Report

	durio_zibethinus_high_sense.contigs
# contigs (>= 0 bp)	927
# contigs (>= 1000 bp)	927
# contigs (>= 5000 bp)	879
# contigs (>= 10000 bp)	646
# contigs (>= 25000 bp)	131
# contigs (>= 50000 bp)	54
Total length (>= 0 bp)	38309010
Total length (>= 1000 bp)	38309010
Total length (>= 5000 bp)	38155775
Total length (>= 10000 bp)	36317569
Total length (>= 25000 bp)	28234394
Total length (>= 50000 bp)	25815779
# contigs	927
Largest contig	2459156
Total length	38309010
Reference length	26551601
GC (%)	31.05
Reference GC (%)	30.98
N50	422311
NG50	748592
N75	23338
NG75	355131
L50	22
LG50	12
L75	152
LG75	24
# misassemblies	274
# misassembled contigs	166
Misassembled contigs length	25558704
# local misassemblies	298
# unaligned mis. contigs	22
# unaligned contigs	372 + 288 part
Unaligned length	6192720
Genome fraction (%)	97.627
Duplication ratio	1.239
# N's per 100 kbp	0.00
# mismatches per 100 kbp	349.21
# indels per 100 kbp	181.54
Largest alignment	1344941
Total aligned length	32097897
NA50	176728
NGA50	296688
NA75	14359
NGA75	159982
LA50	52
LGA50	26
LA75	294
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

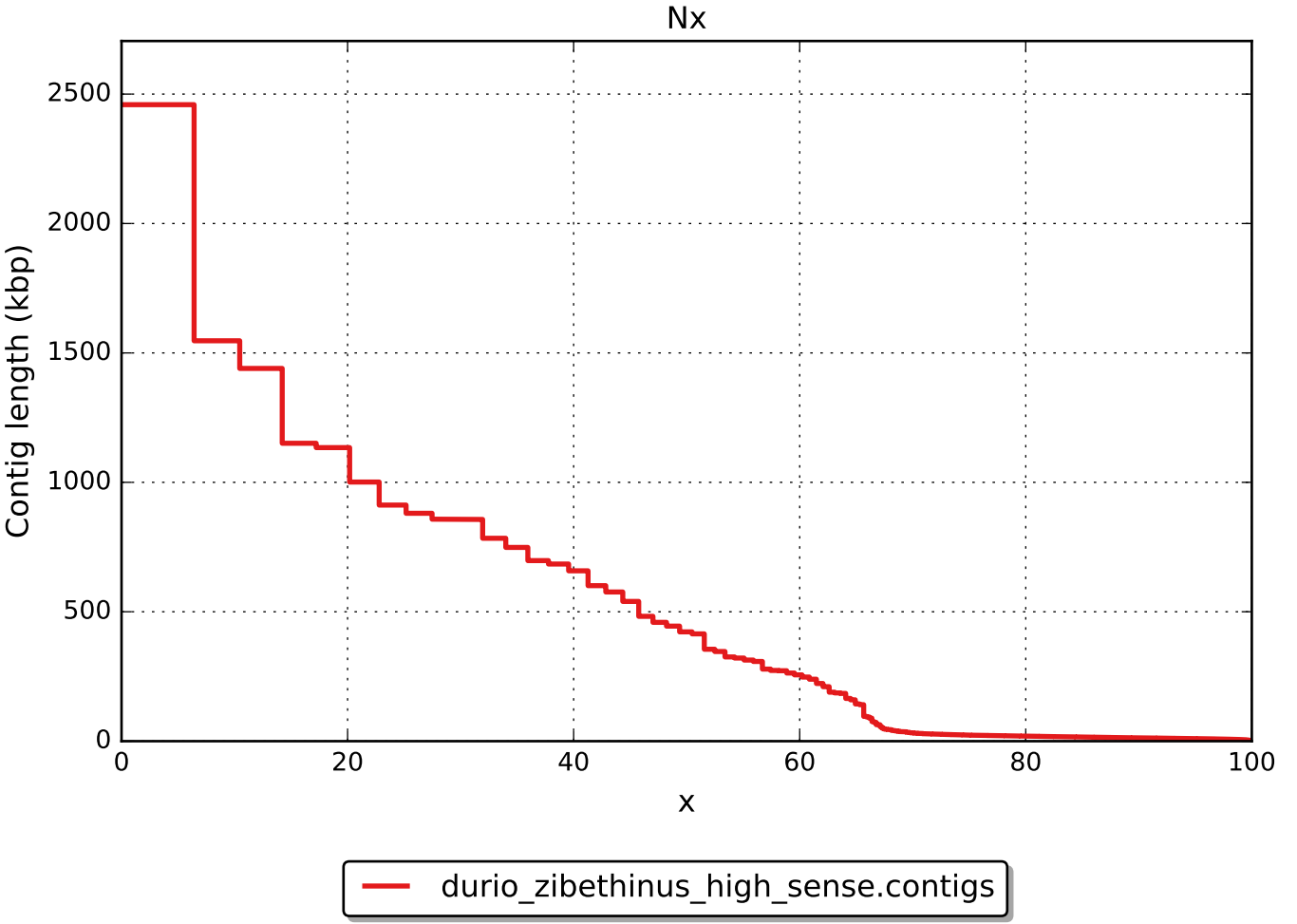
	durio_zibethinus_high_sense.contigs
# misassemblies	274
# relocations	273
# translocations	0
# inversions	1
# misassembled contigs	166
Misassembled contigs length	25558704
# local misassemblies	298
# unaligned mis. contigs	22
# mismatches	90521
# indels	47057
# indels (<= 5 bp)	44596
# indels (> 5 bp)	2461
Indels length	90323

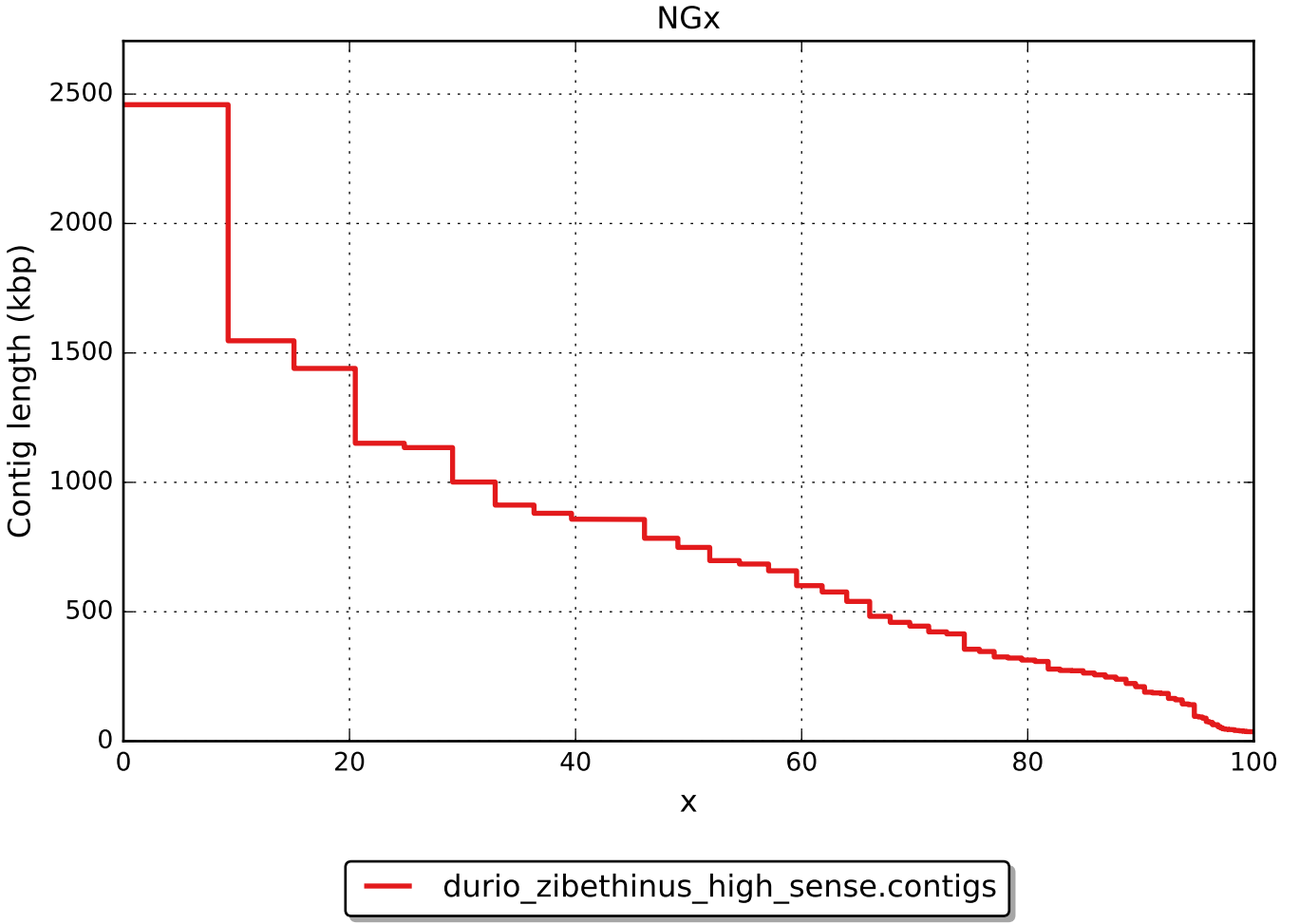
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

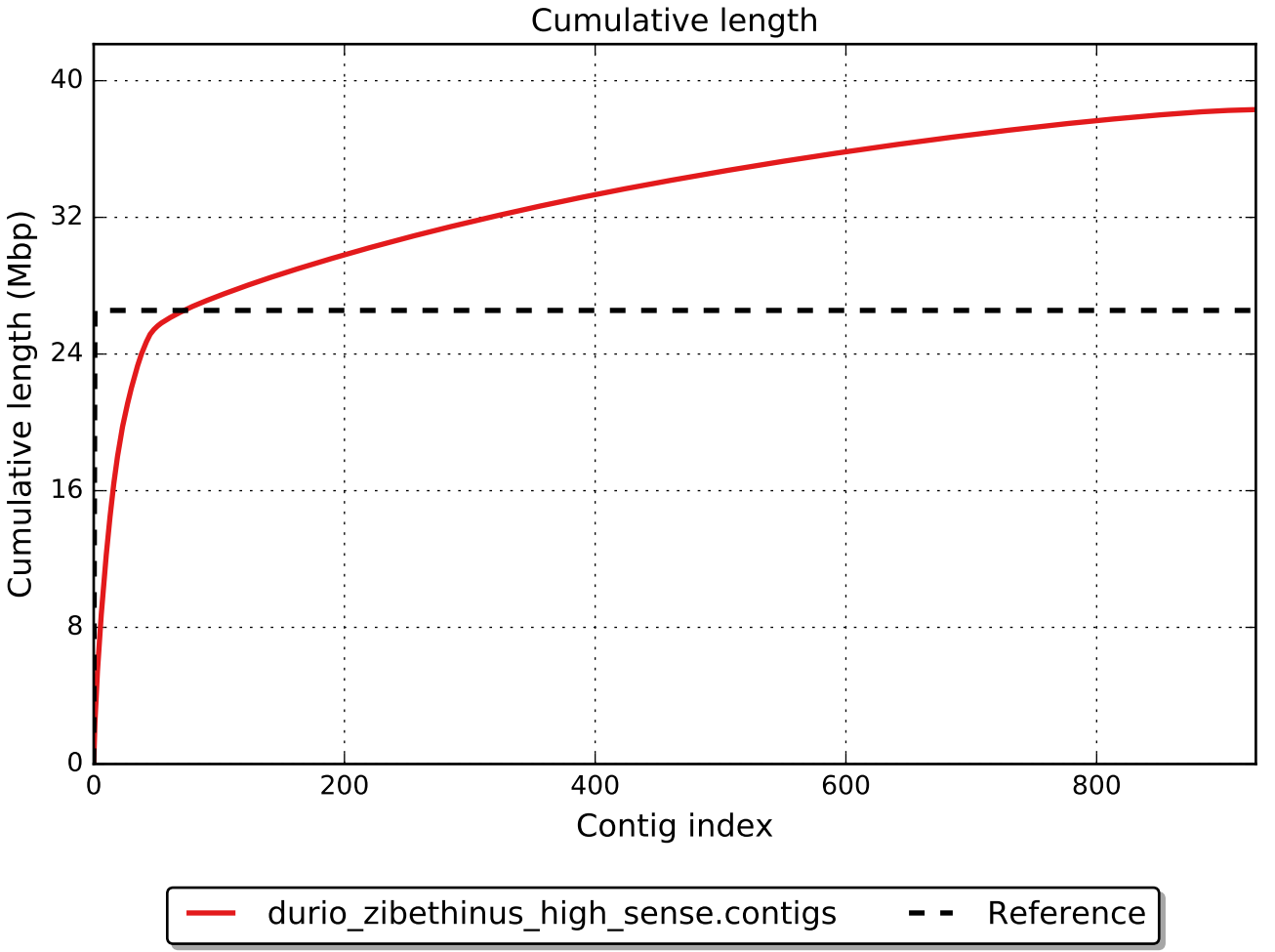
Unaligned report

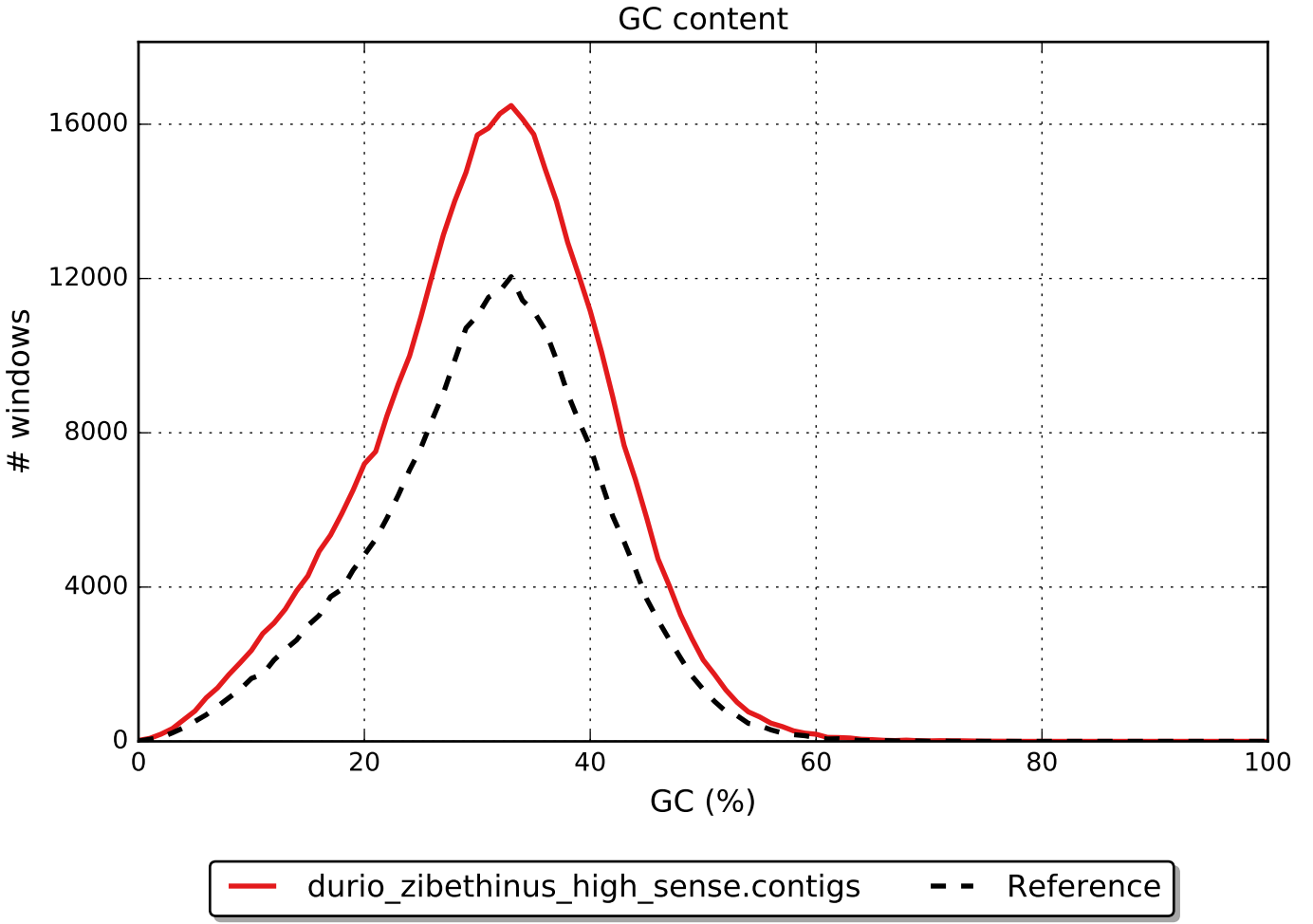
	durio_zibethinus_high_sense.contigs
# fully unaligned contigs	372
Fully unaligned length	3886145
# partially unaligned contigs	288
Partially unaligned length	2306575
# N's	0

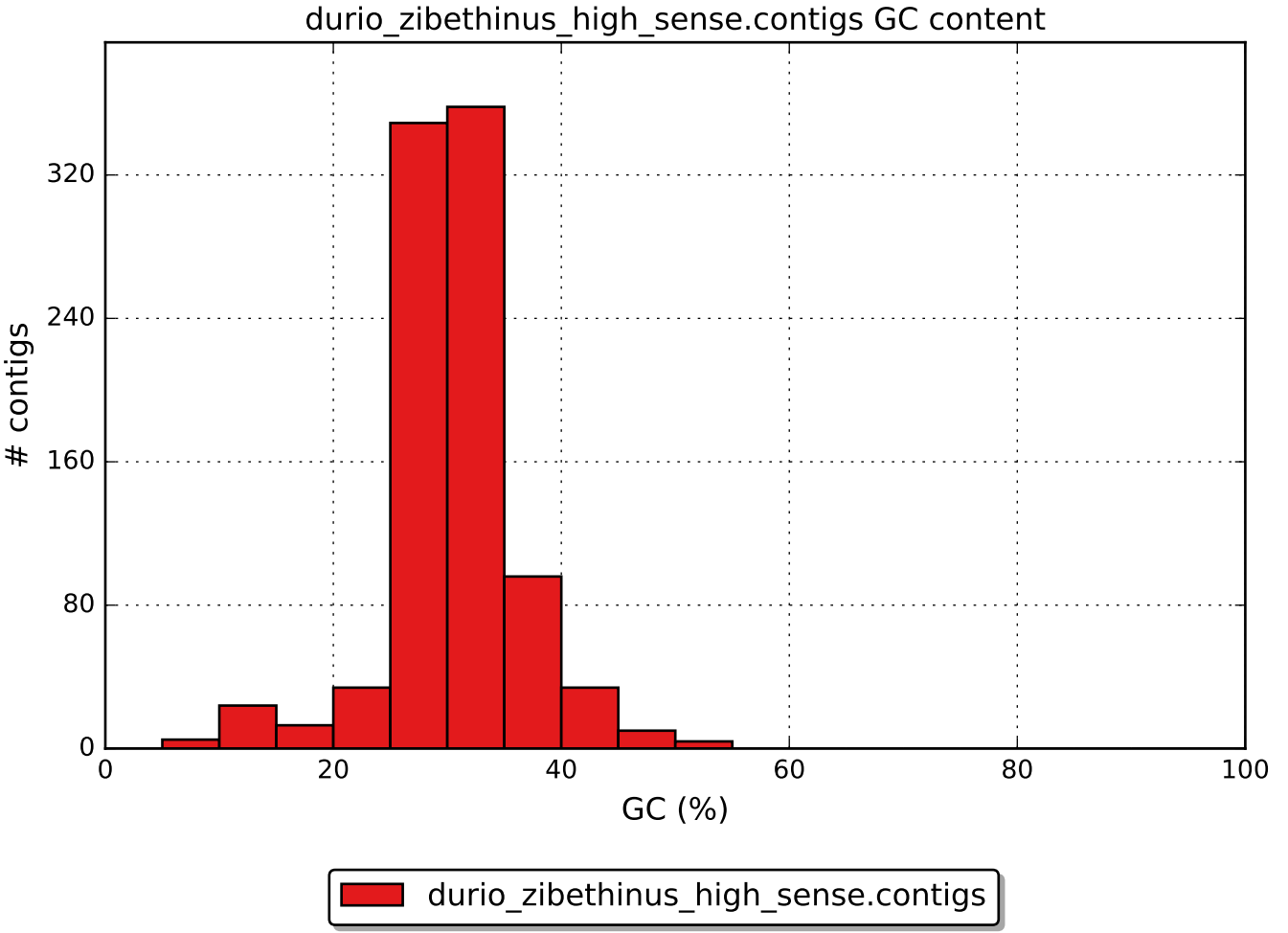
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

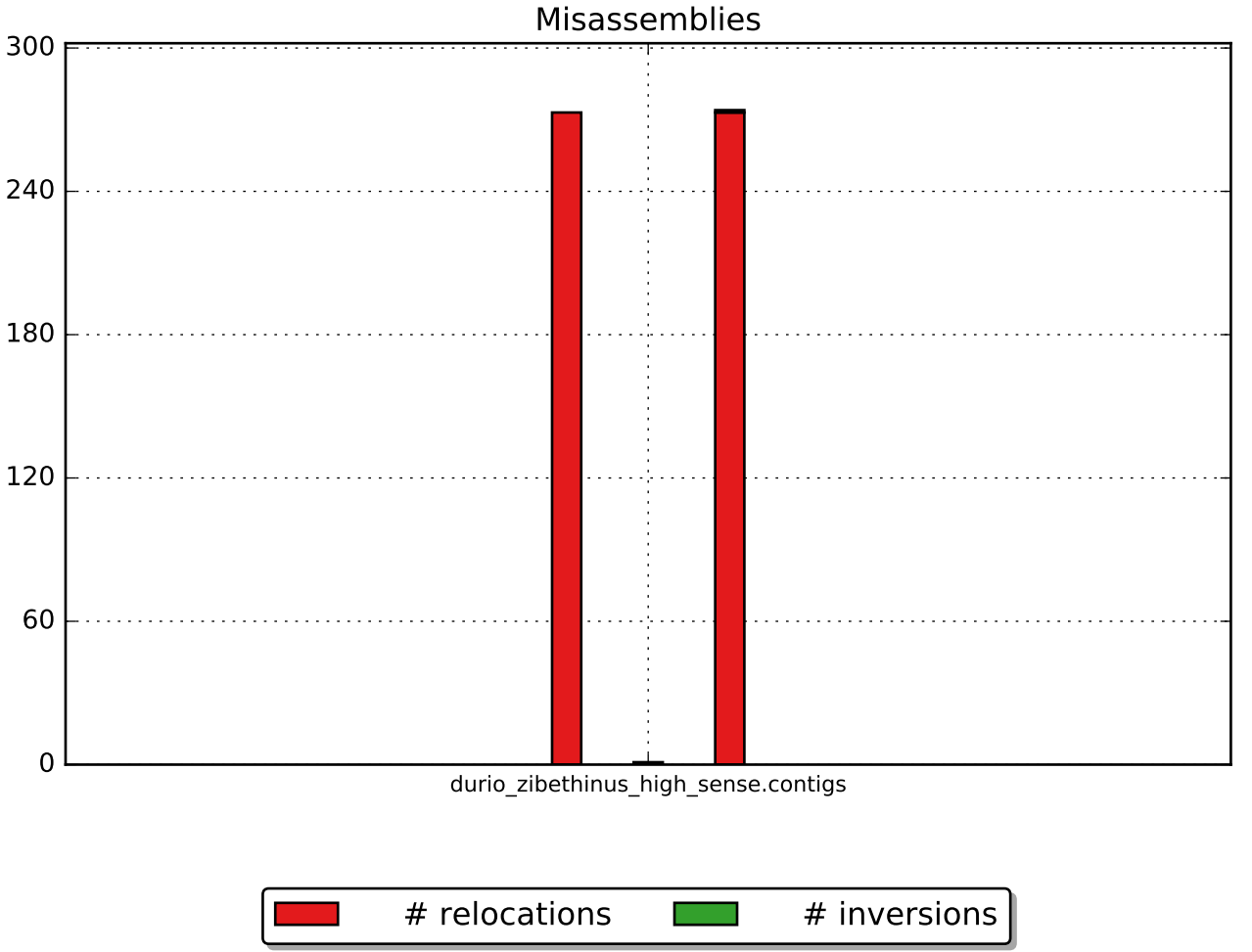

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
durio_zibethinus_high_sense.contigs

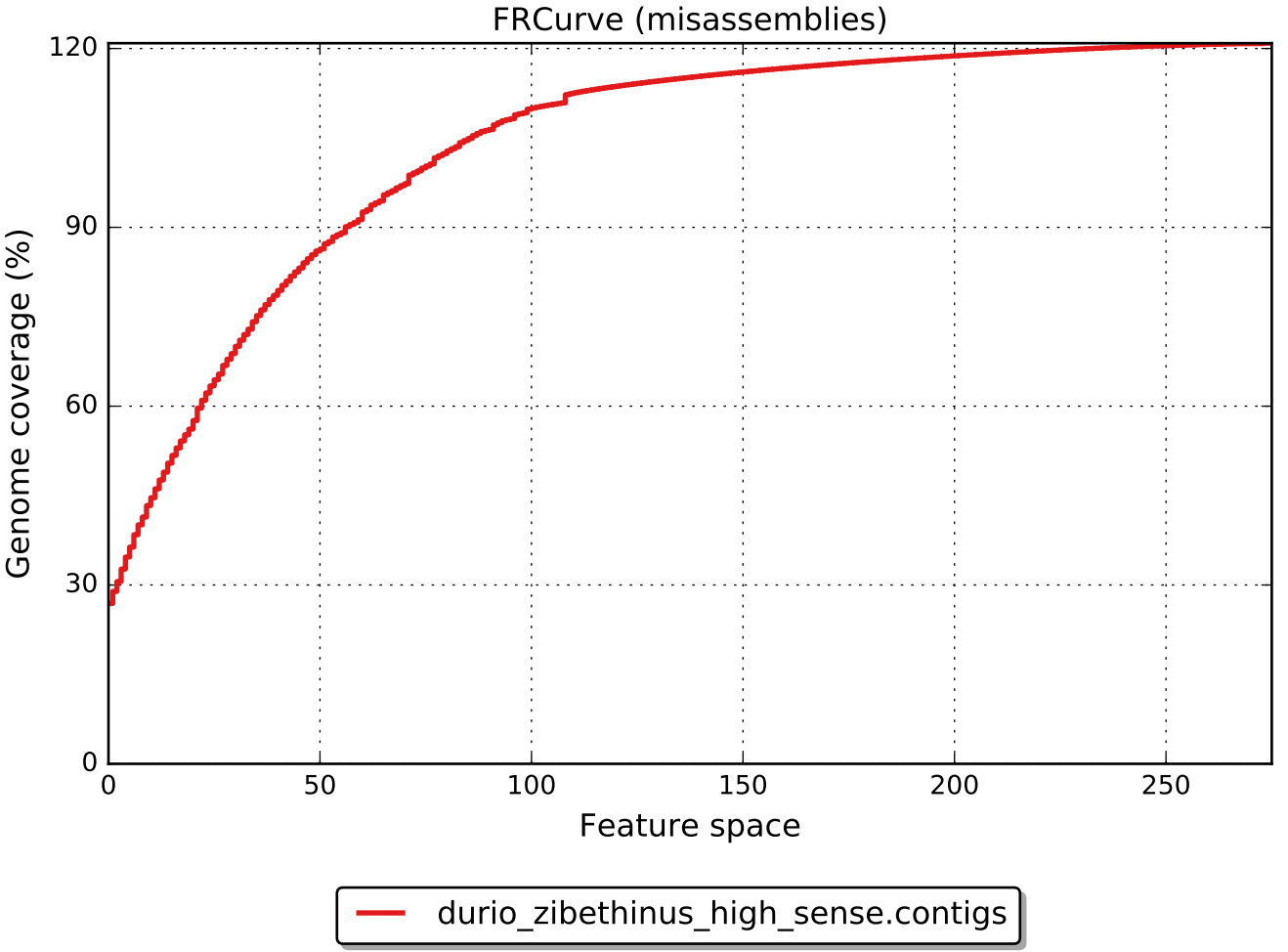

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
durio_zibethinus_high_sense.contigs

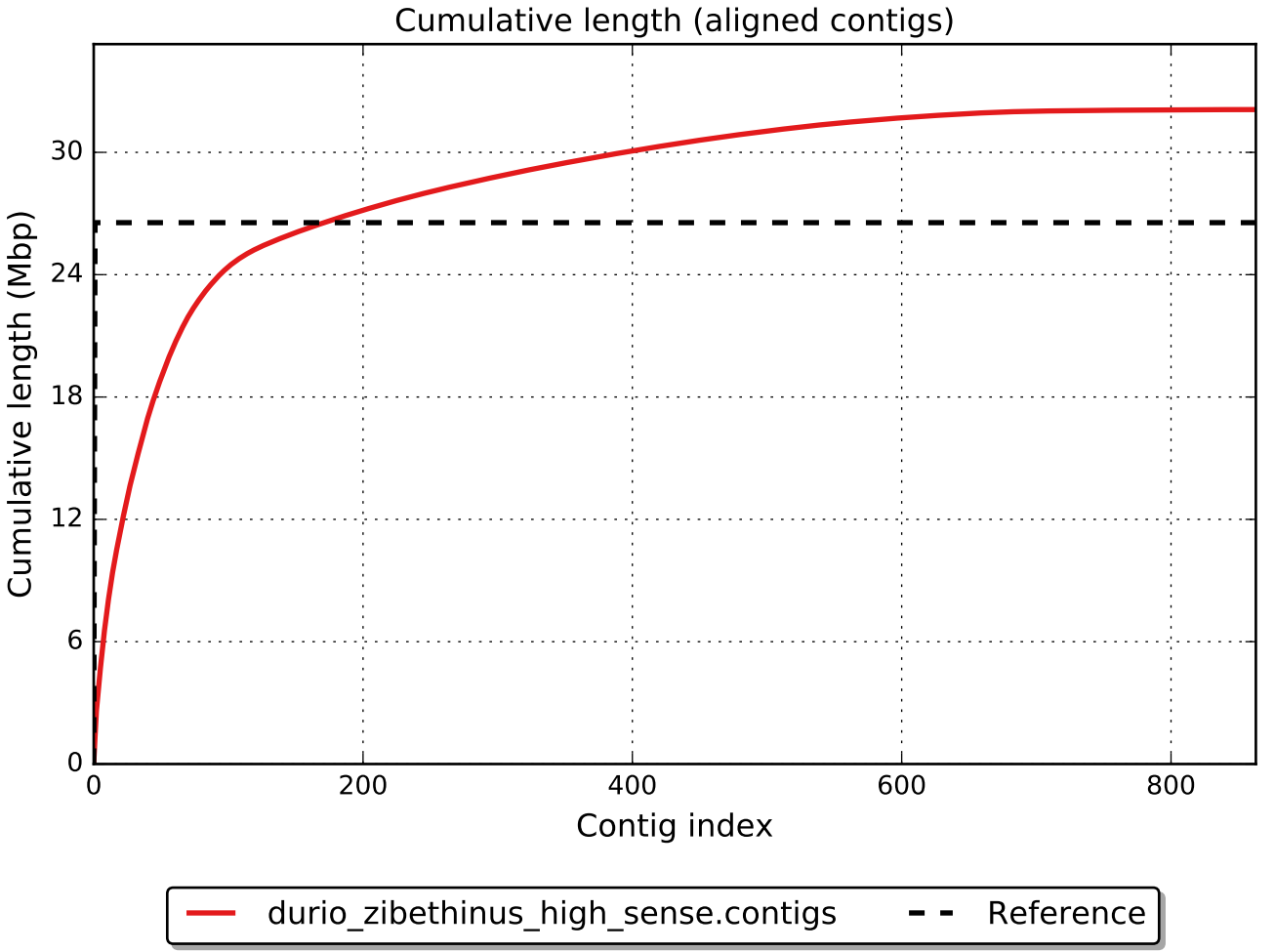

Cumulative length
Cumulative length (Mbp)
40
32
24
16
8
0
0
200
400
600
800
Contig index
durio_zibethinus_high_sense.contigs
Reference

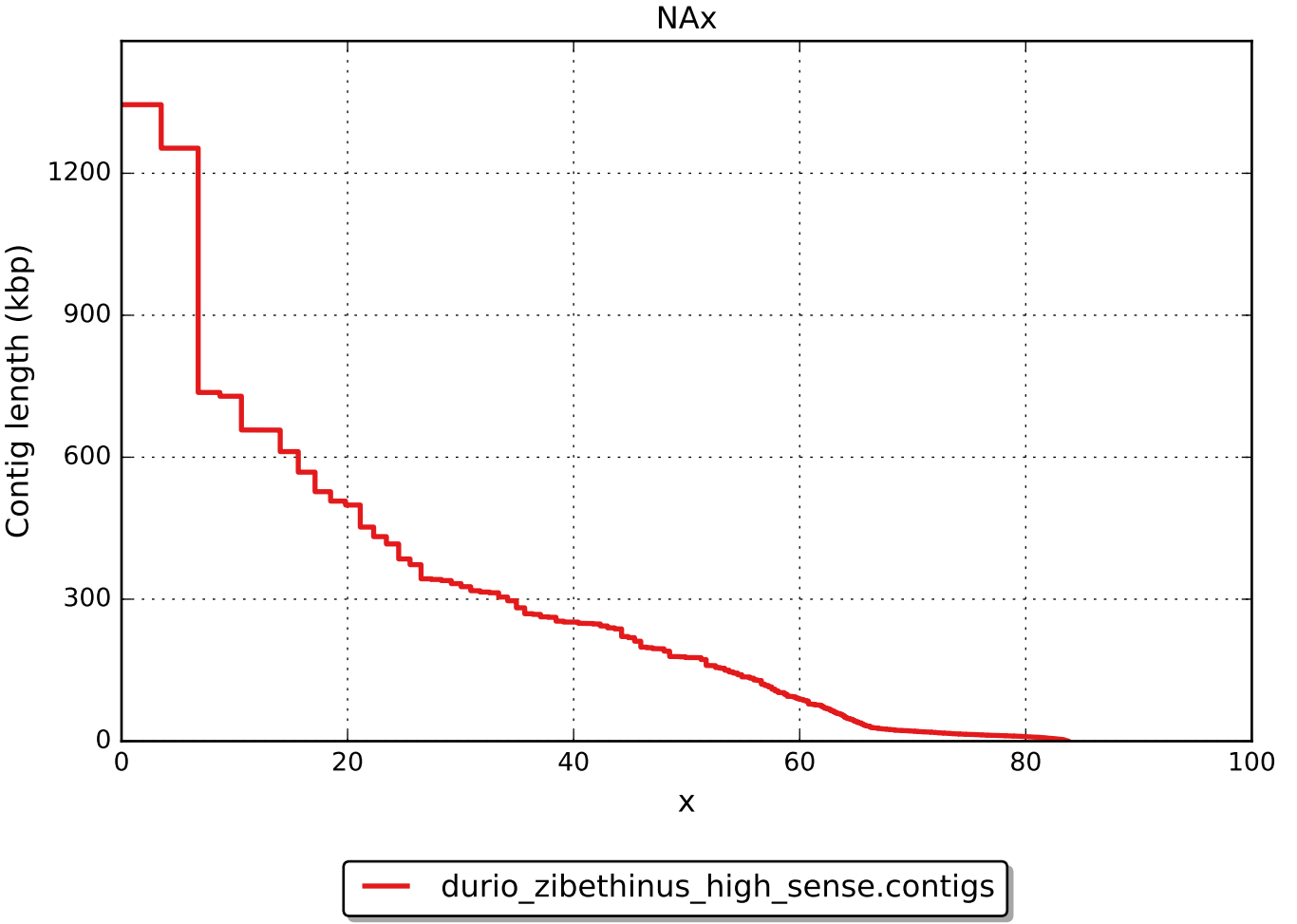

GC content
16000
12000
8000
4000
0
windows
0
20
40
60
80
100
GC (%)
durio_zibethinus_high_sense.contigs
Reference

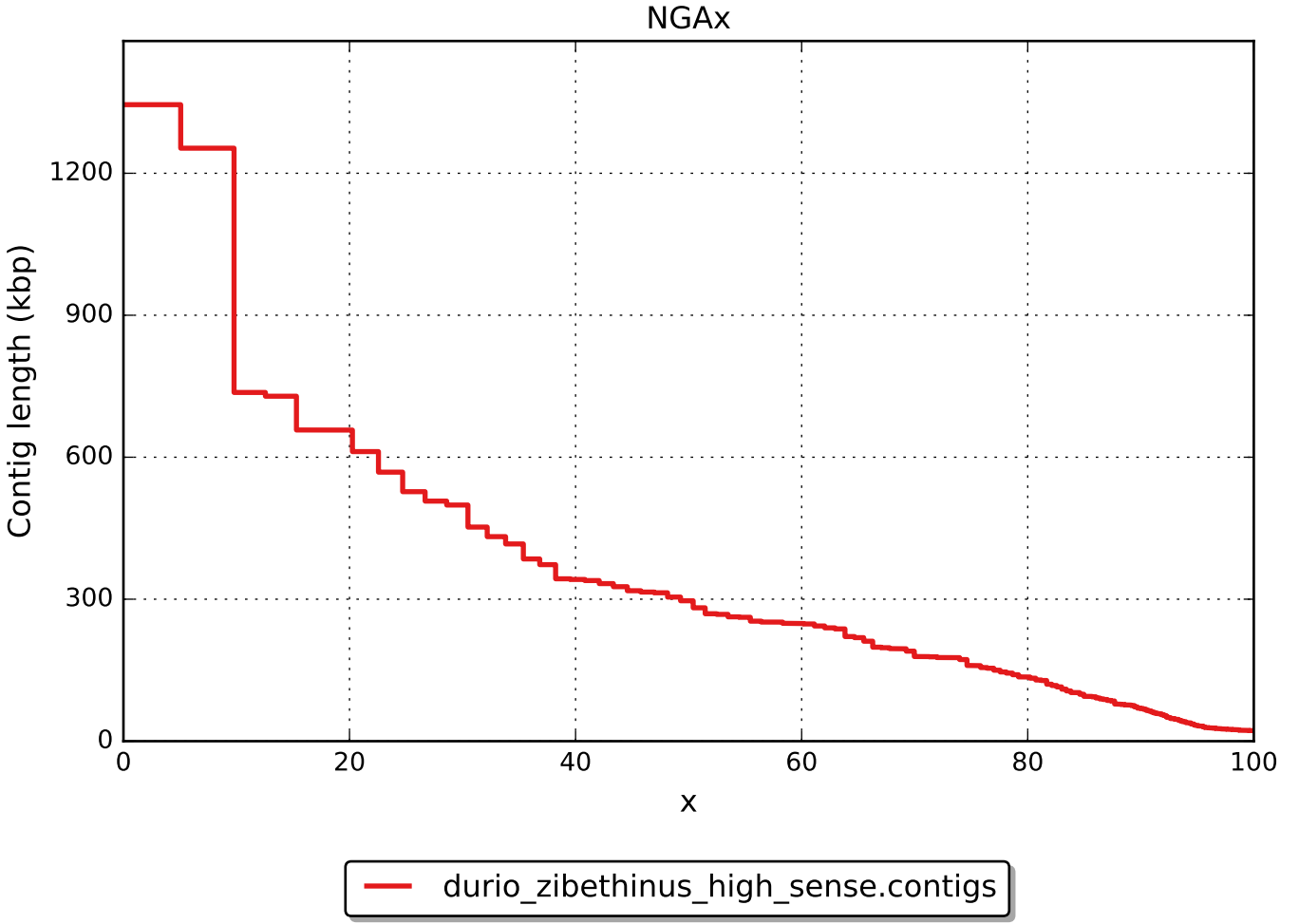

durio_zibethinus_high_sense.contigs GC content
contigs
0
80
160
240
320
0
20
40
60
80
100
GC (%)
durio_zibethinus_high_sense.contigs


Misassemblies
300
240
180
120
60
0
durio_zibethinus_high_sense.contigs
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
120
90
60
30
0
0
50
100
150
200
250
Feature space
durio_zibethinus_high_sense.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
6
12
18
24
30
0
200
400
600
800
Contig index
durio_zibethinus_high_sense.contigs
Reference


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


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