Report

	pilon_pacbio_illumina_combined_genome
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3143327
Total length (>= 1000 bp)	3143327
Total length (>= 5000 bp)	3138937
Total length (>= 10000 bp)	3138937
Total length (>= 25000 bp)	3110386
Total length (>= 50000 bp)	3000076
# contigs	8
Largest contig	2773702
Total length	3143327
Reference length	2765010
GC (%)	37.78
Reference GC (%)	38.11
N50	2773702
NG50	2773702
N75	2773702
NG75	2773702
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2773702
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	5 + 2 part
Unaligned length	325157
Genome fraction (%)	100.000
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.22
Largest alignment	2195416
Total aligned length	2818171
NA50	2195416
NGA50	2195416
NA75	578286
NGA75	2195416
LA50	1
LGA50	1
LA75	2
LGA75	1

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

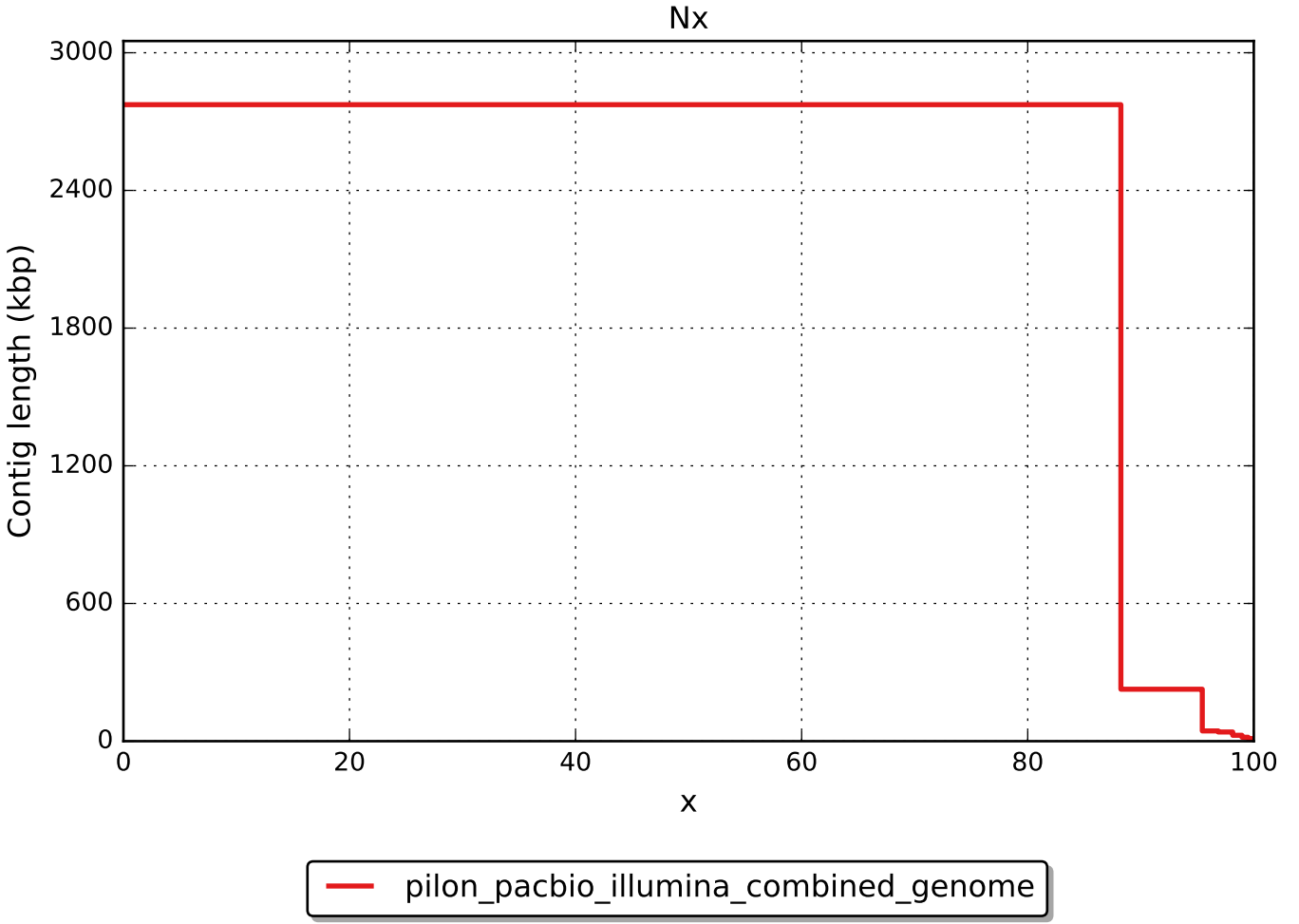
	pilon_pacbio_illumina_combined_genome
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2773702
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	0
# indels	6
# indels (<= 5 bp)	6
# indels (> 5 bp)	0
Indels length	7

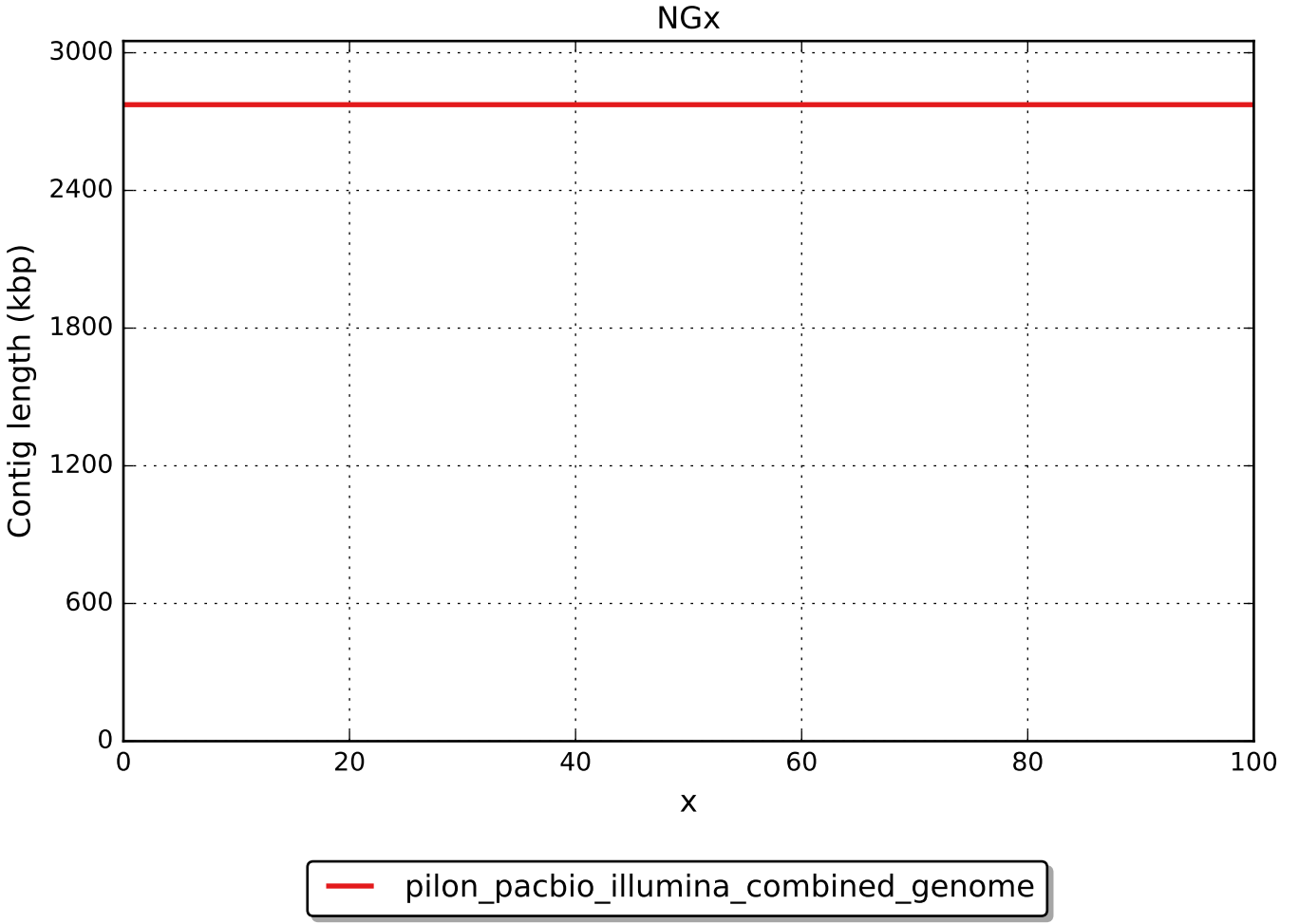
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

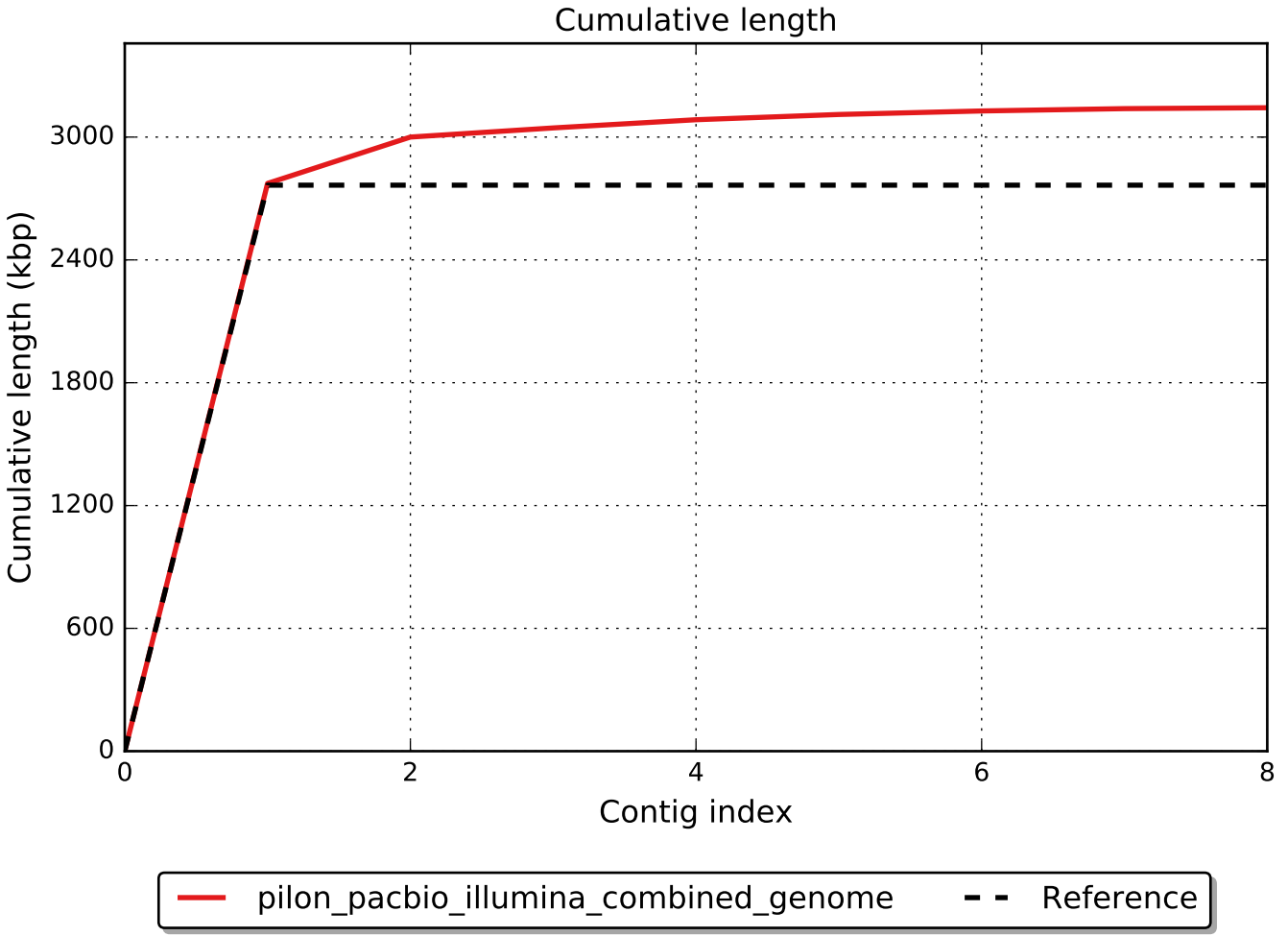
Unaligned report

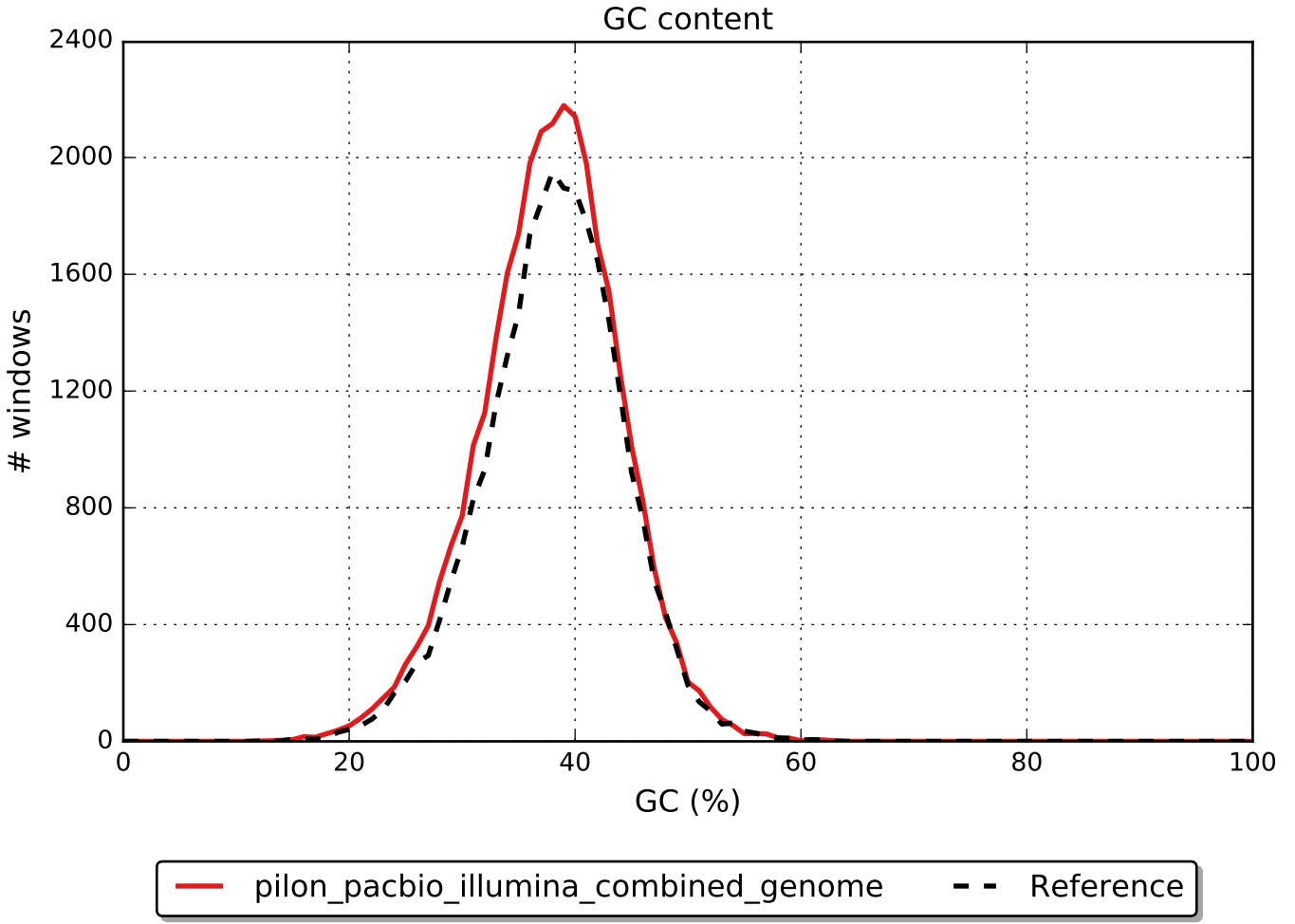
	pilon_pacbio_illumina_combined_genome
# fully unaligned contigs	5
Fully unaligned length	103233
# partially unaligned contigs	2
Partially unaligned length	221924
# N's	0

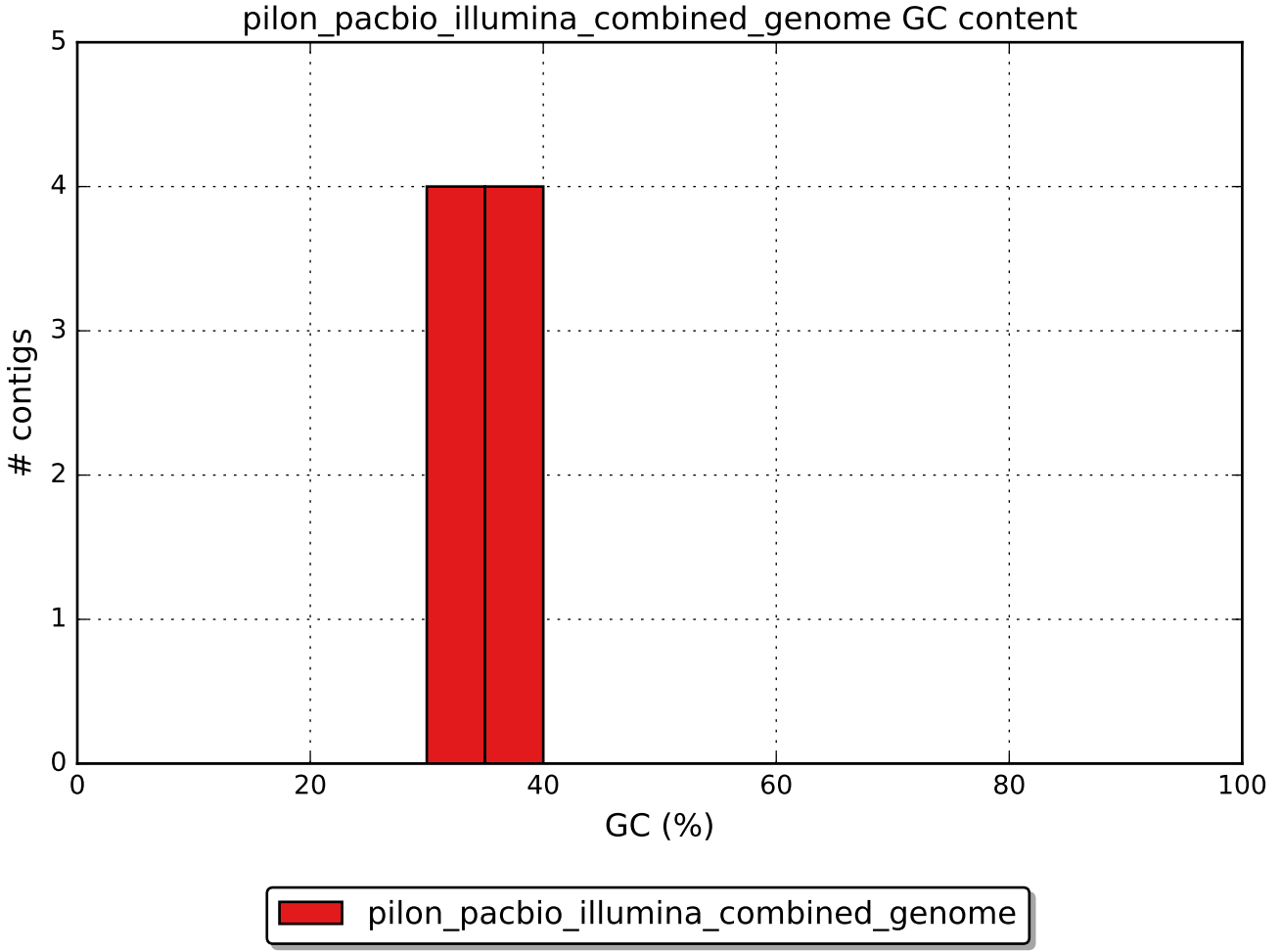
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

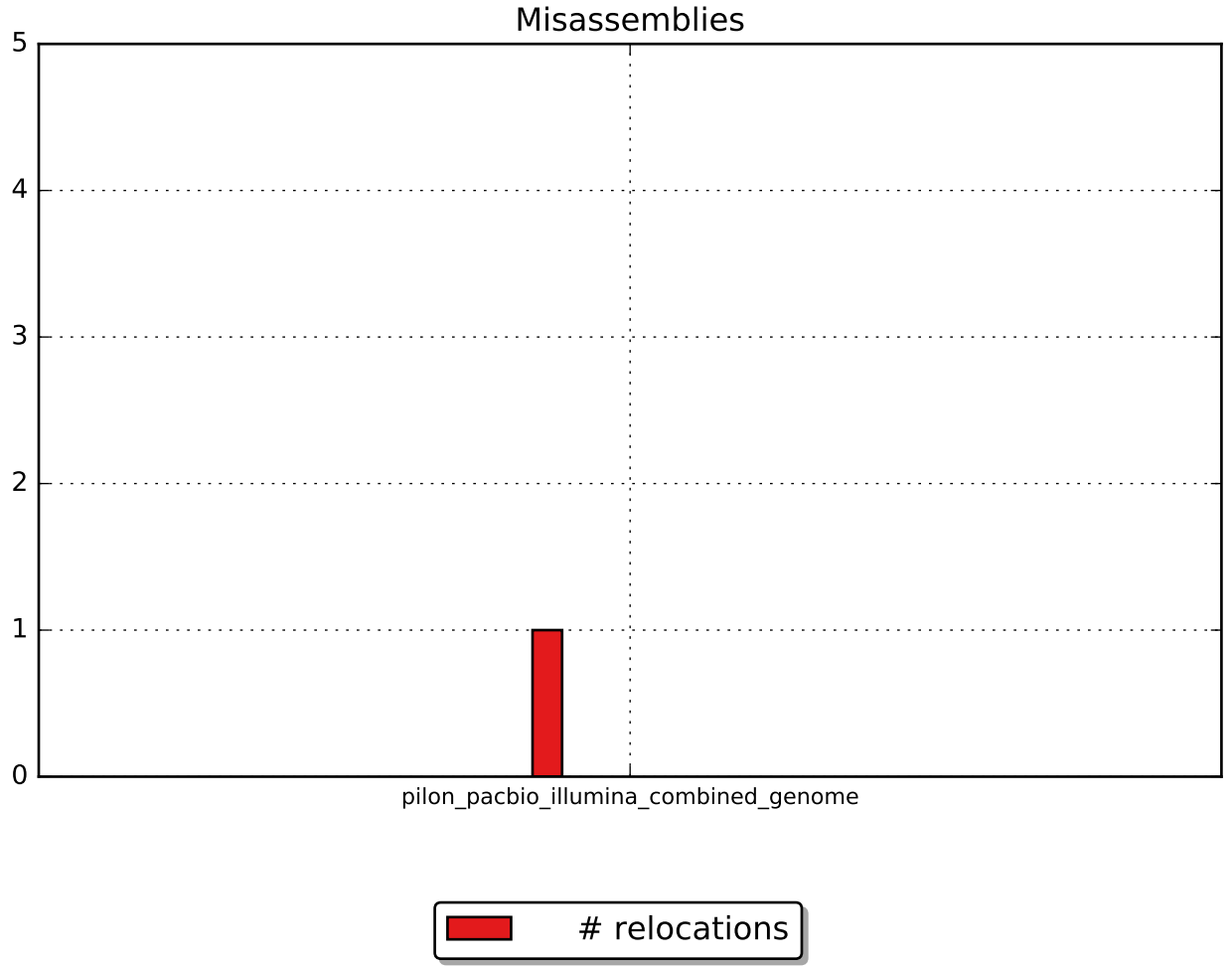

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
pilon_pacbio_illumina_combined_genome

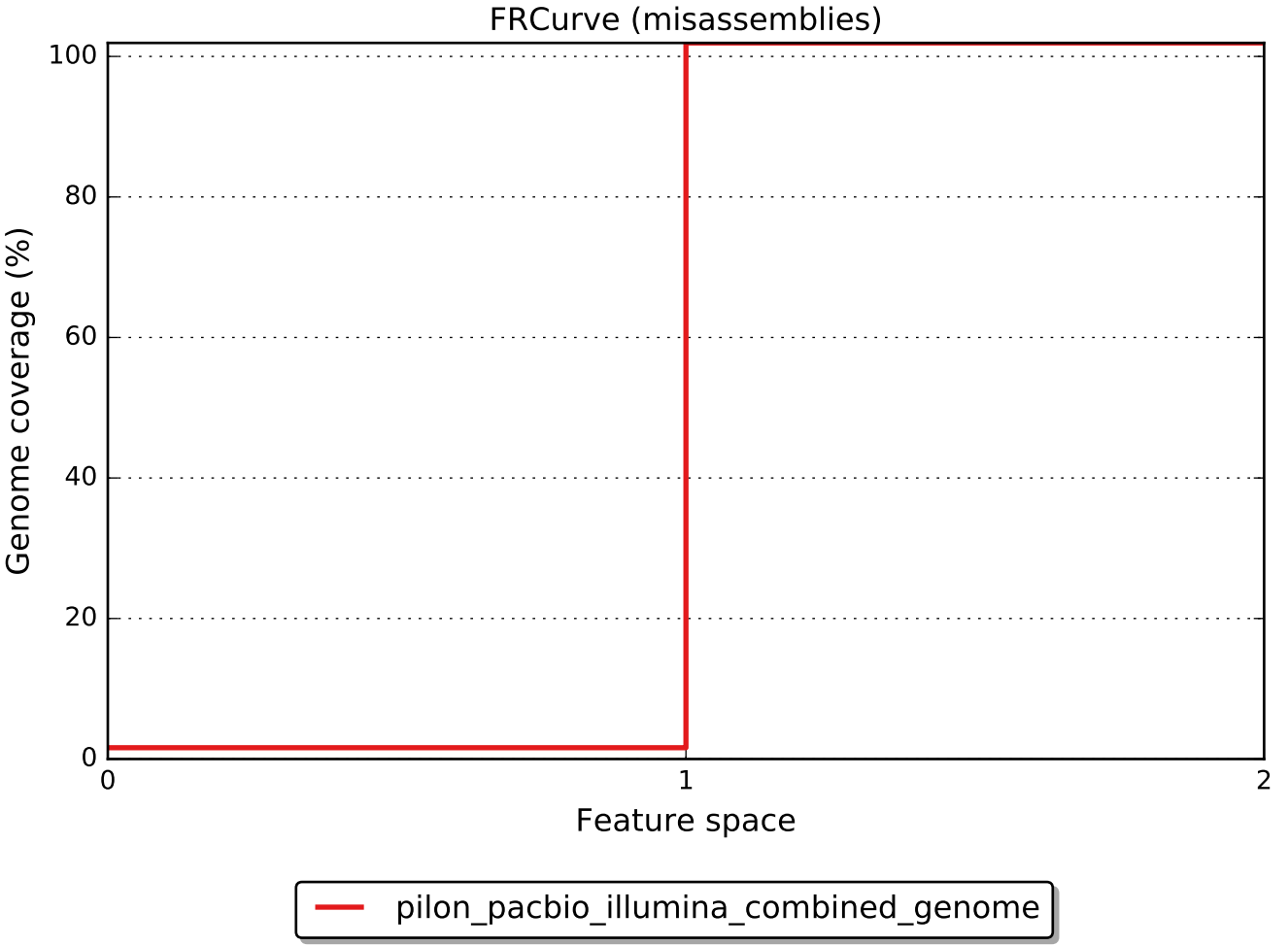

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
pilon_pacbio_illumina_combined_genome

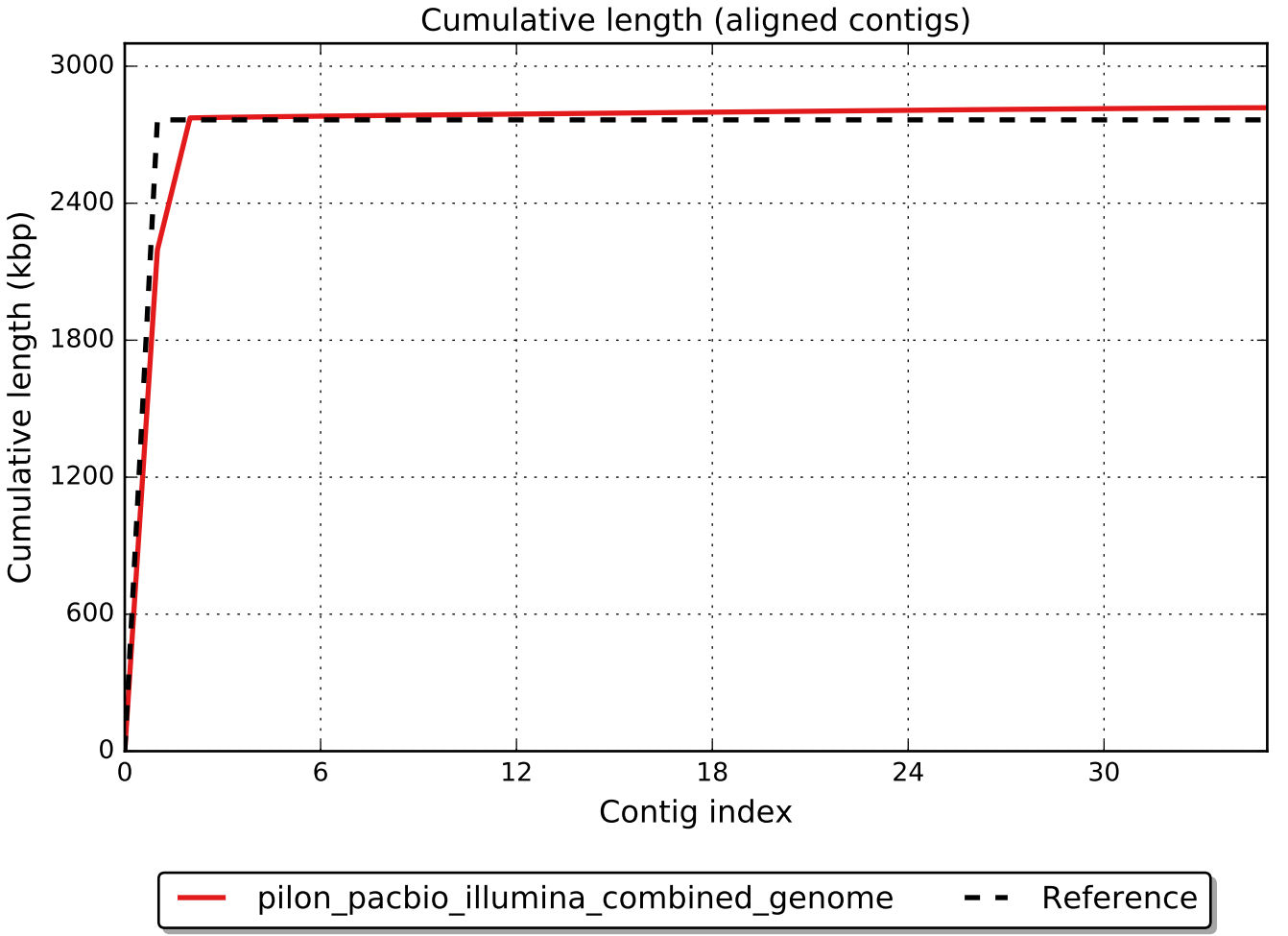

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
Contig index
pilon_pacbio_illumina_combined_genome
Reference

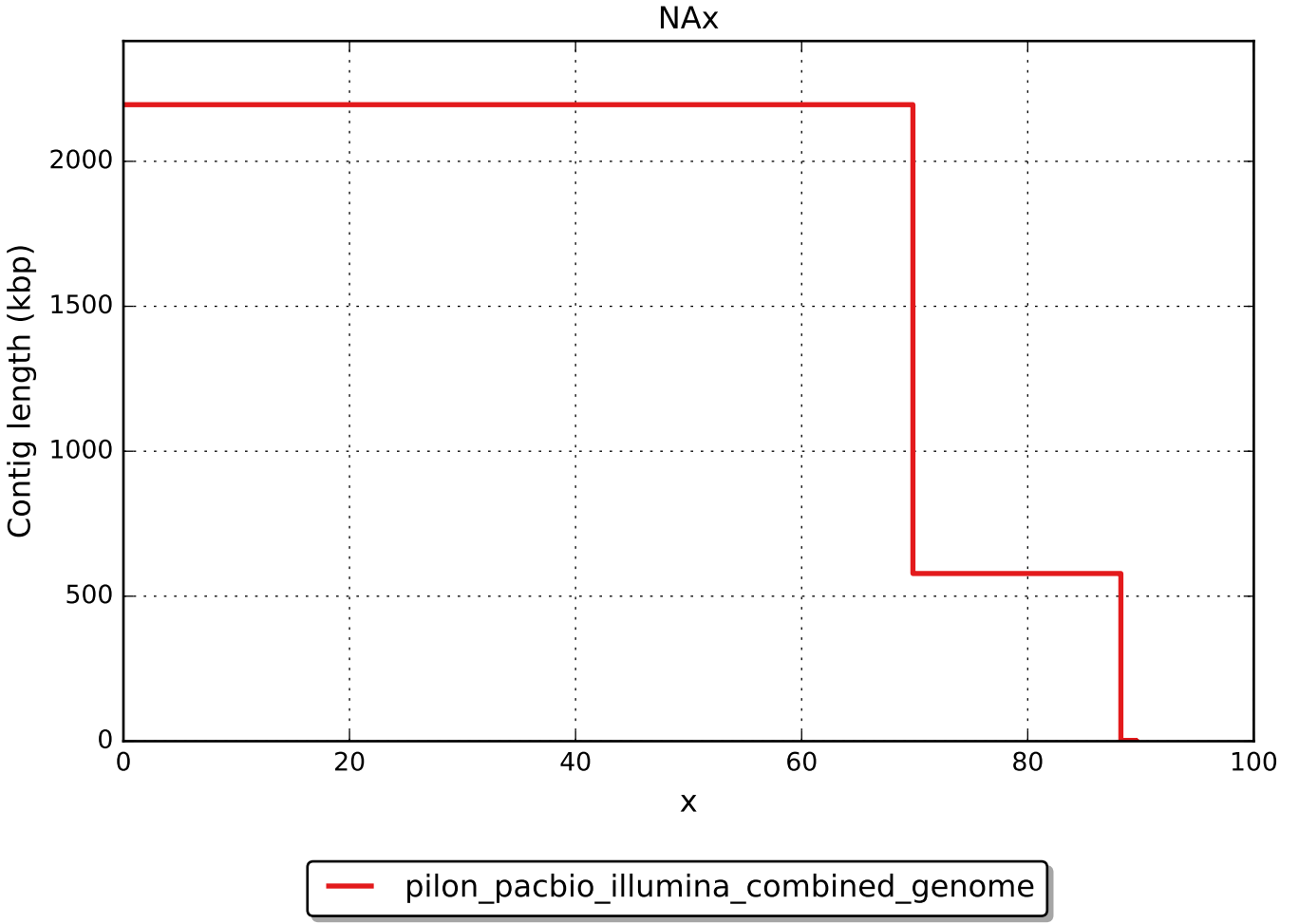

GC content
2400
2000
1600
1200
800
400
0
windows
0
20
40
60
80
100
GC (%)
pilon_pacbio_illumina_combined_genome
Reference

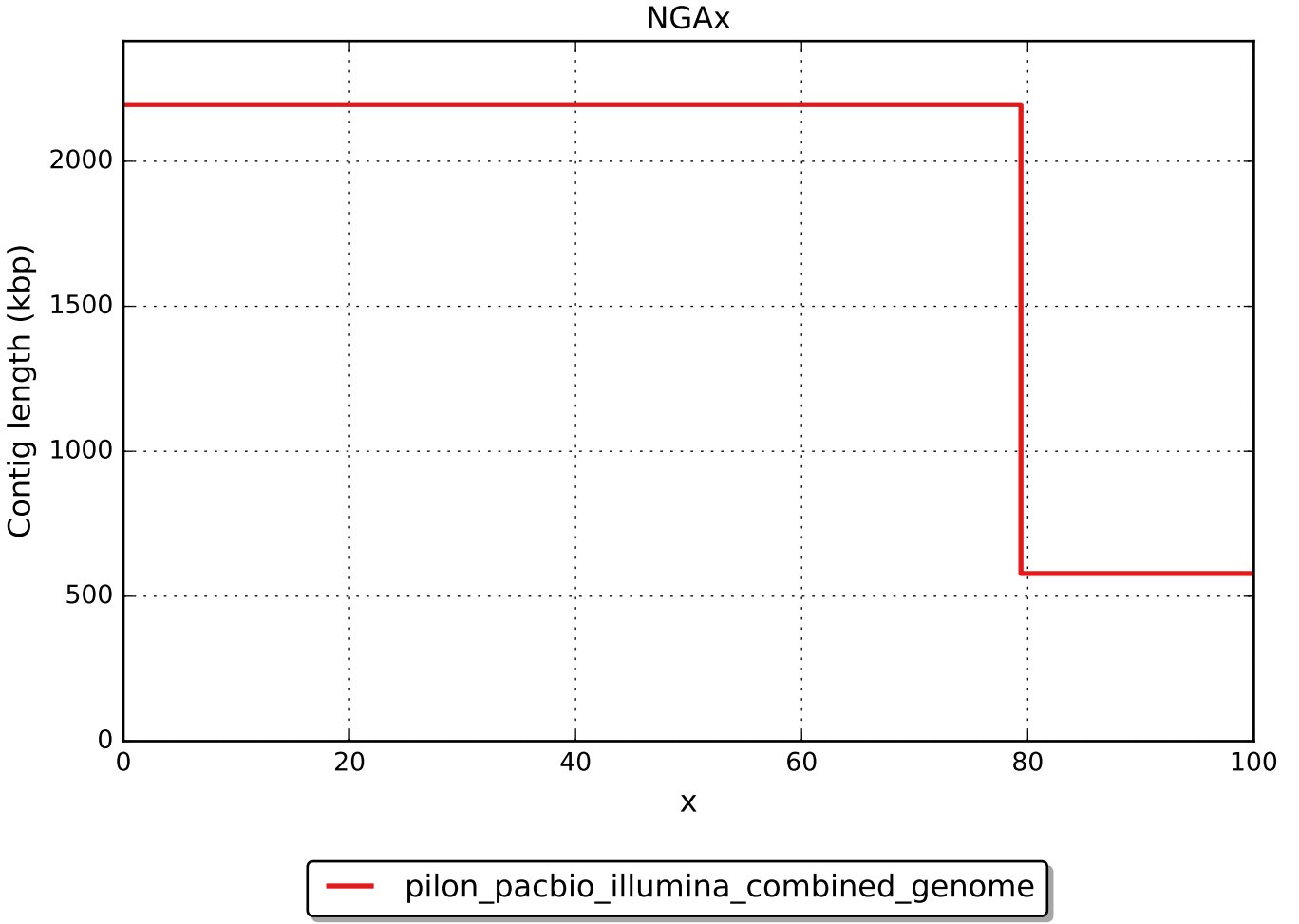

pilon_pacbio_illumina_combined_genome GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
pilon_pacbio_illumina_combined_genome


Misassemblies
5
4
3
2
1
0
pilon_pacbio_illumina_combined_genome
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
pilon_pacbio_illumina_combined_genome


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
6
12
18
24
30
Contig index
pilon_pacbio_illumina_combined_genome
Reference


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


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