Report

| | scaffolds |
|---|---|
| # contigs (>= 1000 bp) | 116 |
| # contigs (>= 5000 bp) | 91 |
| # contigs (>= 10000 bp) | 73 |
| # contigs (>= 25000 bp) | 48 |
| # contigs (>= 50000 bp) | 31 |
| Total length (>= 1000 bp) | 3847604 |
| Total length (>= 5000 bp) | 3784308 |
| Total length (>= 10000 bp) | 3656982 |
| Total length (>= 25000 bp) | 3267331 |
| Total length (>= 50000 bp) | 2692246 |
| # contigs | 124 |
| Largest contig | 161420 |
| Total length | 3853478 |
| Reference length | 4641652 |
| GC (%) | 50.76 |
| Reference GC (%) | 50.78 |
| N50 | 73015 |
| NG50 | 59673 |
| N75 | 35258 |
| NG75 | 15441 |
| L50 | 19 |
| LG50 | 25 |
| L75 | 36 |
| LG75 | 59 |
| # misassemblies | 5 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 310368 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 82.879 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 15.93 |
| # mismatches per 100 kbp | 556.28 |
| # indels per 100 kbp | 0.42 |
| Largest alignment | 142244 |
| NA50 | 72917 |
| NGA50 | 59359 |
| NA75 | 33561 |
| NGA75 | 15351 |
| LA50 | 19 |
| LGA50 | 25 |
| LA75 | 38 |
| LGA75 | 63 |

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

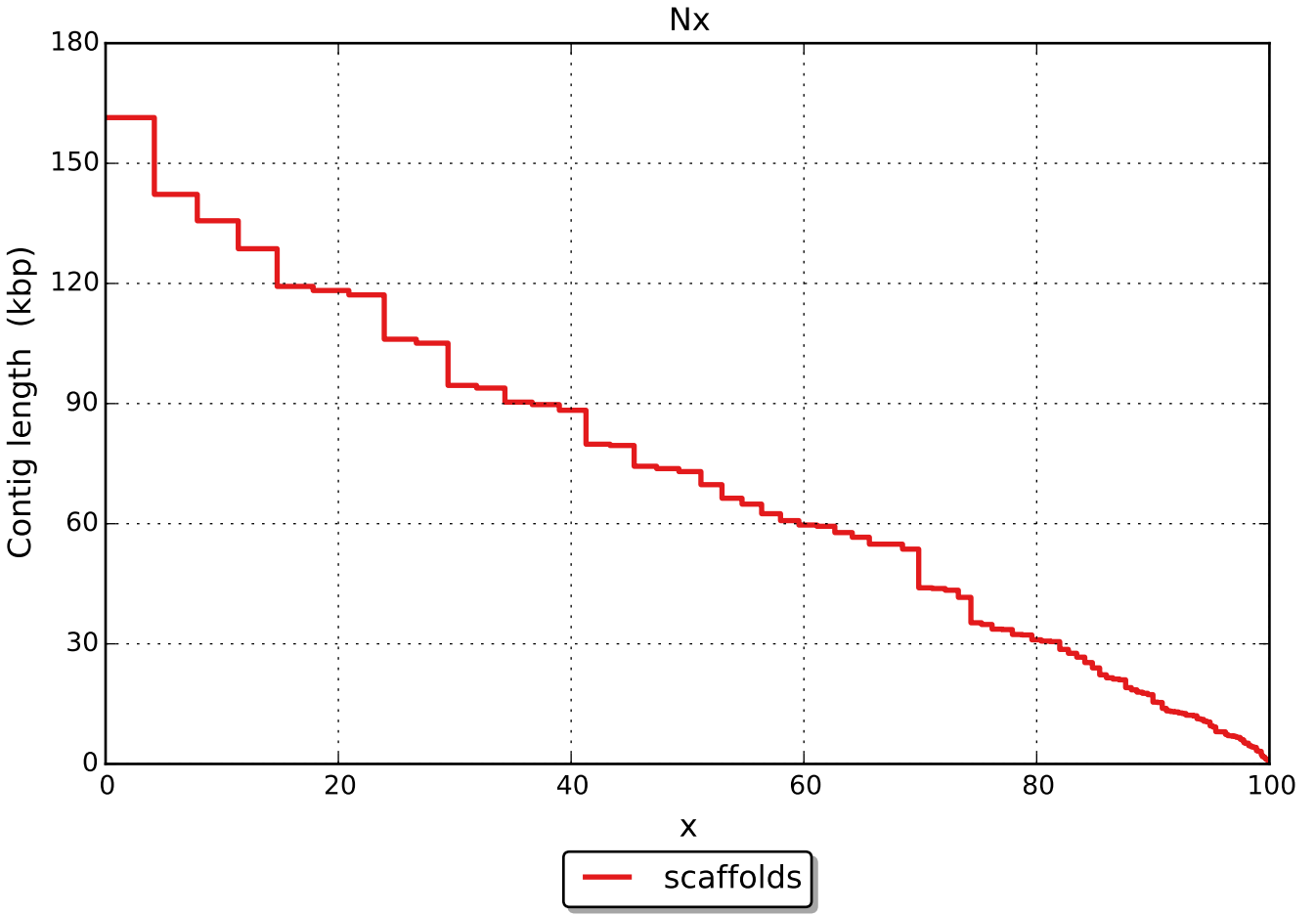
| | scaffolds |
|---|---|
| # misassemblies | 5 |
| # relocations | 4 |
| # translocations | 0 |
| # inversions | 1 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 310368 |
| # local misassemblies | 2 |
| # mismatches | 21400 |
| # indels | 16 |
| # short indels | 14 |
| # long indels | 2 |
| Indels length | 130 |

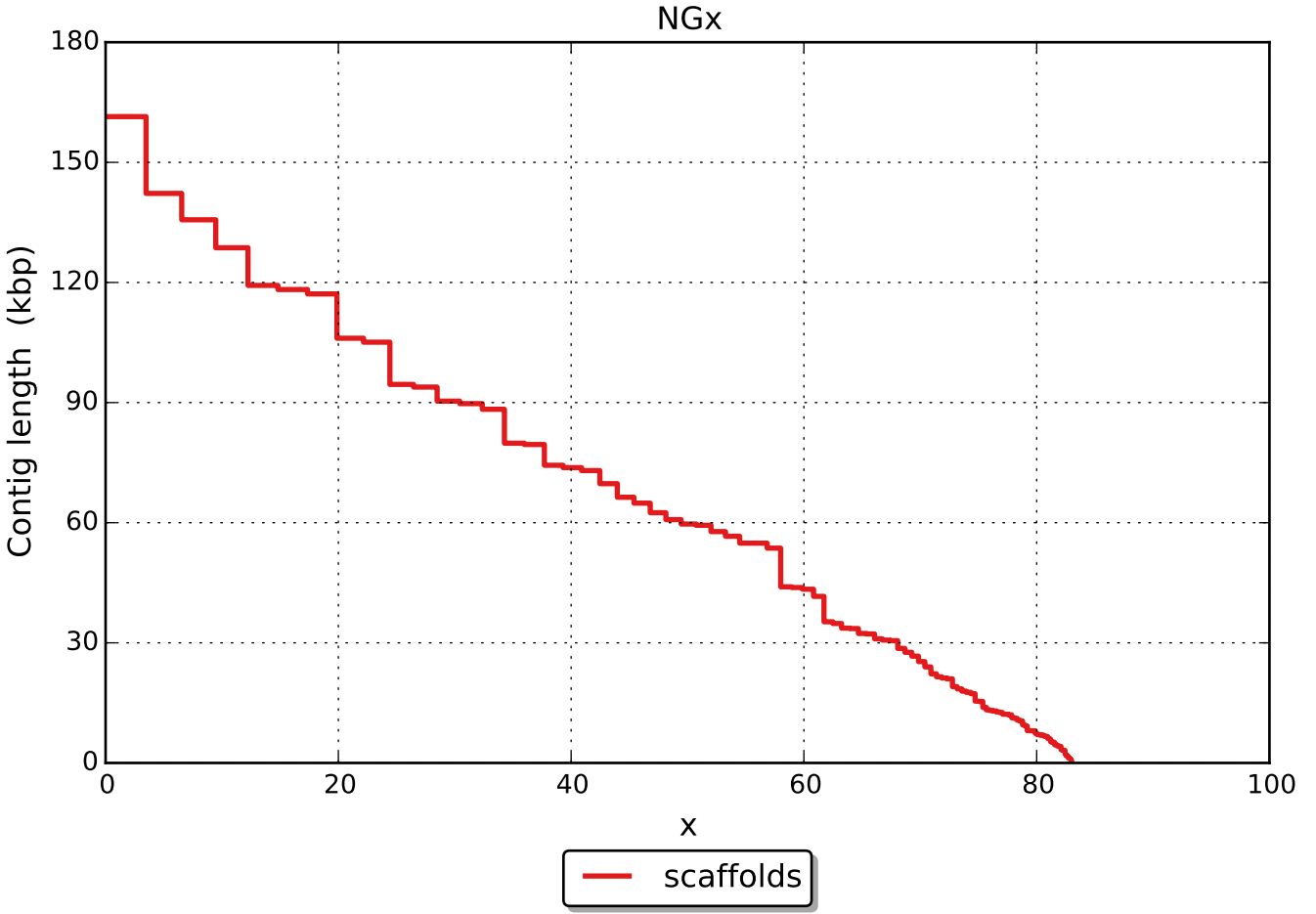
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

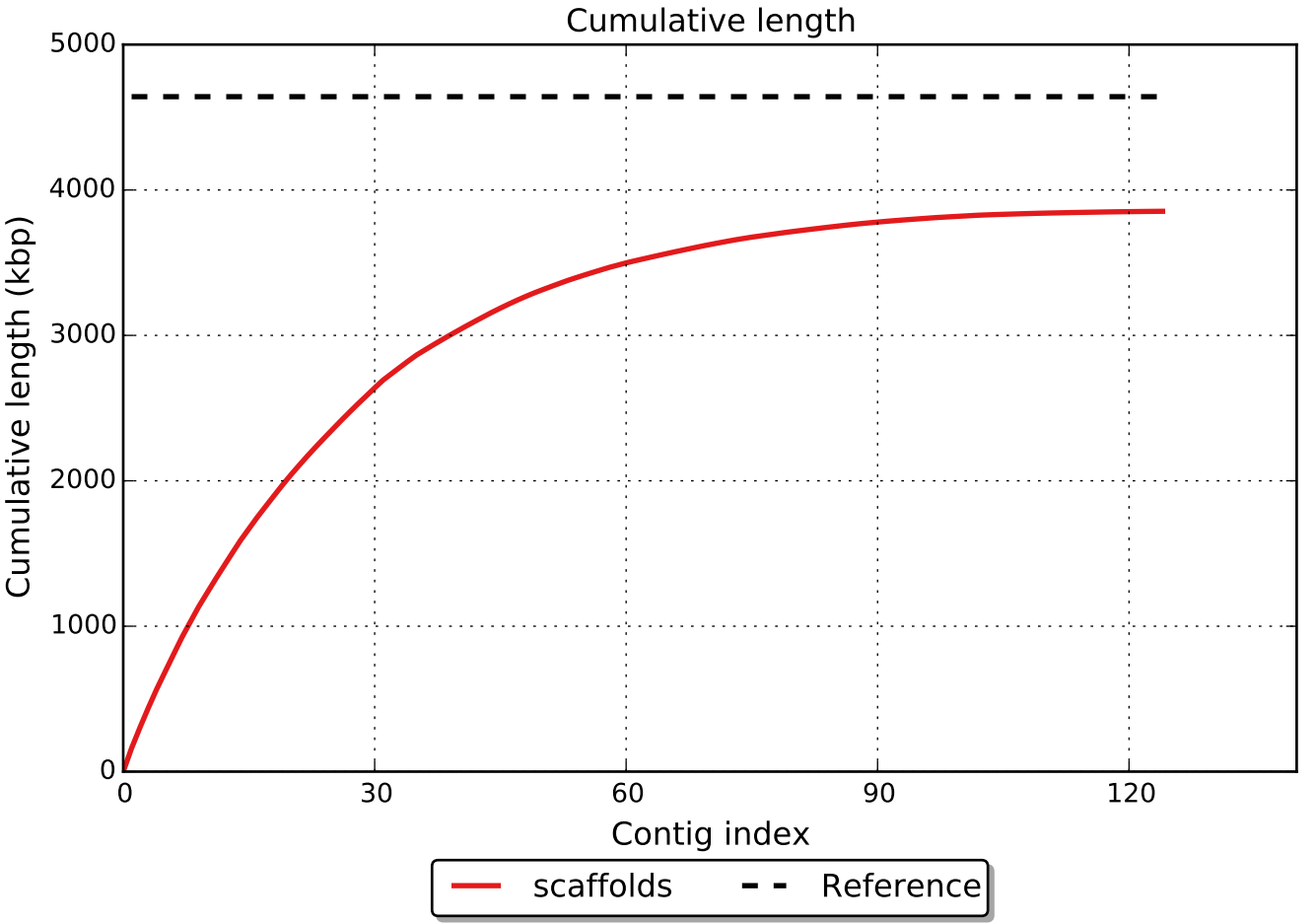
## Unaligned report

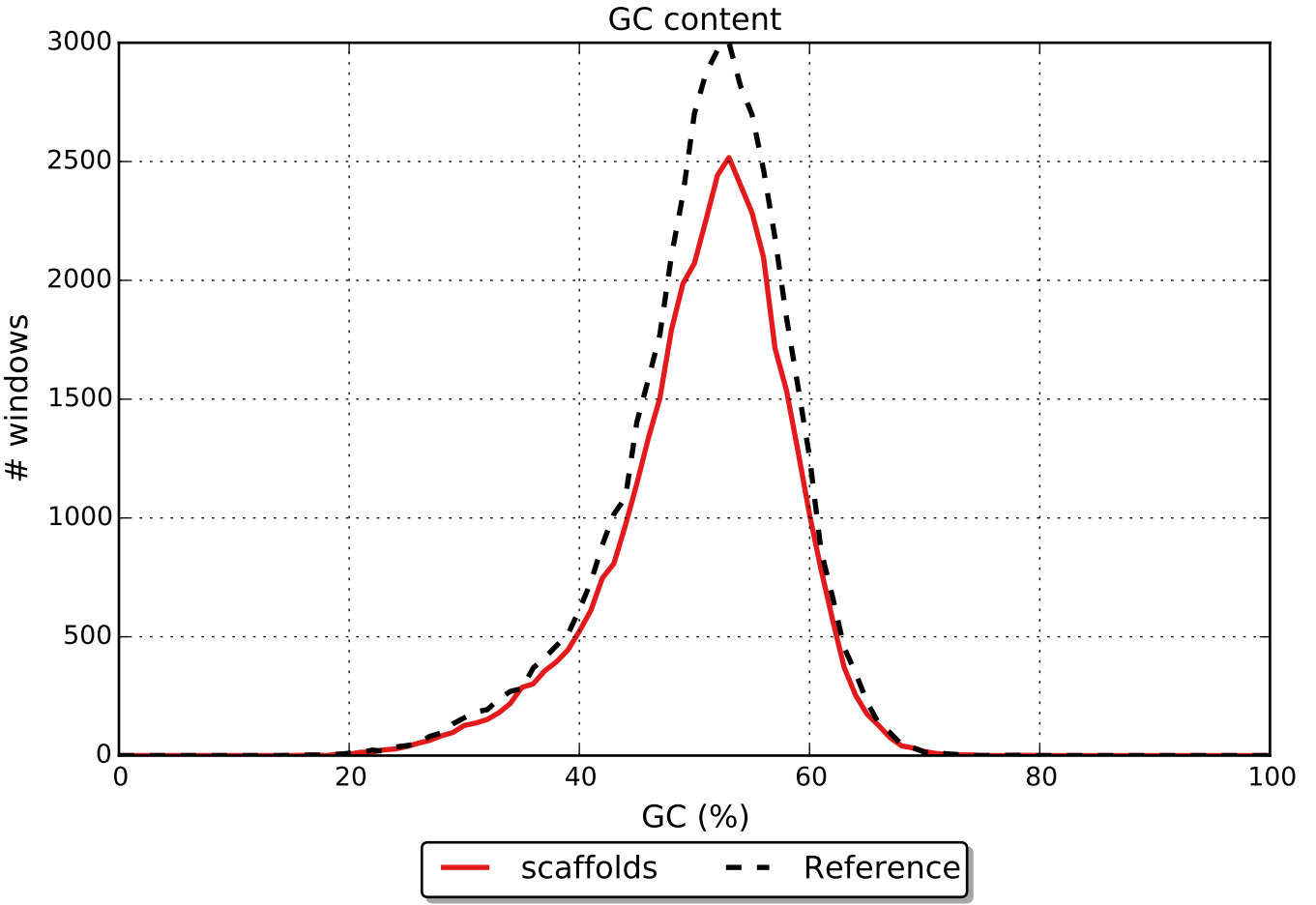
| | scaffolds |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 614 |

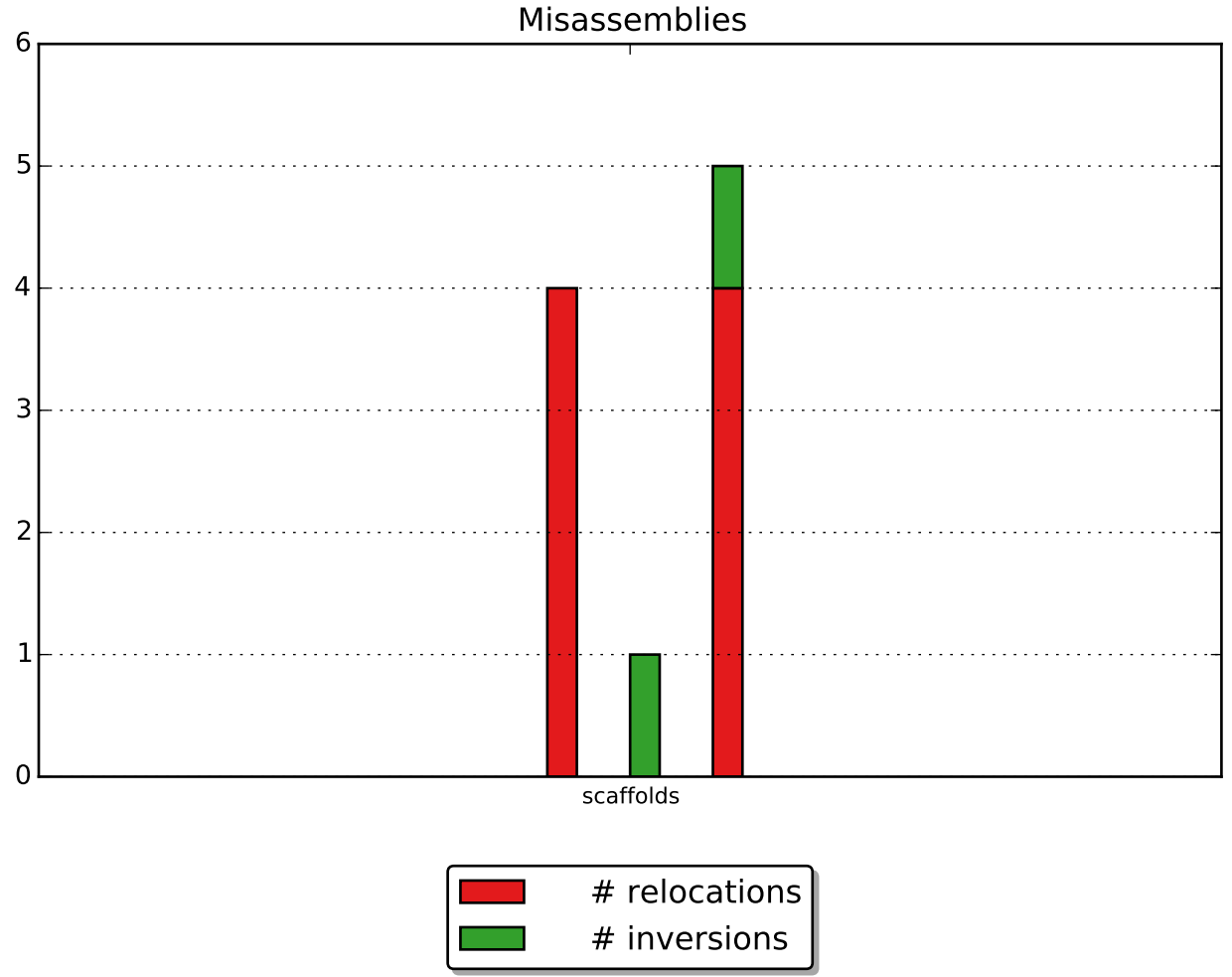
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

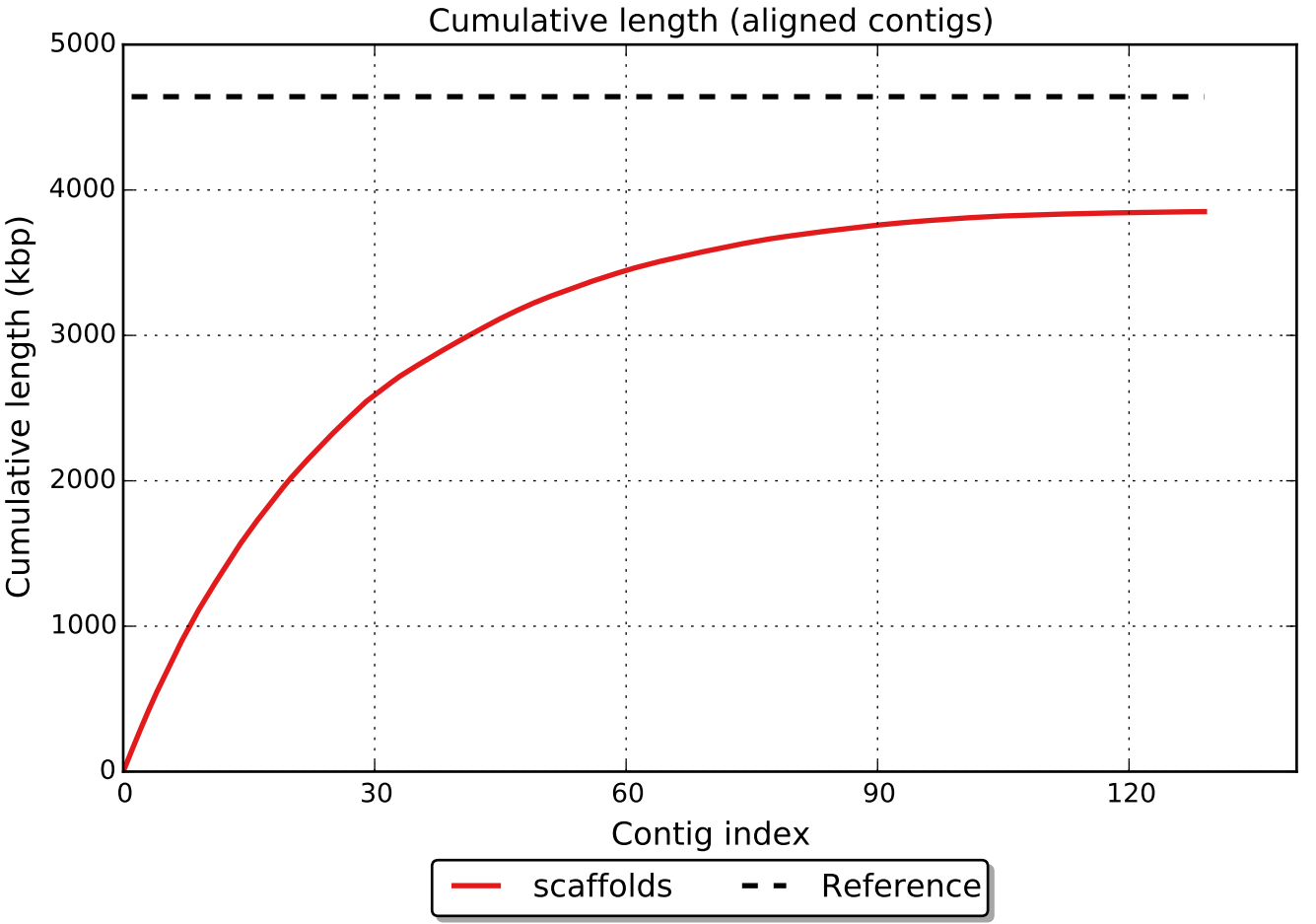

Nx
180
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

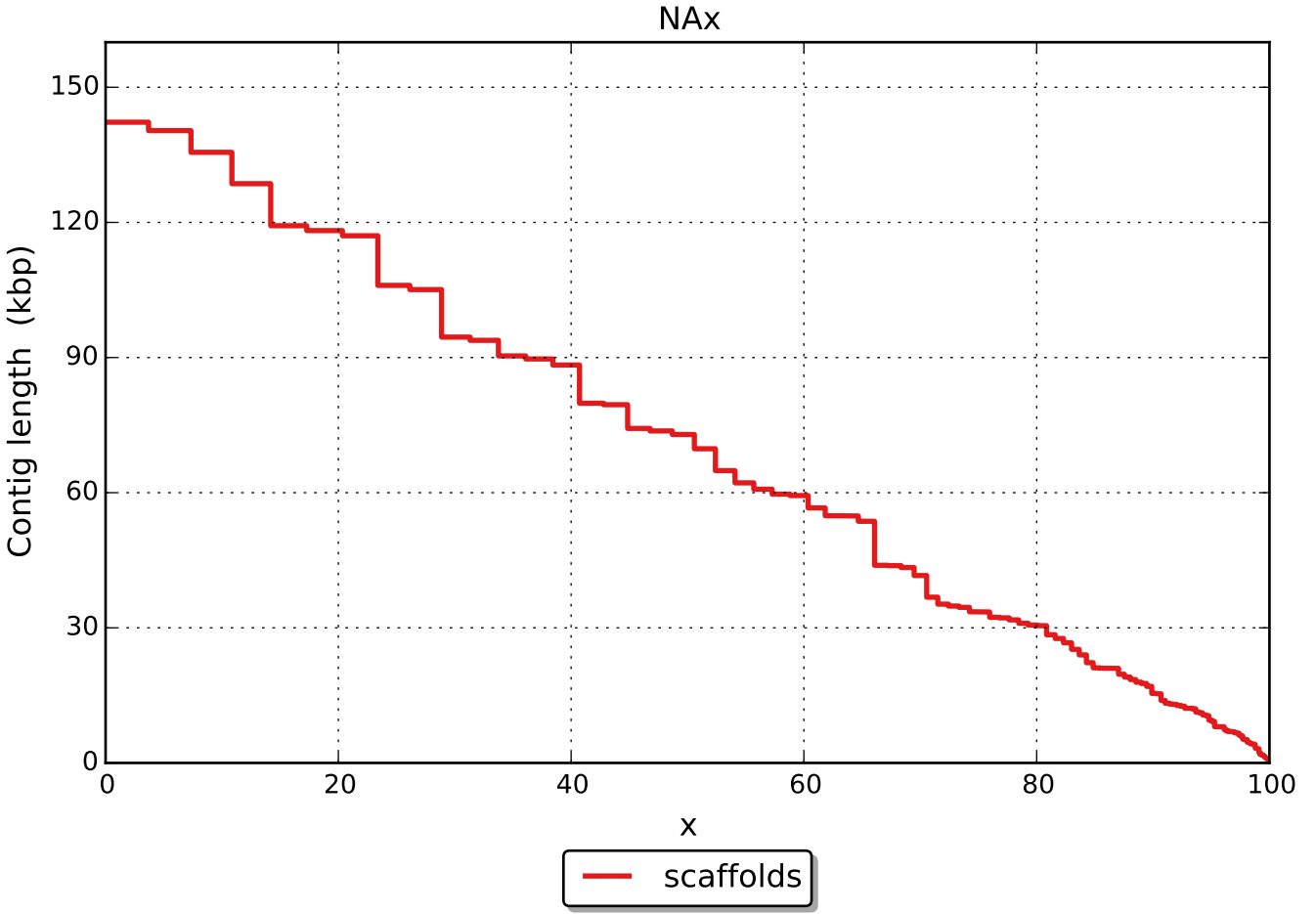

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

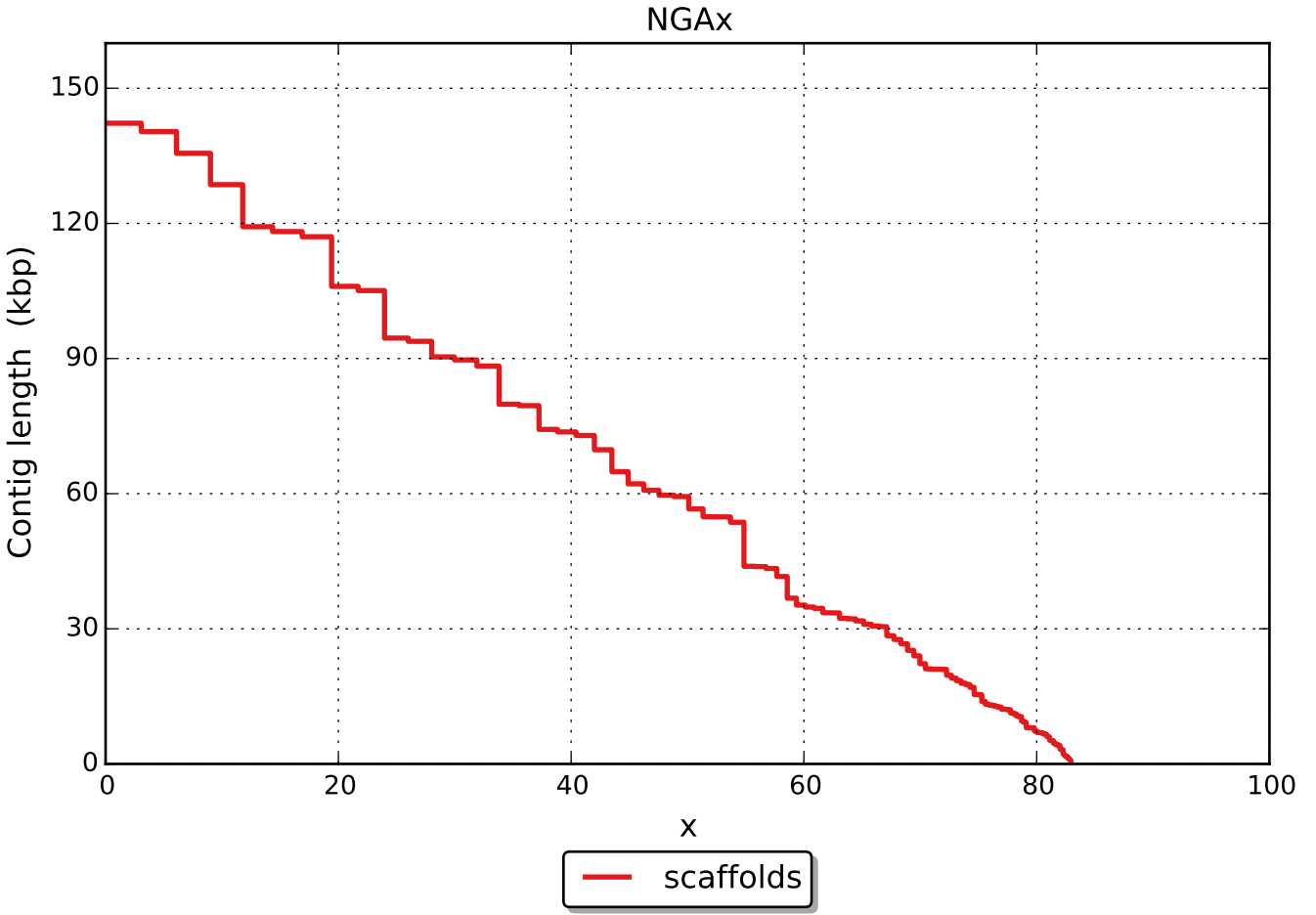

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
scaffolds
Reference


GC content
3000
2500
2000
1500
1000
500
0
# windows
0
20
40
60
80
100
GC (%)
scaffolds
Reference


Misassemblies
6
5
4
3
2
1
0
scaffolds
# relocations
# inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
scaffolds
Reference


NAx
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds