# Report

| | scaffolds |
|---|---|
| # contigs (>= 1000 bp) | 21 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 32323 |
| Total length (>= 5000 bp) | 5456 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 351 |
| Largest contig | 5456 |
| Total length | 243528 |
| Reference length | 4641652 |
| GC (%) | 50.71 |
| Reference GC (%) | 50.79 |
| N50 | 661 |
| N75 | 558 |
| L50 | 136 |
| L75 | 236 |
| # misassemblies | 5 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 5973 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 5 part |
| Unaligned length | 159 |
| Genome fraction (%) | 5.215 |
| Duplication ratio | 1.005 |
| # N's per 100 kbp | 802.78 |
| # mismatches per 100 kbp | 53.70 |
| # indels per 100 kbp | 47.09 |
| Largest alignment | 5416 |
| NA50 | 659 |
| NGA50 | - |
| NA75 | 552 |
| LA50 | 138 |
| LA75 | 239 |

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

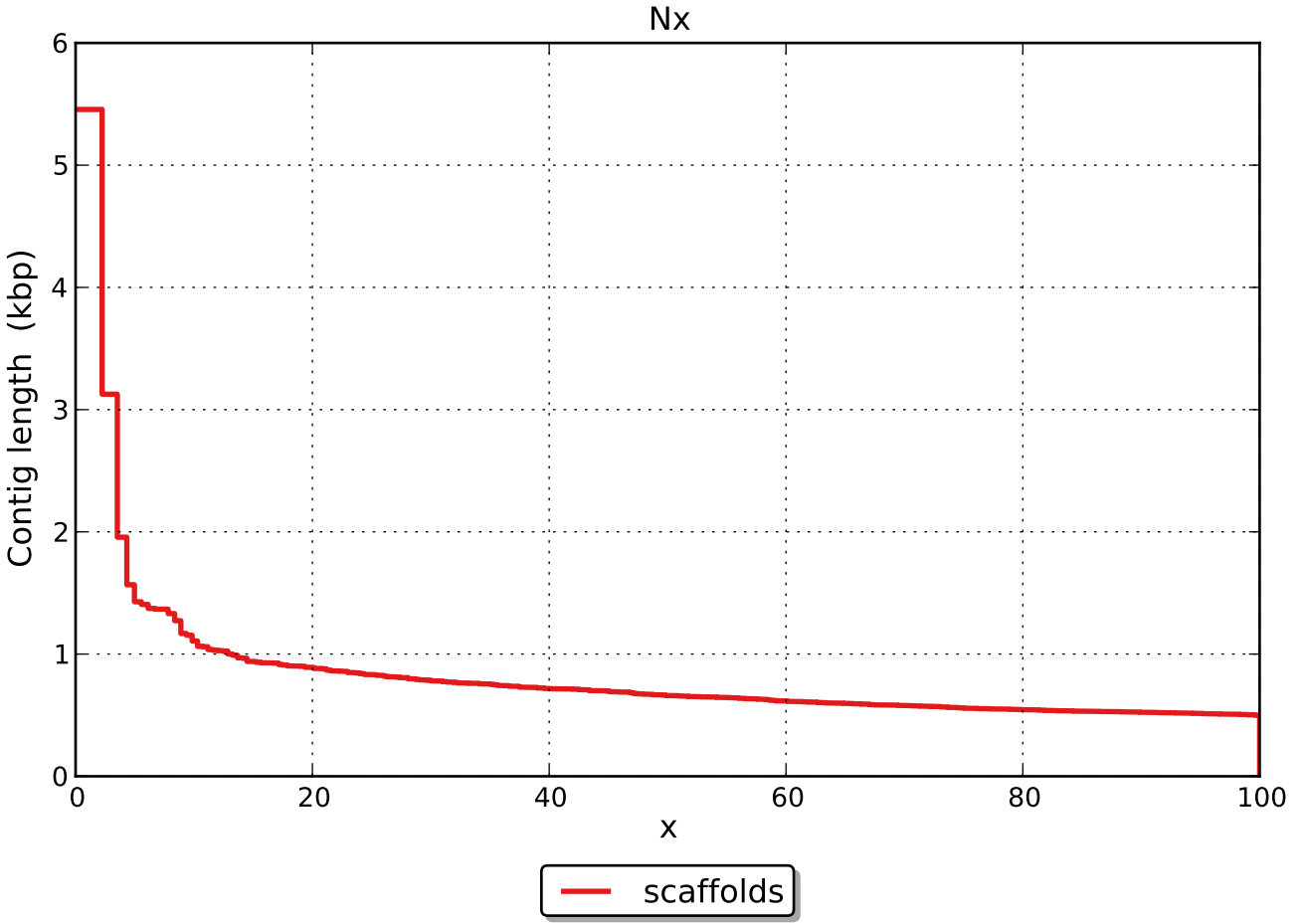
| | scaffolds |
|---|---|
| # misassemblies | 5 |
| # relocations | 5 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 5 |
| Misassembled contigs length | 5973 |
| # local misassemblies | 0 |
| # mismatches | 130 |
| # indels | 114 |
| # short indels | 37 |
| # long indels | 77 |
| Indels length | 1223 |

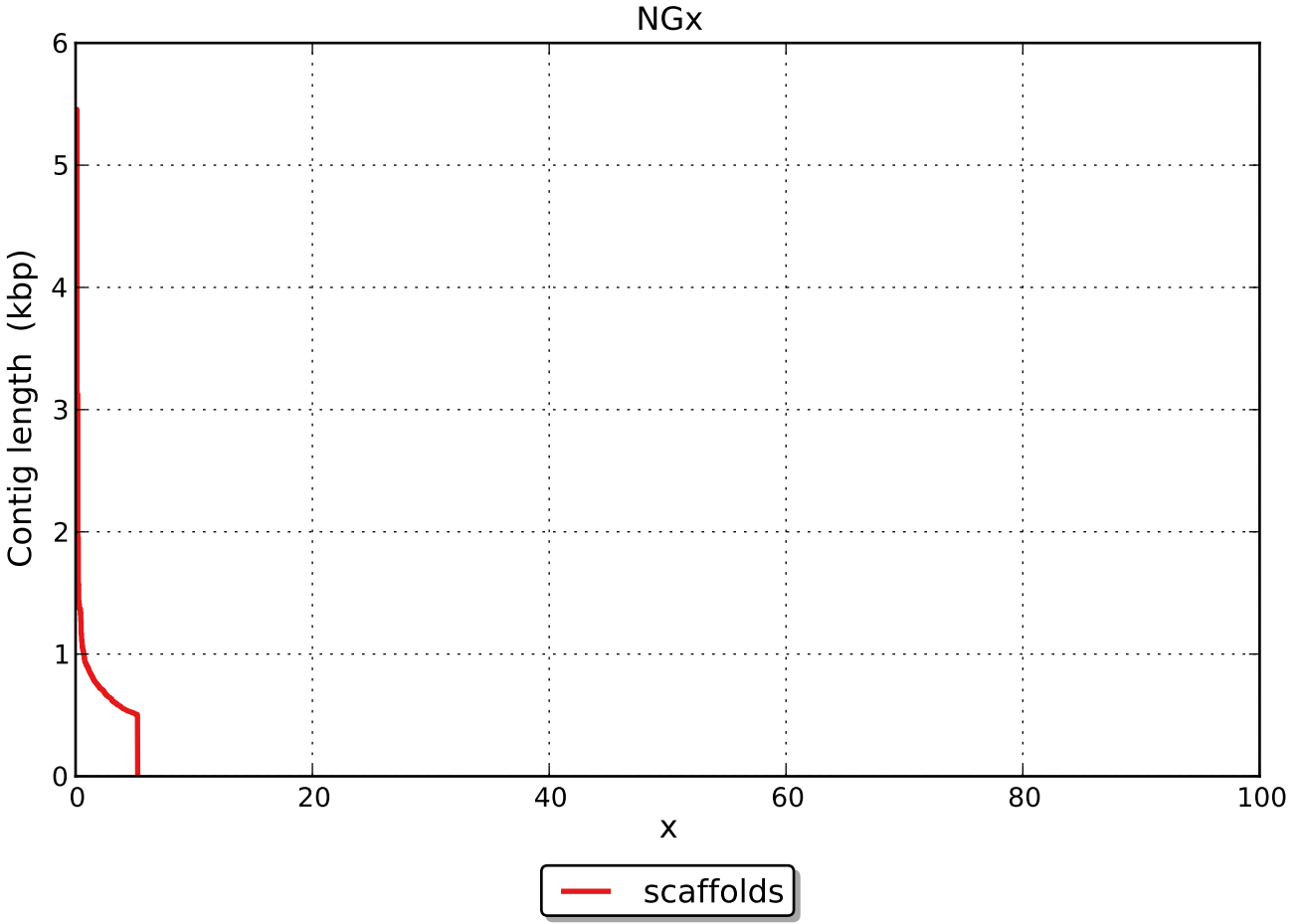
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

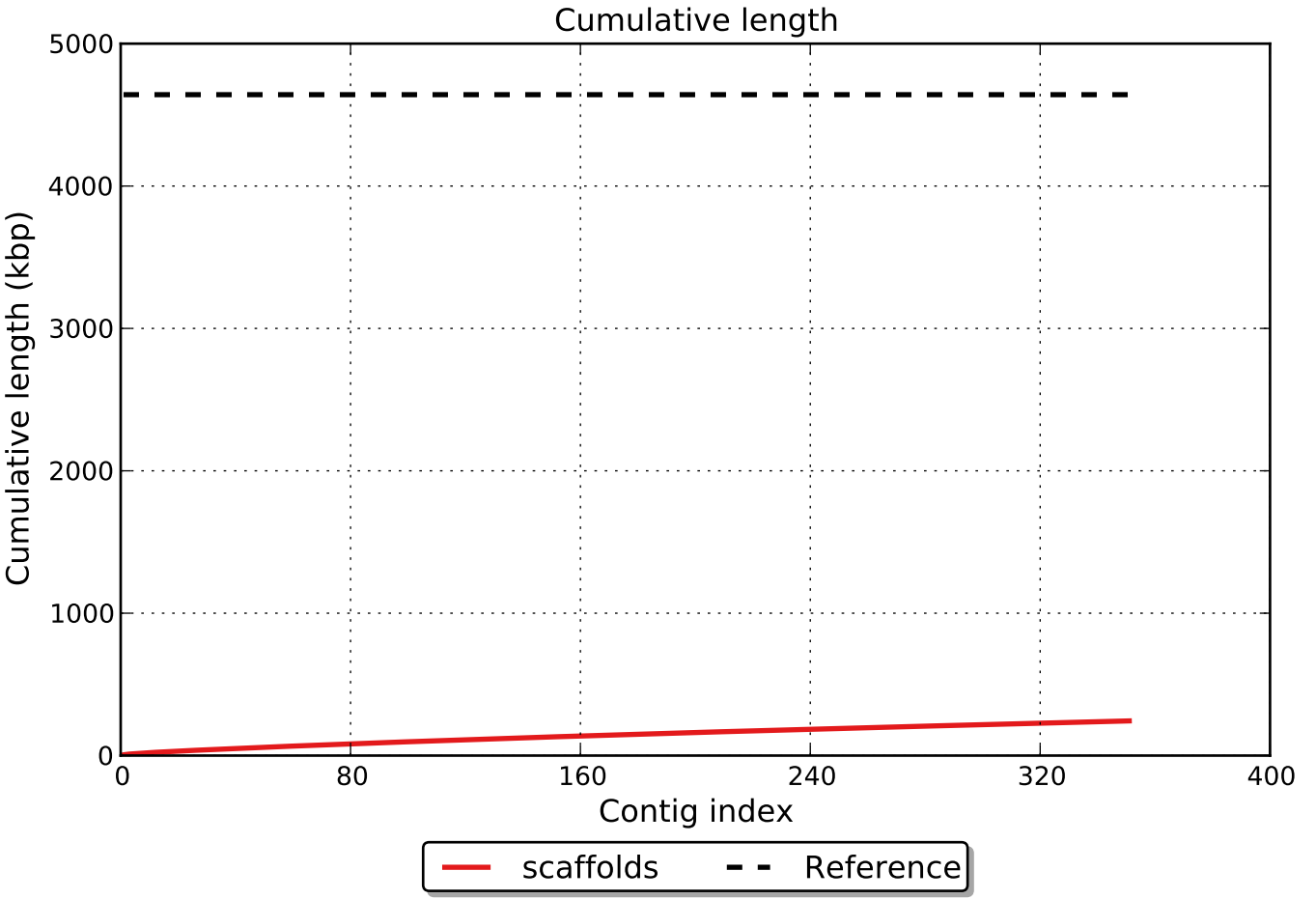
## Unaligned report

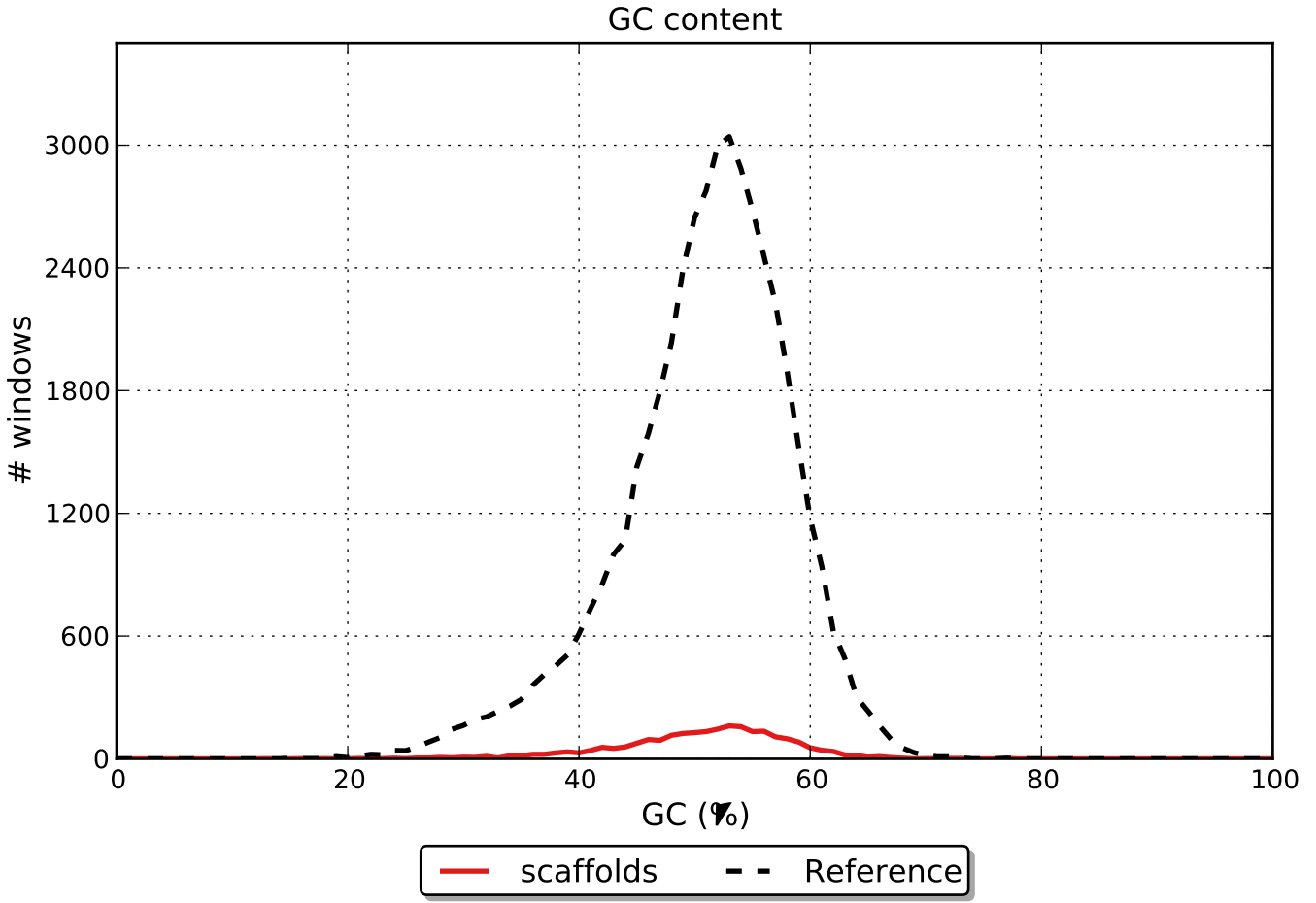
| | scaffolds |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 5 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 159 |
| # N's | 1955 |

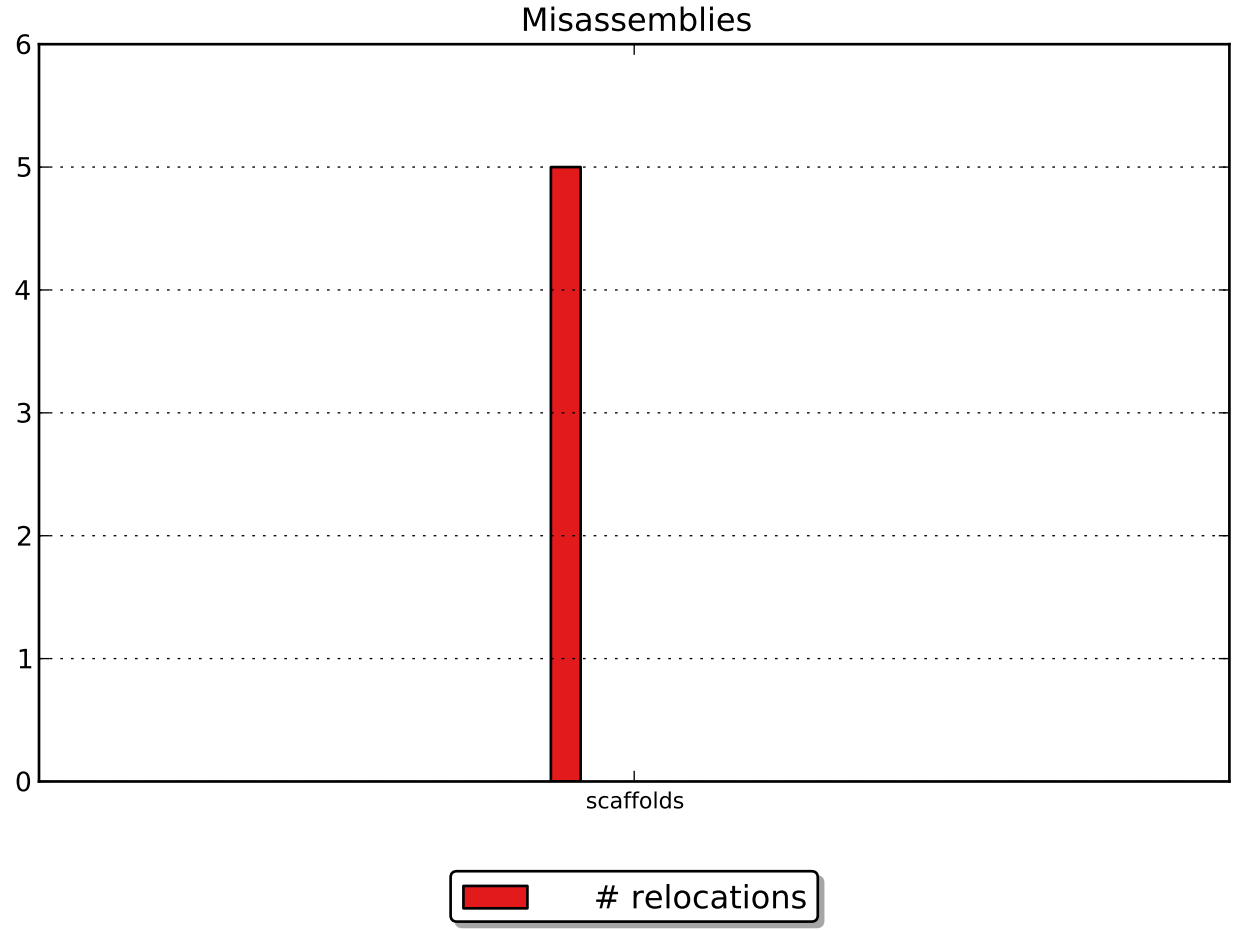
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

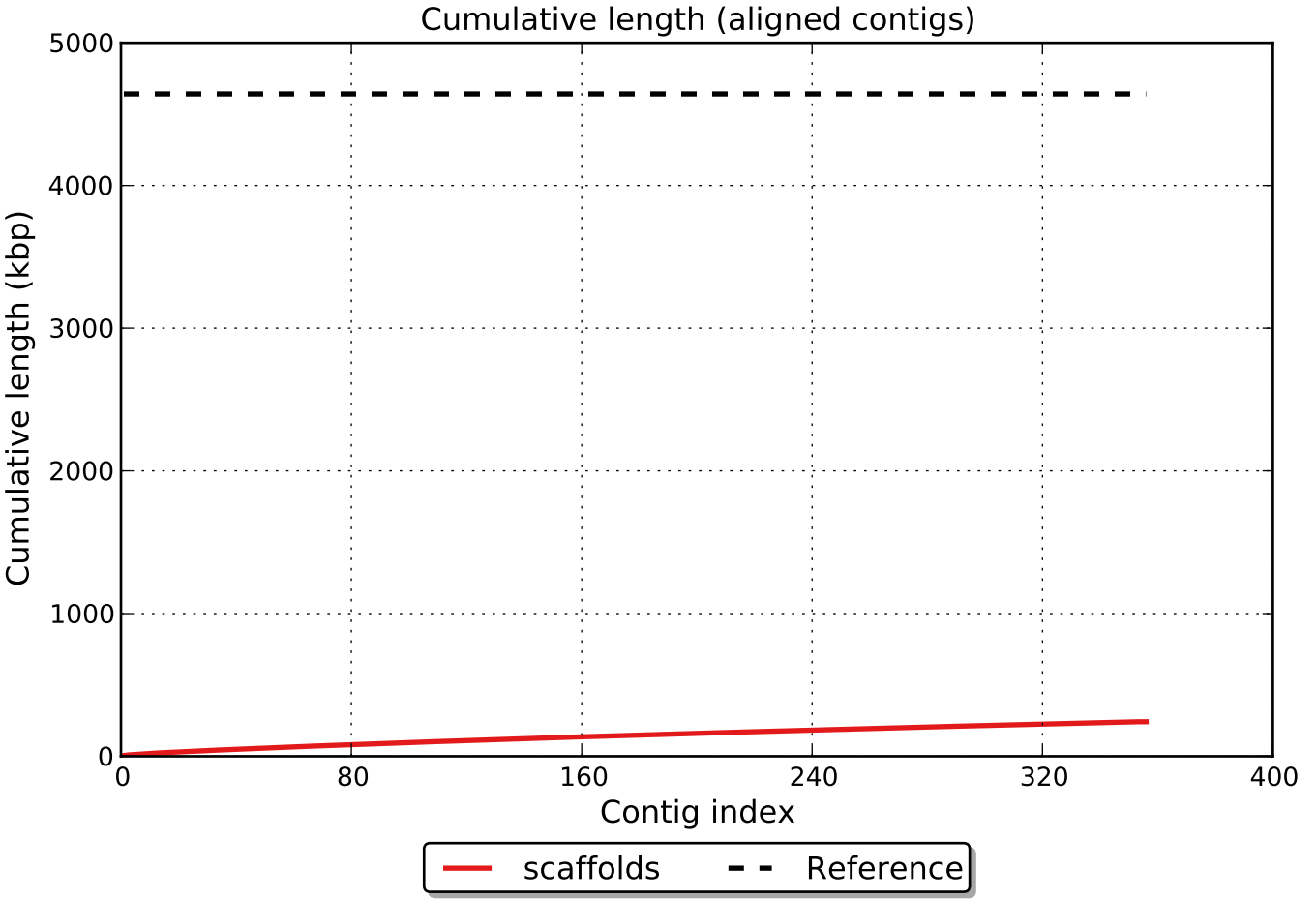

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds

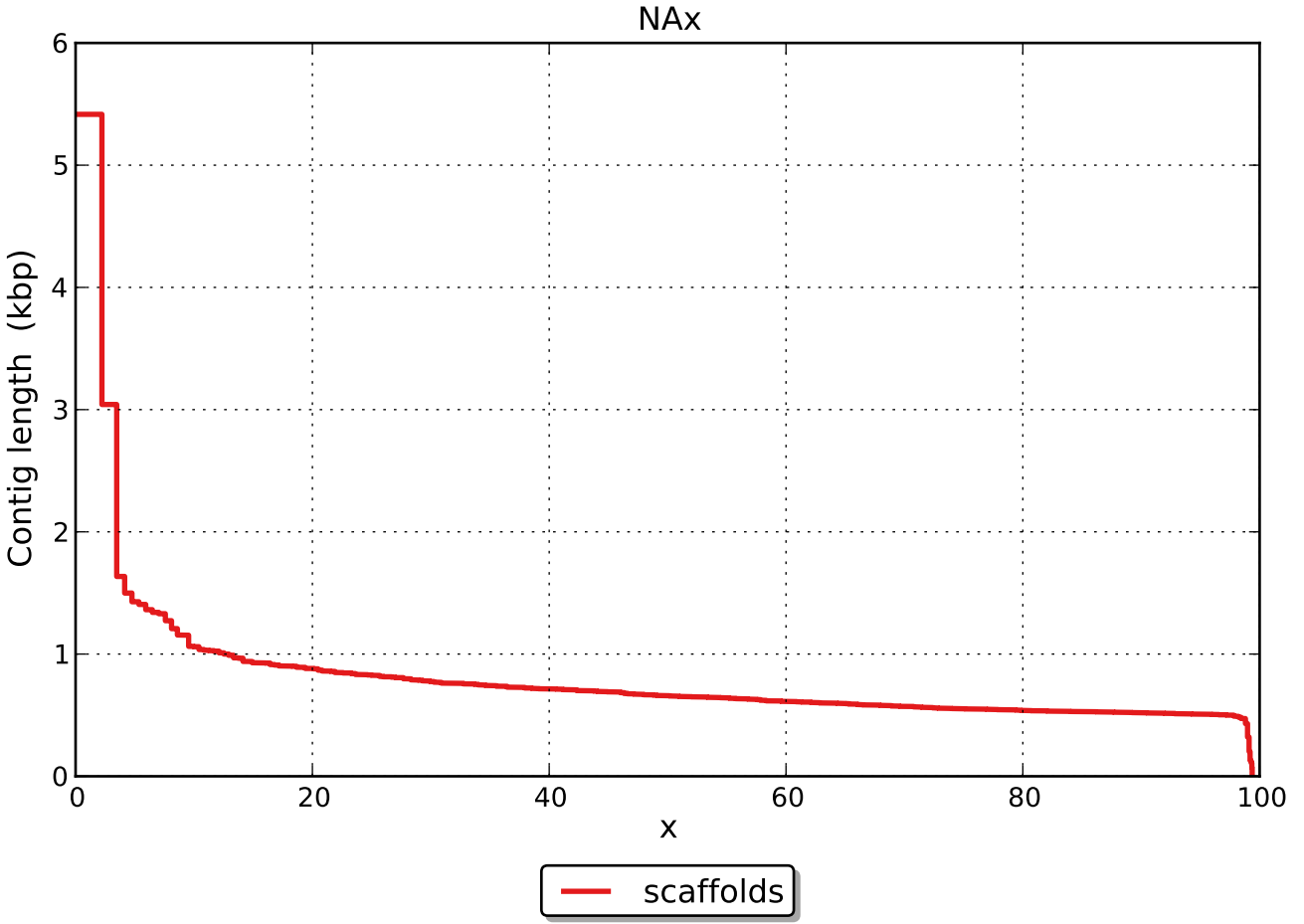

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds

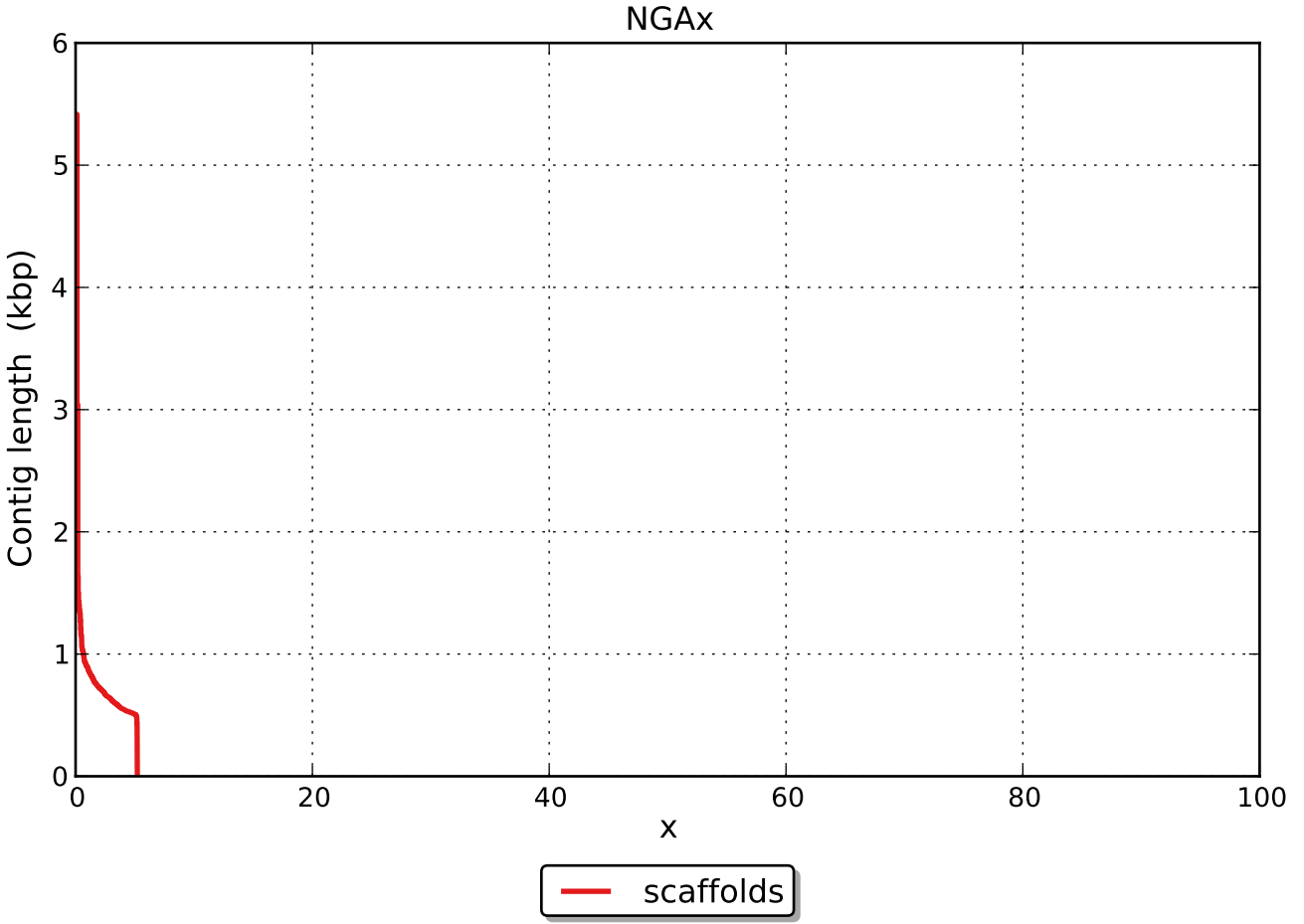

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
scaffolds
Reference


GC content
# windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
scaffolds
Reference


Misassemblies
6
5
4
3
2
1
0
scaffolds
# relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds