Report

	durian_pacbio.contigs
# contigs (>= 0 bp)	522
# contigs (>= 1000 bp)	522
# contigs (>= 5000 bp)	518
# contigs (>= 10000 bp)	456
# contigs (>= 25000 bp)	125
# contigs (>= 50000 bp)	62
Total length (>= 0 bp)	33643051
Total length (>= 1000 bp)	33643051
Total length (>= 5000 bp)	33631824
Total length (>= 10000 bp)	33108986
Total length (>= 25000 bp)	27751758
Total length (>= 50000 bp)	25793356
# contigs	522
Largest contig	2322816
Total length	33643051
Reference length	26551601
GC (%)	31.13
Reference GC (%)	30.98
N50	446658
NG50	549254
N75	84423
NG75	317831
L50	19
LG50	13
L75	54
LG75	27
# misassemblies	233
# misassembled contigs	122
Misassembled contigs length	24524046
# local misassemblies	243
# unaligned mis. contigs	18
# unaligned contigs	154 + 204 part
Unaligned length	4004809
Genome fraction (%)	97.014
Duplication ratio	1.151
# N's per 100 kbp	0.00
# mismatches per 100 kbp	346.87
# indels per 100 kbp	189.21
Largest alignment	1260959
Total aligned length	29628236
NA50	211109
NGA50	281416
NA75	25947
NGA75	131907
LA50	40
LGA50	25
LA75	137
LGA75	59

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

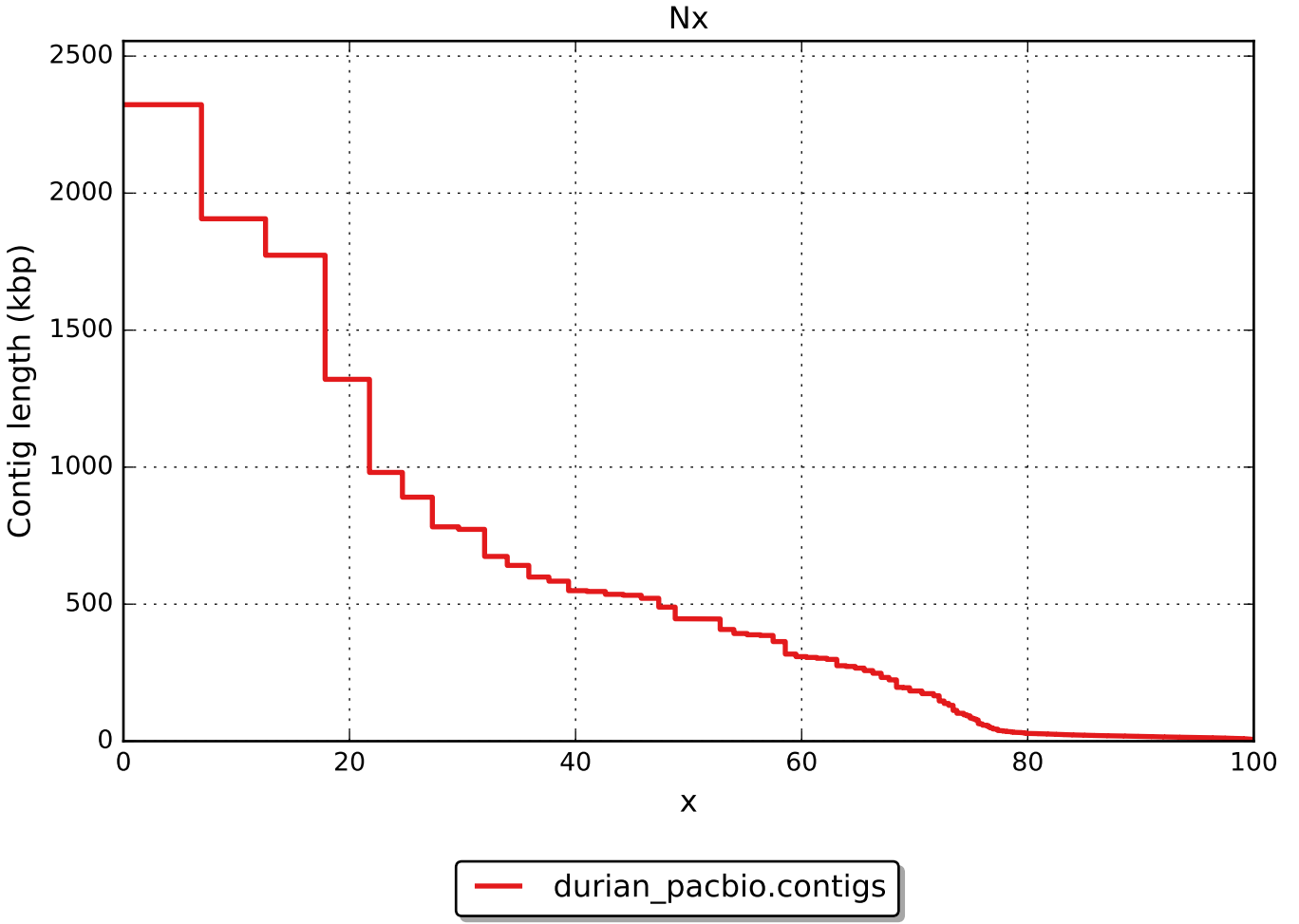
	durian_pacbio.contigs
# misassemblies	233
# relocations	232
# translocations	0
# inversions	1
# misassembled contigs	122
Misassembled contigs length	24524046
# local misassemblies	243
# unaligned mis. contigs	18
# mismatches	89348
# indels	48739
# indels (<= 5 bp)	46271
# indels (> 5 bp)	2468
Indels length	92738

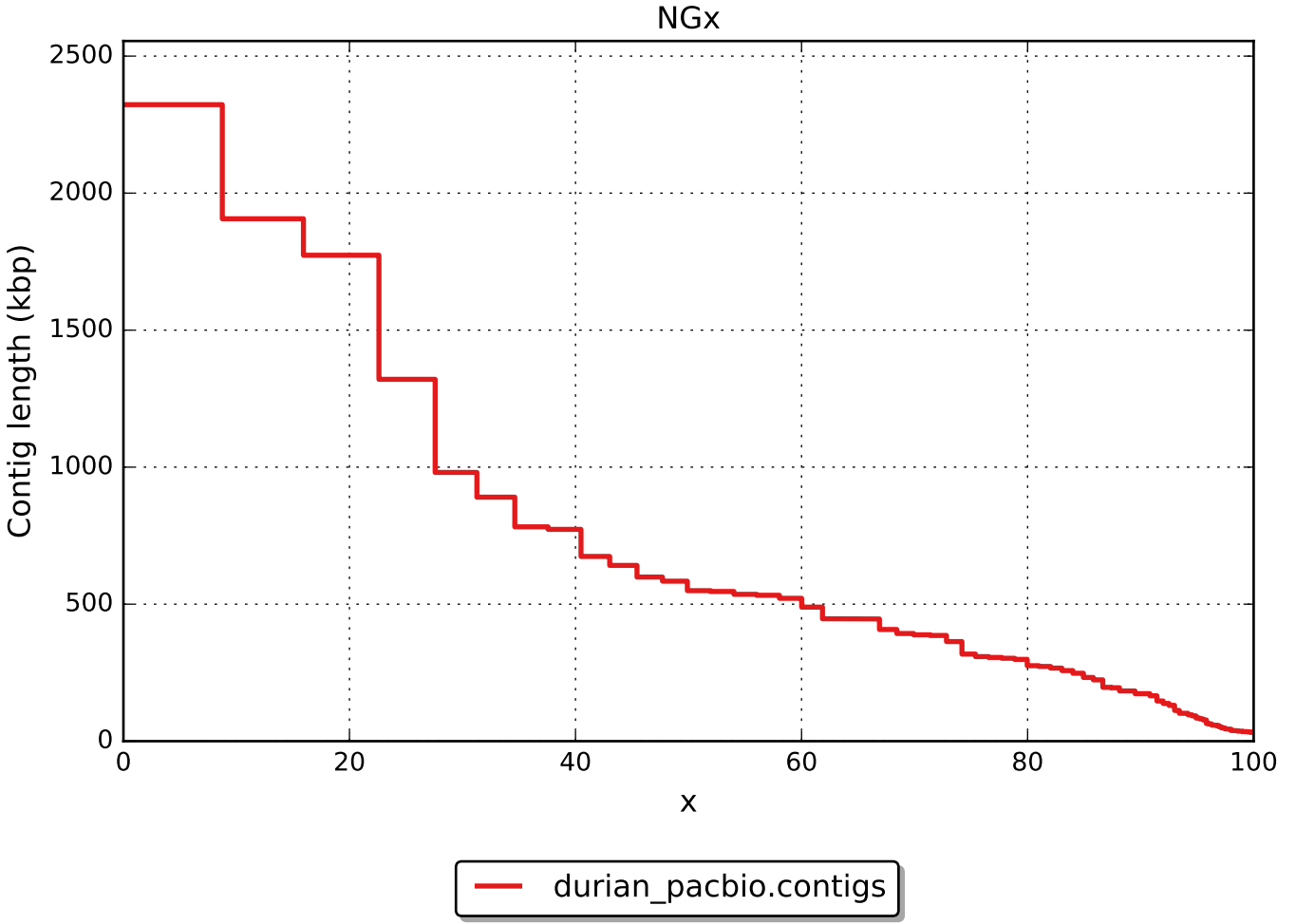
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

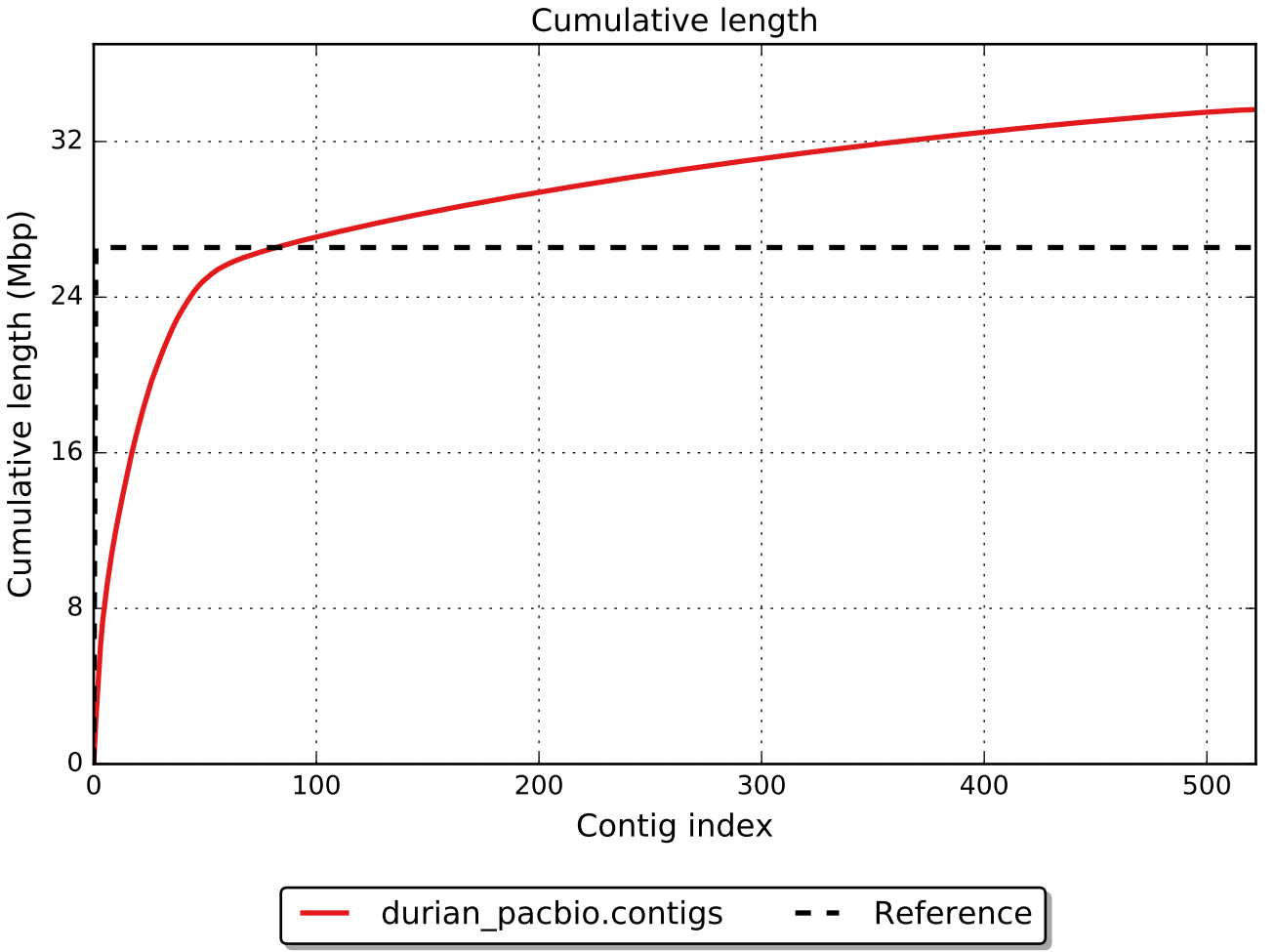
Unaligned report

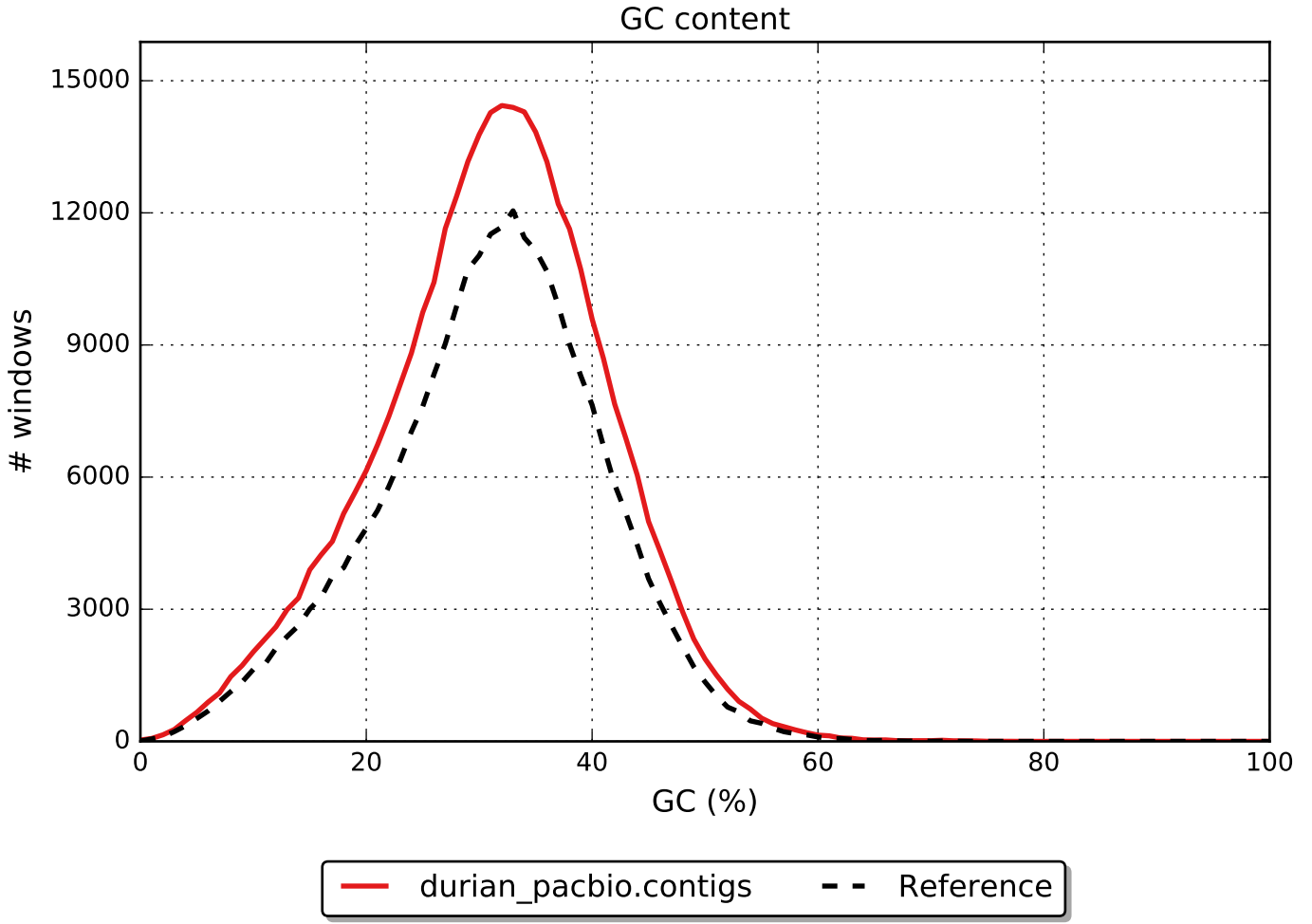
	durian_pacbio.contigs
# fully unaligned contigs	154
Fully unaligned length	2085511
# partially unaligned contigs	204
Partially unaligned length	1919298
# N's	0

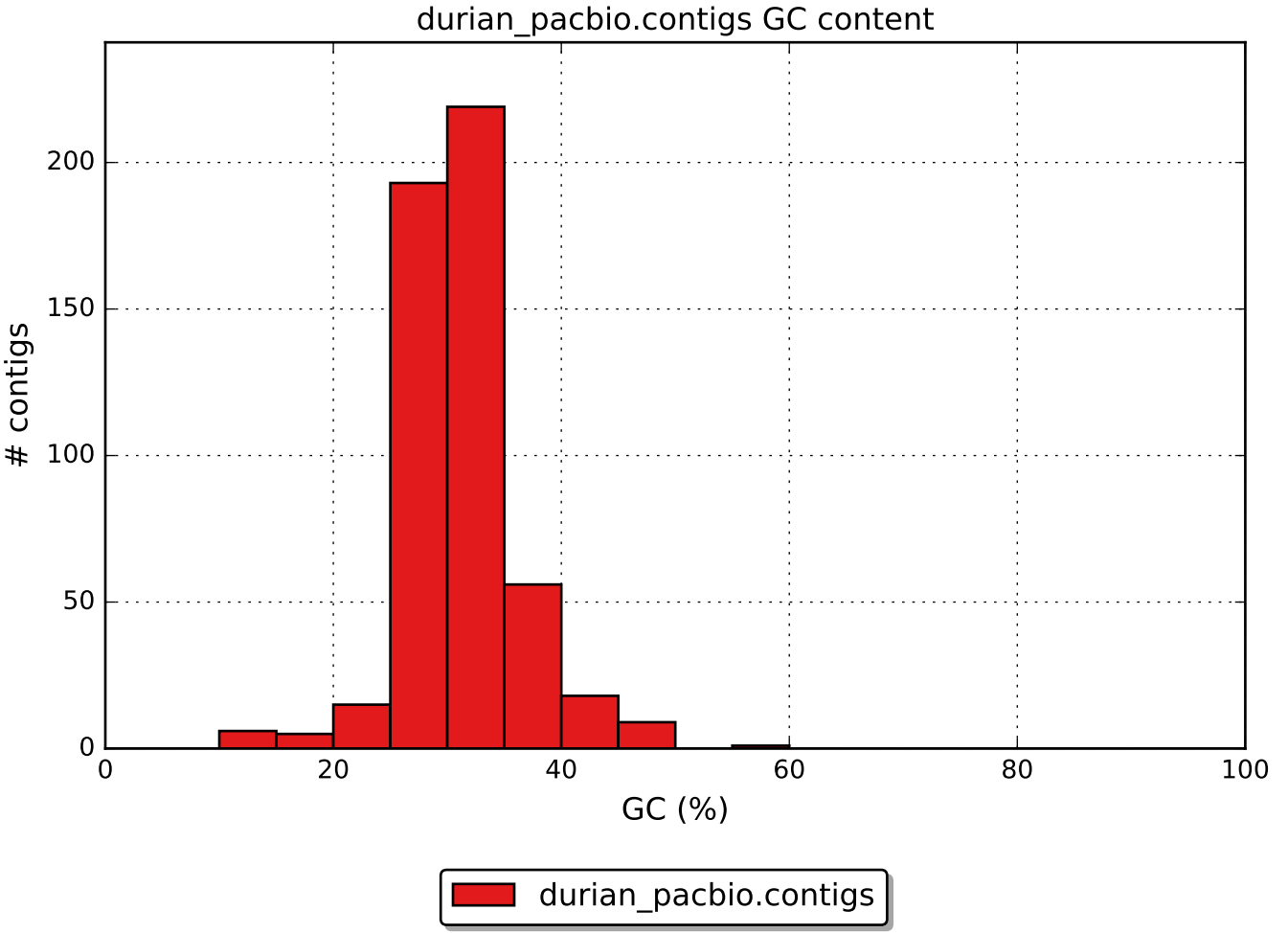
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

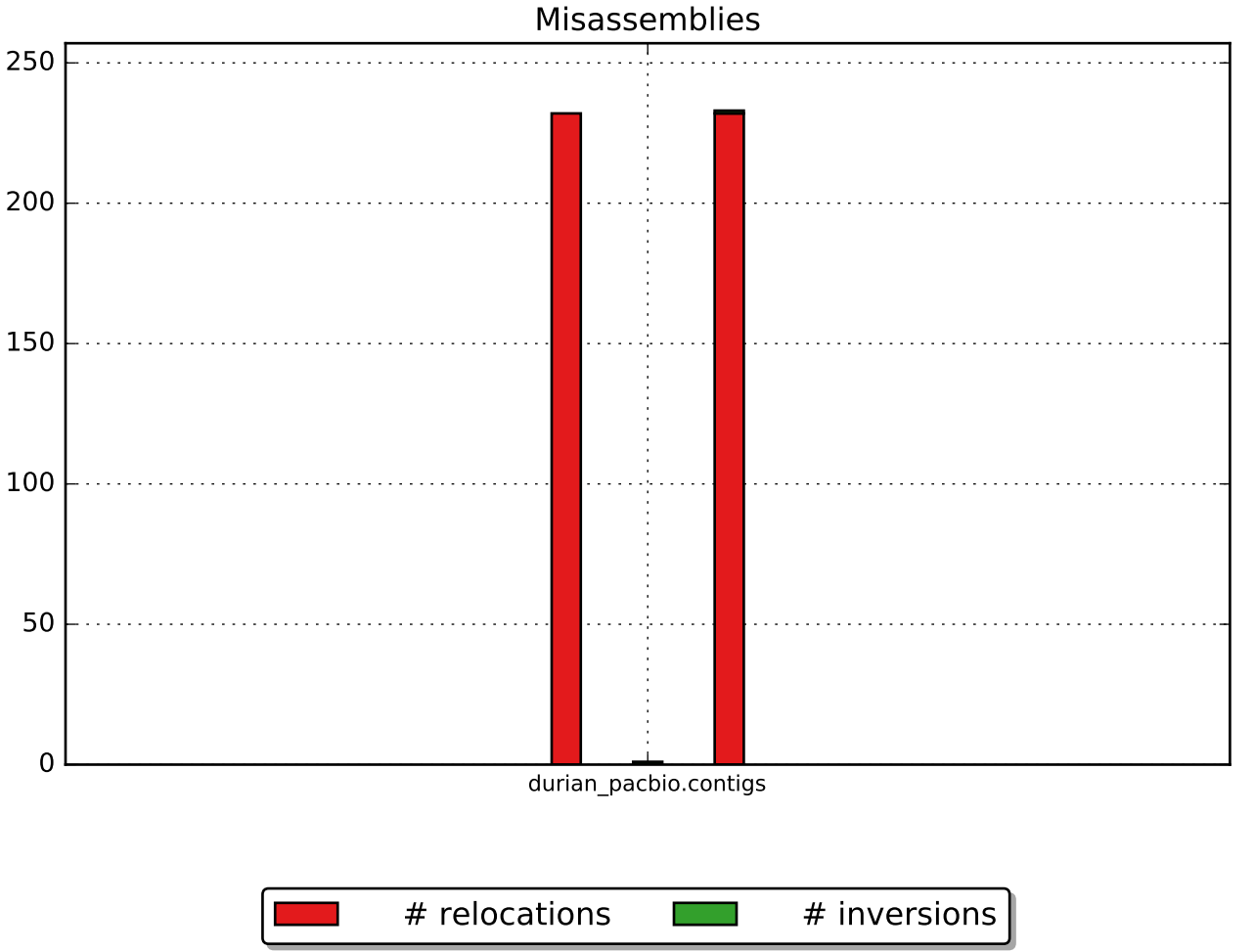

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
durian_pacbio.contigs

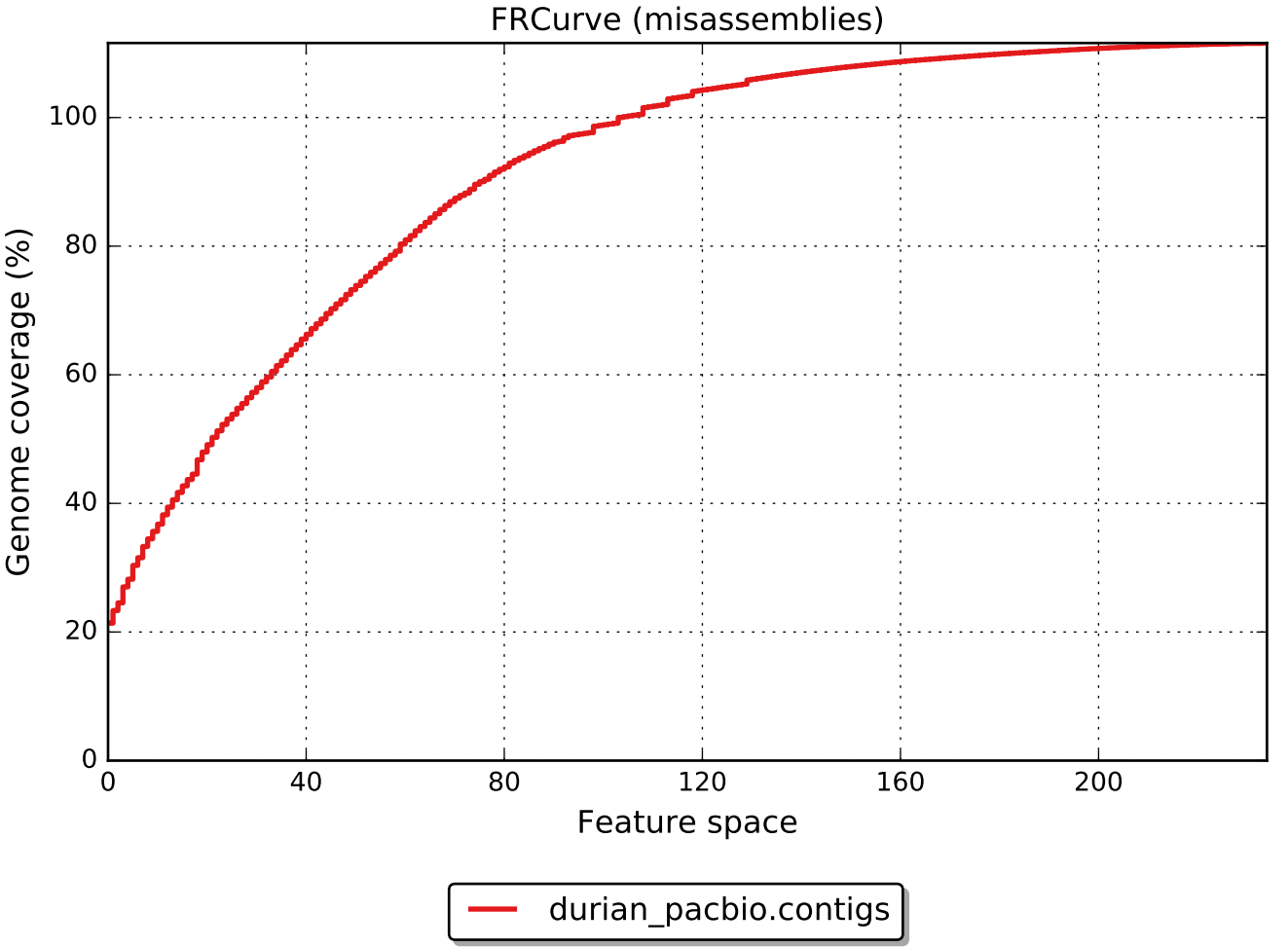

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
durian_pacbio.contigs

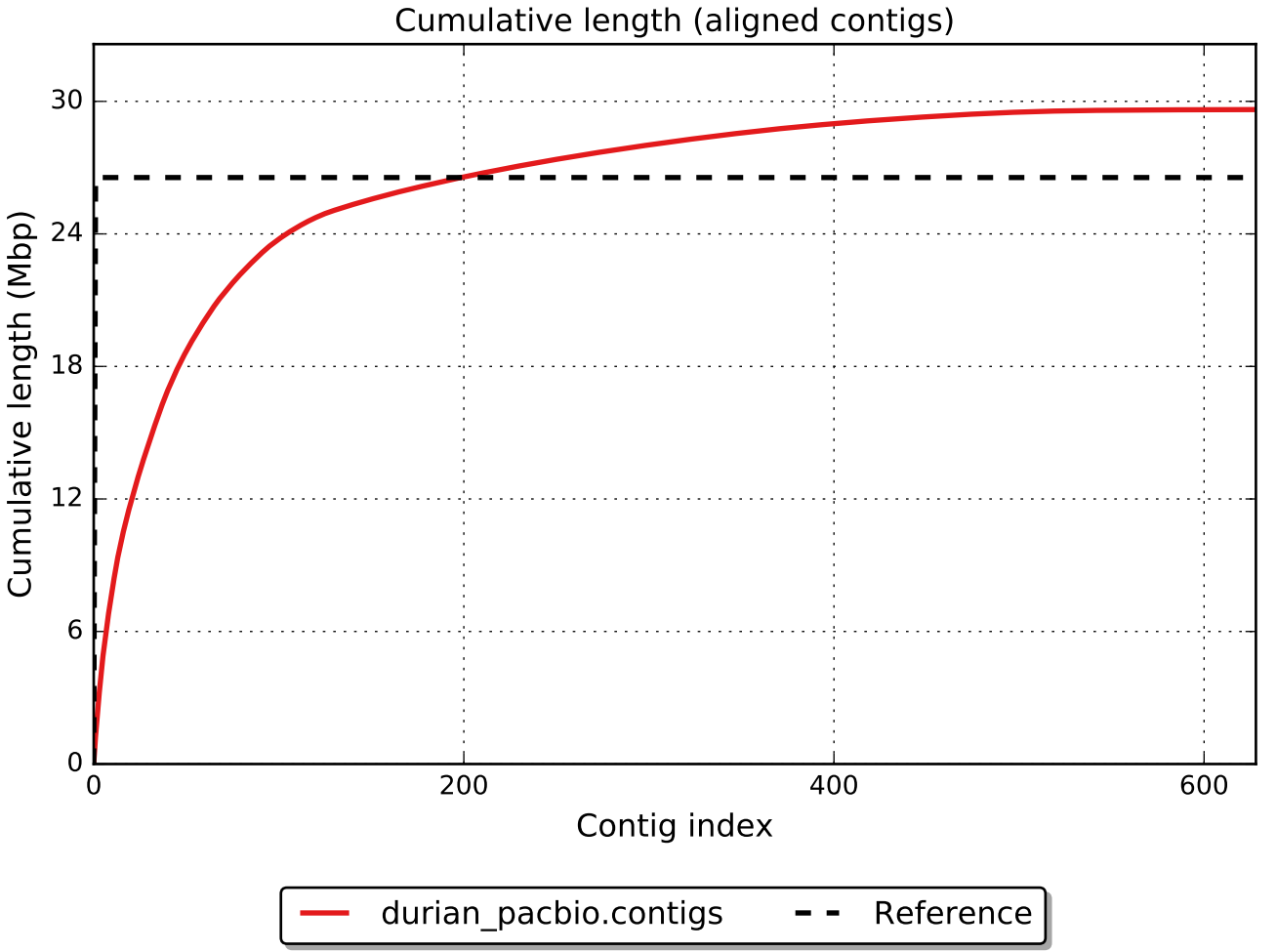

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
100
200
300
400
500
Contig index
durian_pacbio.contigs
Reference

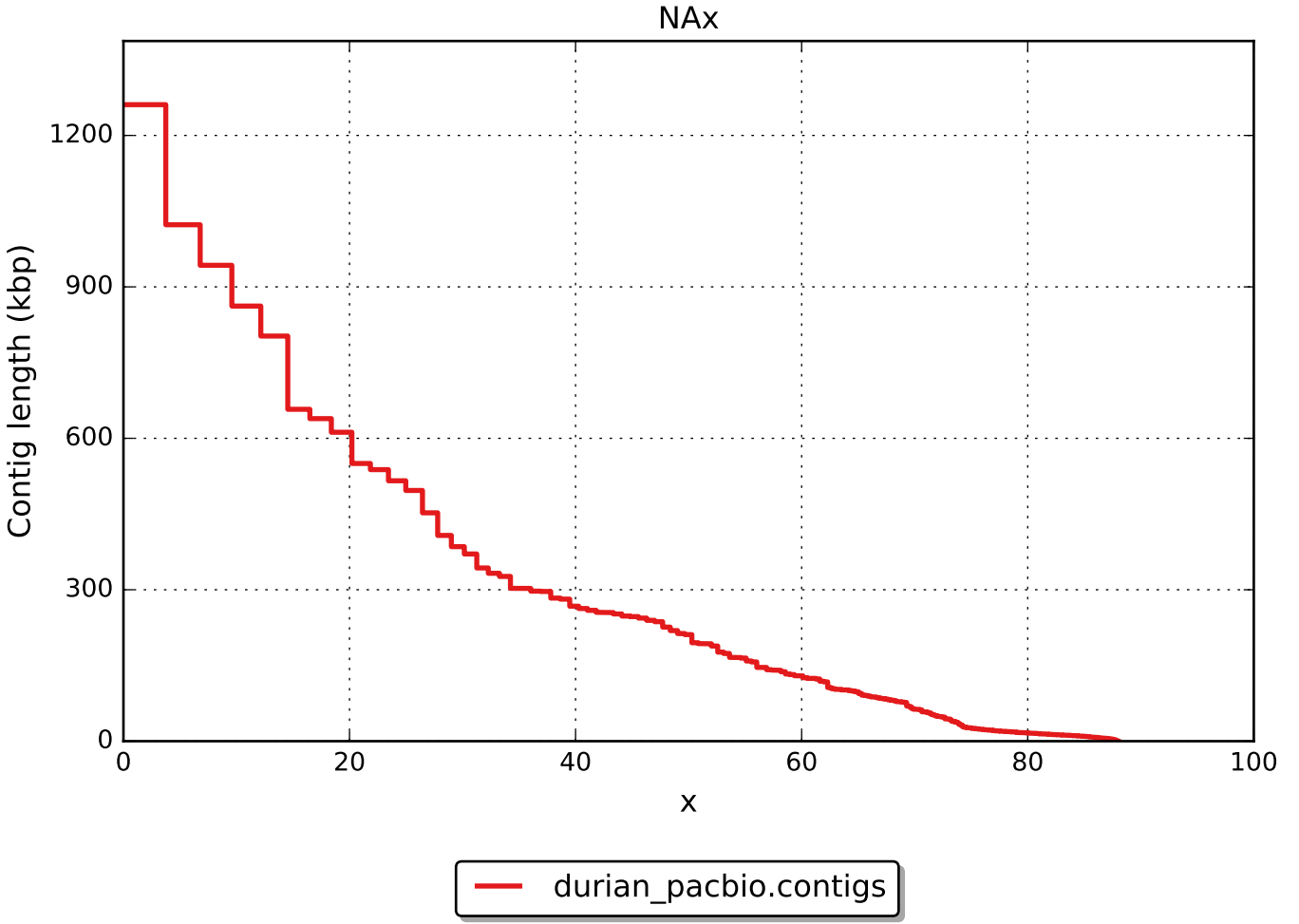

GC content
15000
12000
9000
6000
3000
0
windows
0
20
40
60
80
100
GC (%)
durian_pacbio.contigs
Reference

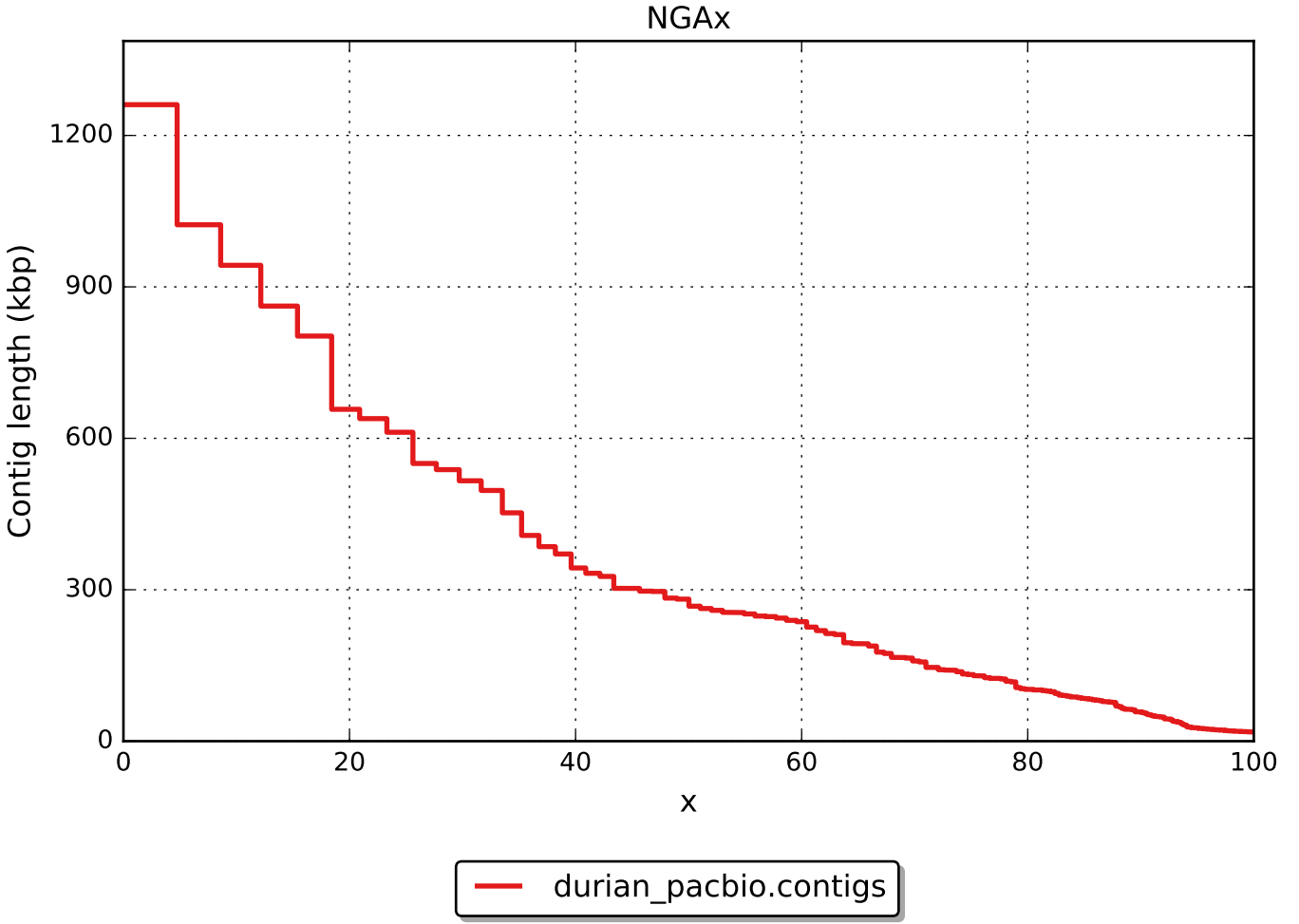

durian_pacbio.contigs GC content
contigs
GC (%)
0
50
100
150
200
0
20
40
60
80
100
durian_pacbio.contigs


Misassemblies
250
200
150
100
50
0
durian_pacbio.contigs
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
40
80
120
160
200
Feature space
durian_pacbio.contigs


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


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


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