Report

	durioz.pilon
# contigs (>= 0 bp)	756
# contigs (>= 1000 bp)	756
# contigs (>= 5000 bp)	676
# contigs (>= 10000 bp)	485
# contigs (>= 25000 bp)	113
# contigs (>= 50000 bp)	39
Total length (>= 0 bp)	29794825
Total length (>= 1000 bp)	29794825
Total length (>= 5000 bp)	29537469
Total length (>= 10000 bp)	28058760
Total length (>= 25000 bp)	22246790
Total length (>= 50000 bp)	19856769
# contigs	756
Largest contig	3001067
Total length	29794825
Reference length	24162007
GC (%)	31.64
Reference GC (%)	33.51
N50	574099
NG50	880685
N75	24350
NG75	193700
L50	13
LG50	9
L75	118
LG75	22
# misassemblies	168
# misassembled contigs	86
Misassembled contigs length	18564751
# local misassemblies	255
# unaligned mis. contigs	15
# unaligned contigs	312 + 189 part
Unaligned length	4731663
Genome fraction (%)	85.862
Duplication ratio	1.208
# N's per 100 kbp	0.00
# mismatches per 100 kbp	324.72
# indels per 100 kbp	118.16
Largest alignment	2720121
Total aligned length	25048671
NA50	185895
NGA50	281398
NA75	16717
NGA75	67325
LA50	31
LGA50	19
LA75	211
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

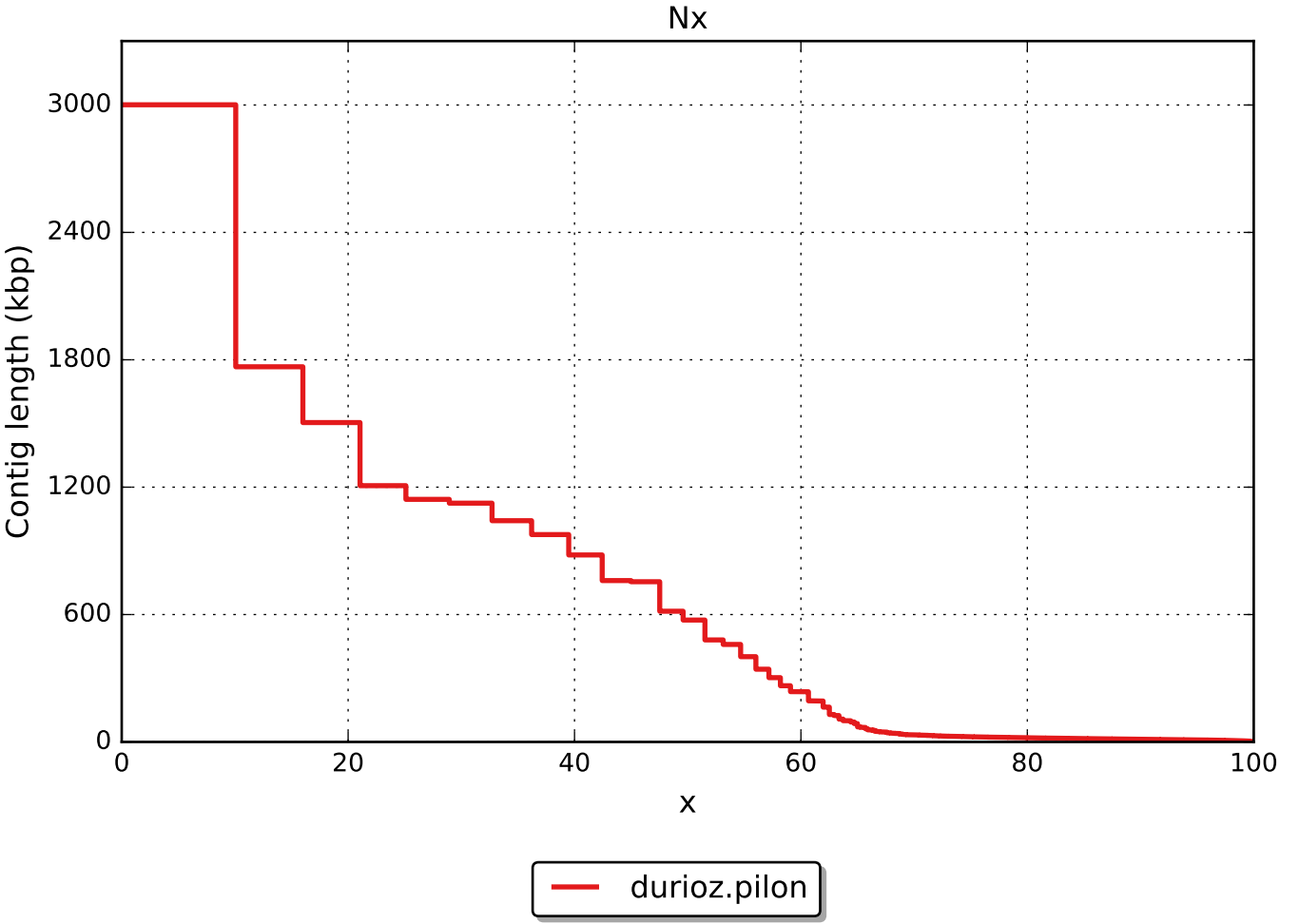
	durioz.pilon
# misassemblies	168
# relocations	166
# translocations	0
# inversions	2
# misassembled contigs	86
Misassembled contigs length	18564751
# local misassemblies	255
# unaligned mis. contigs	15
# mismatches	67367
# indels	24514
# indels (<= 5 bp)	22964
# indels (> 5 bp)	1550
Indels length	51851

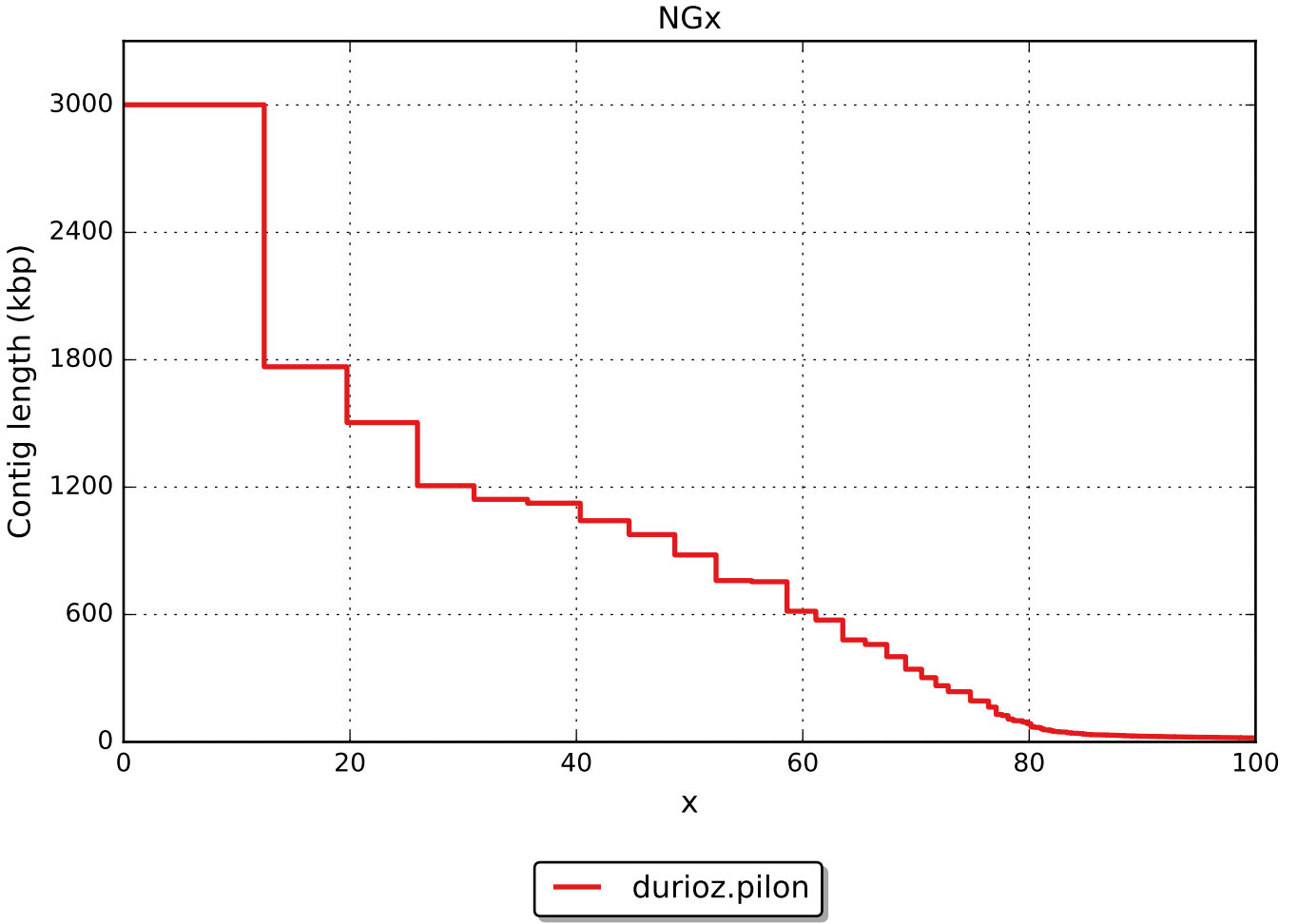
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

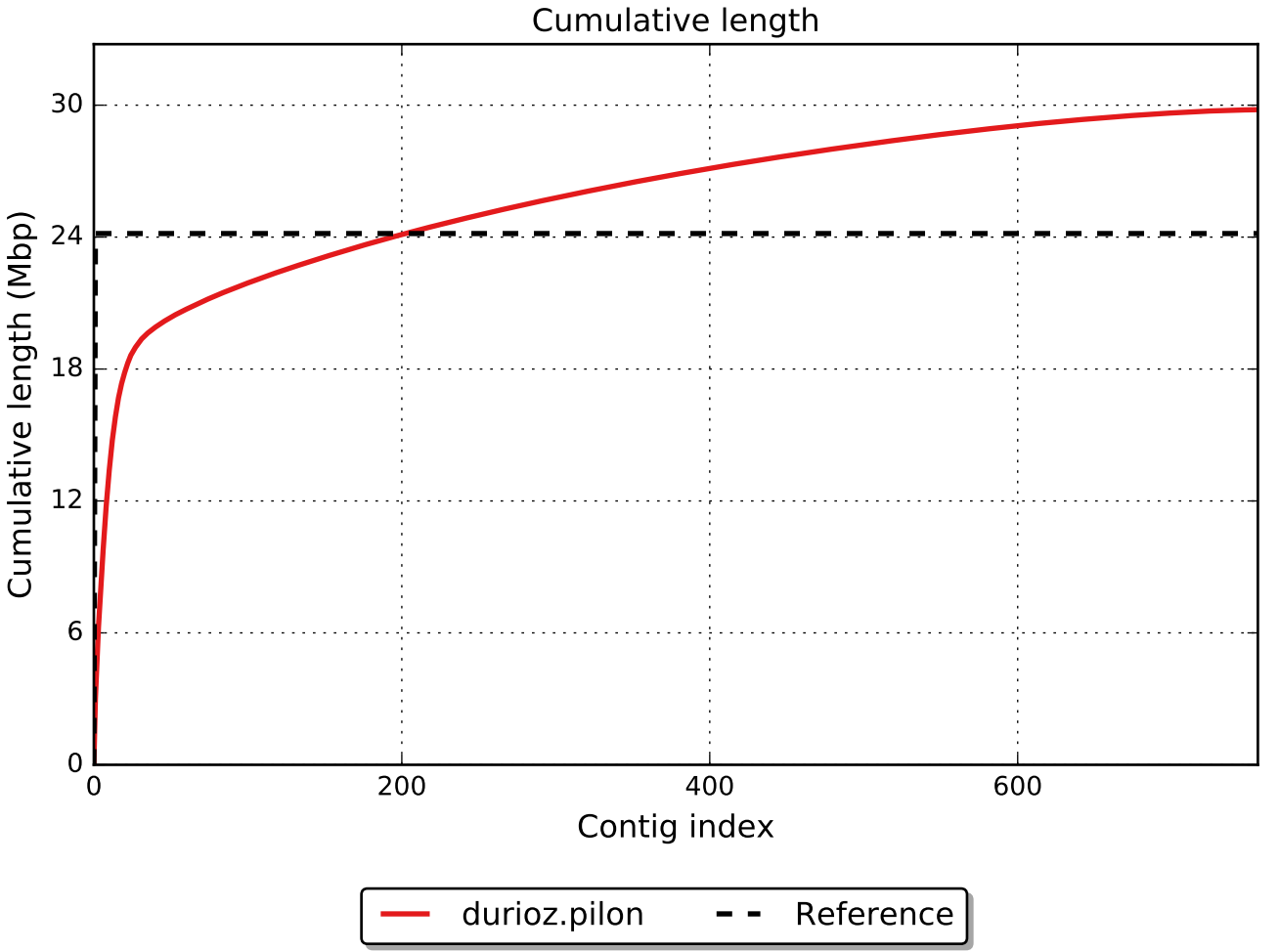
Unaligned report

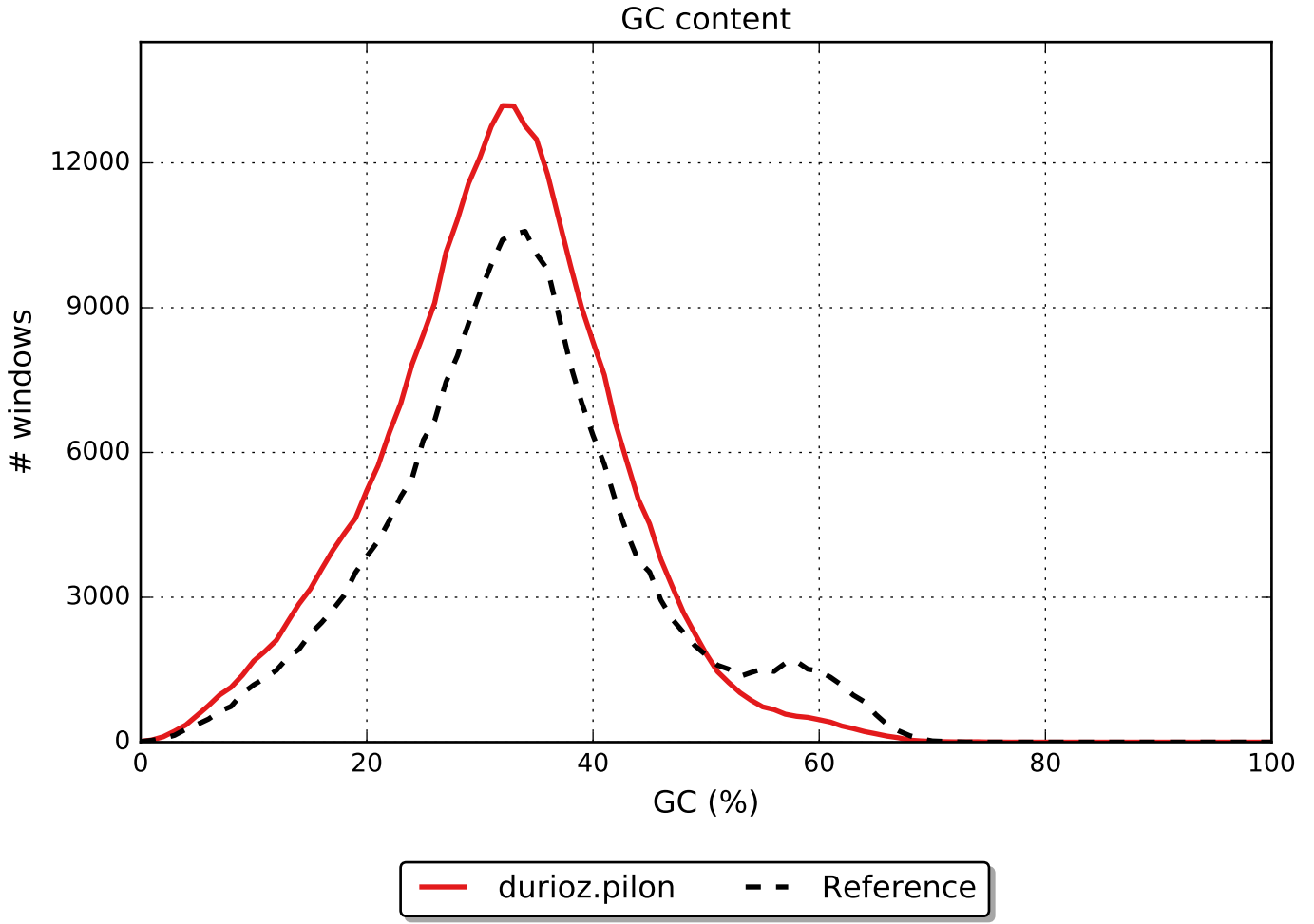
	durioz.pilon
# fully unaligned contigs	312
Fully unaligned length	3072667
# partially unaligned contigs	189
Partially unaligned length	1658996
# N's	0

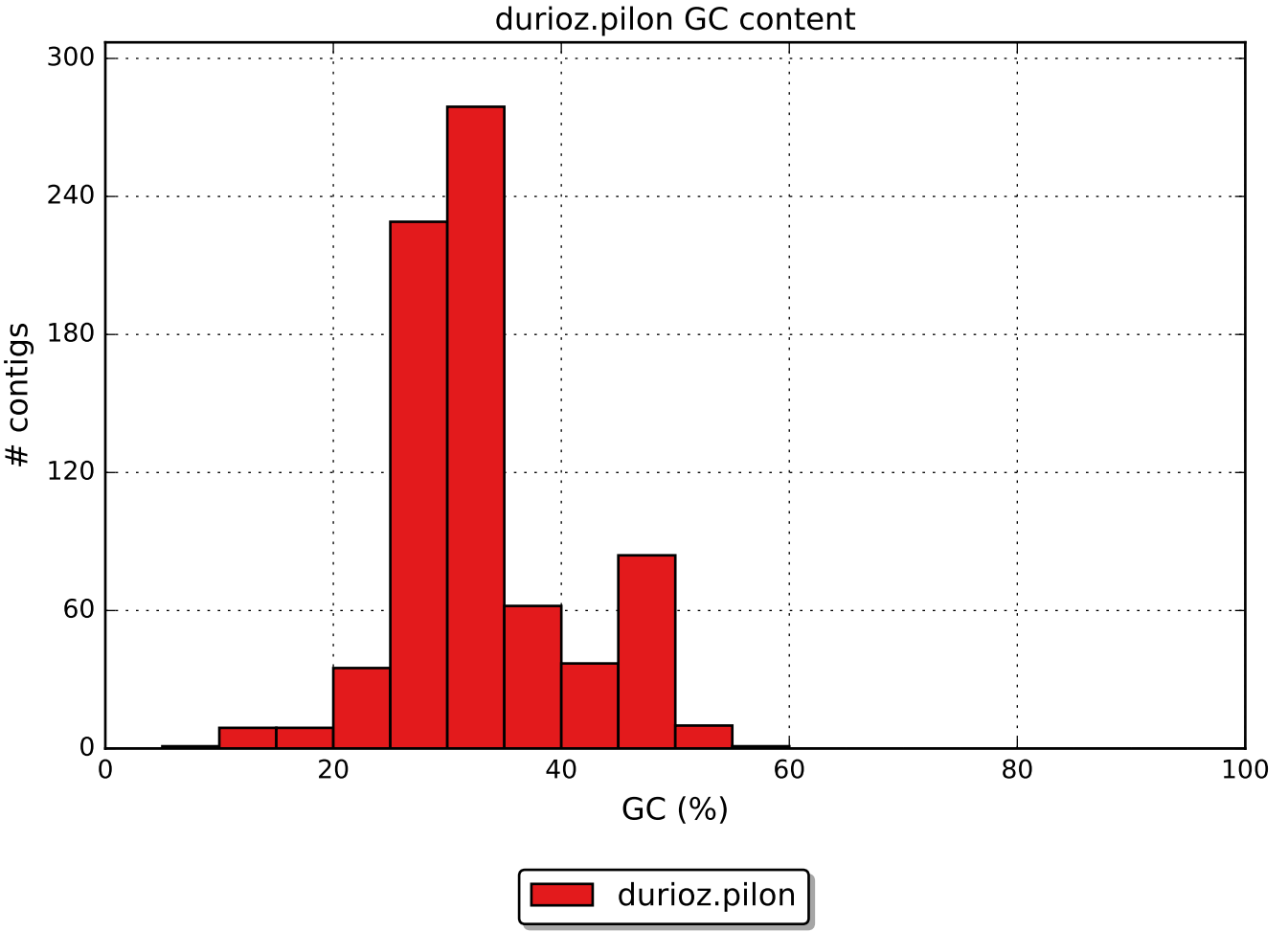
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

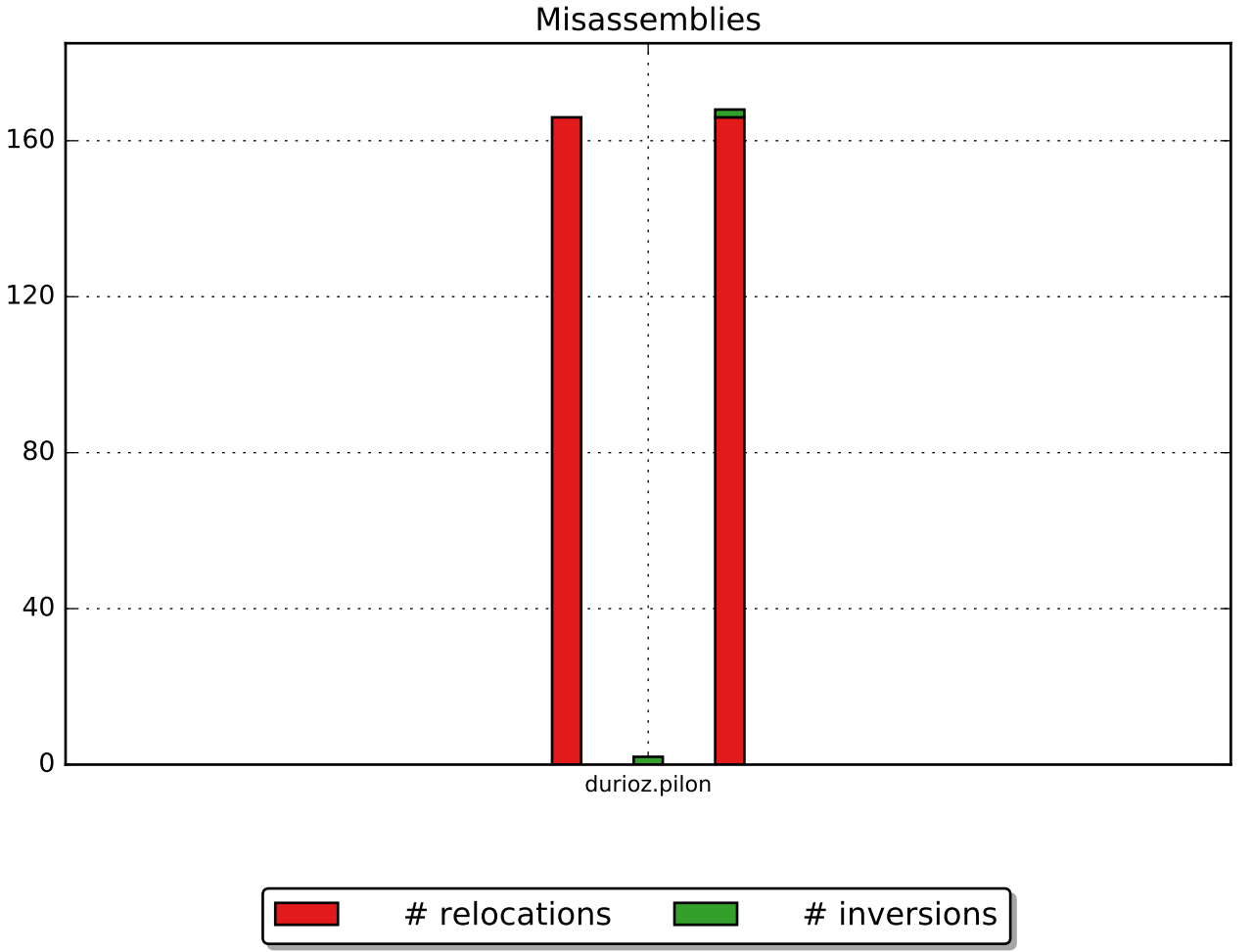

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
durioz.pilon

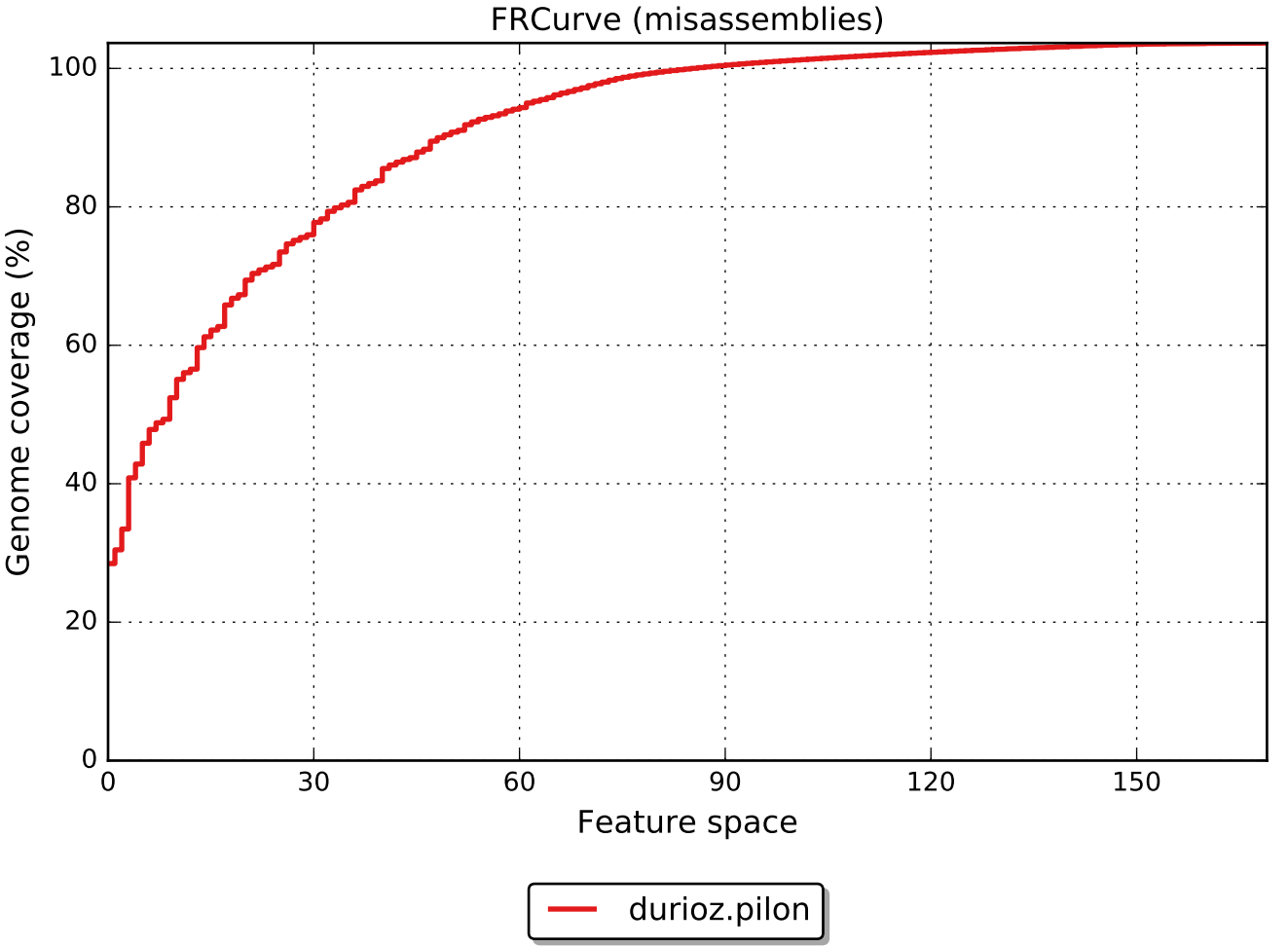

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
durioz.pilon

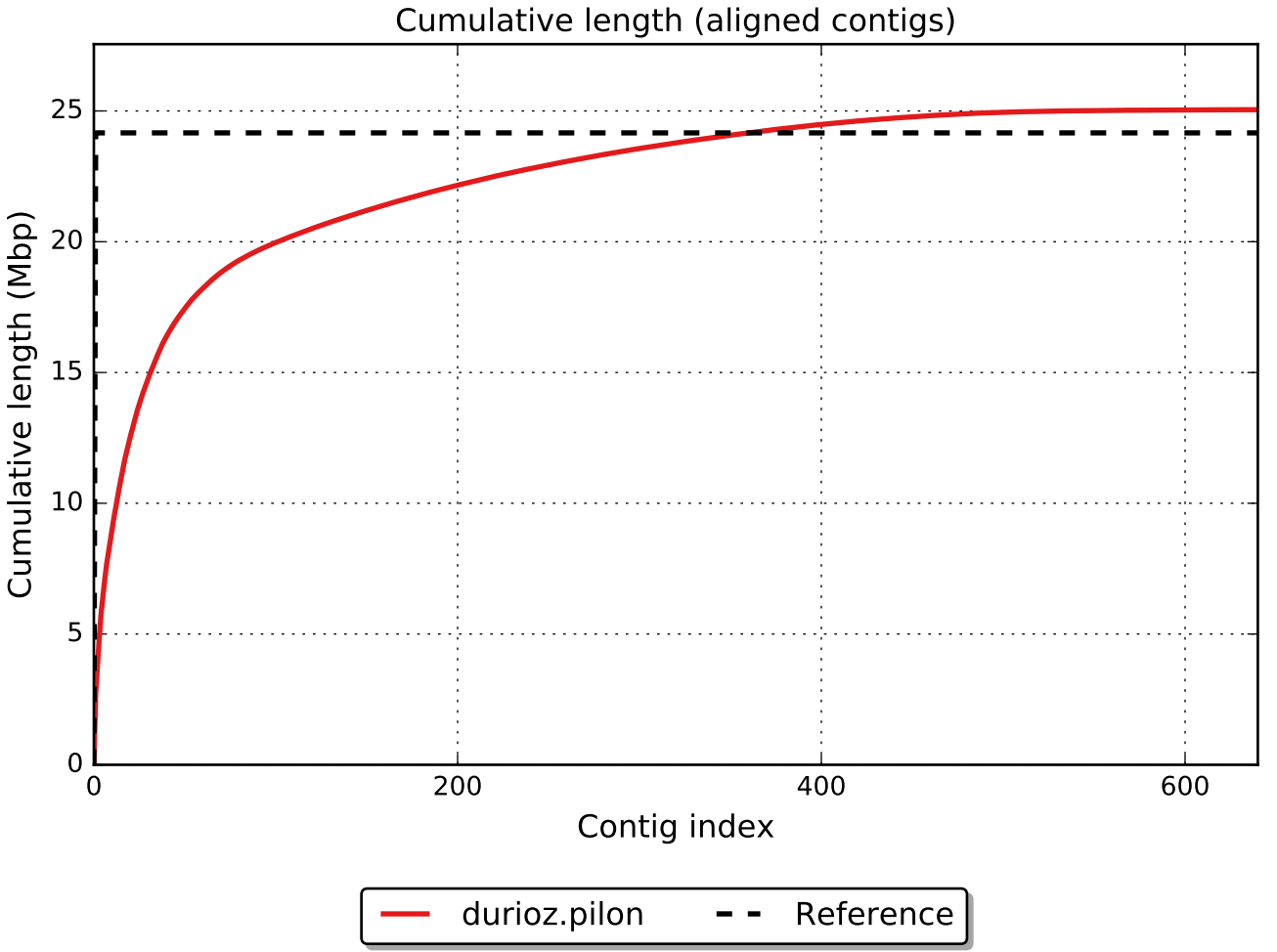

Cumulative length
Cumulative length (Mbp)
30
24
18
12
6
0
0
200
400
600
Contig index
durioz.pilon
Reference

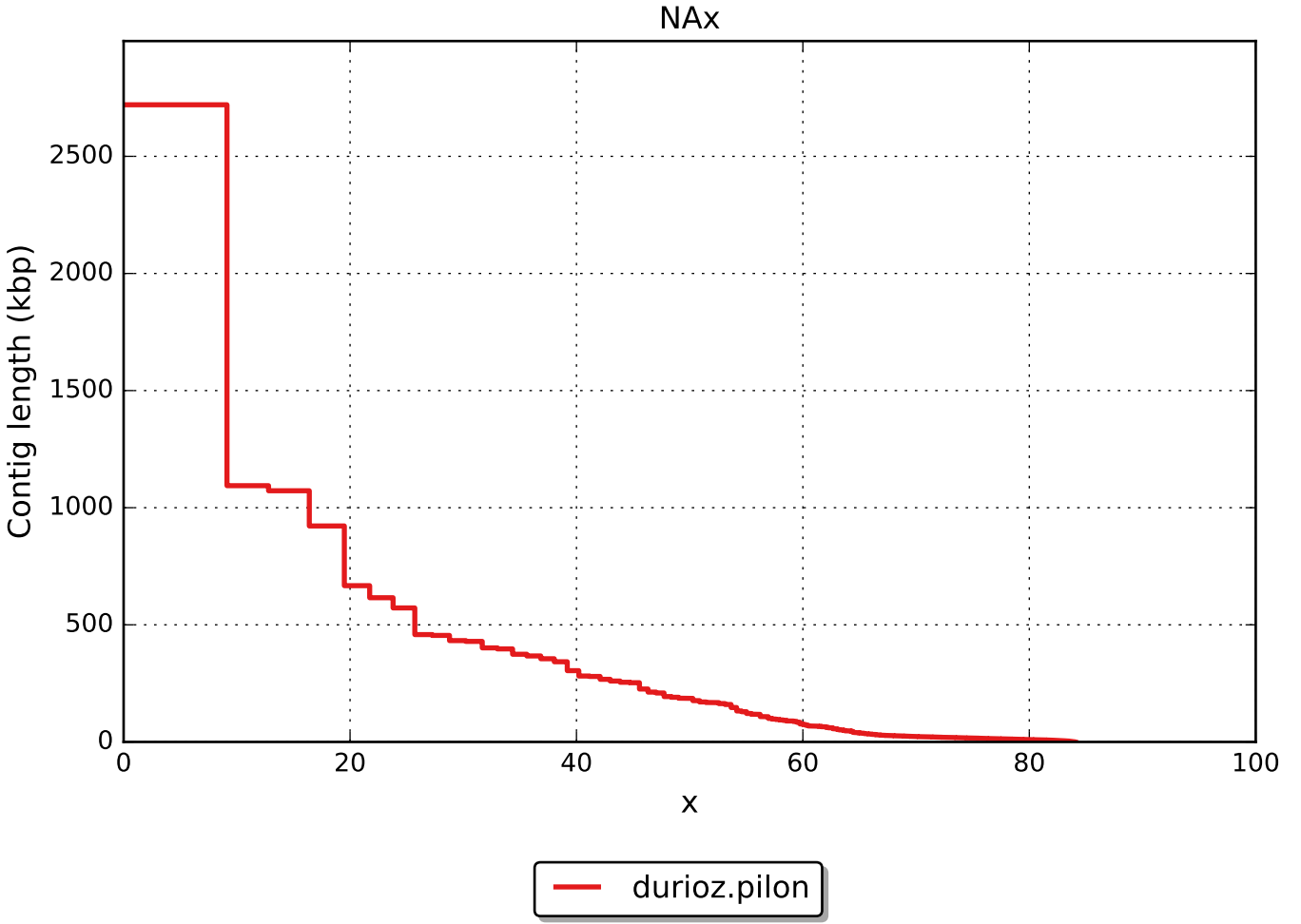

GC content
windows
GC (%)
0
3000
6000
9000
12000
0
20
40
60
80
100
durioz.pilon
Reference

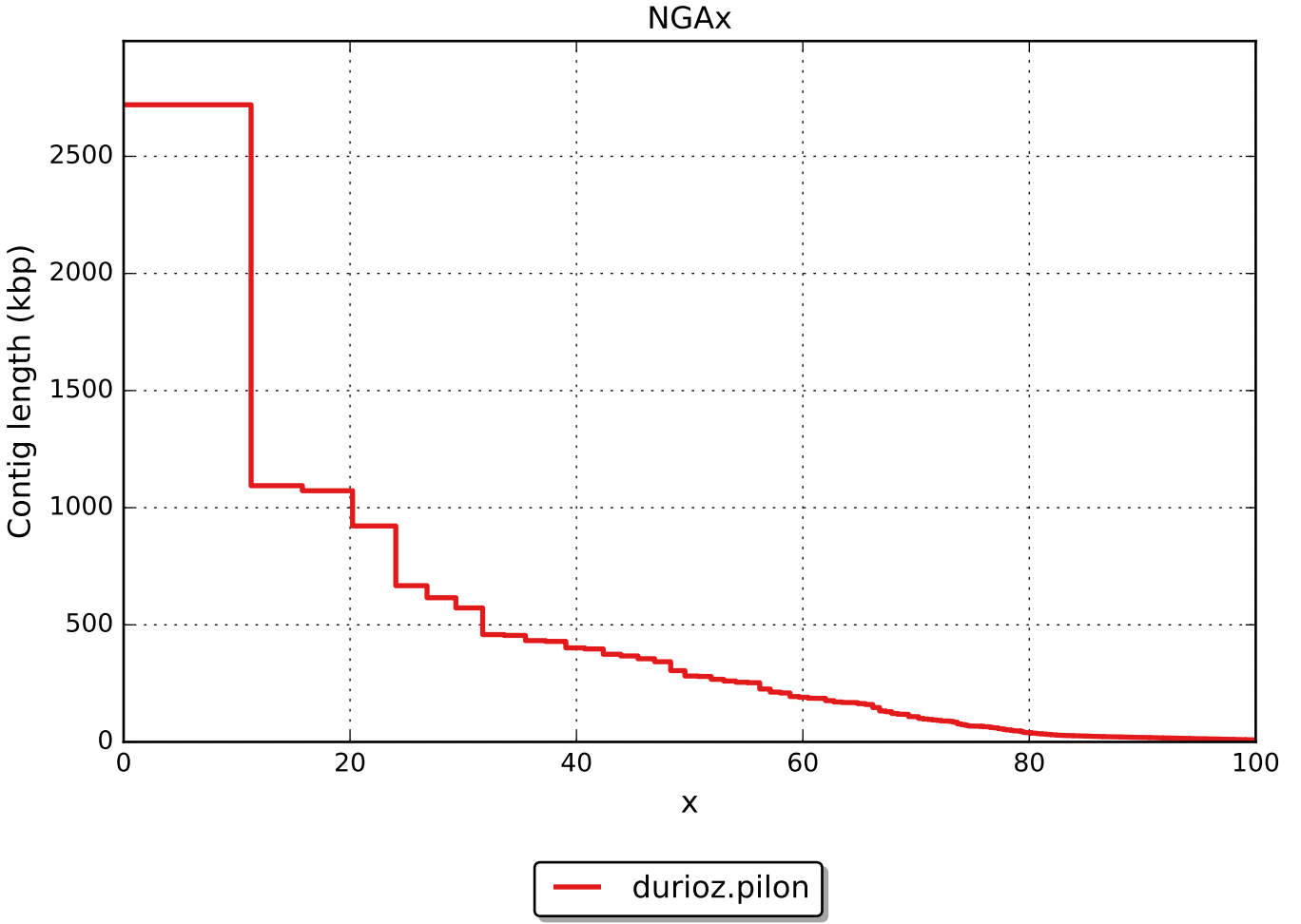

durioz.pilon GC content
300
240
180
120
60
0
contigs
0
20
40
60
80
100
GC (%)
durioz.pilon


Misassemblies
160
120
80
40
0
durioz.pilon
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
30
60
90
120
150
Feature space
durioz.pilon


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
5
10
15
20
25
0
200
400
600
Contig index
durioz.pilon
Reference


NAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
durioz.pilon


NGAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
durioz.pilon