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	3140603
GC (%)	37.73
Reference GC (%)	37.68
N50	2775725
NG50	2775725
N75	2775725
NG75	2775725
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	28
# misassembled contigs	7
Misassembled contigs length	3133856
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.422
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.45
# indels per 100 kbp	2.49
Largest alignment	840747
Total aligned length	3163756
NA50	500611
NGA50	500611
NA75	164597
NGA75	164597
LA50	3
LGA50	3
LA75	5
LGA75	5

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

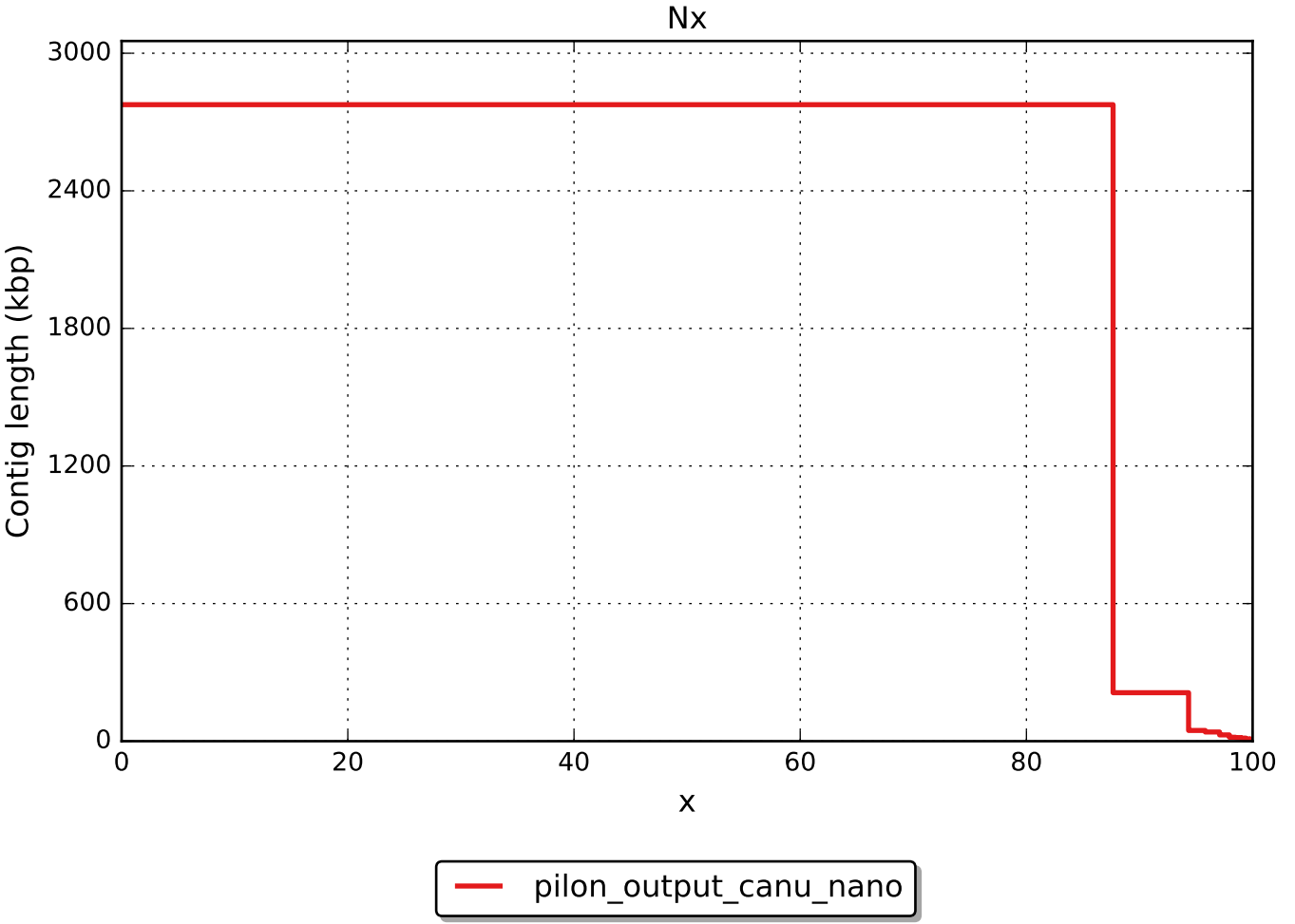
	pilon_output_canu_nano
# misassemblies	28
# relocations	7
# translocations	21
# inversions	0
# misassembled contigs	7
Misassembled contigs length	3133856
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	725
# indels	77
# indels (<= 5 bp)	73
# indels (> 5 bp)	4
Indels length	117

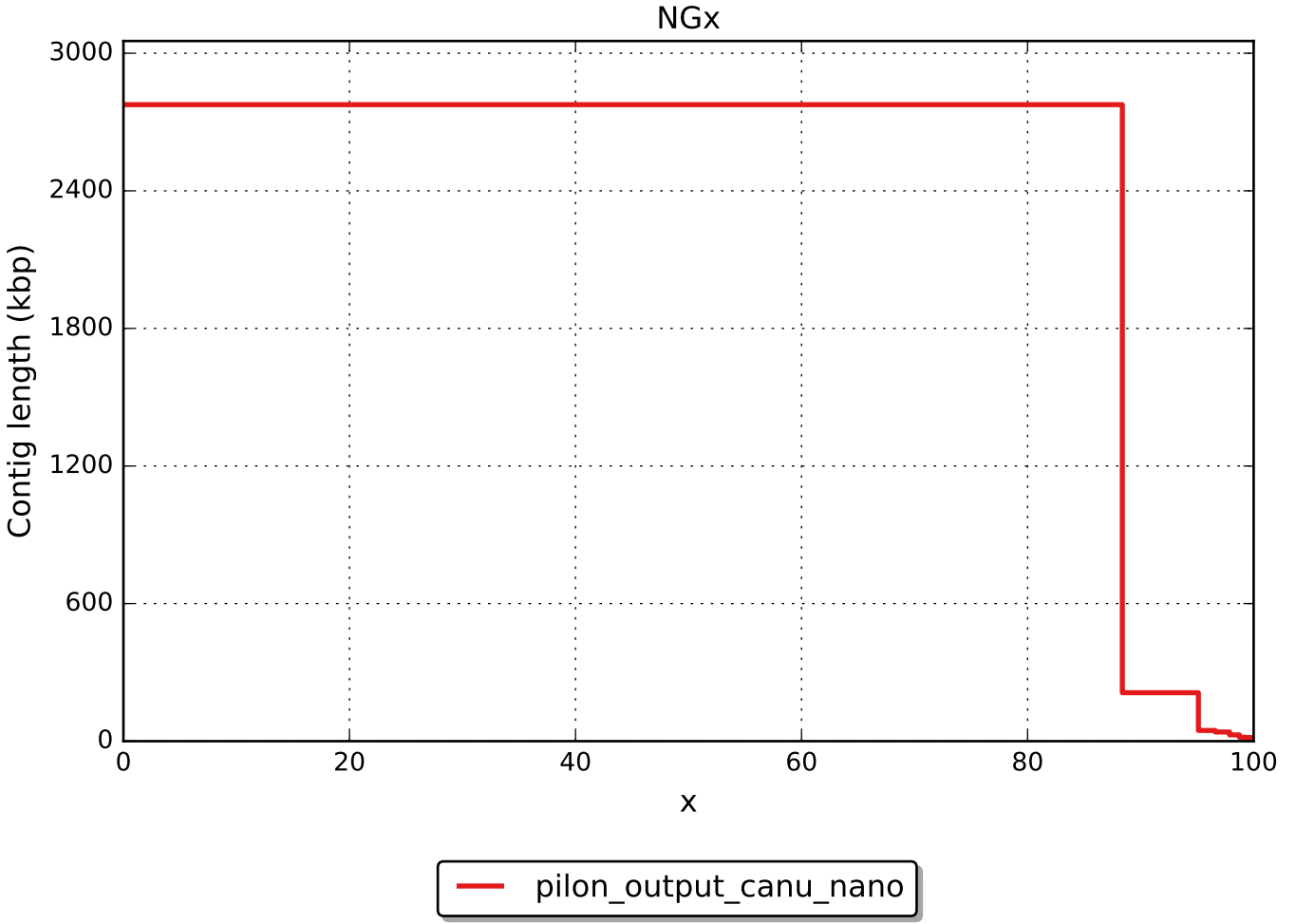
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

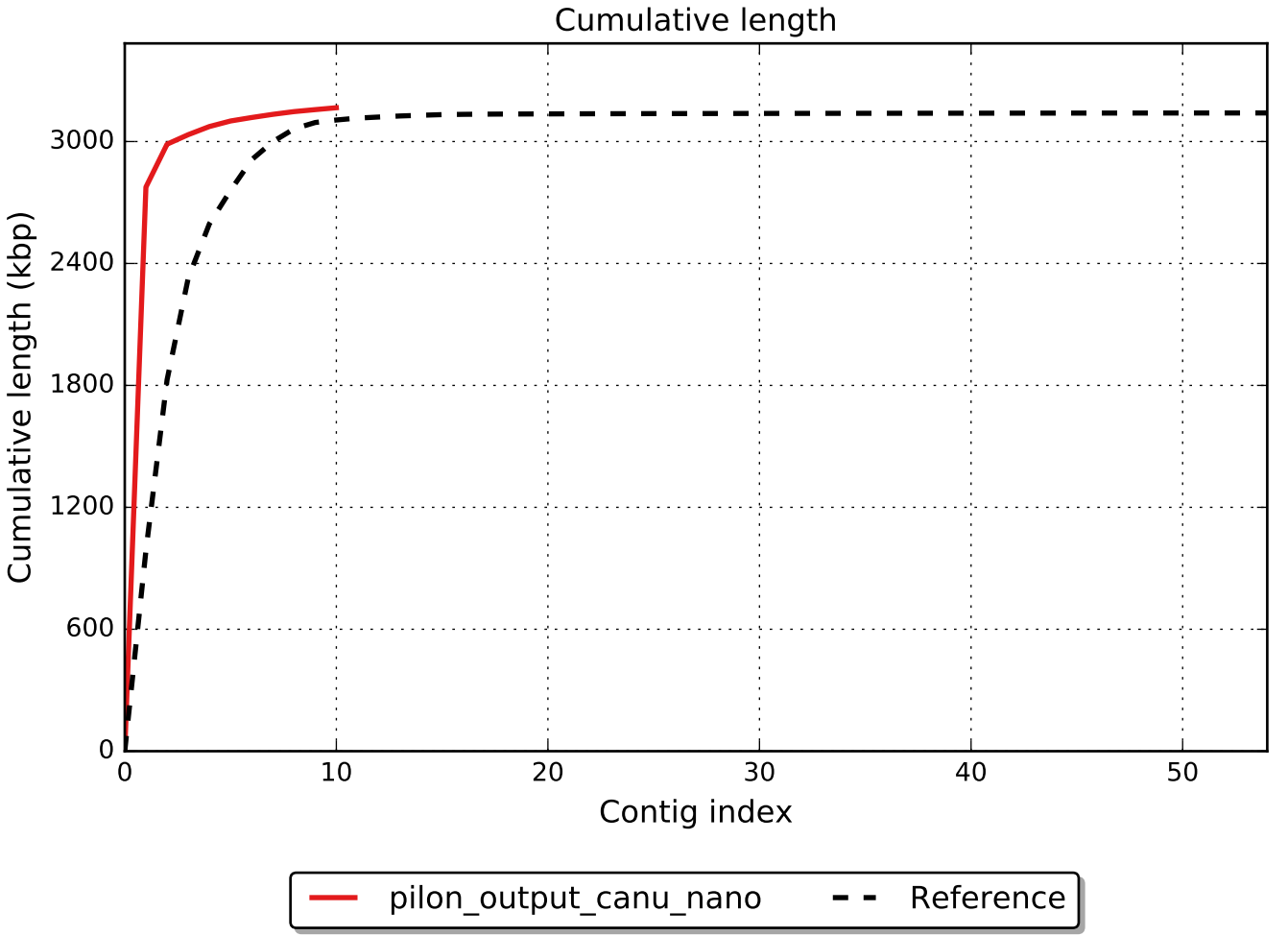
Unaligned report

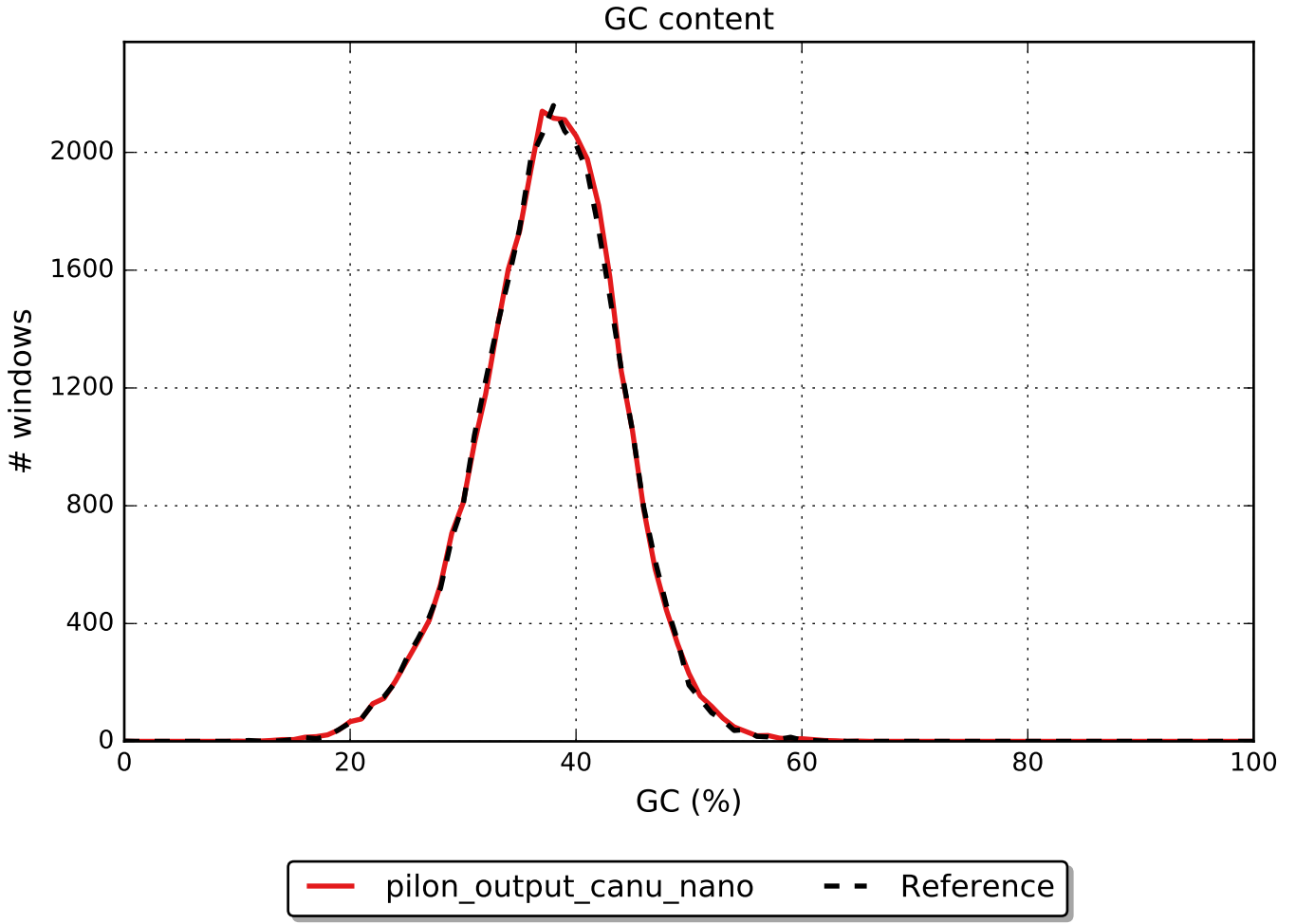
	pilon_output_canu_nano
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

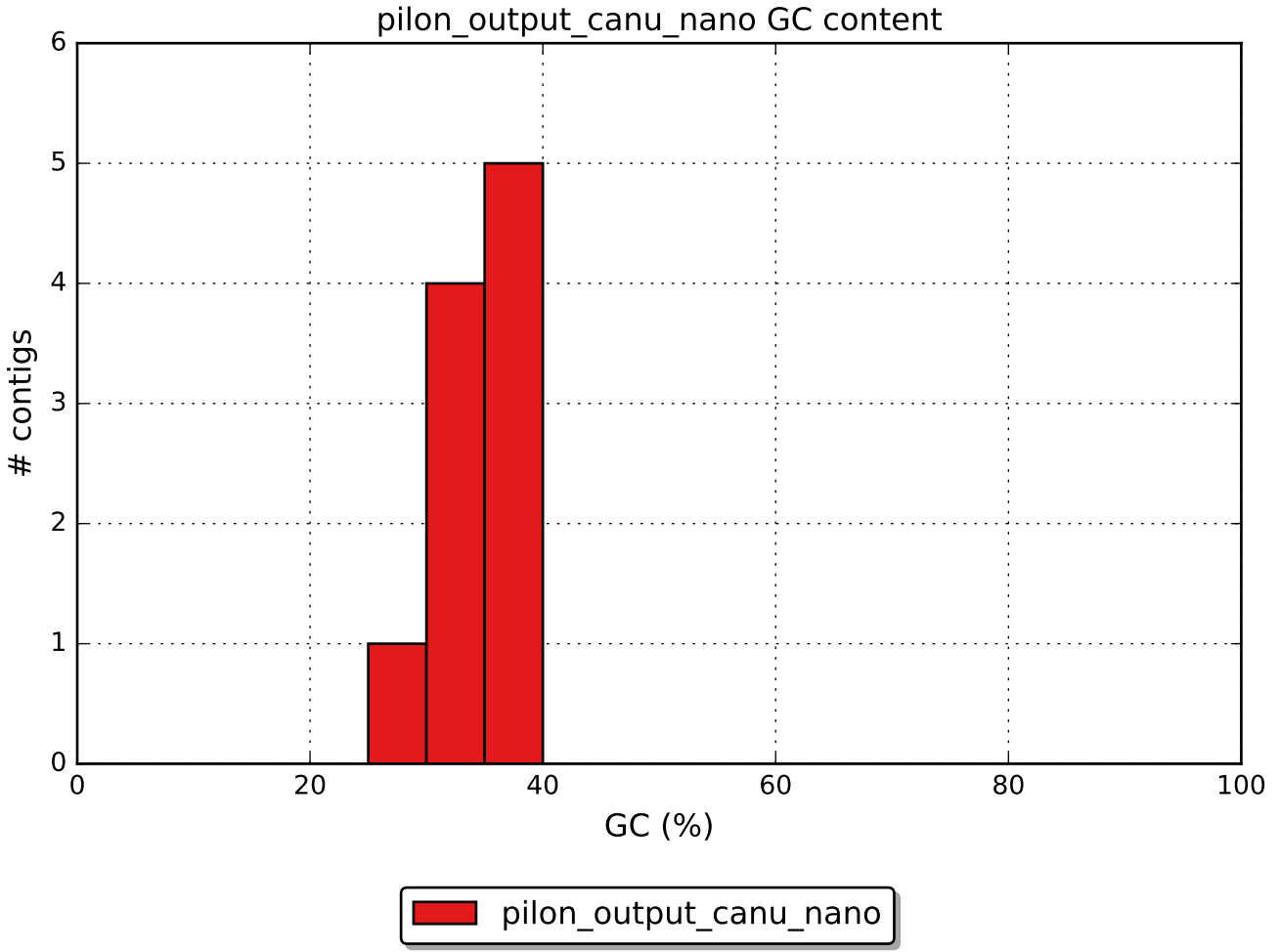
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

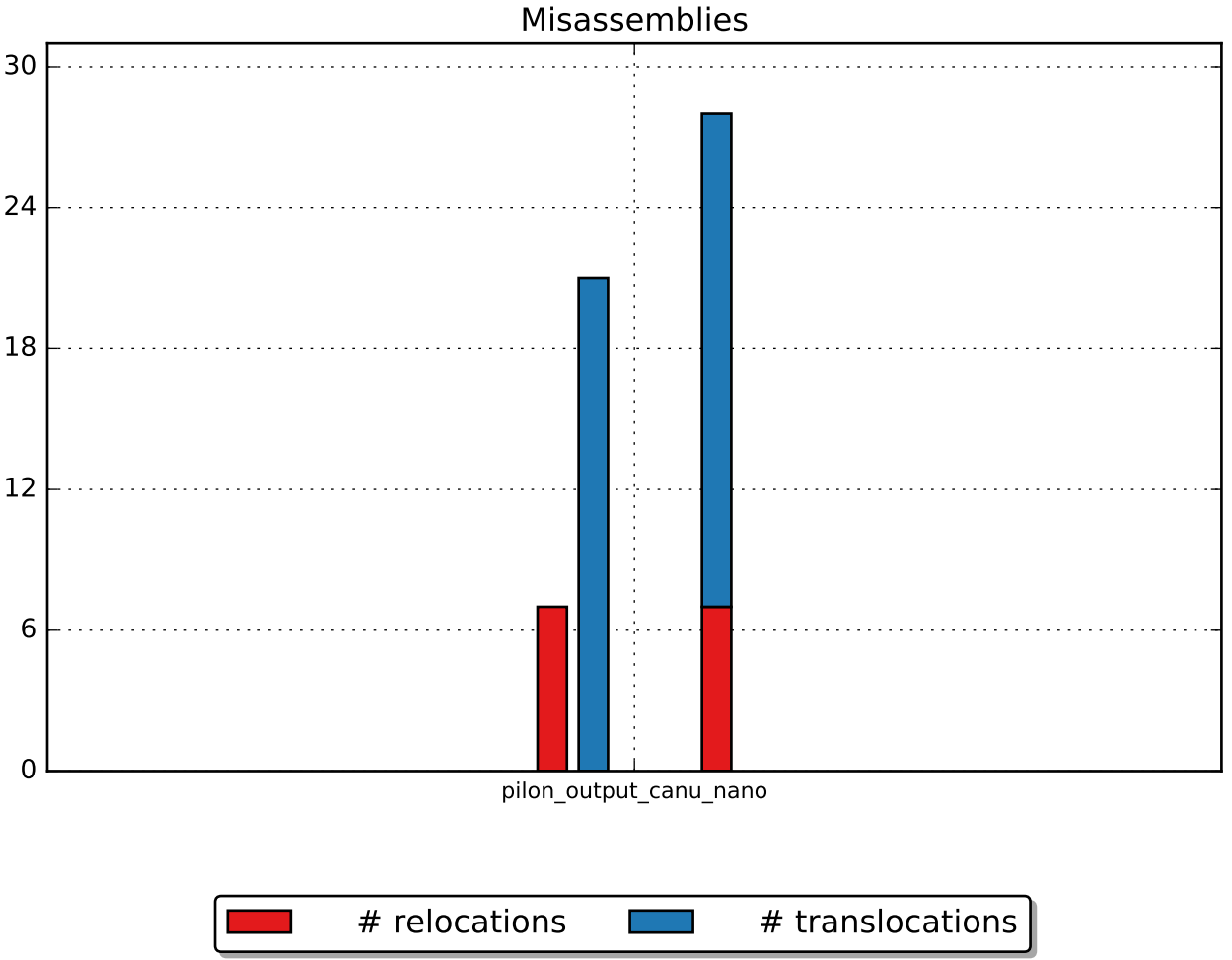

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
pilon_output_canu_nano

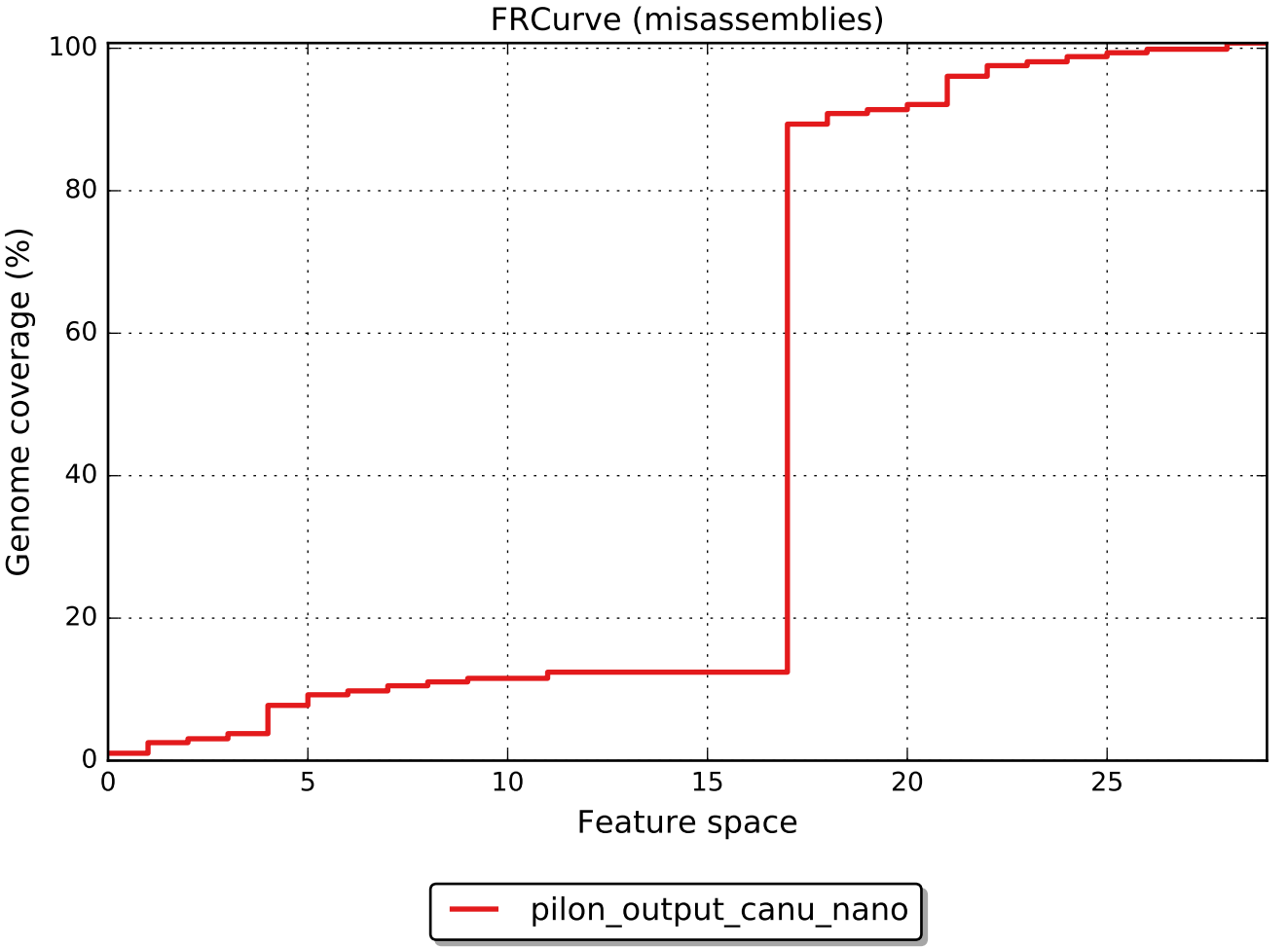

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
pilon_output_canu_nano

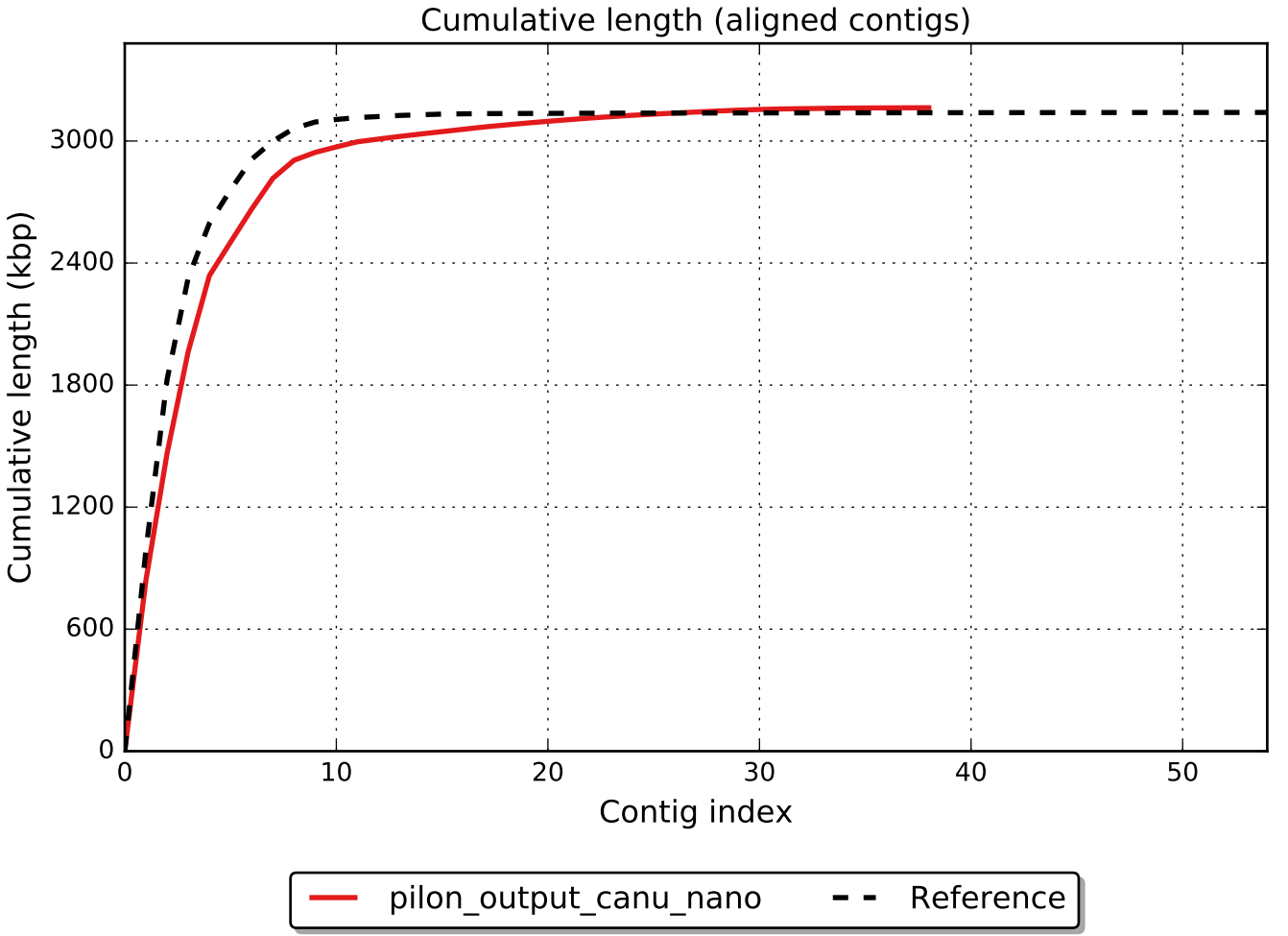

Cumulative length
Cumulative length (kbp)
0
600
1200
1800
2400
3000
0
10
20
30
40
50
Contig index
pilon_output_canu_nano
Reference

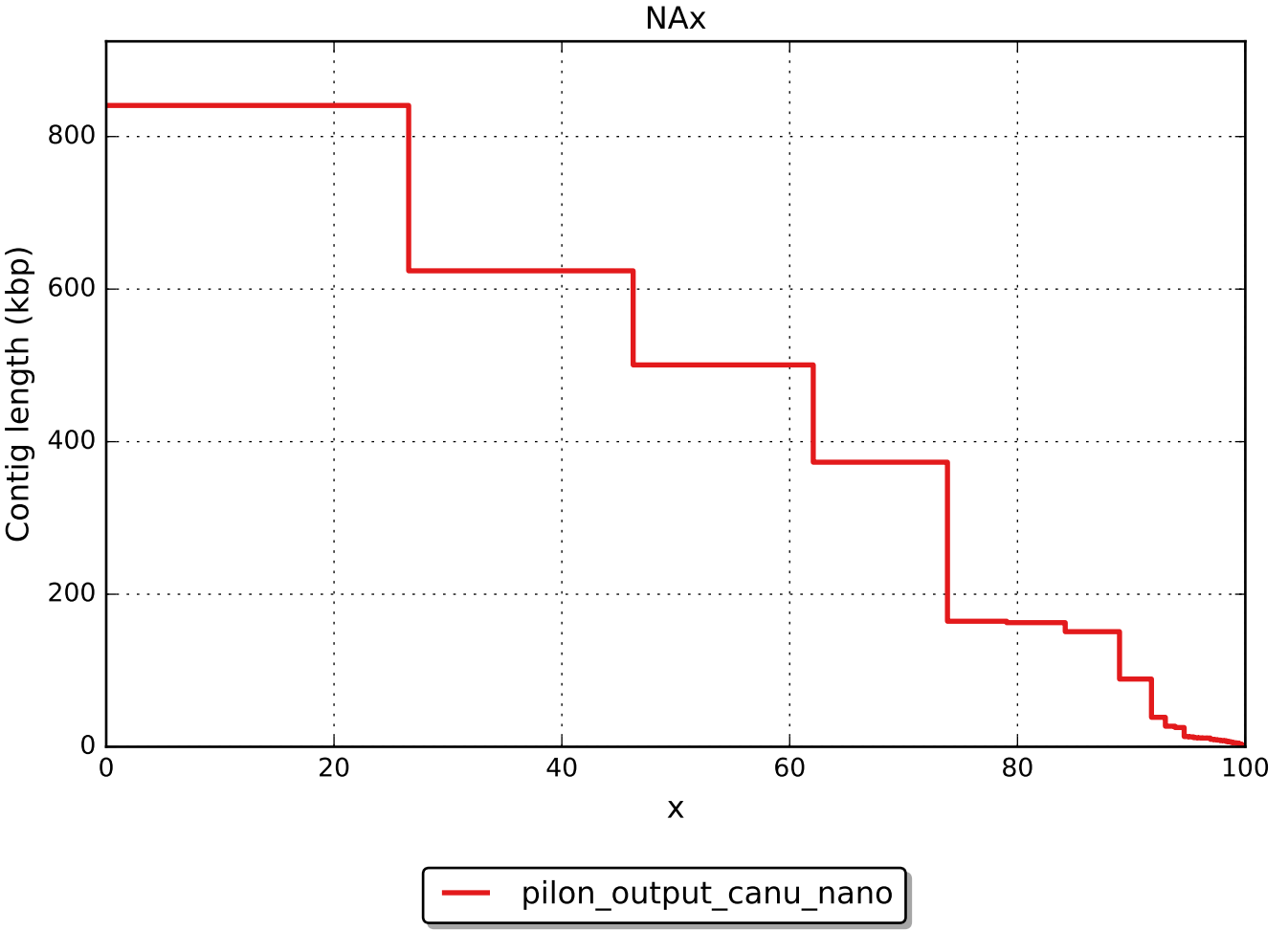

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
pilon_output_canu_nano
Reference

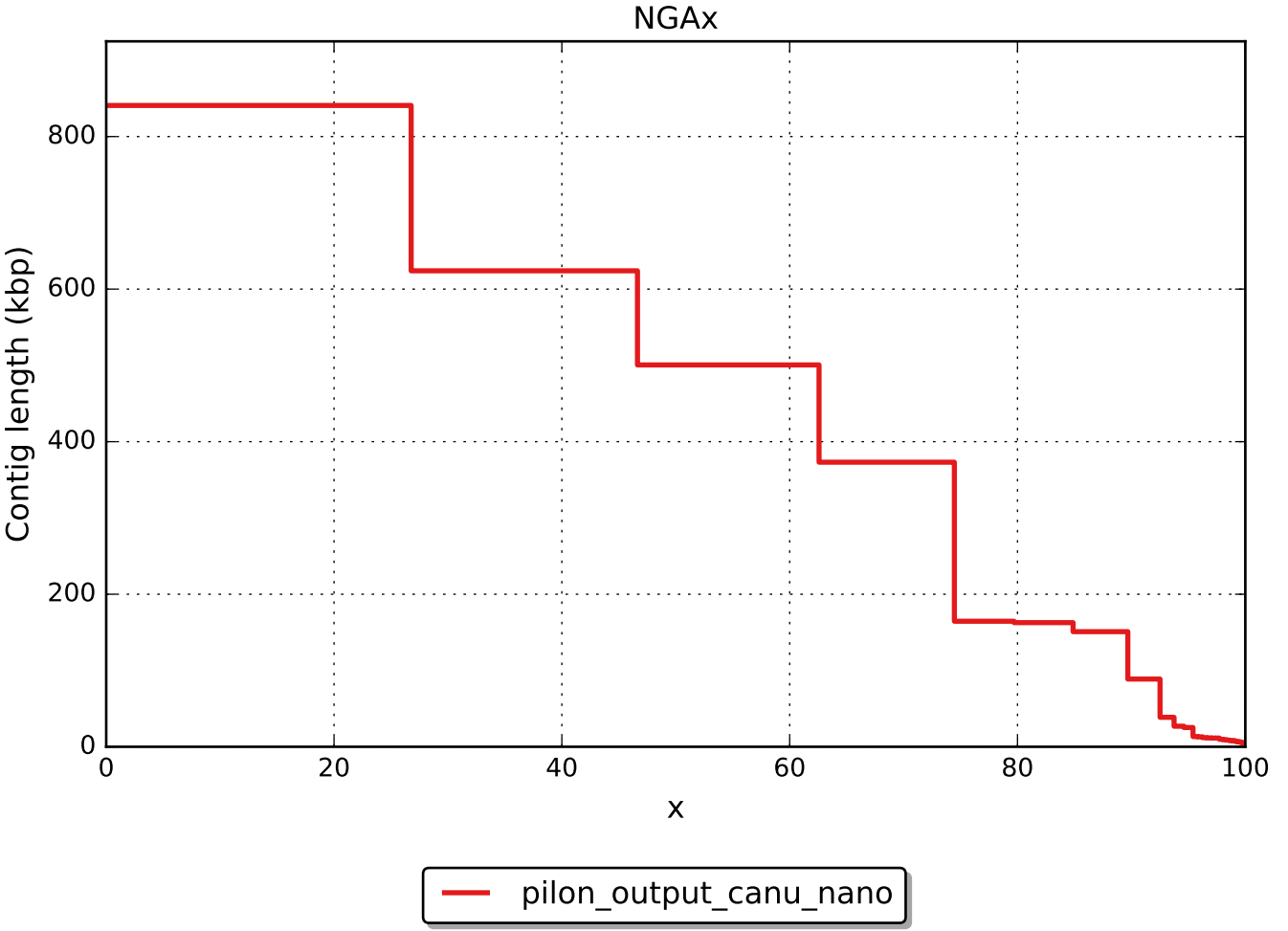

pilon_output_canu_nano GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
pilon_output_canu_nano


Misassemblies
30
24
18
12
6
0
pilon_output_canu_nano
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
5
10
15
20
25
pilon_output_canu_nano


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
600
1200
1800
2400
3000
0
10
20
30
40
50
Contig index
pilon_output_canu_nano
Reference


NAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
pilon_output_canu_nano


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
pilon_output_canu_nano