Report

	pilon_output_canu_nano
# contigs (>= 0 bp)	10
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3166347
Total length (>= 1000 bp)	3166347
Total length (>= 5000 bp)	3166347
Total length (>= 10000 bp)	3147255
Total length (>= 25000 bp)	3101136
Total length (>= 50000 bp)	2987086
# contigs	10
Largest contig	2775725
Total length	3166347
Reference length	3052572
GC (%)	37.73
Reference GC (%)	37.87
N50	2775725
NG50	2775725
N75	2775725
NG75	2775725
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	159
# misassembled contigs	6
Misassembled contigs length	3043001
# local misassemblies	19
# unaligned mis. contigs	3
# unaligned contigs	1 + 7 part
Unaligned length	368648
Genome fraction (%)	87.353
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	172.51
# indels per 100 kbp	13.65
Largest alignment	209807
Total aligned length	2797360
NA50	107749
NGA50	109975
NA75	15950
NGA75	22829
LA50	11
LGA50	10
LA75	33
LGA75	28

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

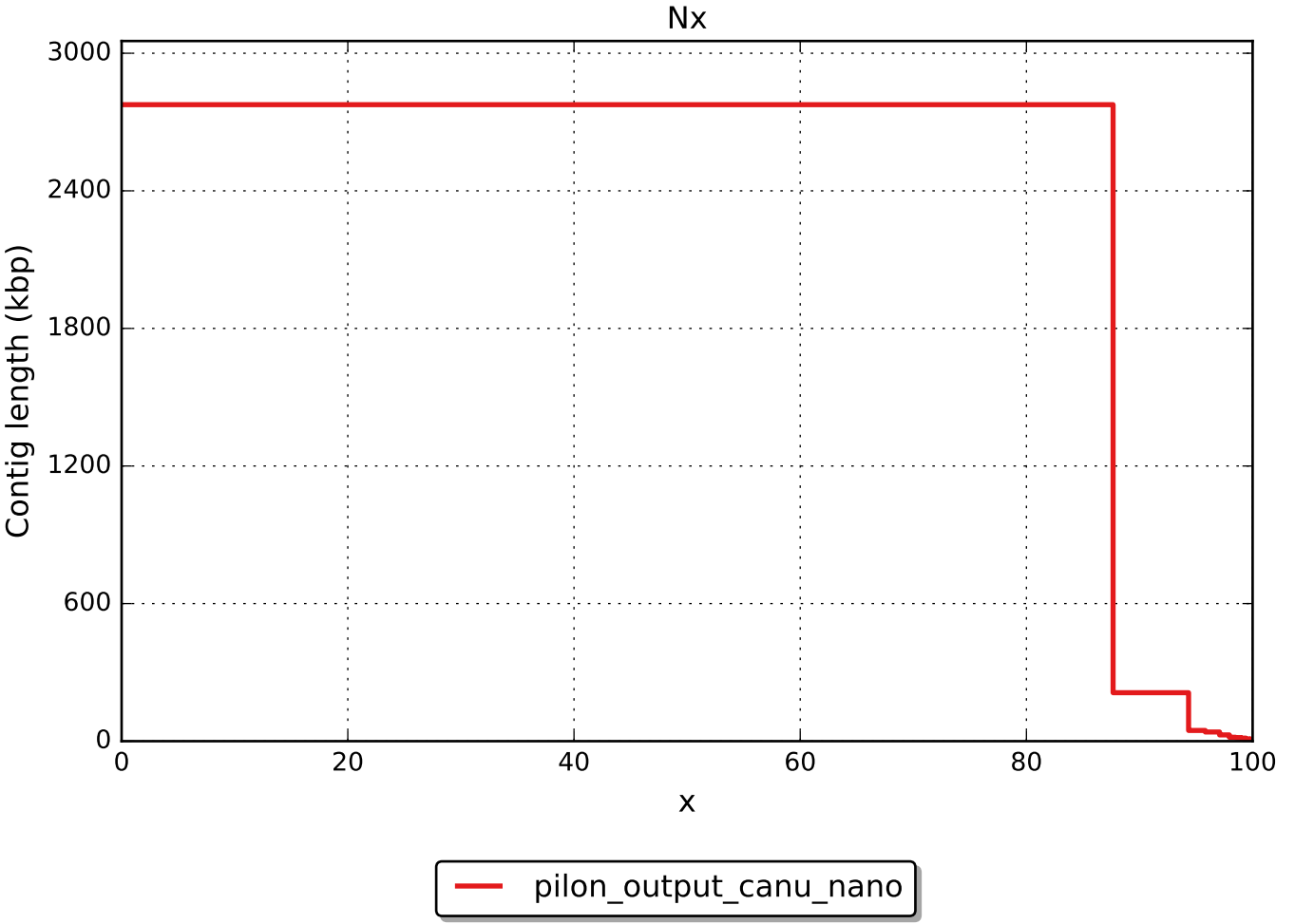
	pilon_output_canu_nano
# misassemblies	159
# relocations	101
# translocations	58
# inversions	0
# misassembled contigs	6
Misassembled contigs length	3043001
# local misassemblies	19
# unaligned mis. contigs	3
# mismatches	4600
# indels	364
# indels (<= 5 bp)	348
# indels (> 5 bp)	16
Indels length	785

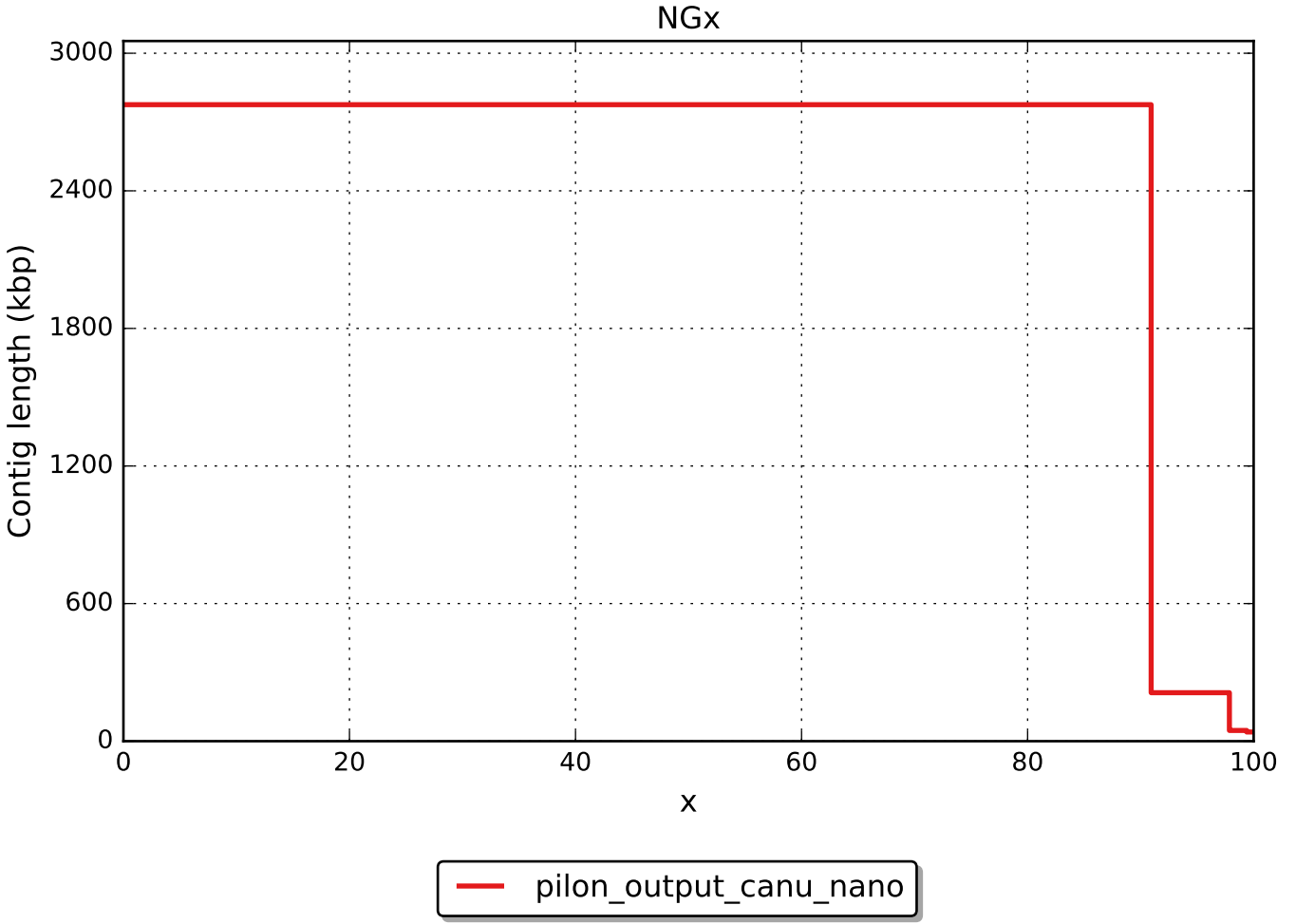
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

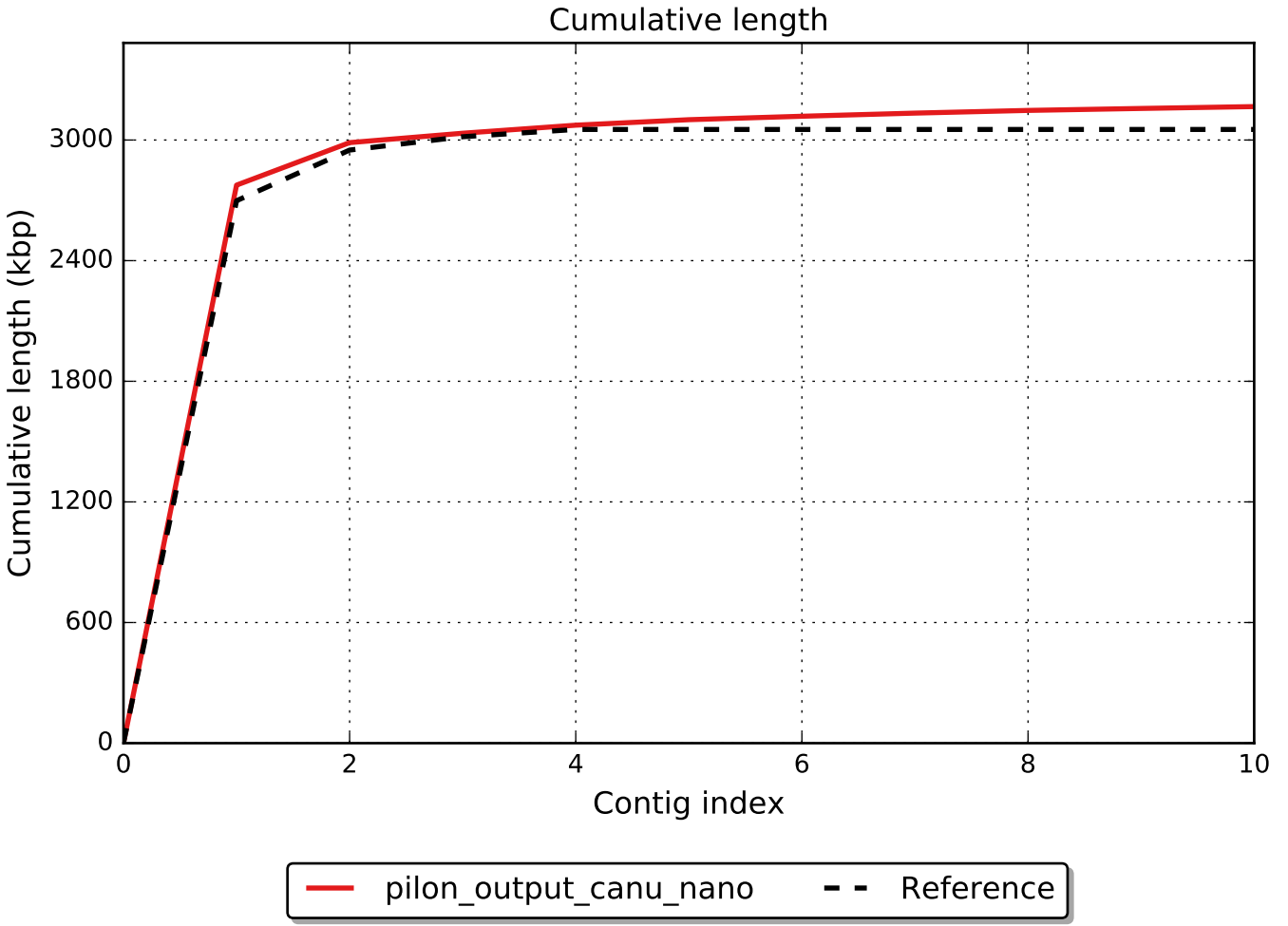
Unaligned report

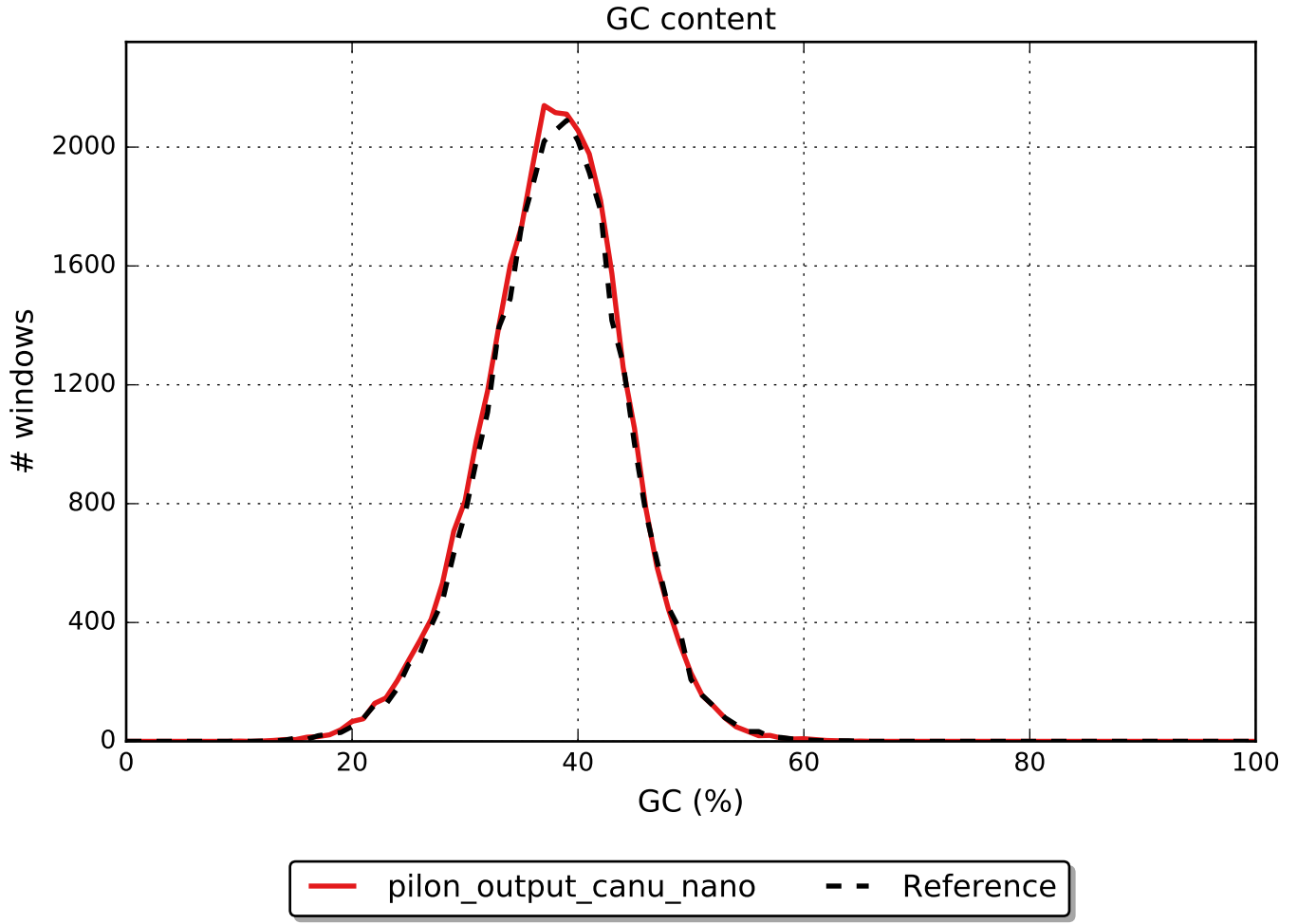
	pilon_output_canu_nano
# fully unaligned contigs	1
Fully unaligned length	9296
# partially unaligned contigs	7
Partially unaligned length	359352
# N's	0

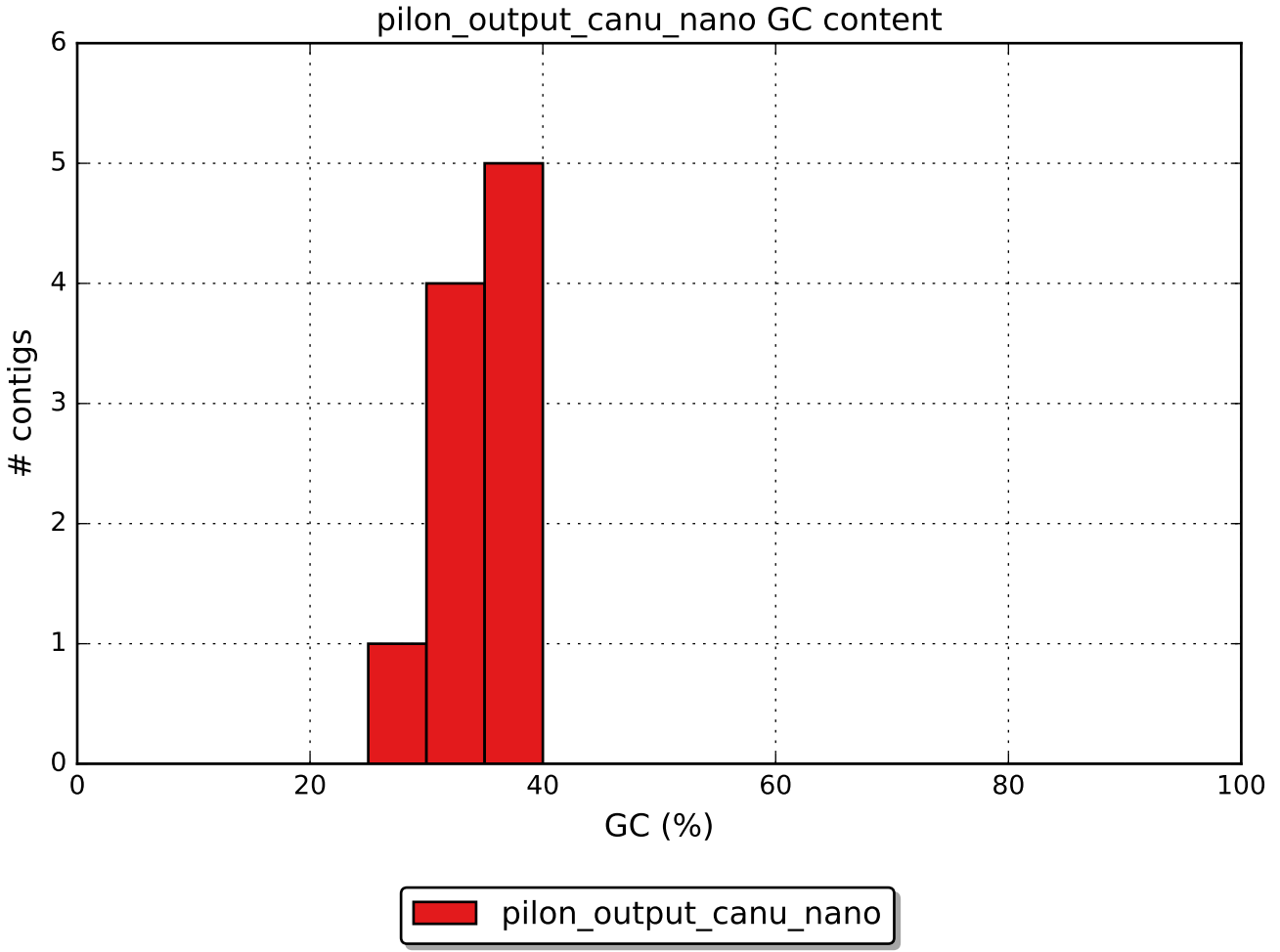
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

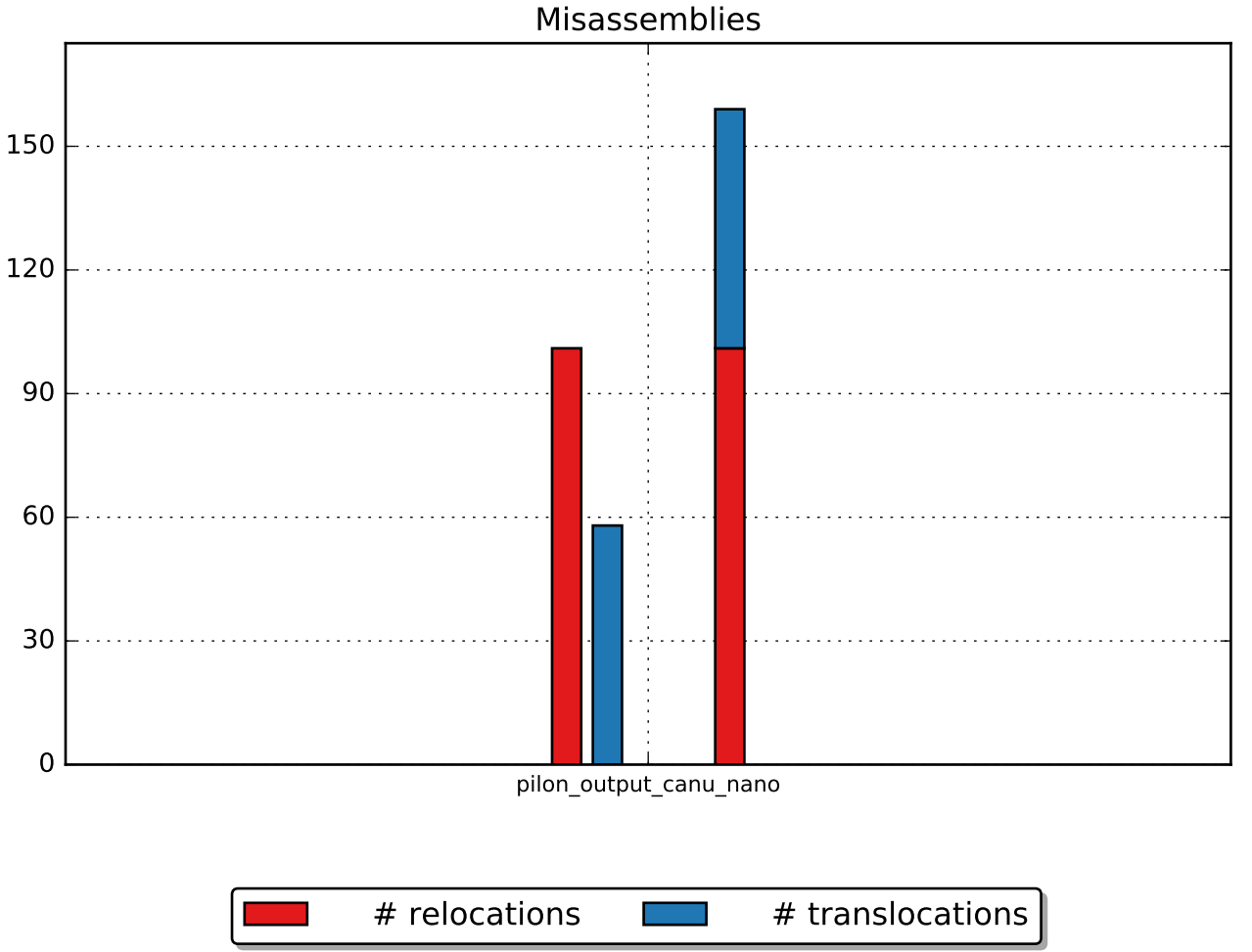

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
pilon_output_canu_nano

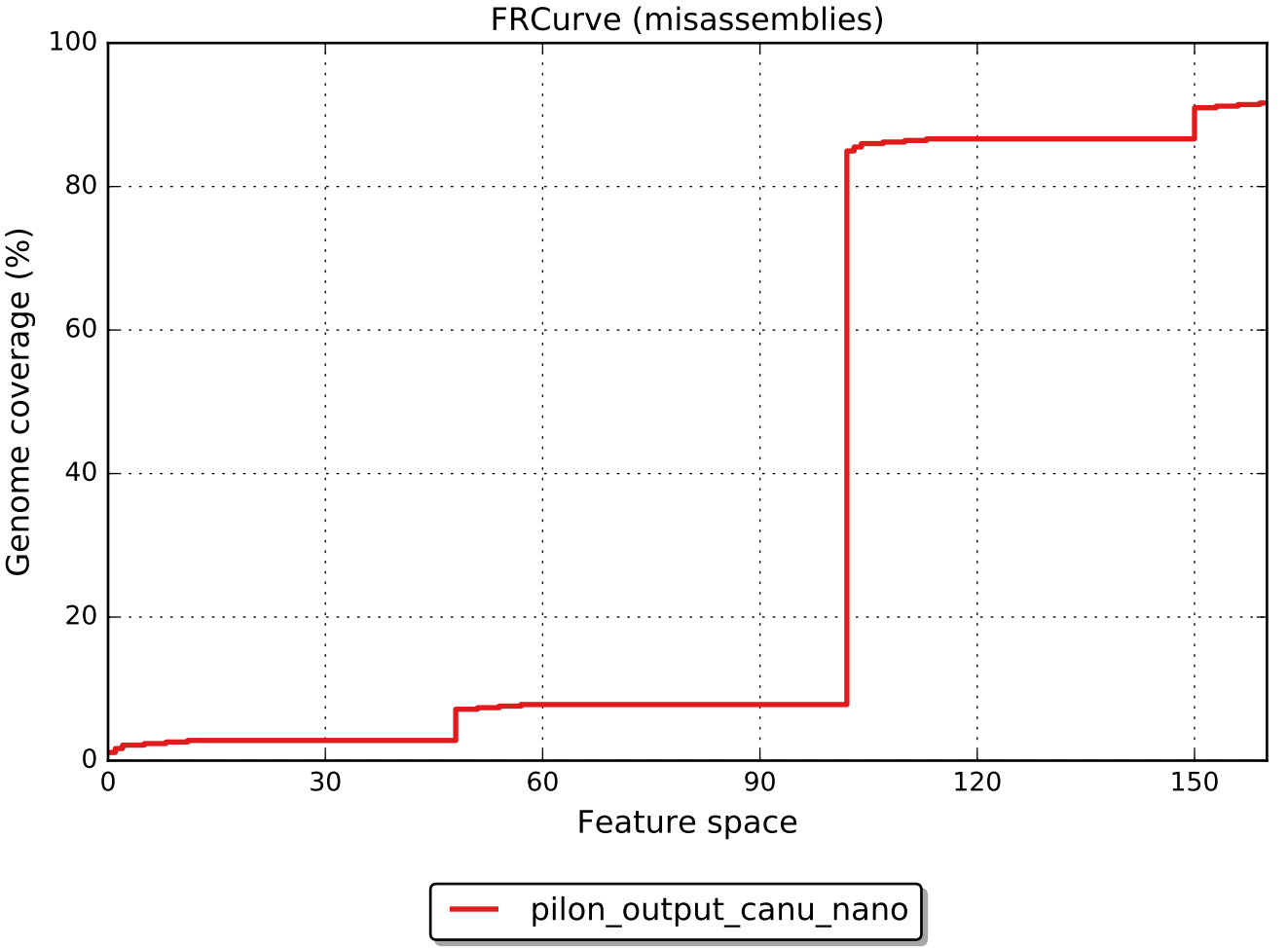

NGx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
pilon_output_canu_nano

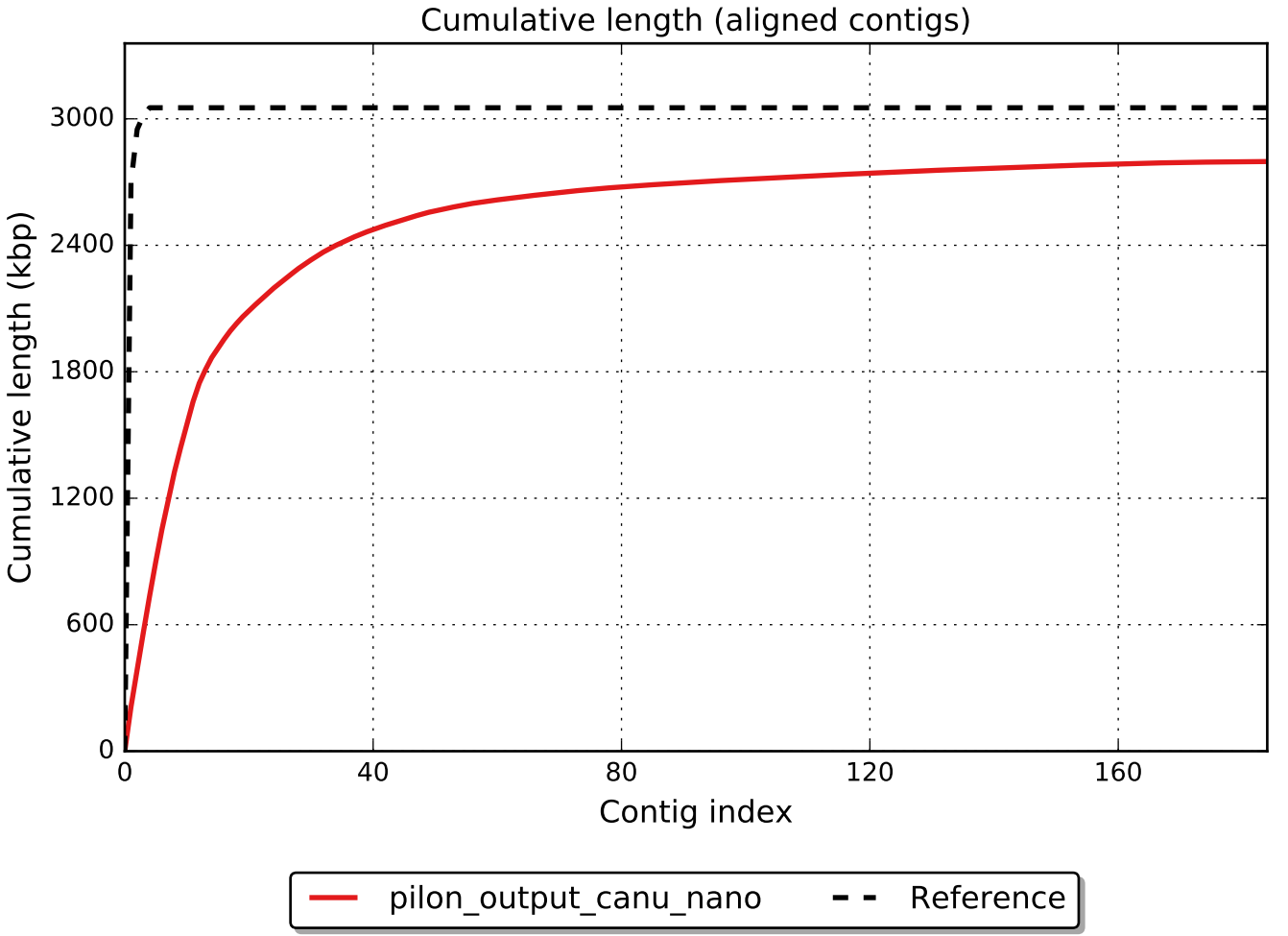

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
10
Contig index
pilon_output_canu_nano
Reference

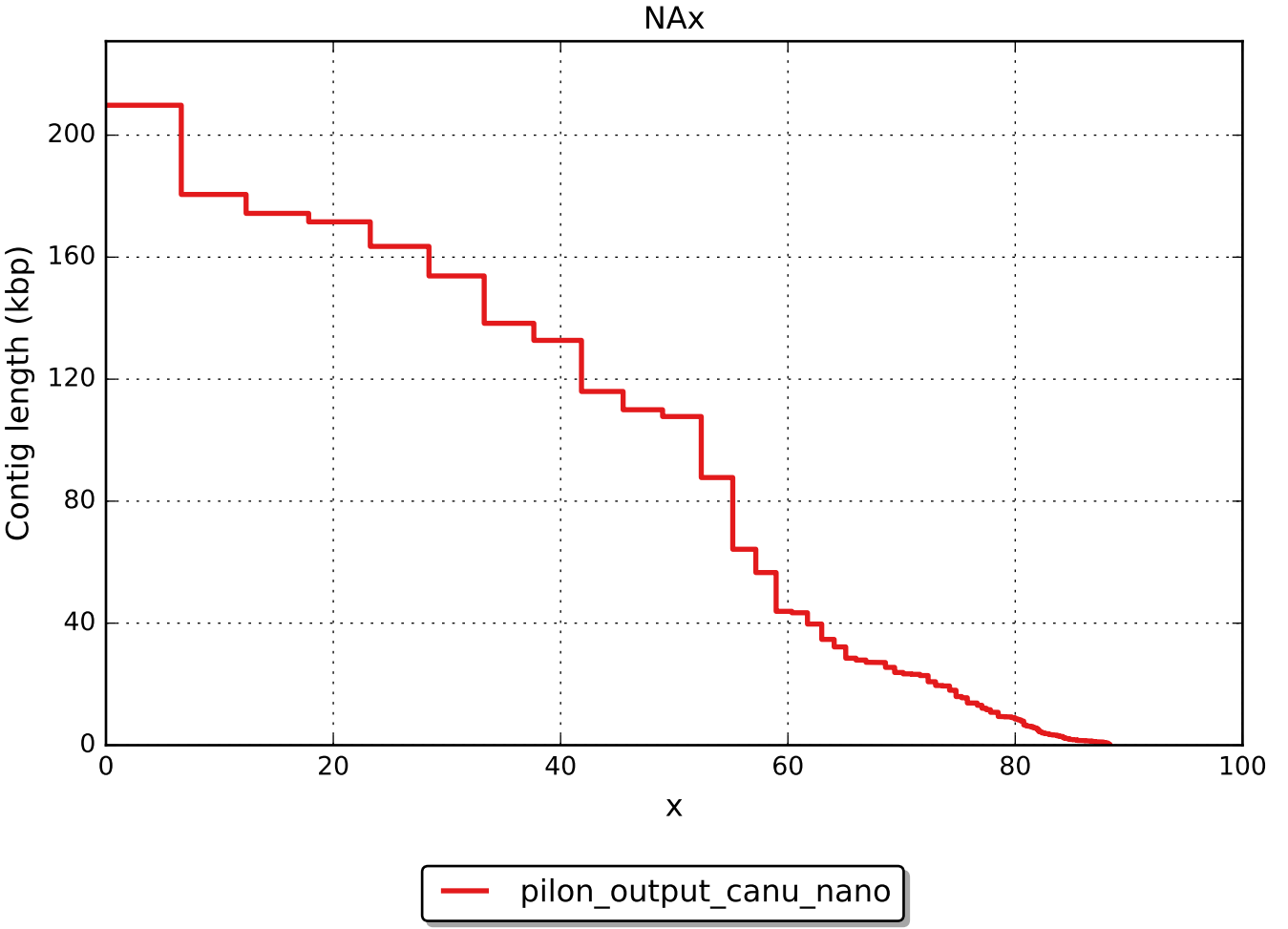

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
pilon_output_canu_nano
Reference

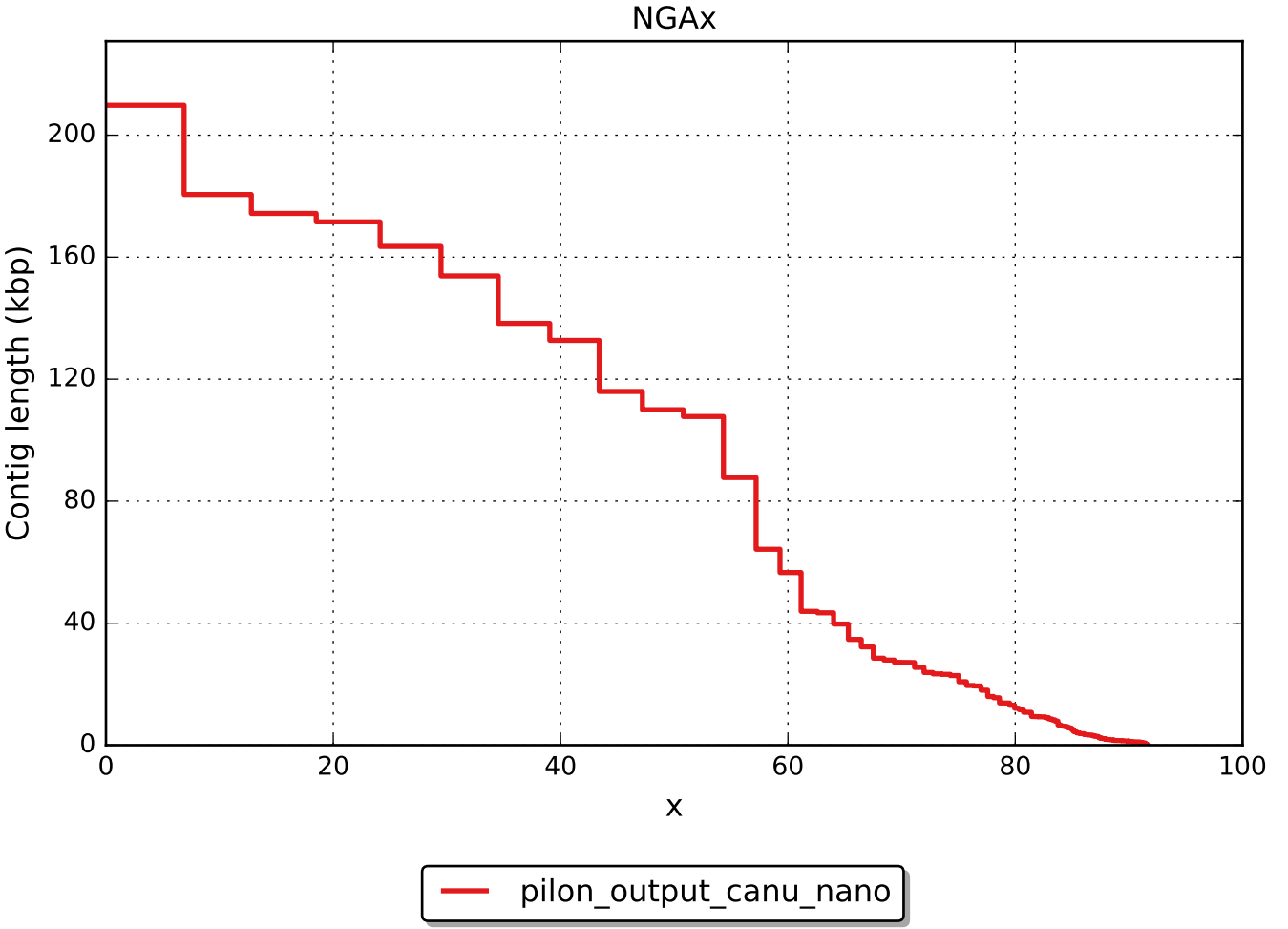

pilon_output_canu_nano GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
pilon_output_canu_nano


Misassemblies
150
120
90
60
30
0
pilon_output_canu_nano
relocations
translocations


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
40
80
120
160
Contig index
pilon_output_canu_nano
Reference


NAx
Contig length (kbp)
0
40
80
120
160
200
0
20
40
60
80
100
x
pilon_output_canu_nano


NGAx
Contig length (kbp)
0
40
80
120
160
200
0
20
40
60
80
100
x
pilon_output_canu_nano