# Report

| | durio_zibethinus.contigs |
|---|---|
| # contigs (>= 0 bp) | 981 |
| # contigs (>= 1000 bp) | 981 |
| # contigs (>= 5000 bp) | 896 |
| # contigs (>= 10000 bp) | 590 |
| # contigs (>= 25000 bp) | 137 |
| # contigs (>= 50000 bp) | 64 |
| Total length (>= 0 bp) | 37535010 |
| Total length (>= 1000 bp) | 37535010 |
| Total length (>= 5000 bp) | 37271620 |
| Total length (>= 10000 bp) | 34971779 |
| Total length (>= 25000 bp) | 28025466 |
| Total length (>= 50000 bp) | 25759419 |
| # contigs | 981 |
| Largest contig | 1979337 |
| Total length | 37535010 |
| Reference length | 26551601 |
| GC (%) | 30.97 |
| Reference GC (%) | 30.98 |
| N50 | 380819 |
| NG50 | 546284 |
| N75 | 24321 |
| NG75 | 354531 |
| L50 | 27 |
| LG50 | 14 |
| L75 | 143 |
| LG75 | 30 |
| # misassemblies | 241 |
| # misassembled contigs | 134 |
| Misassembled contigs length | 23180502 |
| # local misassemblies | 266 |
| # unaligned mis. contigs | 19 |
| # unaligned contigs | 534 + 260 part |
| Unaligned length | 7130522 |
| Genome fraction (%) | 97.251 |
| Duplication ratio | 1.177 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 349.44 |
| # indels per 100 kbp | 187.13 |
| Largest alignment | 1260946 |
| Total aligned length | 30389958 |
| NA50 | 158876 |
| NGA50 | 281393 |
| NA75 | 12978 |
| NGA75 | 129274 |
| LA50 | 49 |
| LGA50 | 25 |
| LA75 | 289 |
| LGA75 | 57 |

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

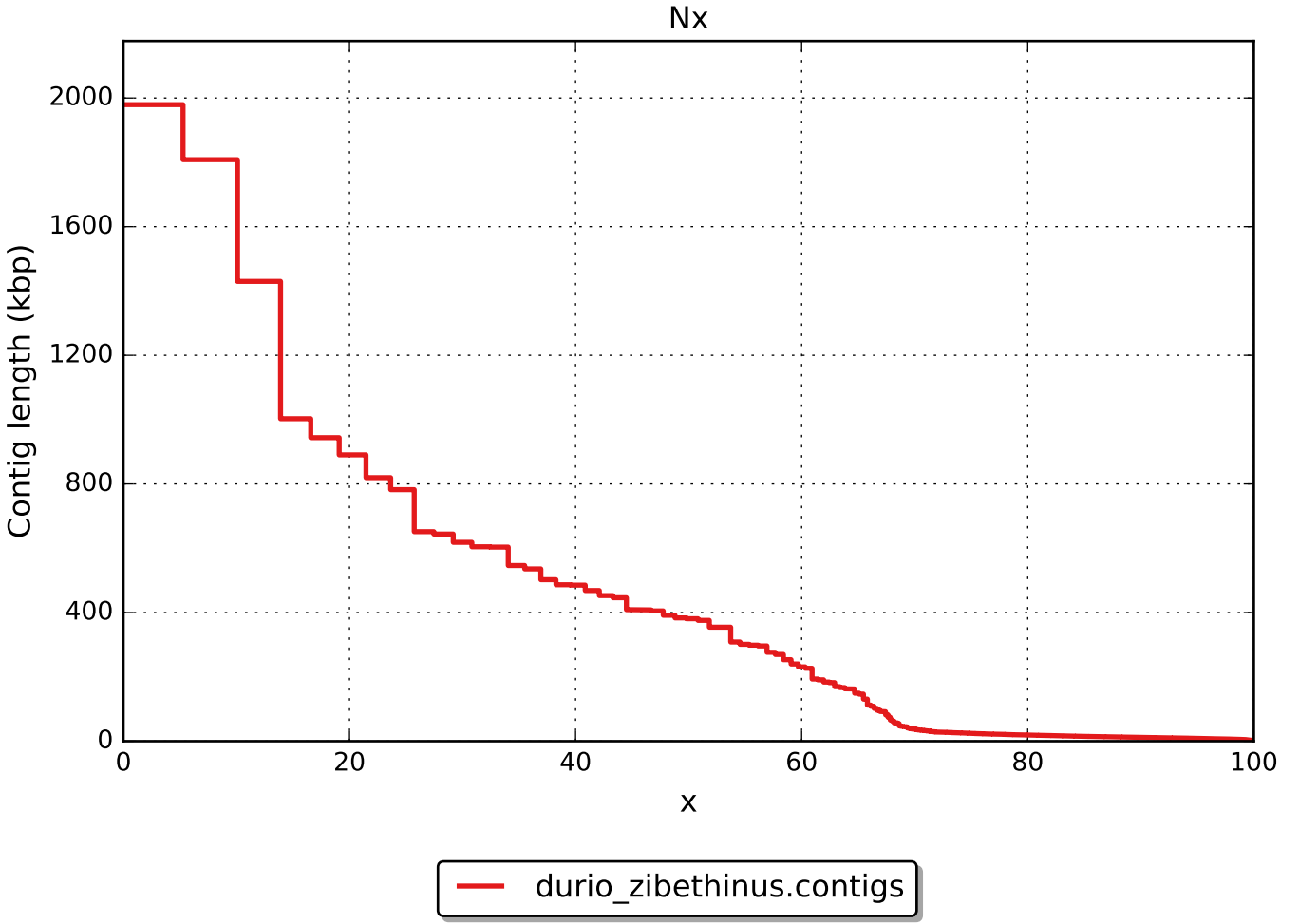
| | durio_zibethinus.contigs |
|---|---|
| # misassemblies | 241 |
| # relocations | 240 |
| # translocations | 0 |
| # inversions | 1 |
| # misassembled contigs | 134 |
| Misassembled contigs length | 23180502 |
| # local misassemblies | 266 |
| # unaligned mis. contigs | 19 |
| # mismatches | 90232 |
| # indels | 48319 |
| # indels (<= 5 bp) | 45887 |
| # indels (> 5 bp) | 2432 |
| Indels length | 92411 |

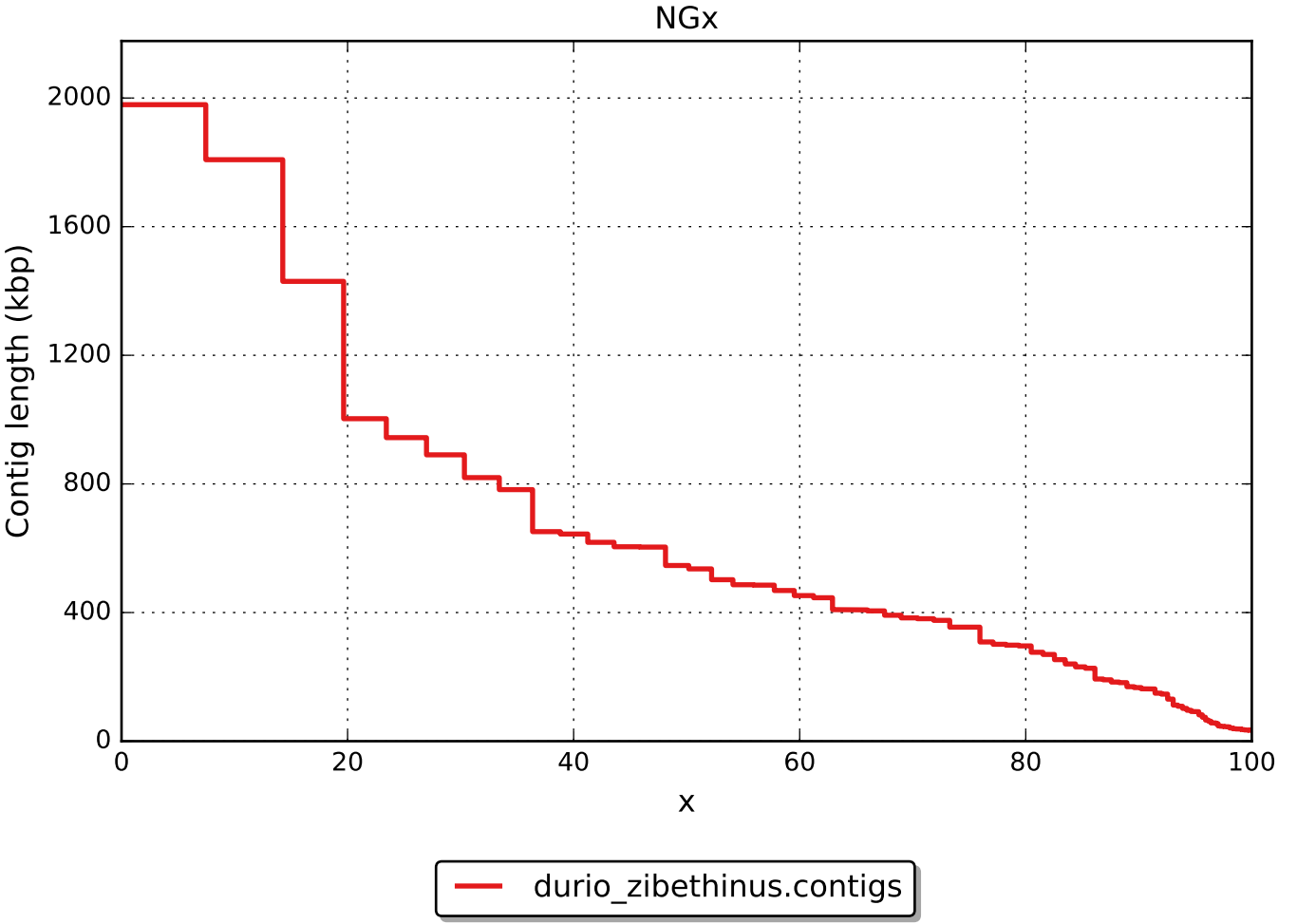
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

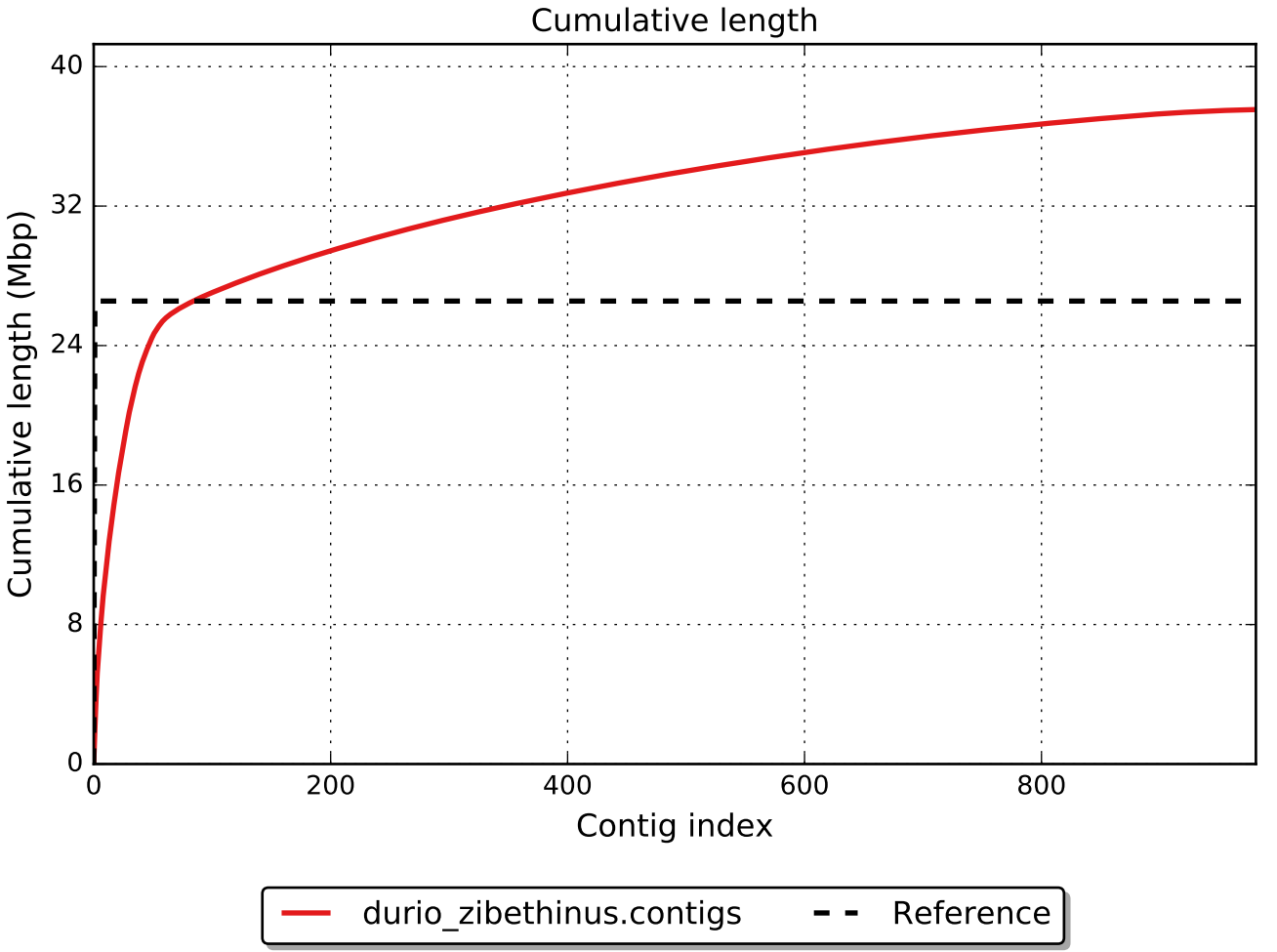
# Unaligned report

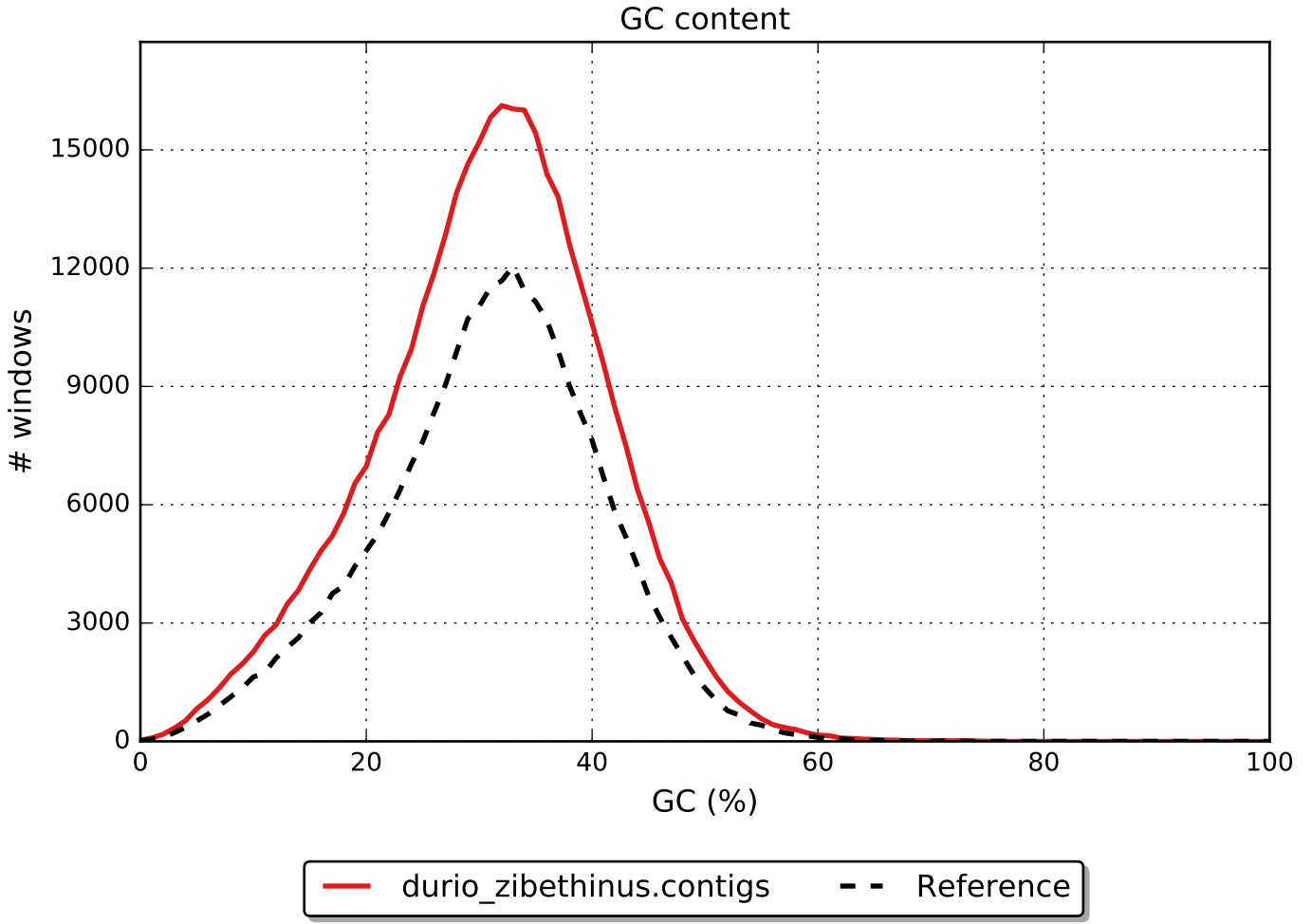
| | durio_zibethinus.contigs |
|---|---|
| # fully unaligned contigs | 534 |
| Fully unaligned length | 4975588 |
| # partially unaligned contigs | 260 |
| Partially unaligned length | 2154934 |
| # N's | 0 |

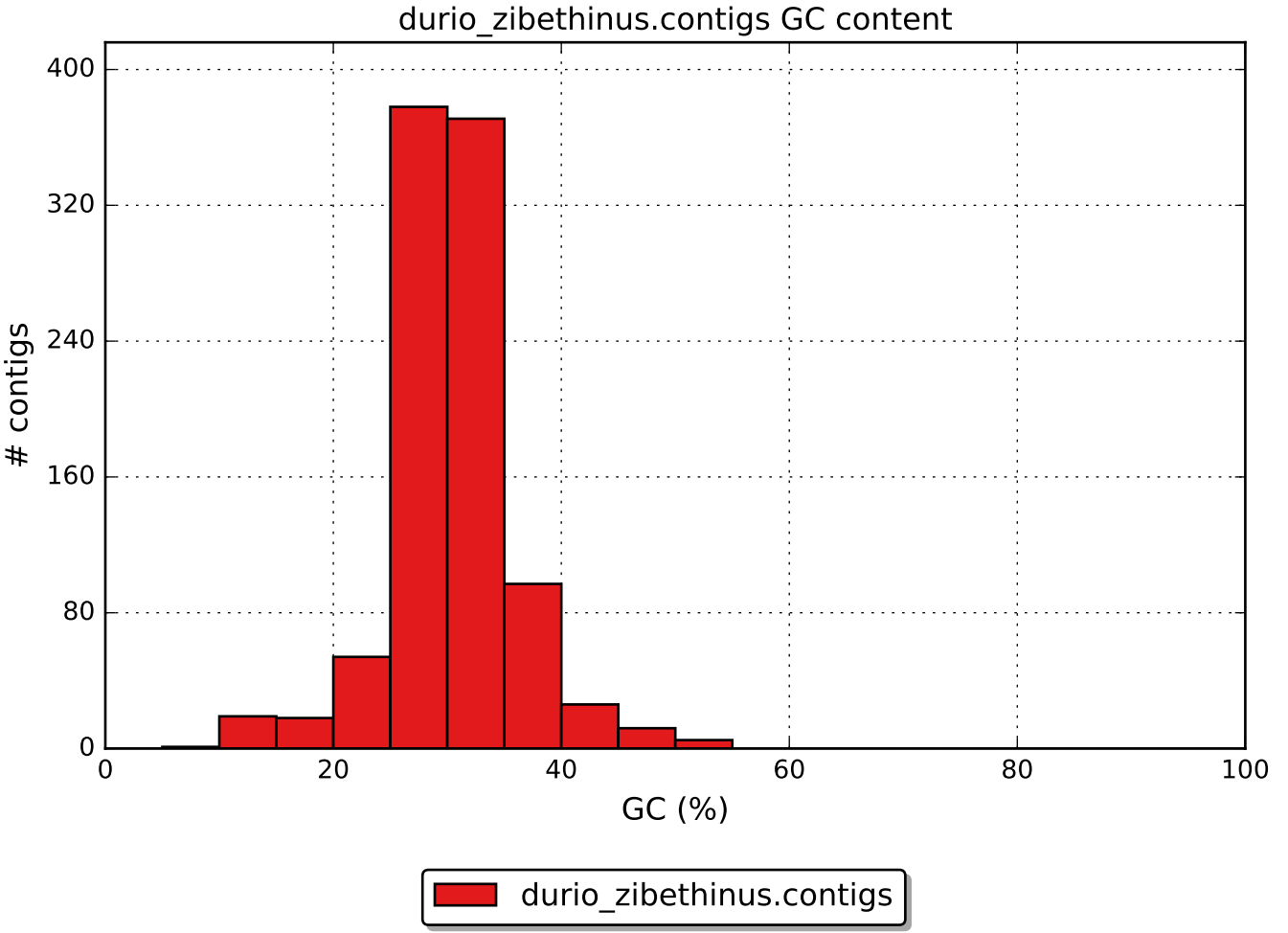
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

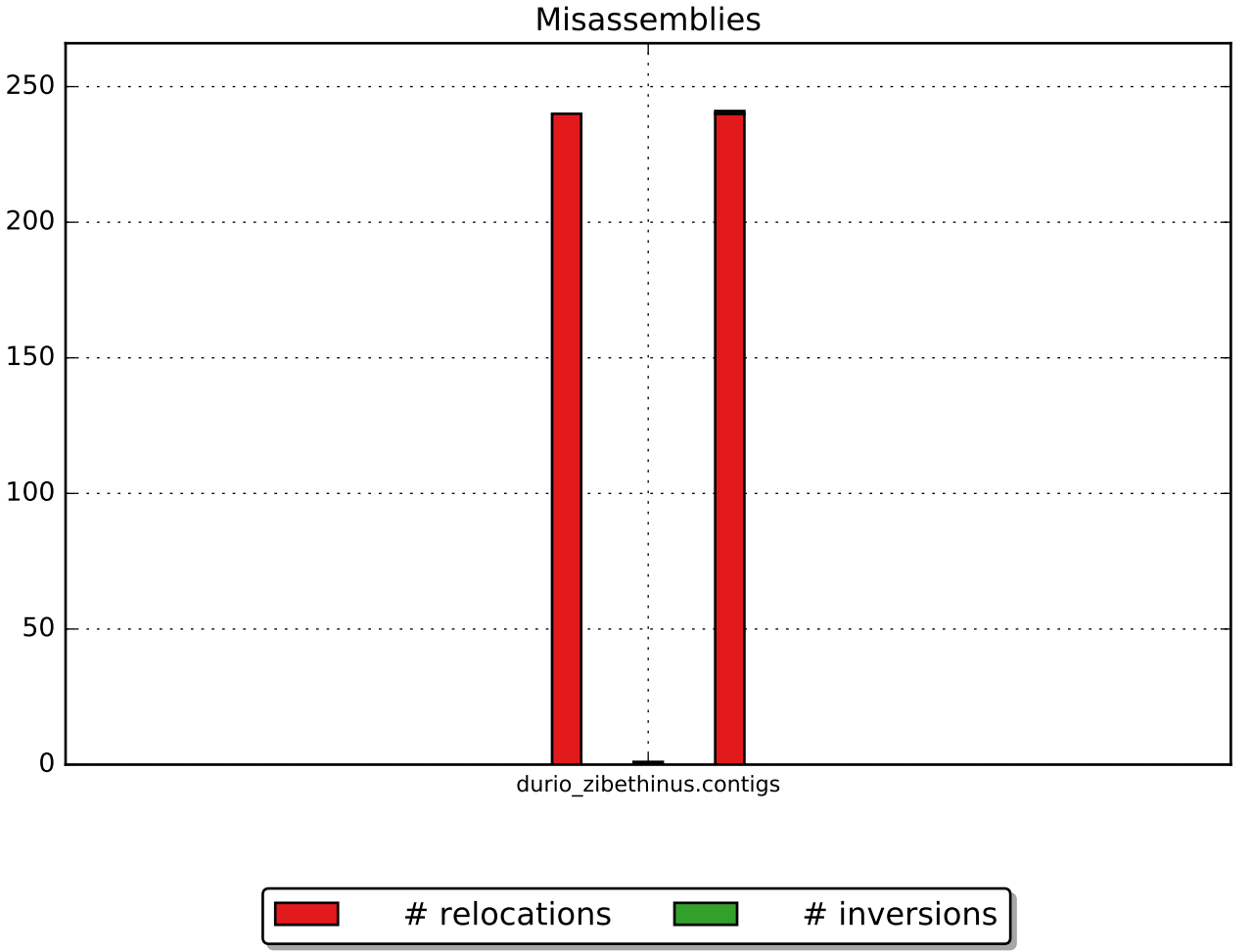

Nx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
durio_zibethinus.contigs

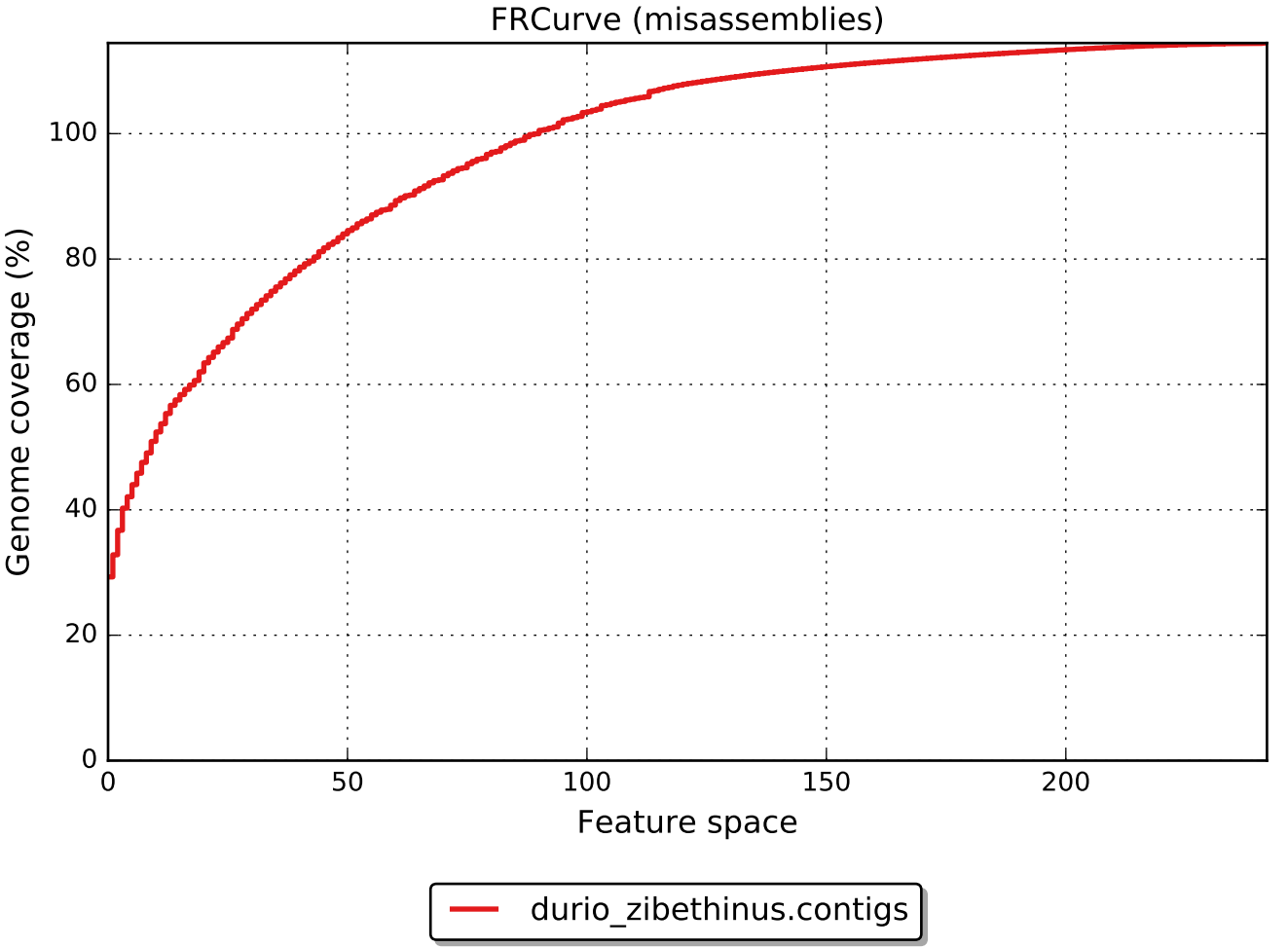

NGx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
durio_zibethinus.contigs

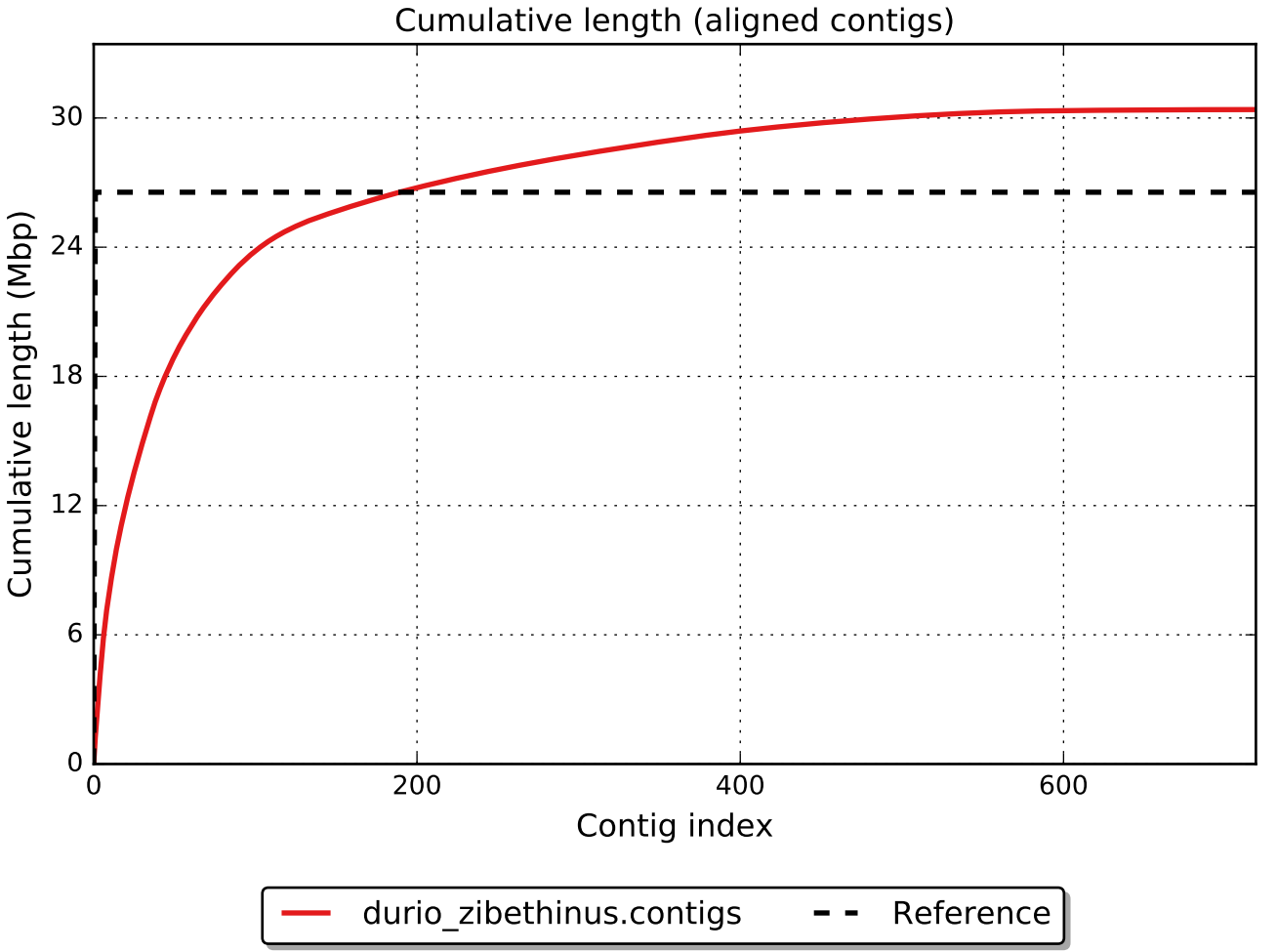

Cumulative length
Cumulative length (Mbp)
40
32
24
16
8
0
0
200
400
600
800
Contig index
durio_zibethinus.contigs
Reference

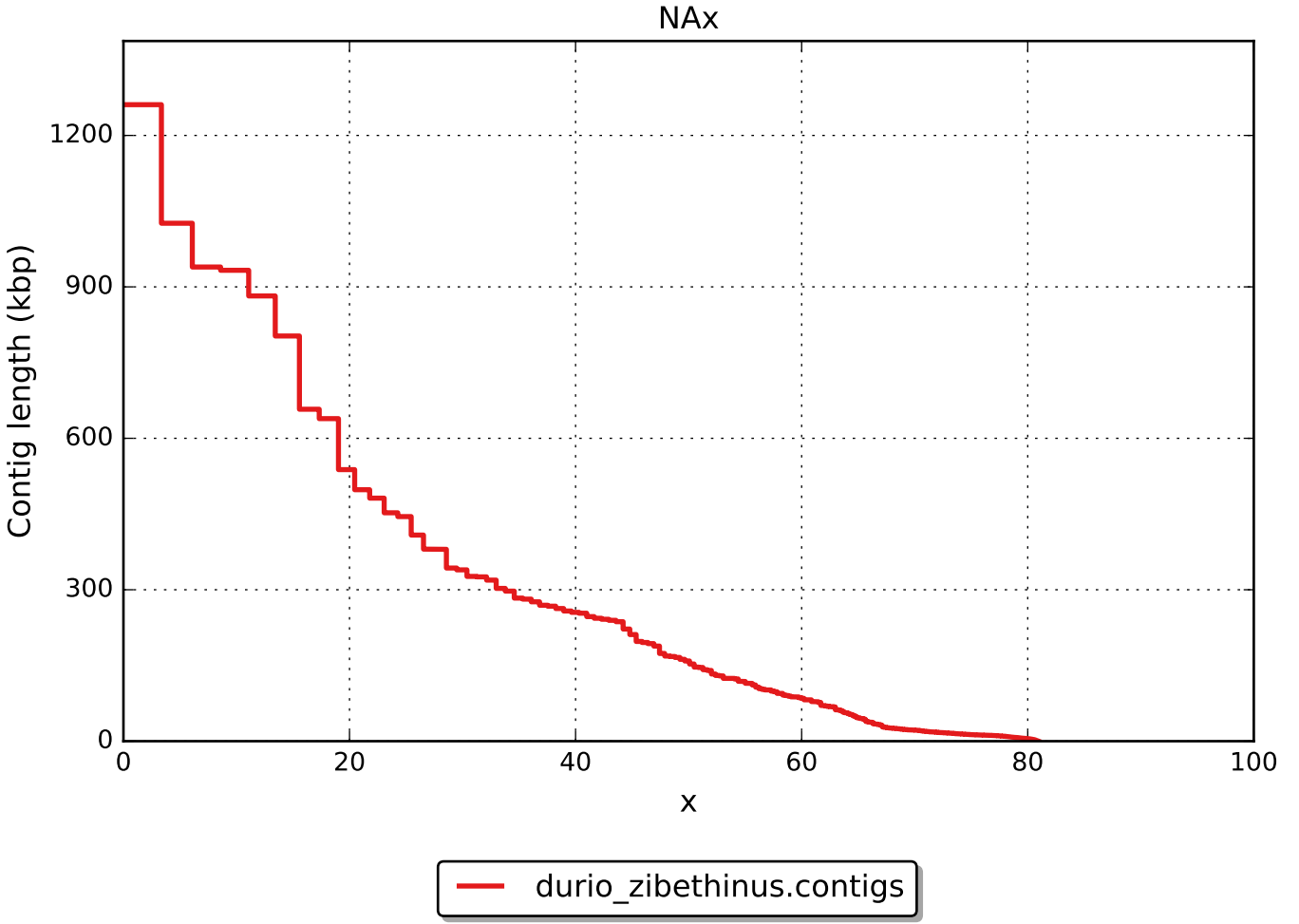

GC content
# windows
15000
12000
9000
6000
3000
0
0
20
40
60
80
100
GC (%)
durio_zibethinus.contigs
Reference

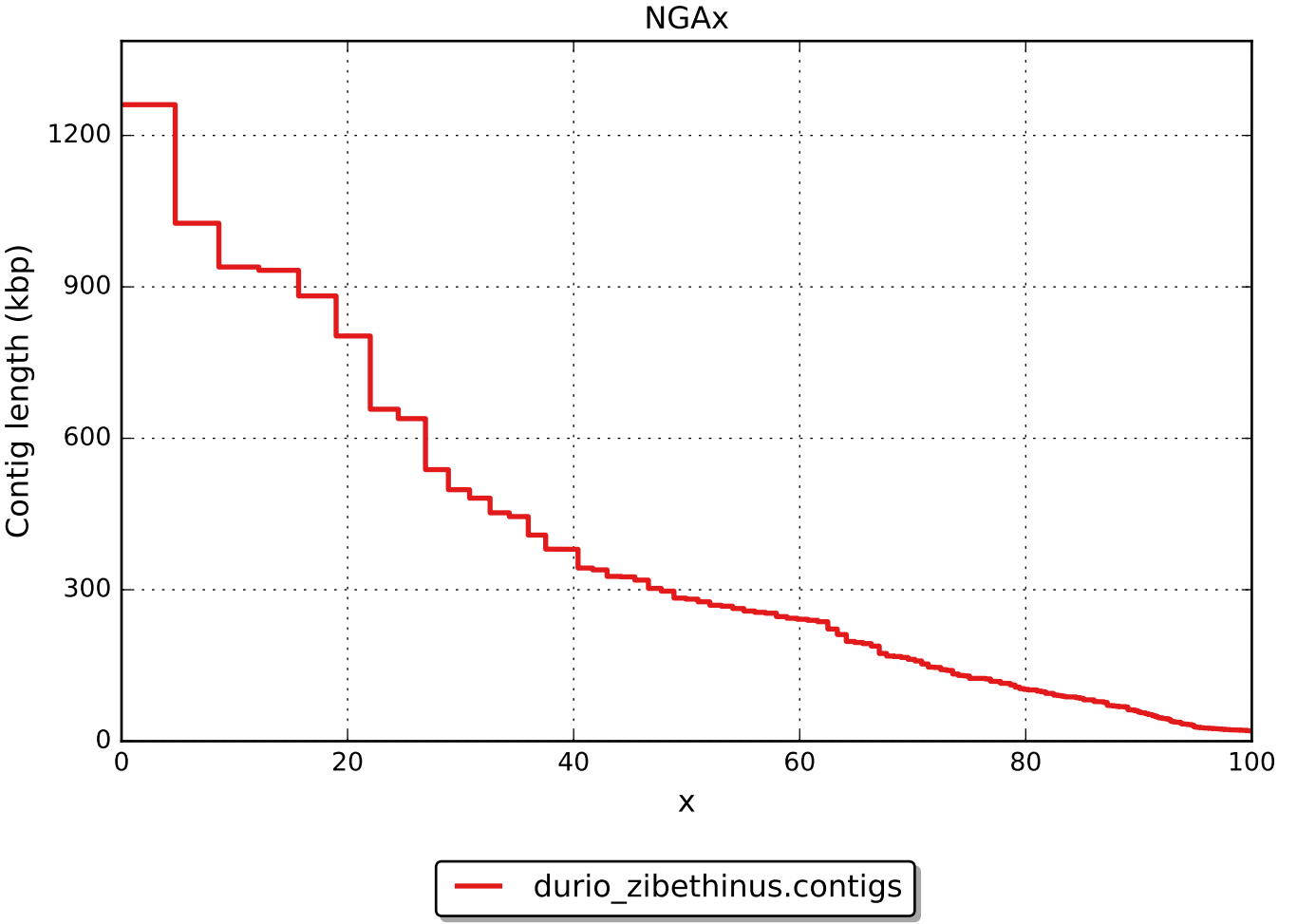

durio_zibethinus.contigs GC content
400
320
240
160
80
0
# contigs
0
20
40
60
80
100
GC (%)
durio_zibethinus.contigs


Misassemblies
250
200
150
100
50
0
durio_zibethinus.contigs
# relocations
# inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
50
100
150
200
Feature space
durio_zibethinus.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
6
12
18
24
30
0
200
400
600
Contig index
durio_zibethinus.contigs
Reference


NAx
Contig length (kbp)
1200
900
600
300
0
0
20
40
60
80
100
x
durio_zibethinus.contigs


NGAx
Contig length (kbp)
1200
900
600
300
0
0
20
40
60
80
100
x
durio_zibethinus.contigs