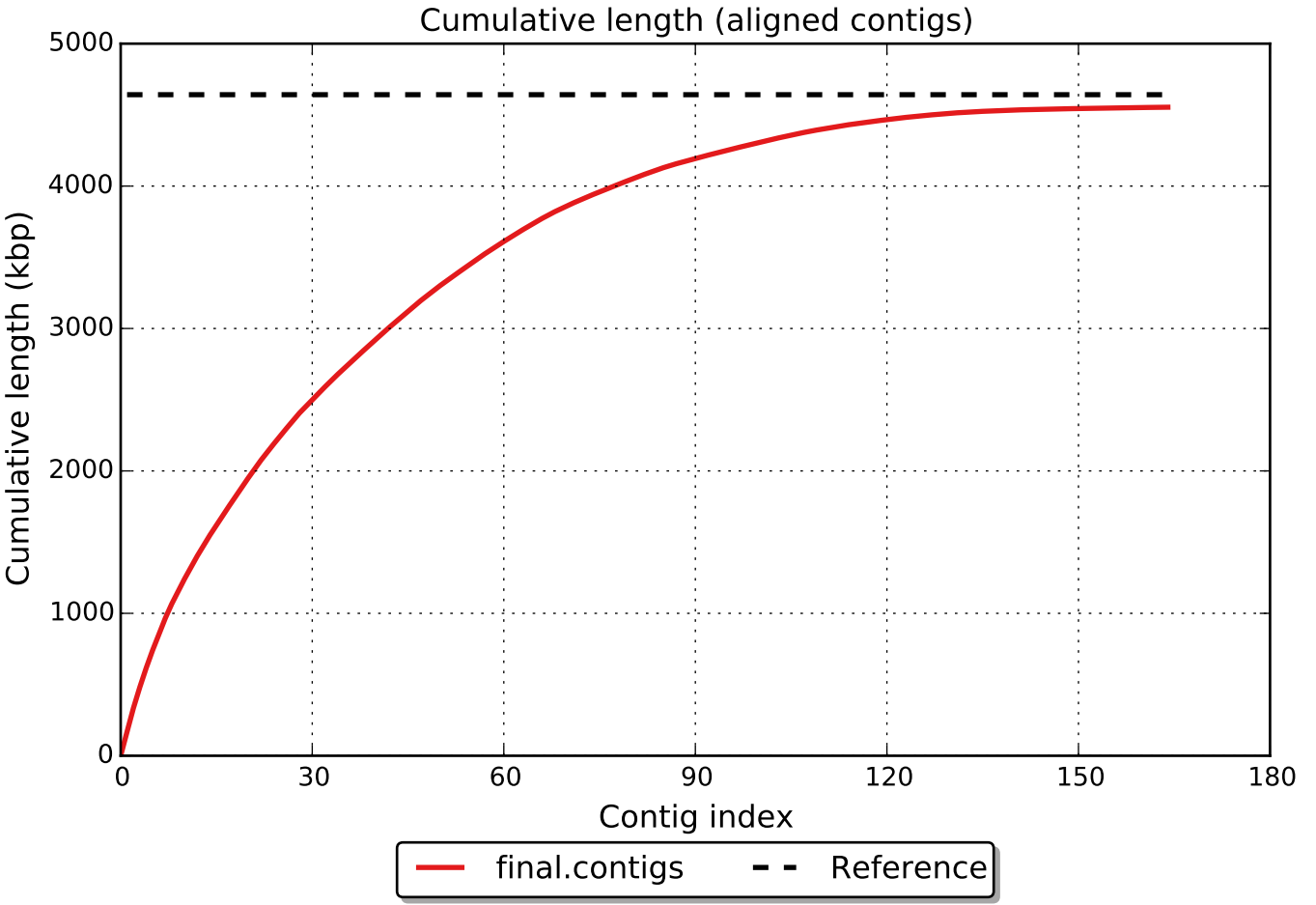

Nx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

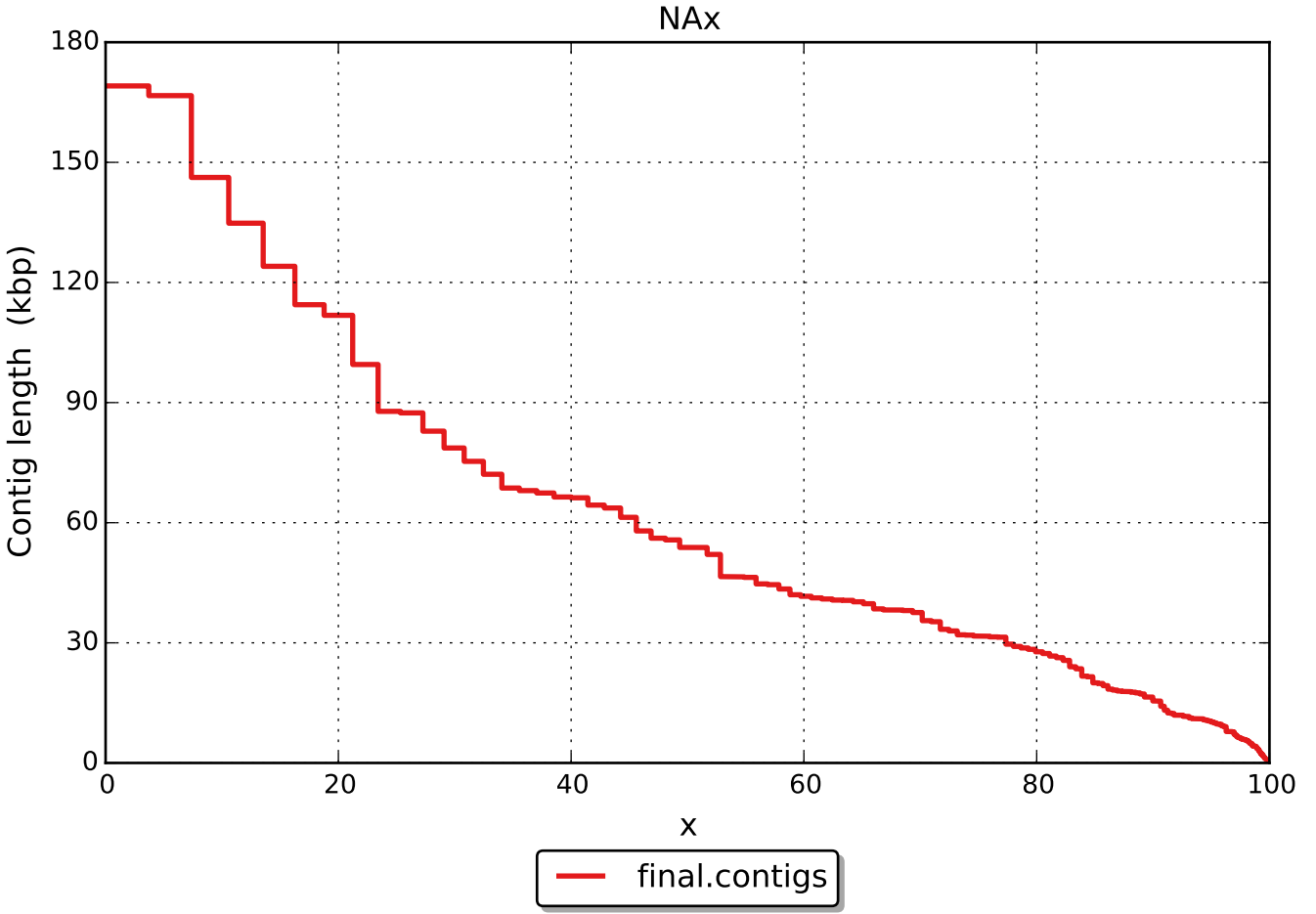

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

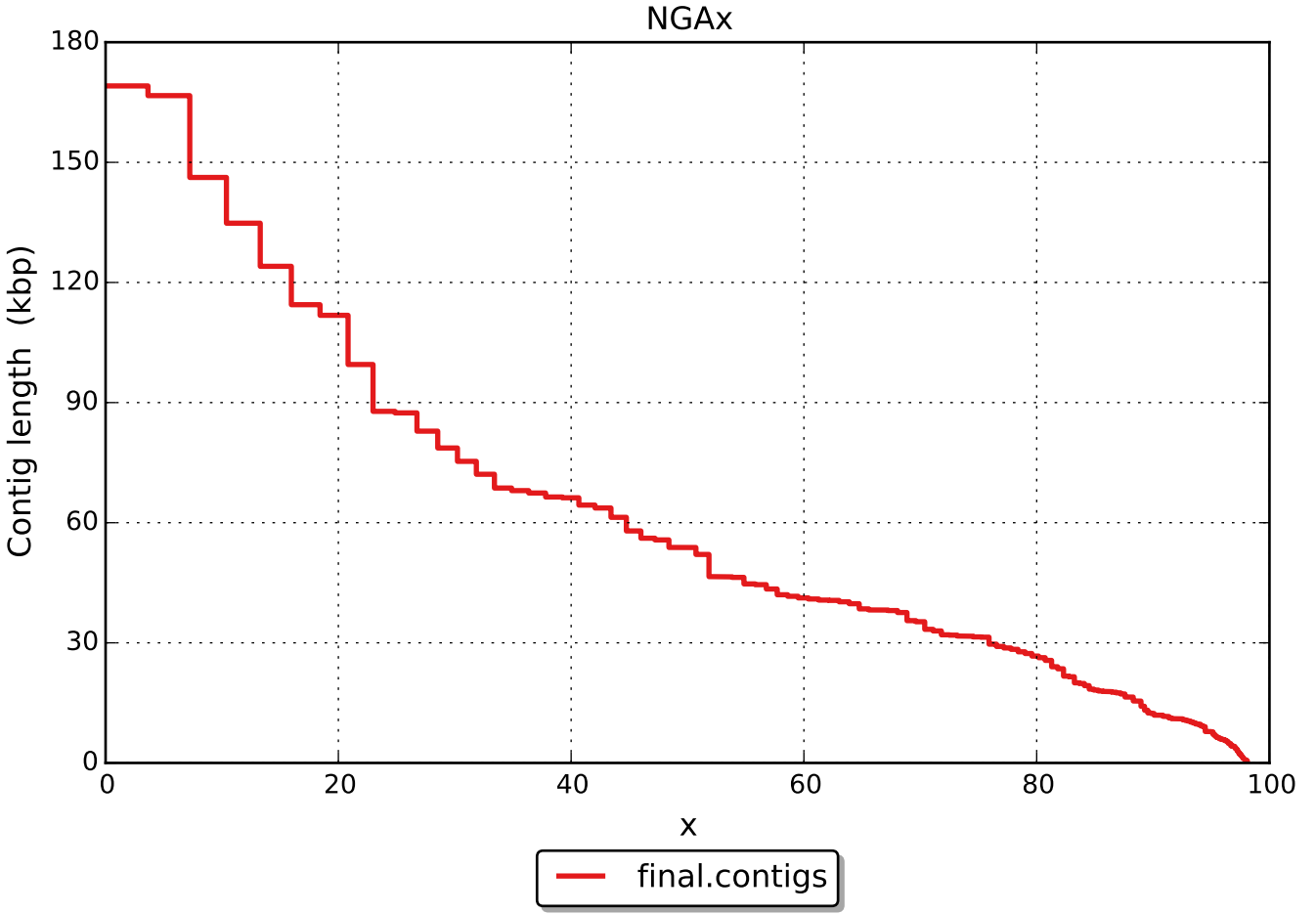

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
180
Contig index
final.contigs
Reference


GC content
# windows
3000
2400
1800
1200
600
0
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 (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
180
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGAx
180
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs