Report

	Durio_zibe_PilonPolished
# contigs (>= 0 bp)	655
# contigs (>= 1000 bp)	655
# contigs (>= 5000 bp)	634
# contigs (>= 10000 bp)	497
# contigs (>= 25000 bp)	157
# contigs (>= 50000 bp)	81
Total length (>= 0 bp)	31333134
Total length (>= 1000 bp)	31333134
Total length (>= 5000 bp)	31270716
Total length (>= 10000 bp)	30154949
Total length (>= 25000 bp)	24695717
Total length (>= 50000 bp)	22084286
# contigs	655
Largest contig	2182778
Total length	31333134
Reference length	23775123
GC (%)	31.05
Reference GC (%)	30.18
N50	287196
NG50	412228
N75	33670
NG75	162939
L50	26
LG50	15
L75	116
LG75	36
# misassemblies	171
# misassembled contigs	102
Misassembled contigs length	15257209
# local misassemblies	233
# unaligned mis. contigs	7
# unaligned contigs	286 + 186 part
Unaligned length	5731771
Genome fraction (%)	94.671
Duplication ratio	1.137
# N's per 100 kbp	0.00
# mismatches per 100 kbp	305.20
# indels per 100 kbp	133.12
Largest alignment	2007280
Total aligned length	25587050
NA50	125398
NGA50	265789
NA75	16179
NGA75	96962
LA50	46
LGA50	25
LA75	225
LGA75	65

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

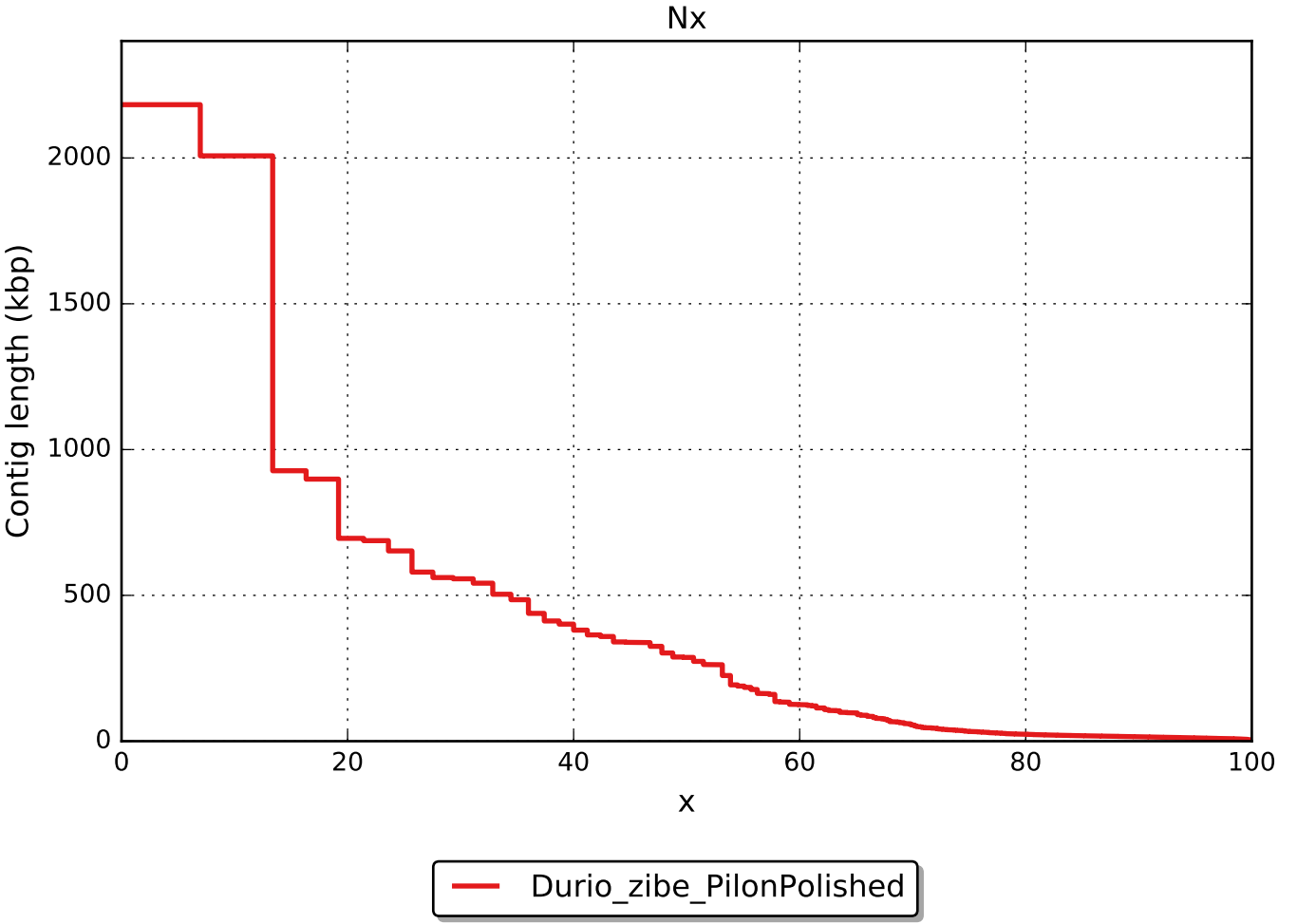
	Durio_zibe_PilonPolished
# misassemblies	171
# relocations	170
# translocations	0
# inversions	1
# misassembled contigs	102
Misassembled contigs length	15257209
# local misassemblies	233
# unaligned mis. contigs	7
# mismatches	68694
# indels	29964
# indels (<= 5 bp)	28198
# indels (> 5 bp)	1766
Indels length	61728

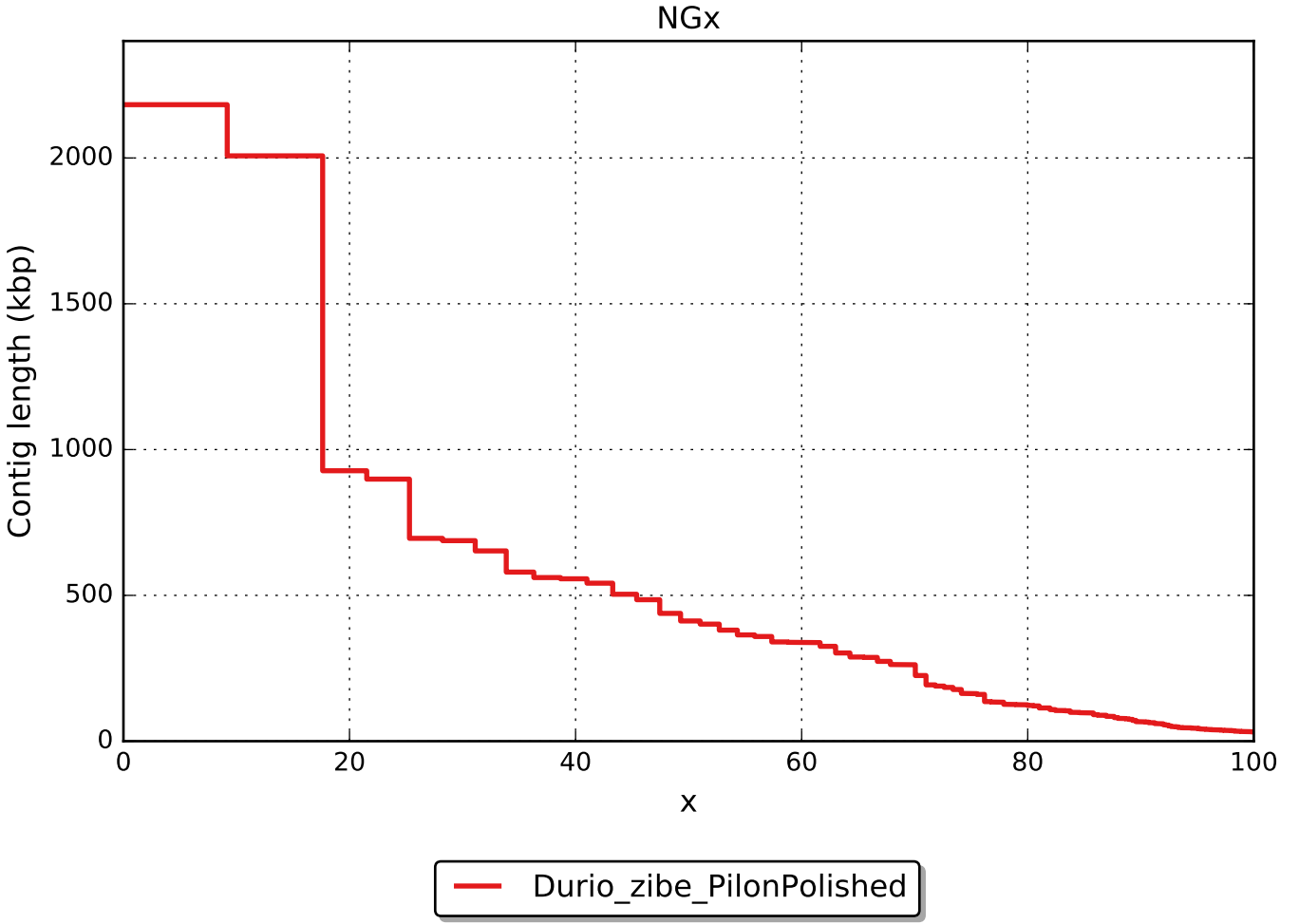
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

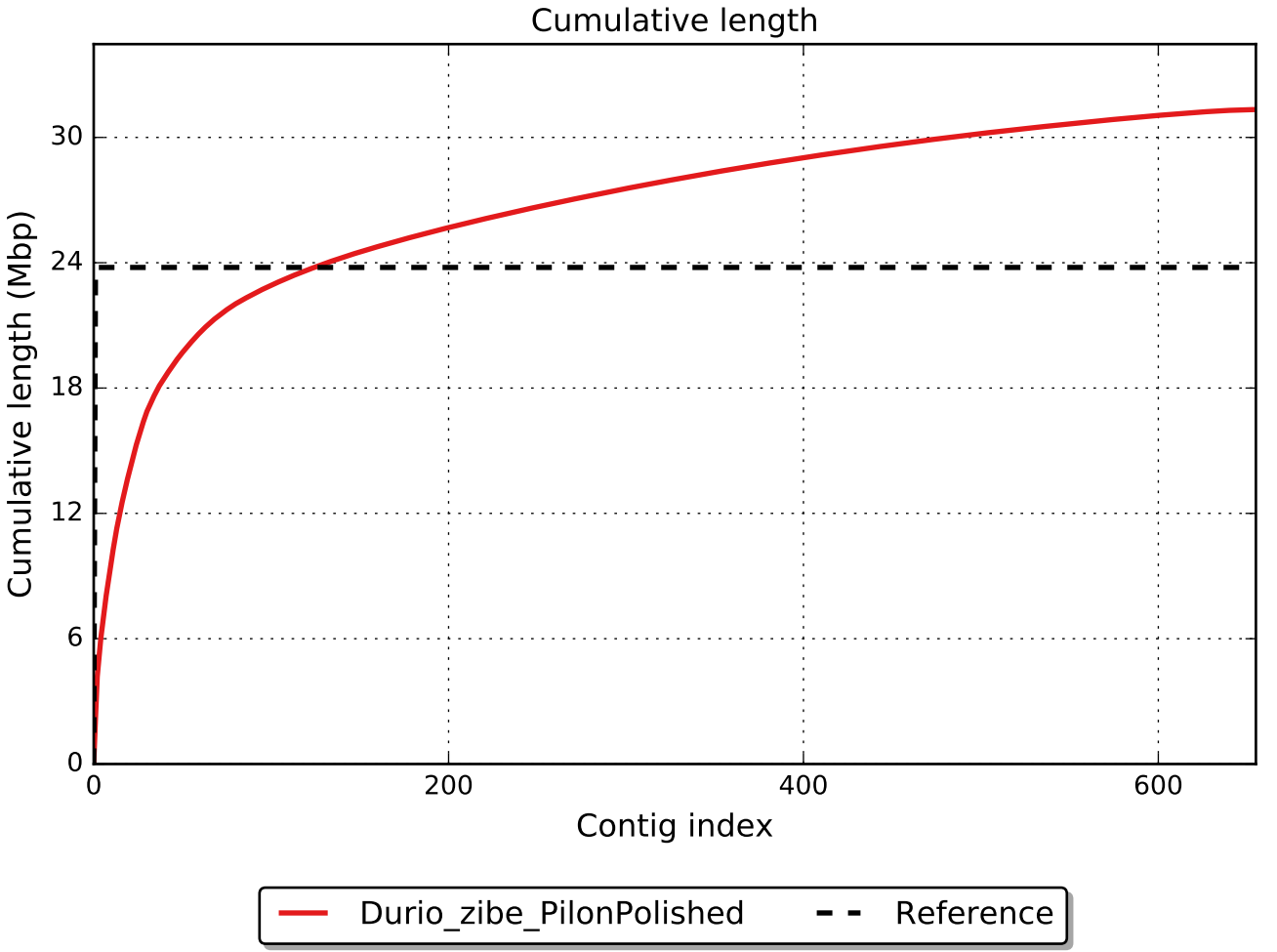
Unaligned report

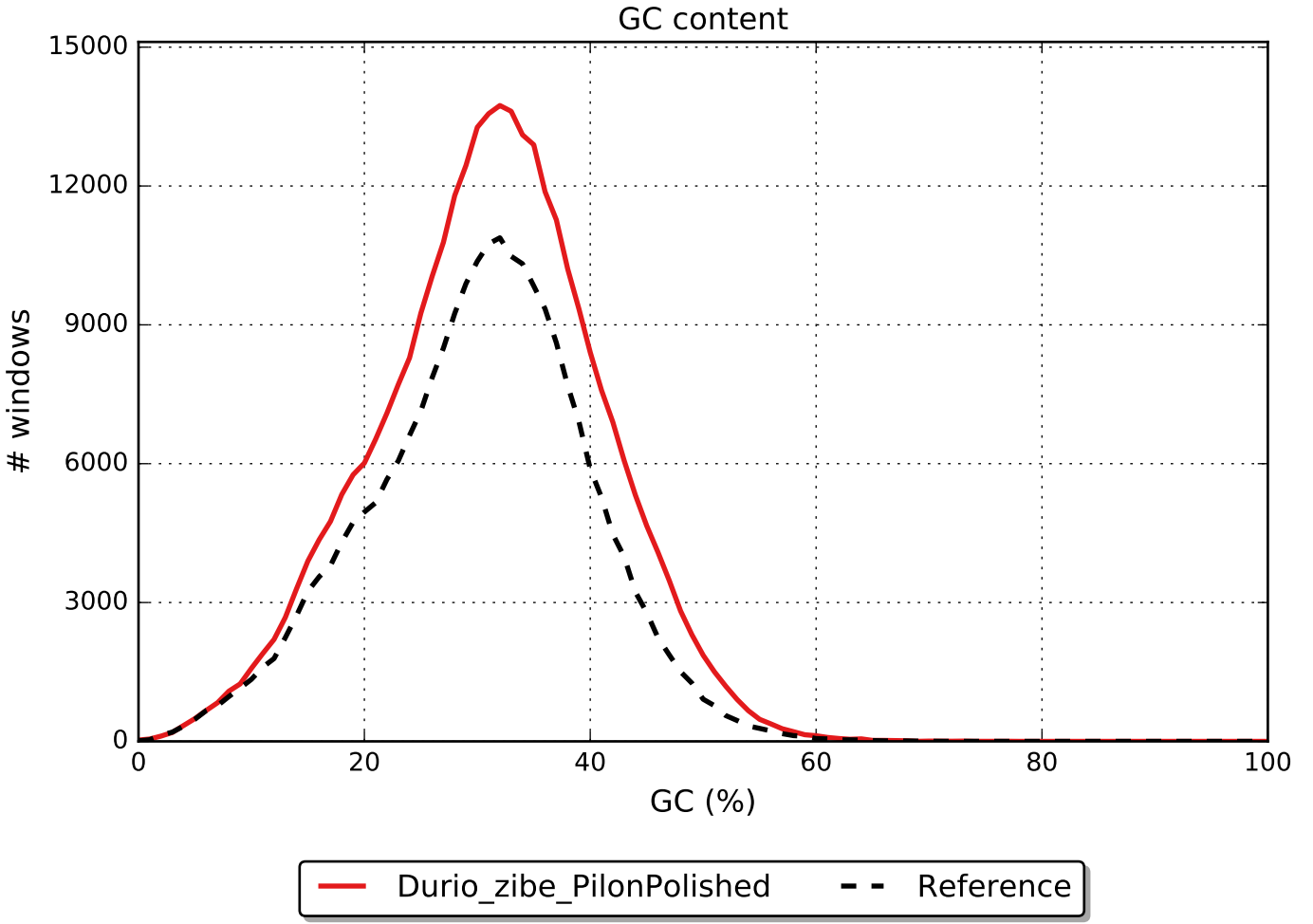
	Durio_zibe_PilonPolished
# fully unaligned contigs	286
Fully unaligned length	3883912
# partially unaligned contigs	186
Partially unaligned length	1847859
# N's	0

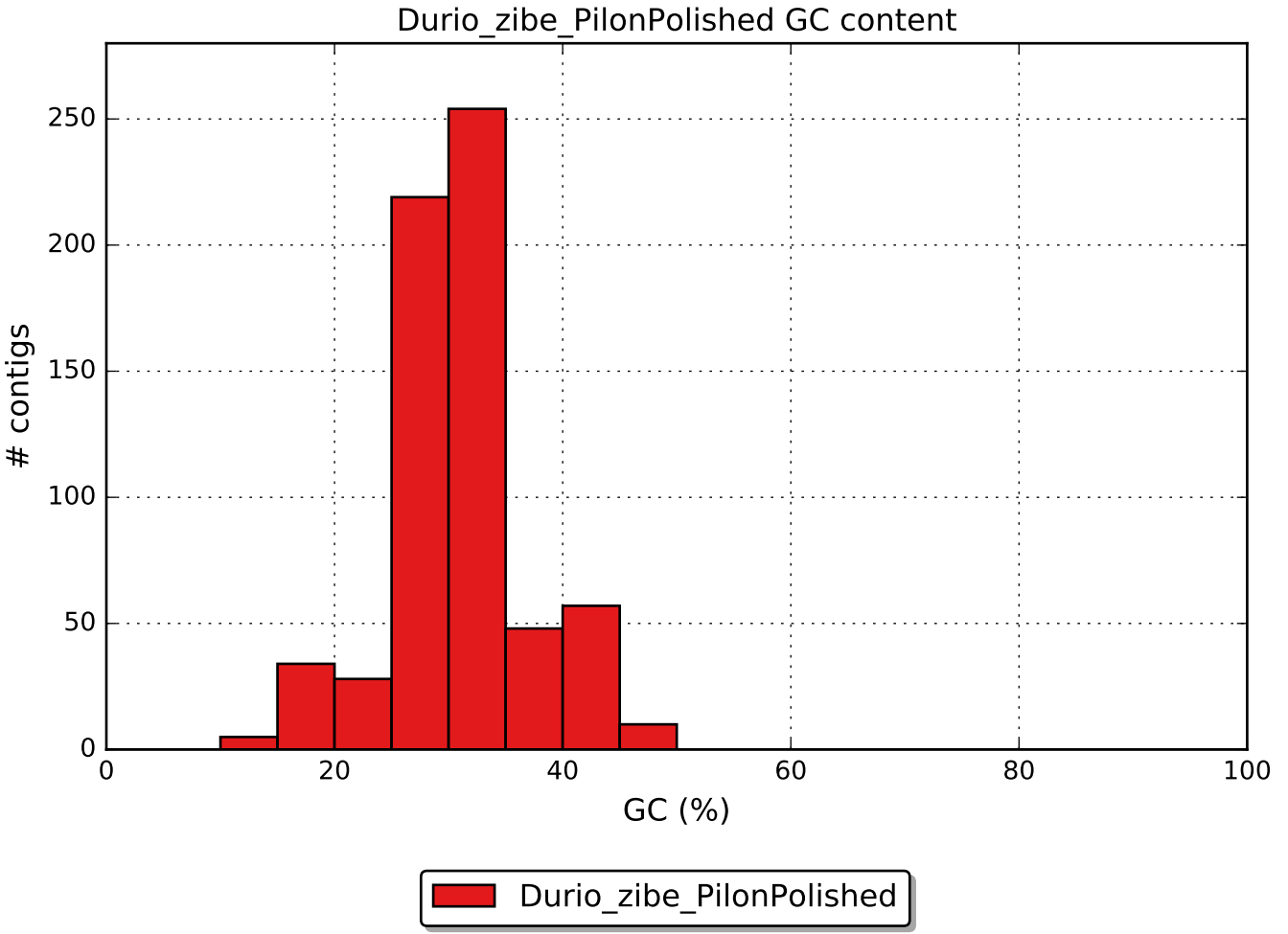
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

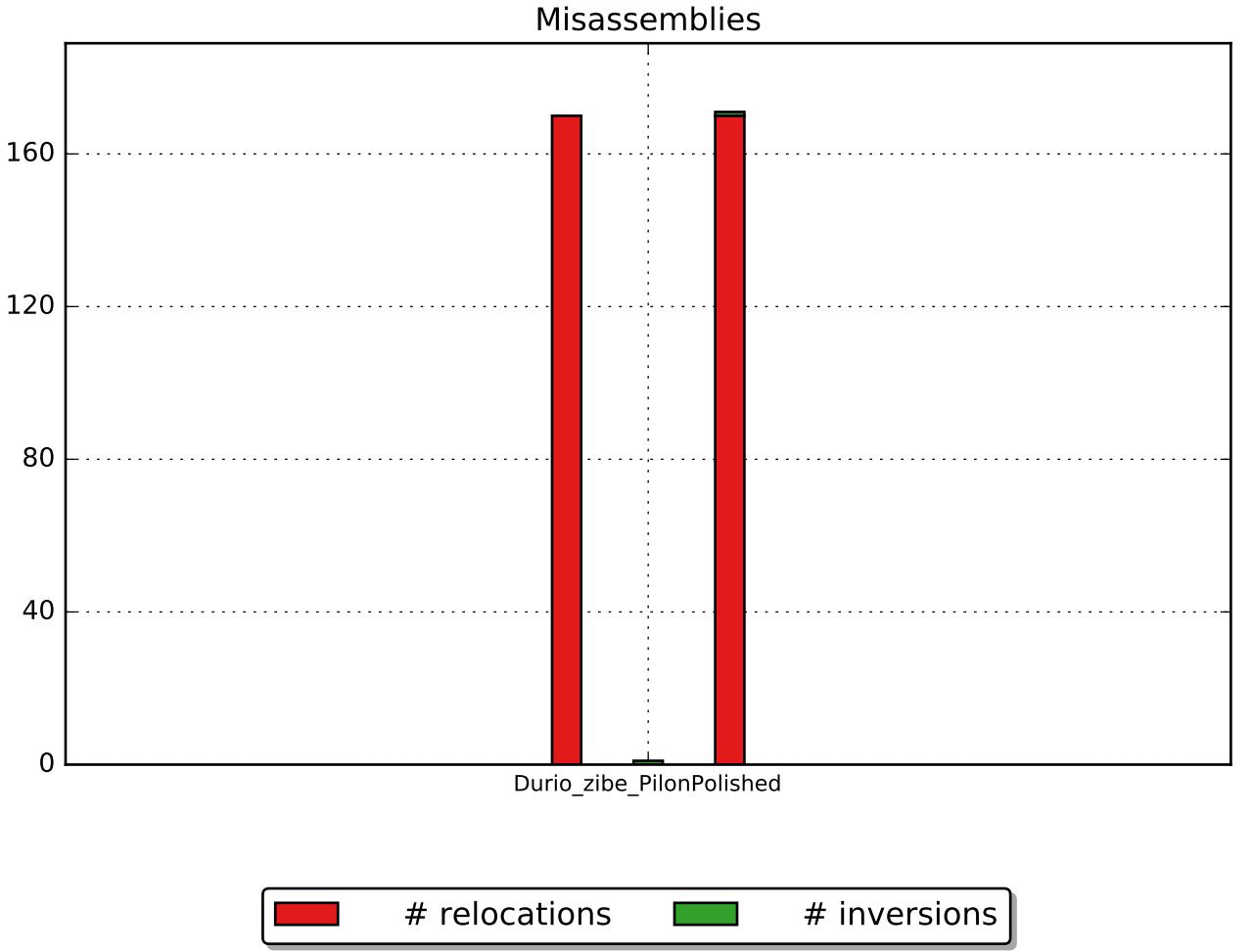

Nx
Contig length (kbp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
Durio_zibe_PilonPolished

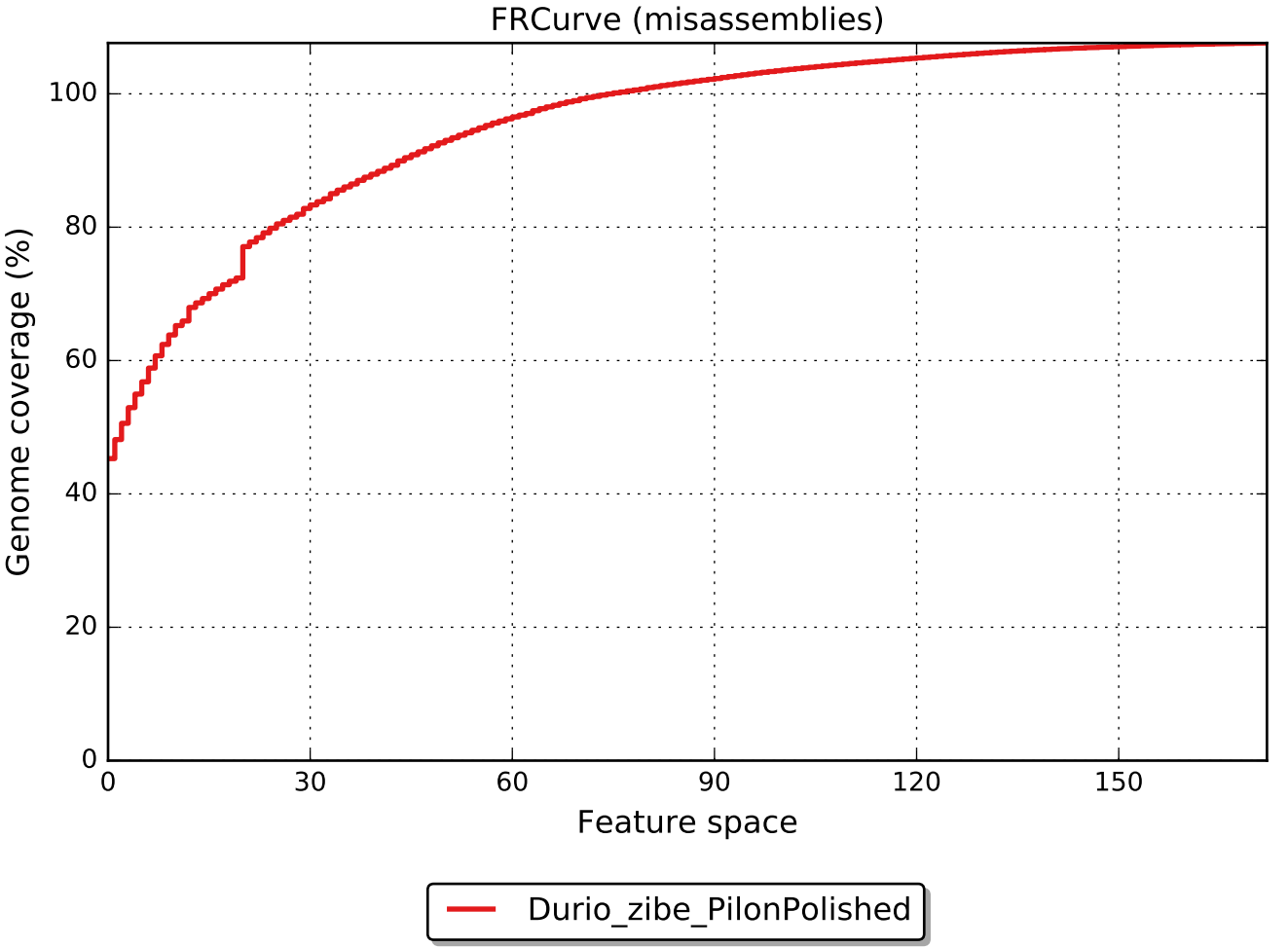

NGx
Contig length (kbp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
Durio_zibe_PilonPolished

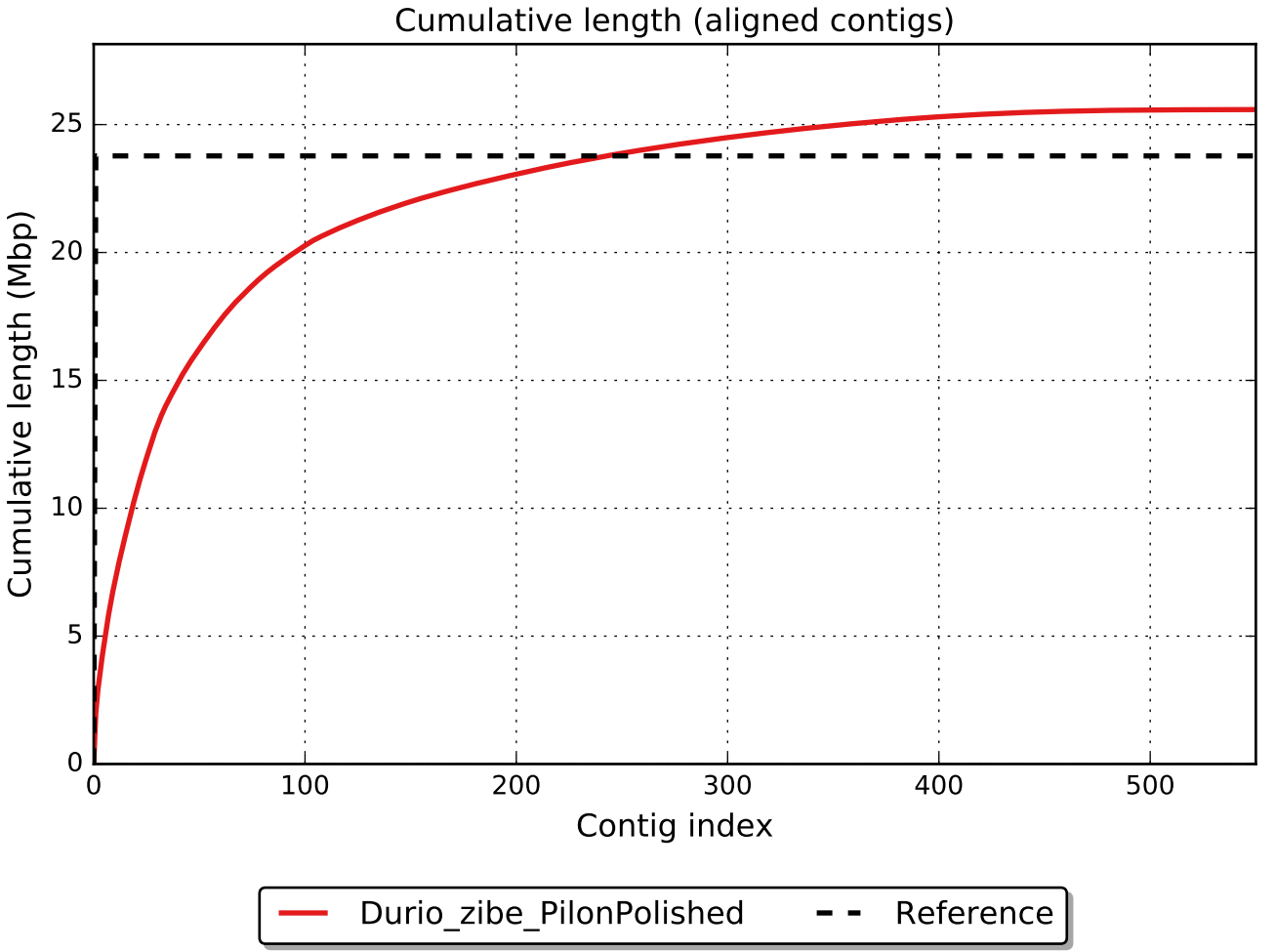

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
200
400
600
Contig index
Durio_zibe_PilonPolished
Reference

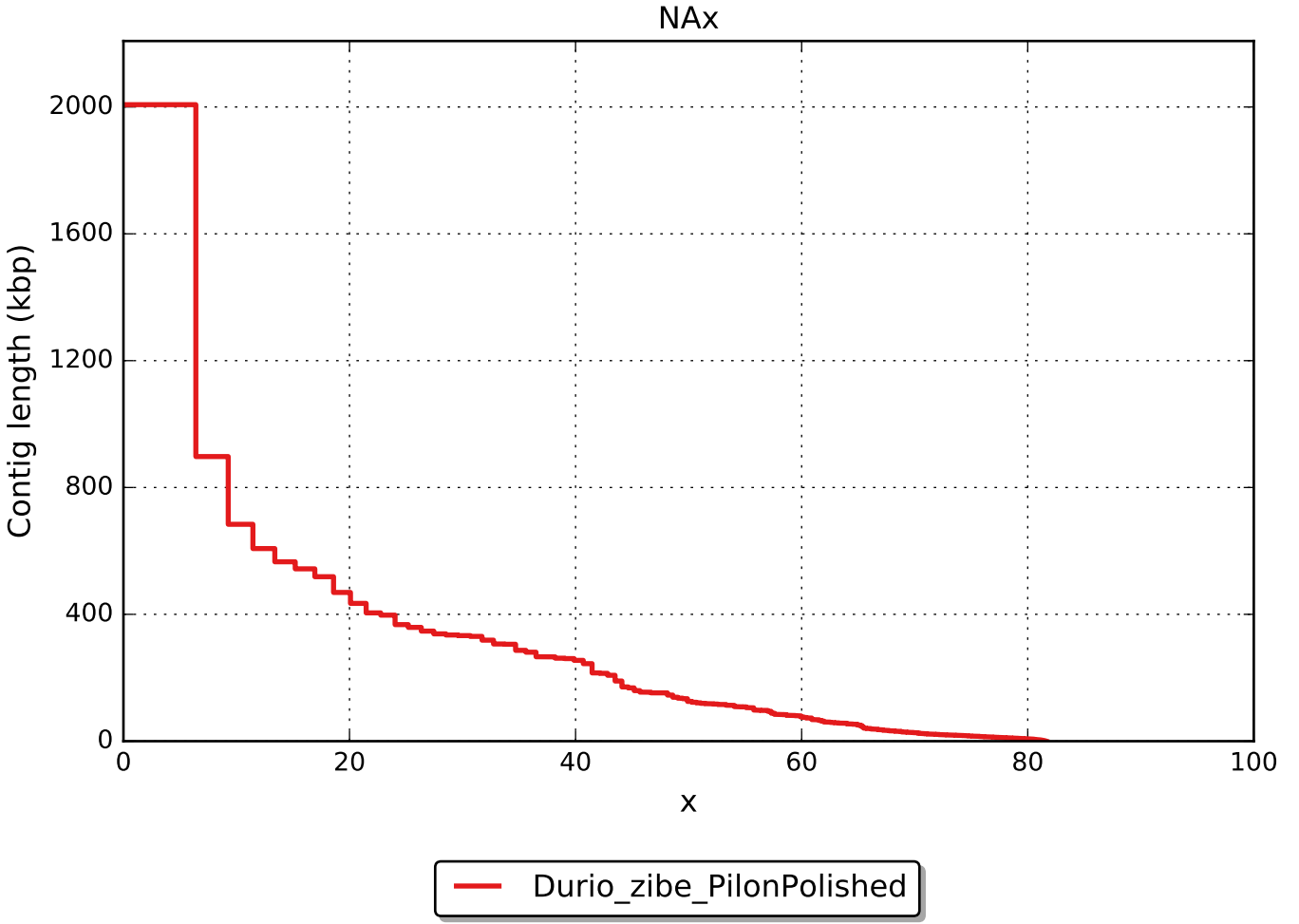

GC content
15000
12000
9000
6000
3000
0
windows
0
20
40
60
80
100
GC (%)
Durio_zibe_PilonPolished
Reference

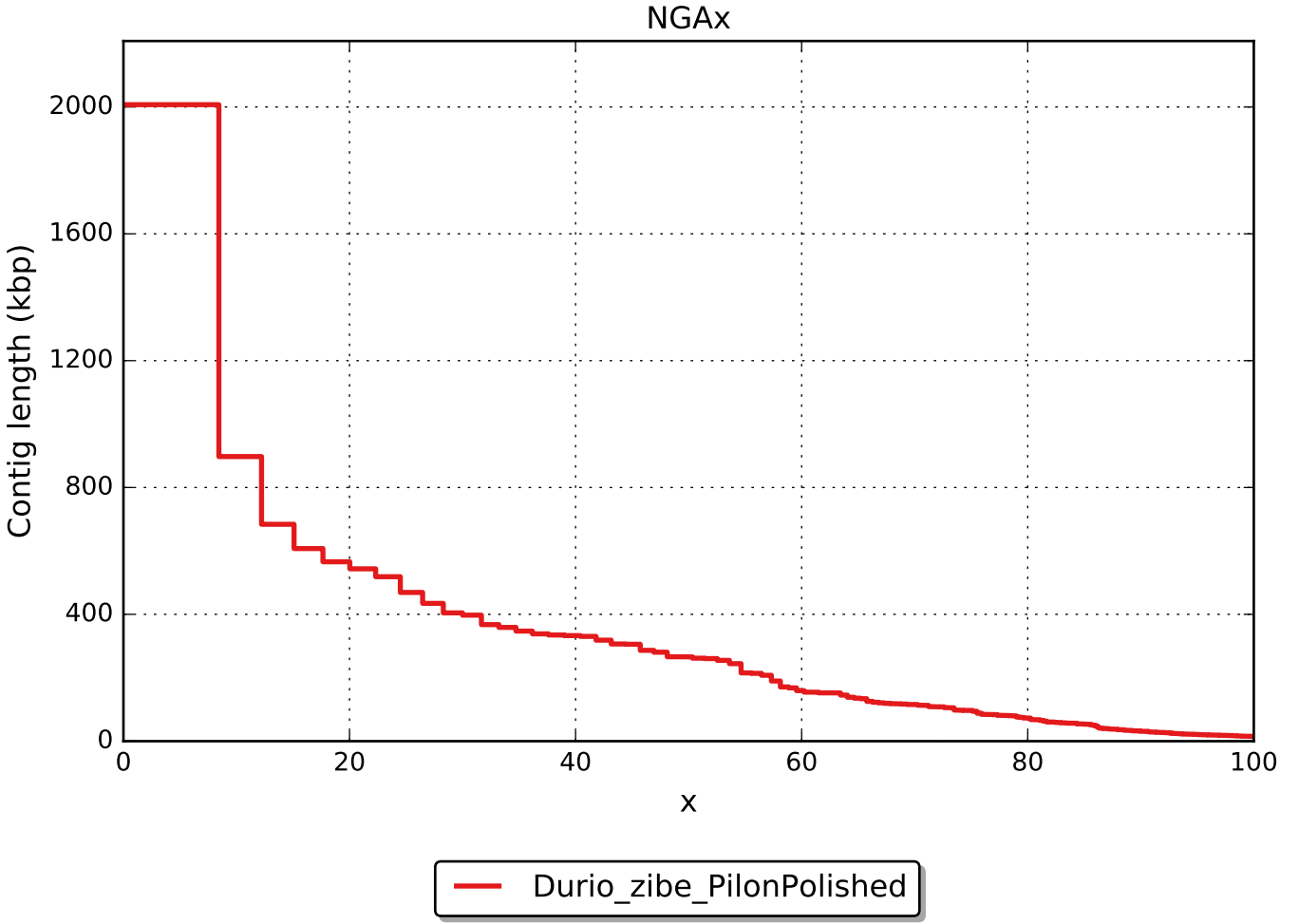

Durio_zibe_PilonPolished GC content
contigs
GC (%)
0
50
100
150
200
250
0
20
40
60
80
100
Durio_zibe_PilonPolished


Misassemblies
160
120
80
40
0
Durio_zibe_PilonPolished
relocations
inversions


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
5
10
15
20
25
0
100
200
300
400
500
Contig index
Durio_zibe_PilonPolished
Reference


NAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
Durio_zibe_PilonPolished


NGAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
Durio_zibe_PilonPolished