Report

	pilon
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3141050
Total length (>= 1000 bp)	3141050
Total length (>= 5000 bp)	3141050
Total length (>= 10000 bp)	3132750
Total length (>= 25000 bp)	3103593
Total length (>= 50000 bp)	2992680
# contigs	8
Largest contig	2773703
Total length	3141050
Reference length	1753437
GC (%)	37.78
Reference GC (%)	37.94
N50	2773703
NG50	2773703
N75	2773703
NG75	2773703
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	31
# misassembled contigs	2
Misassembled contigs length	2782003
# local misassemblies	4
# unaligned mis. contigs	1
# unaligned contigs	4 + 4 part
Unaligned length	1265371
Genome fraction (%)	100.000
Duplication ratio	1.070
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.29
Largest alignment	1183847
Total aligned length	1875680
NA50	578286
NGA50	1183847
NGA75	578286
LA50	2
LGA50	1
LGA75	2

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

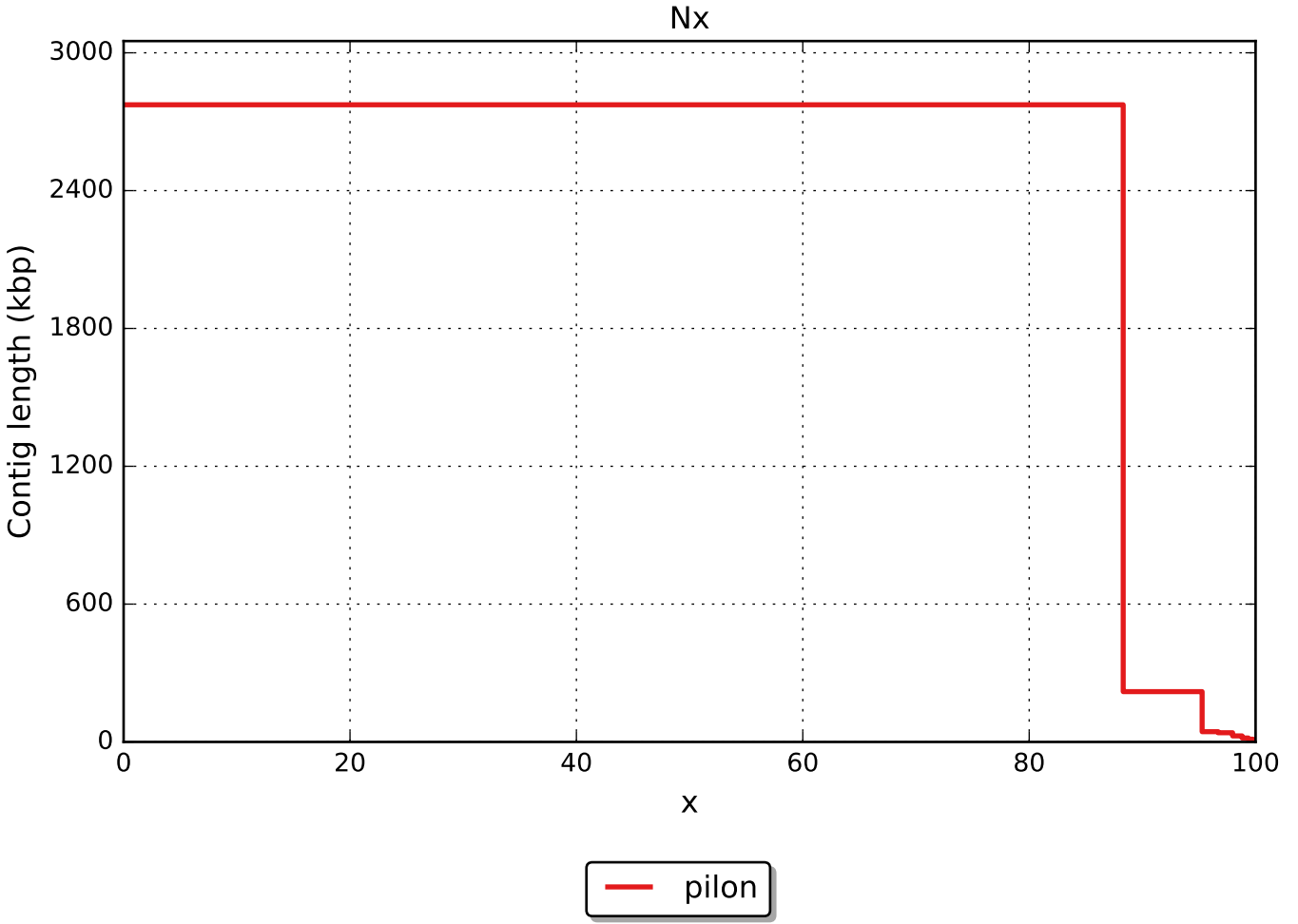
	pilon
# misassemblies	31
# relocations	31
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	2782003
# local misassemblies	4
# unaligned mis. contigs	1
# mismatches	0
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	5

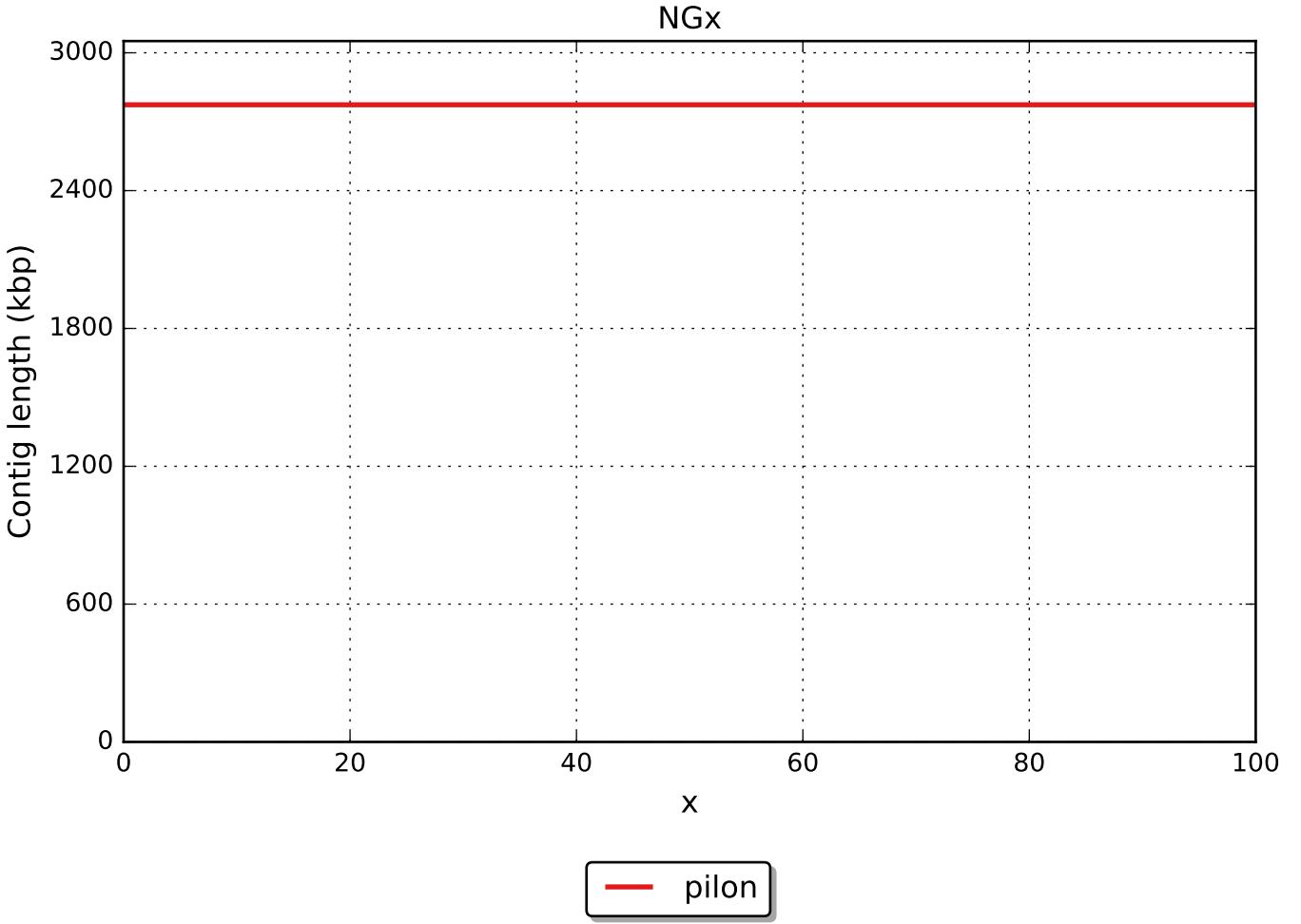
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

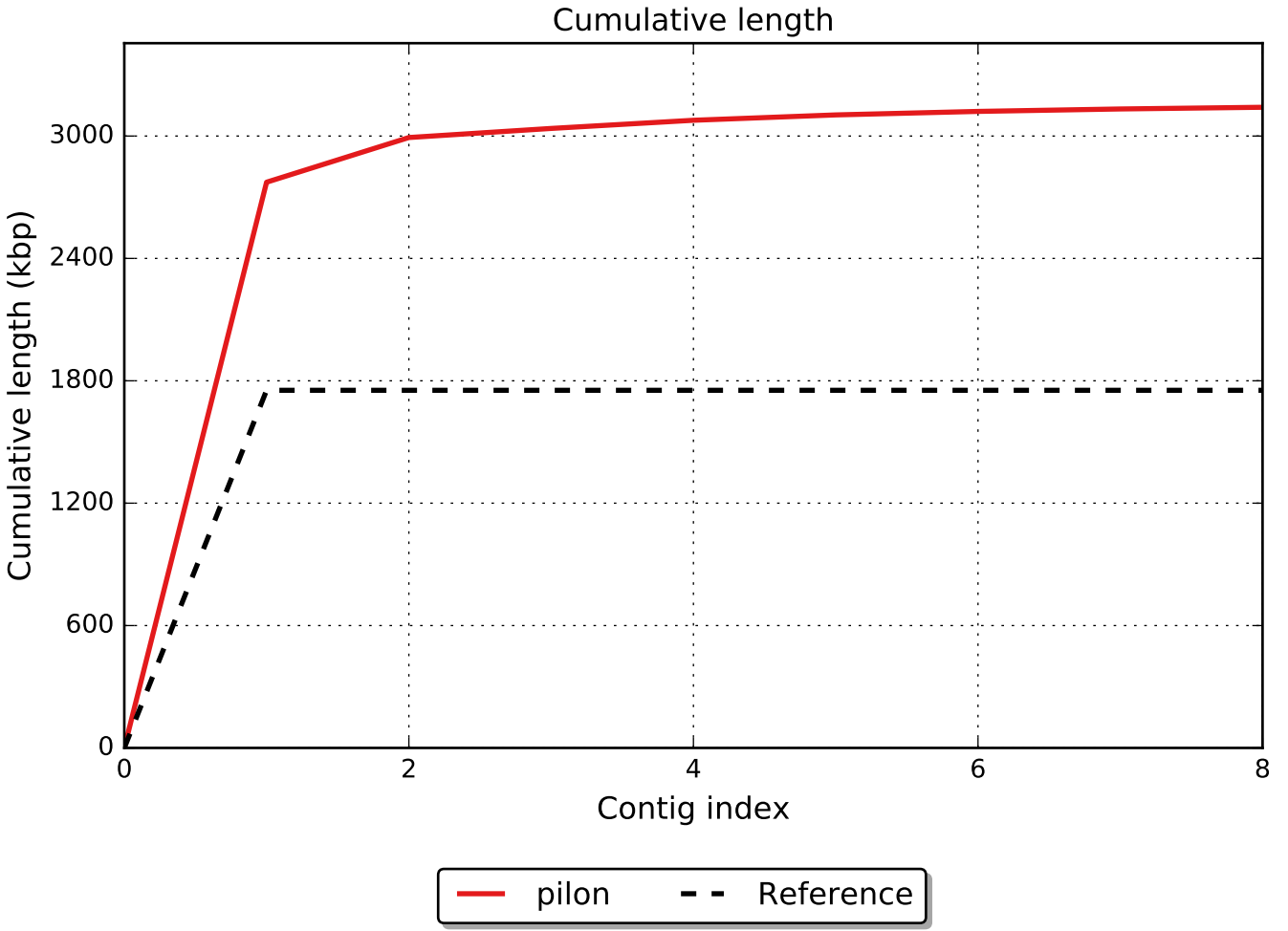
Unaligned report

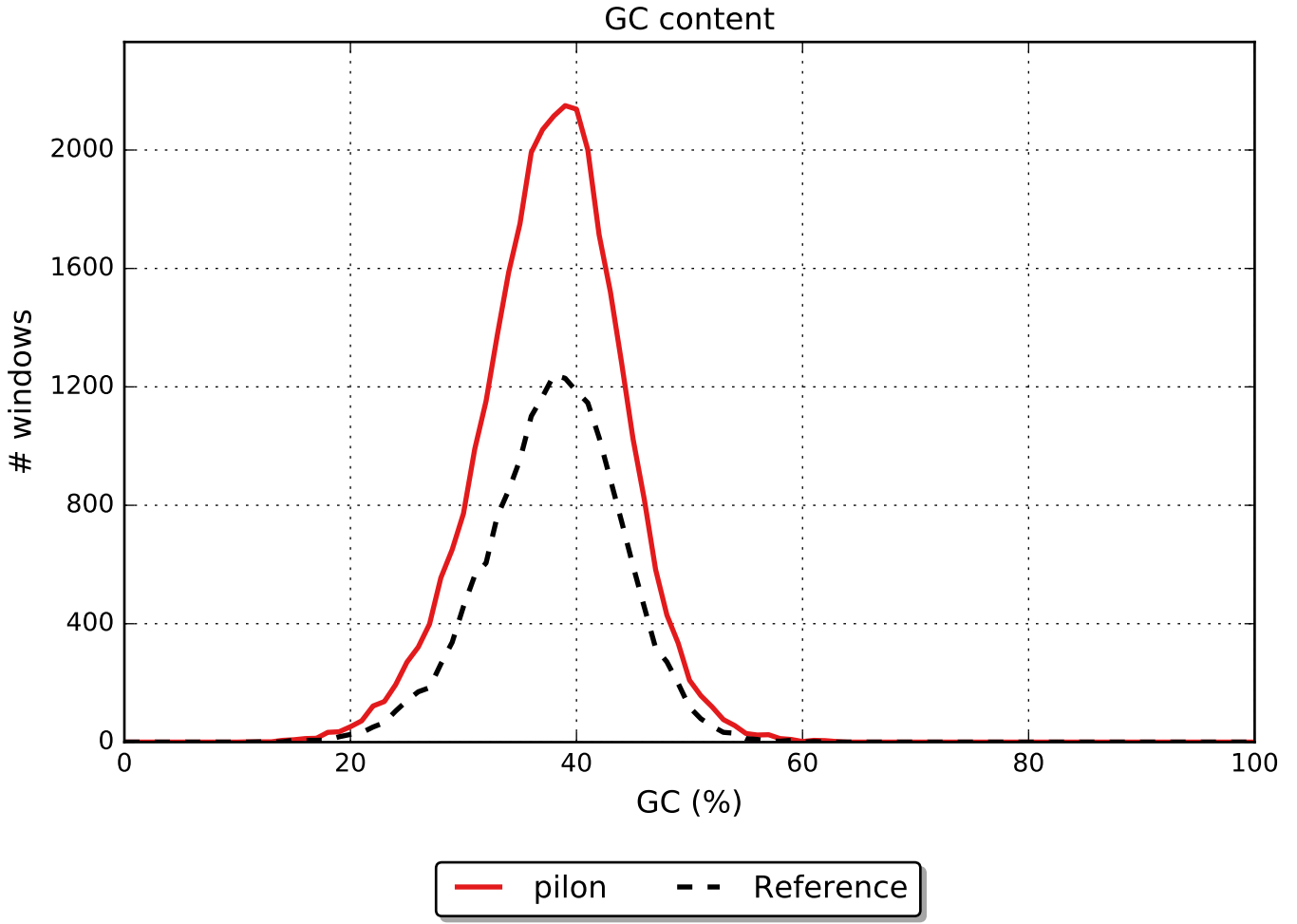
	pilon
# fully unaligned contigs	4
Fully unaligned length	100053
# partially unaligned contigs	4
Partially unaligned length	1165318
# N's	0

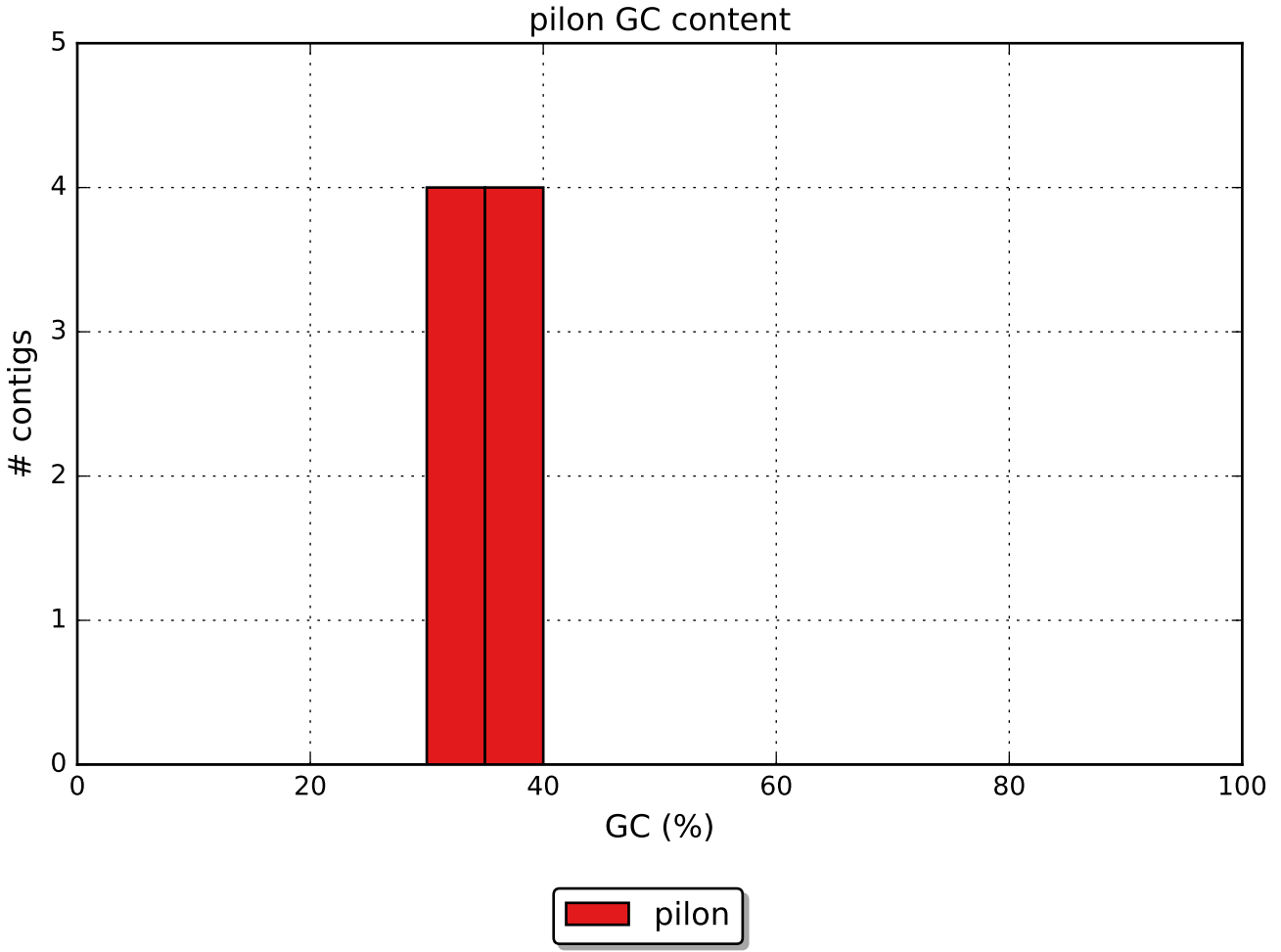
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

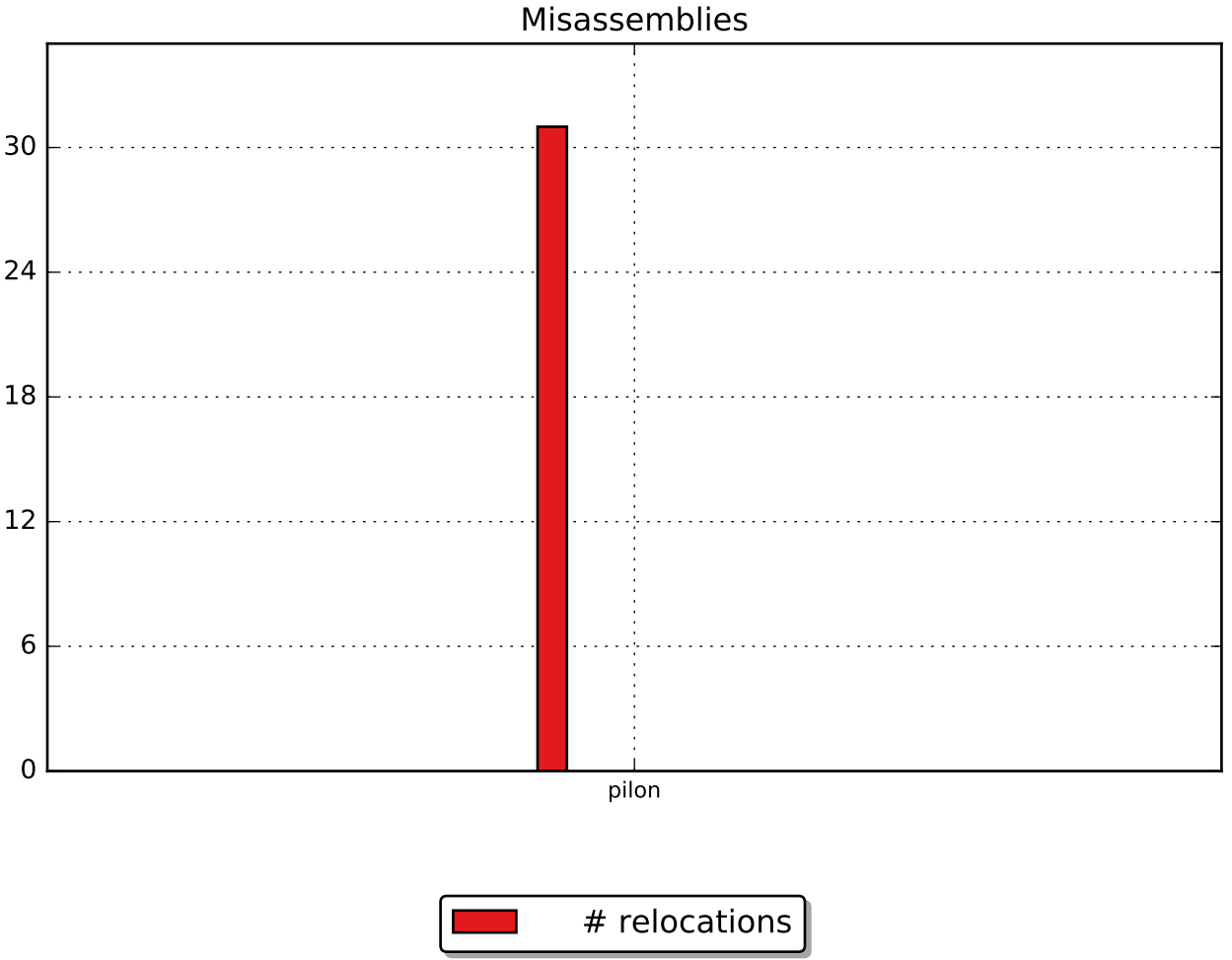

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
pilon

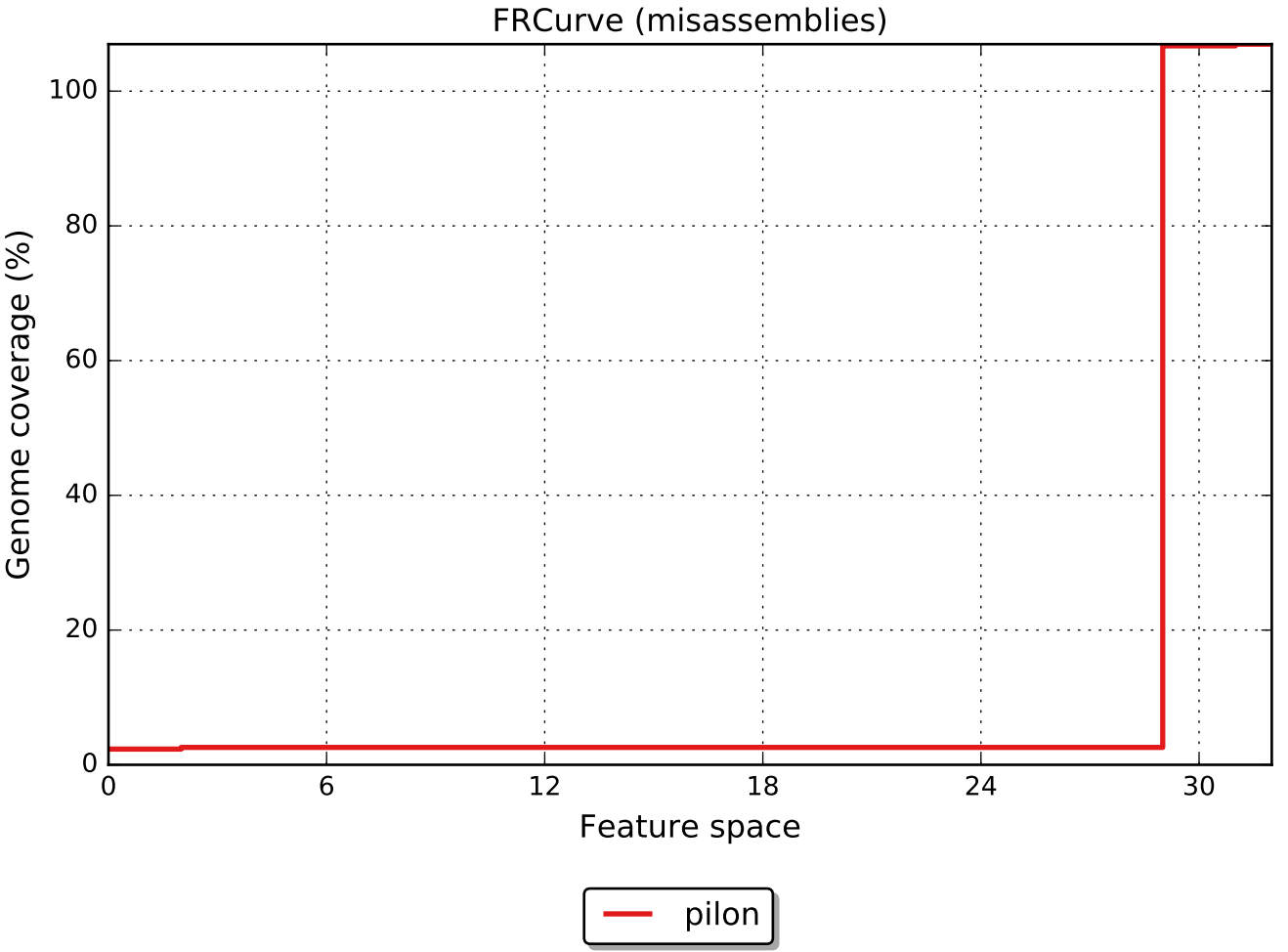

NGx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
pilon

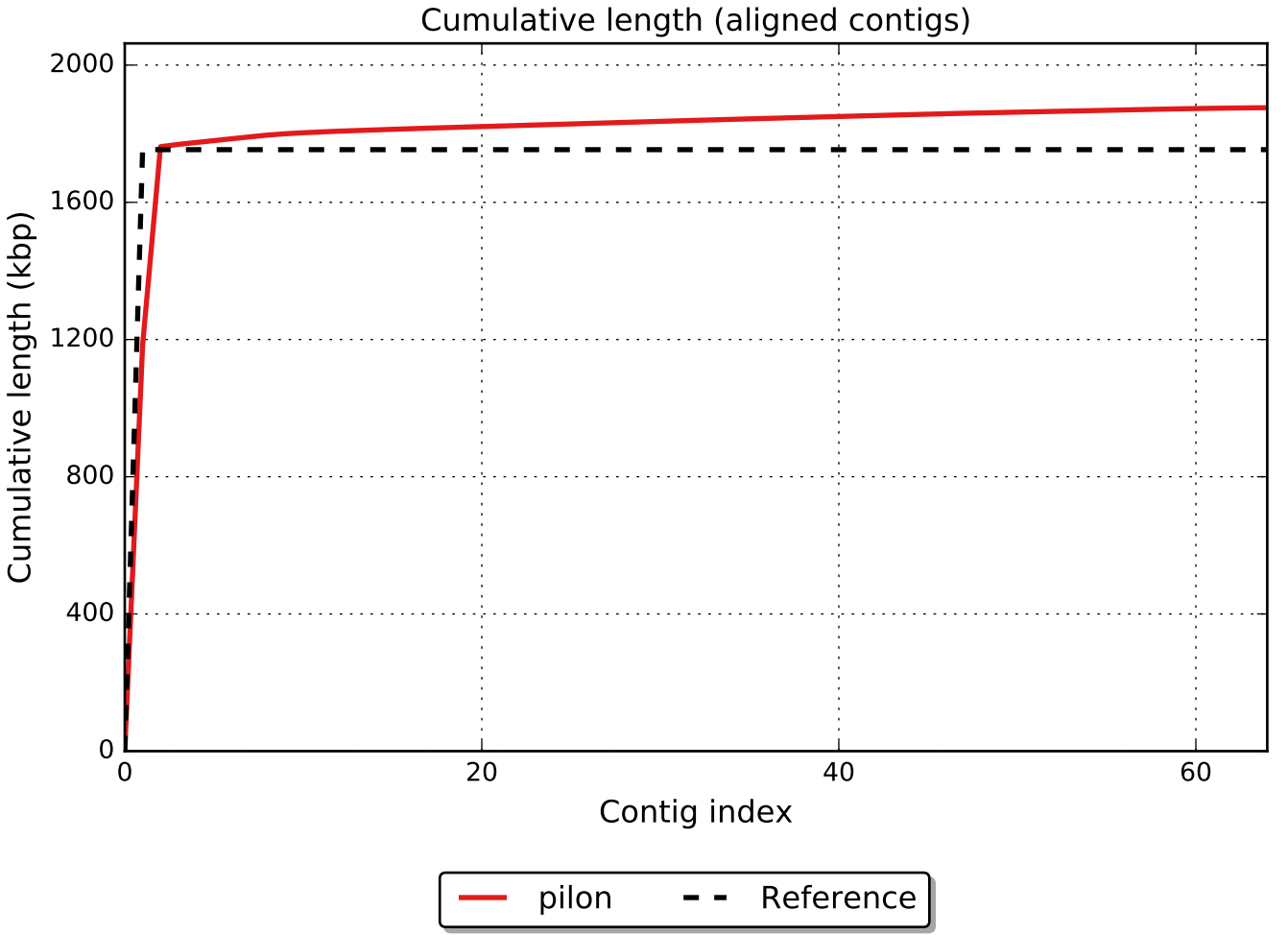

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
Contig index
pilon
Reference

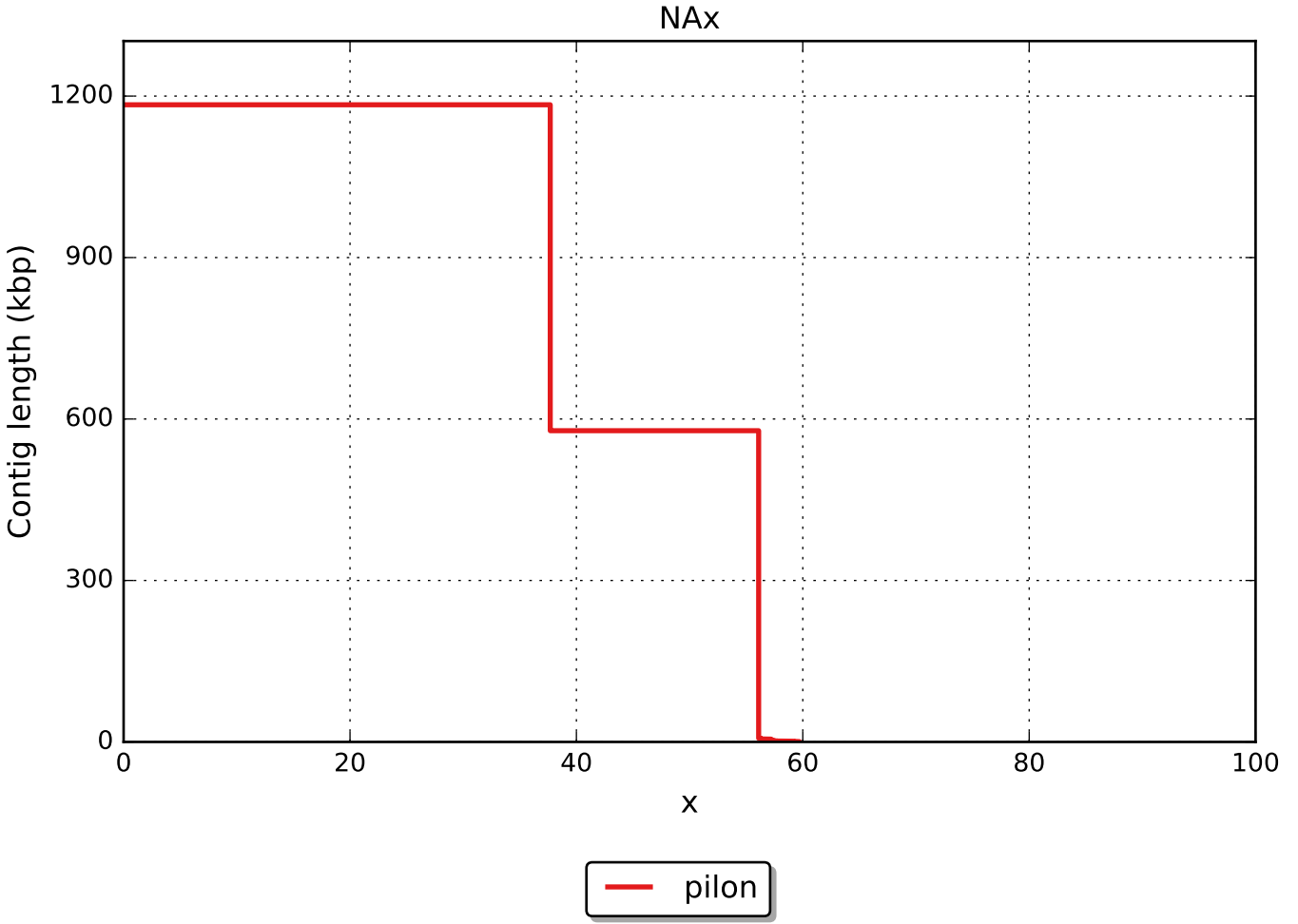

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
pilon
Reference

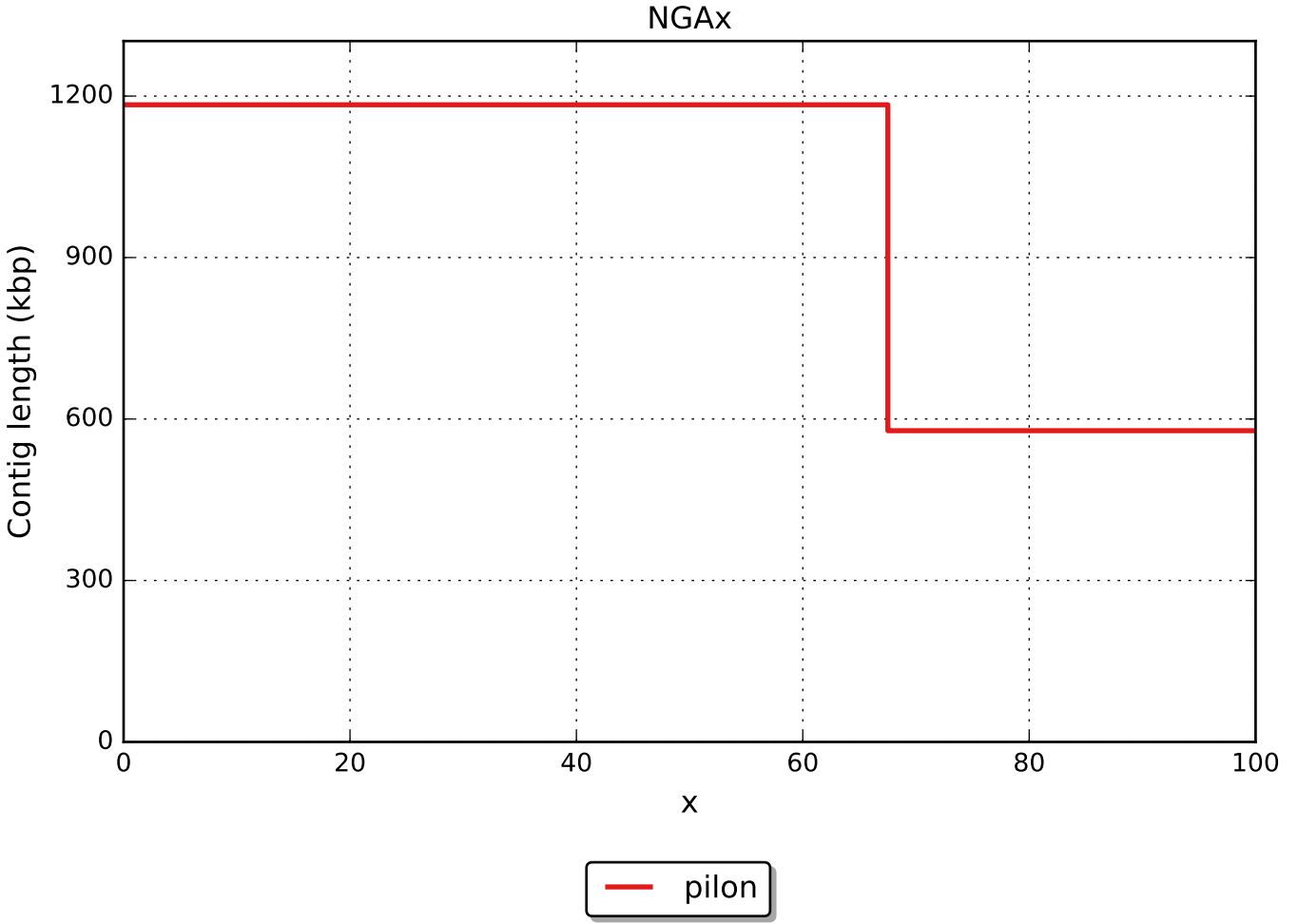

pilon GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
pilon


Misassemblies
30
24
18
12
6
0
pilon
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
6
12
18
24
30
Feature space
pilon


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
Contig index
pilon
Reference


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


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