Report

	06.fixstart
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2546872
Total length (>= 1000 bp)	2546872
Total length (>= 5000 bp)	2546872
Total length (>= 10000 bp)	2546872
Total length (>= 25000 bp)	2546872
Total length (>= 50000 bp)	2546872
# contigs	1
Largest contig	2546872
Total length	2546872
Reference length	2610531
GC (%)	54.22
Reference GC (%)	54.14
N50	2546872
NG50	2546872
N75	2546872
NG75	2546872
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2546872
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.566
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.12
# indels per 100 kbp	6.60
Largest alignment	1463849
Total aligned length	2546872
NA50	1463849
NGA50	1463849
NA75	1083023
NGA75	1083023
LA50	1
LGA50	1
LA75	2
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

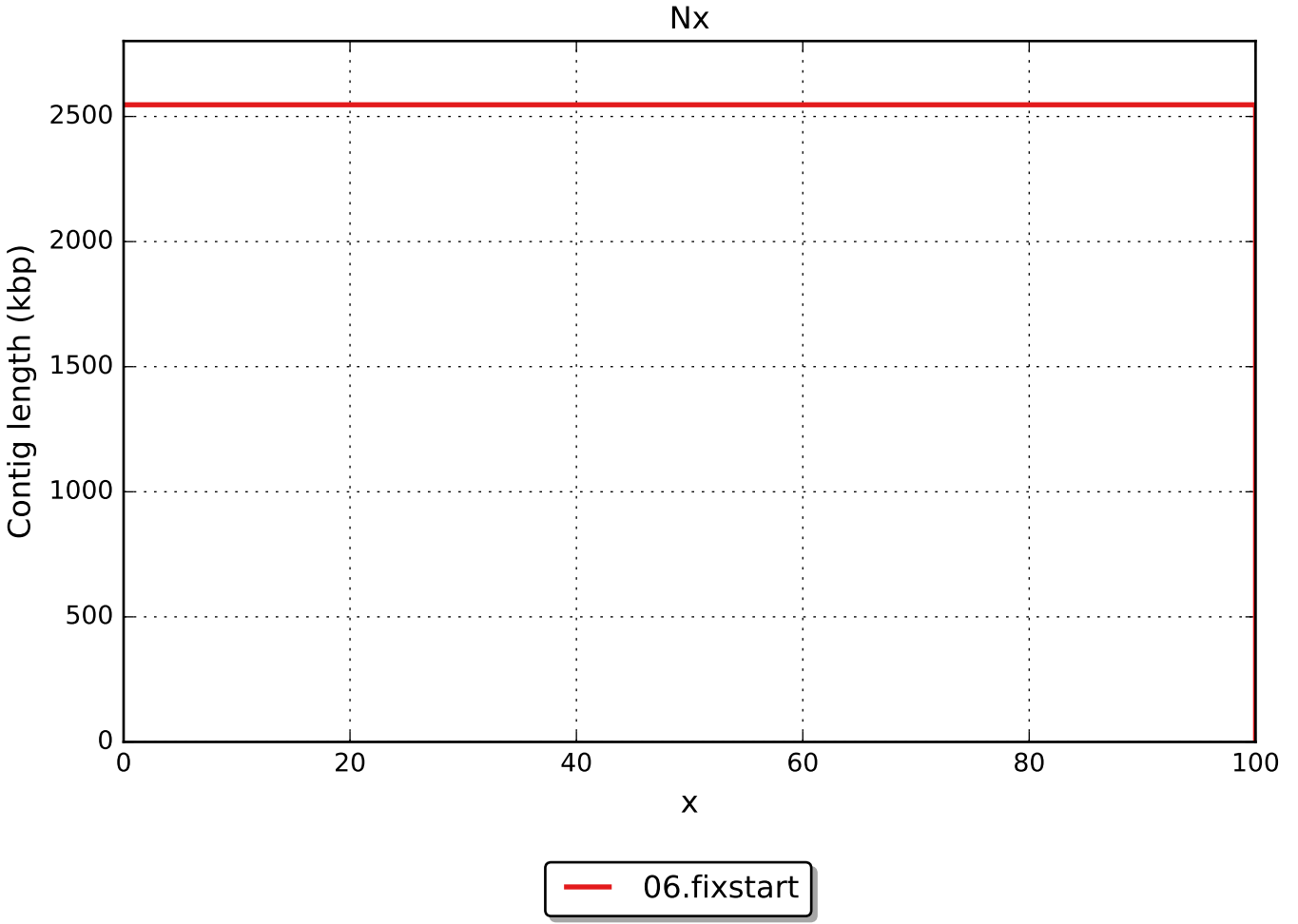
	06.fixstart
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2546872
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	3
# indels	168
# indels (<= 5 bp)	168
# indels (> 5 bp)	0
Indels length	173

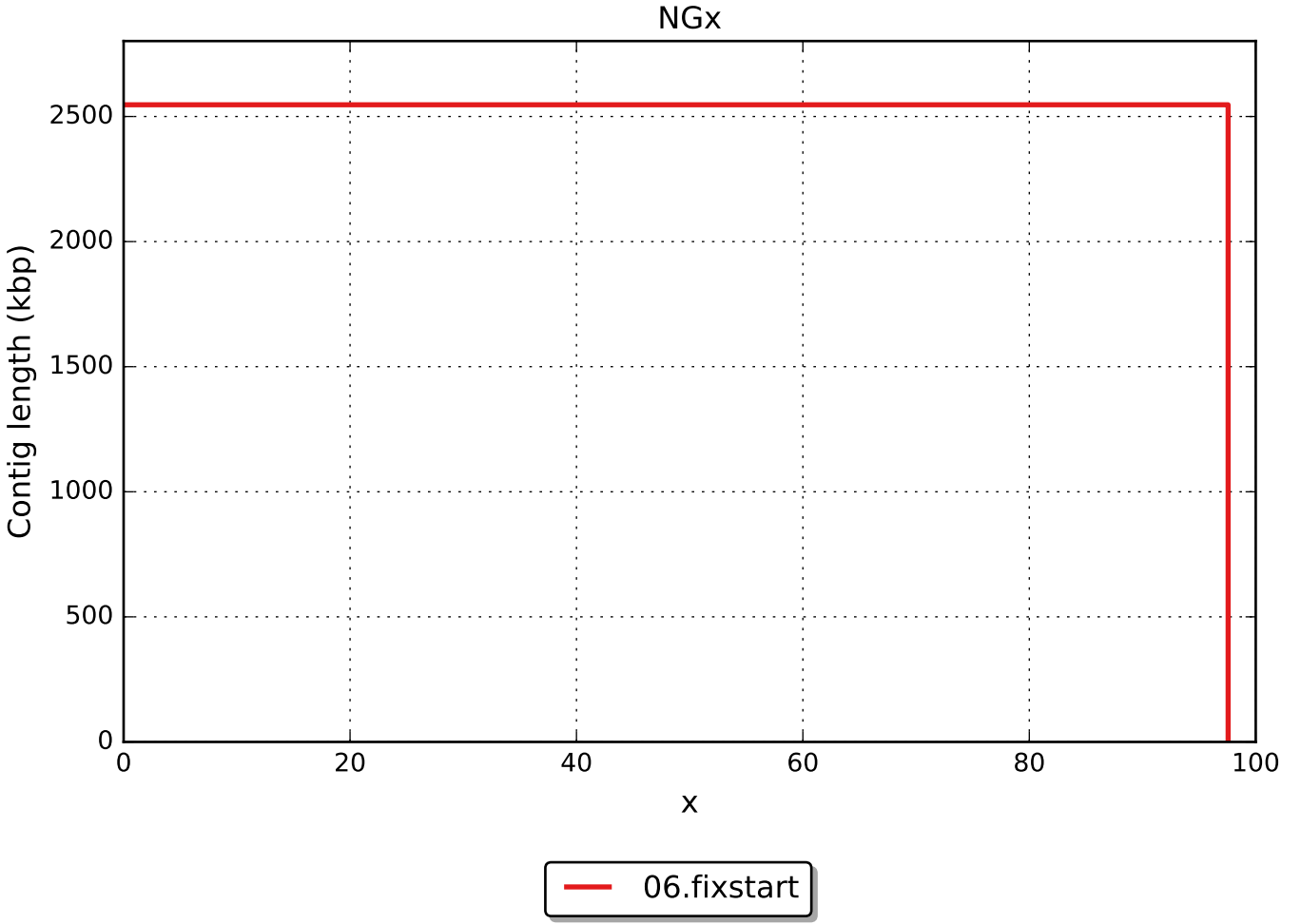
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

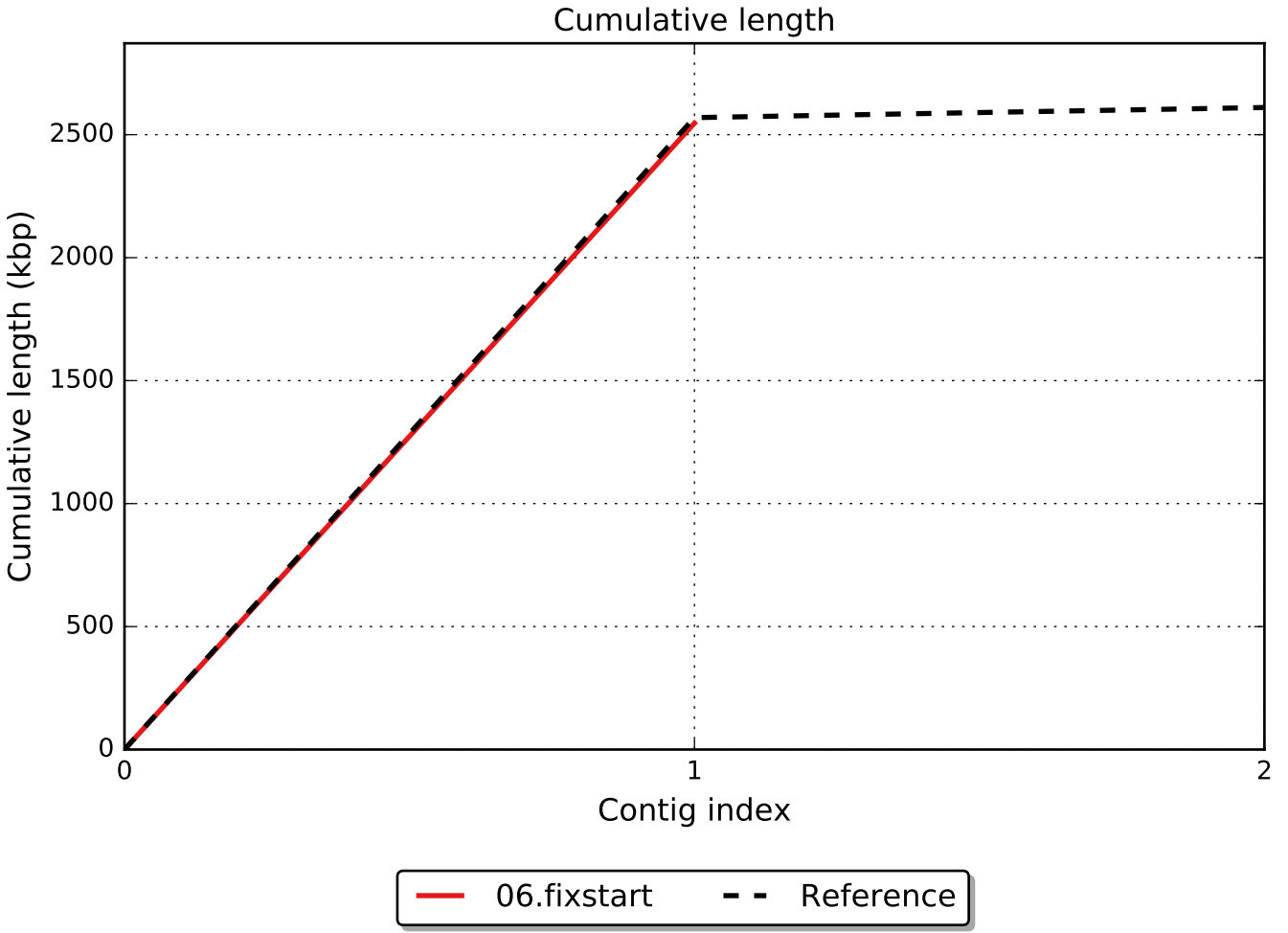
Unaligned report

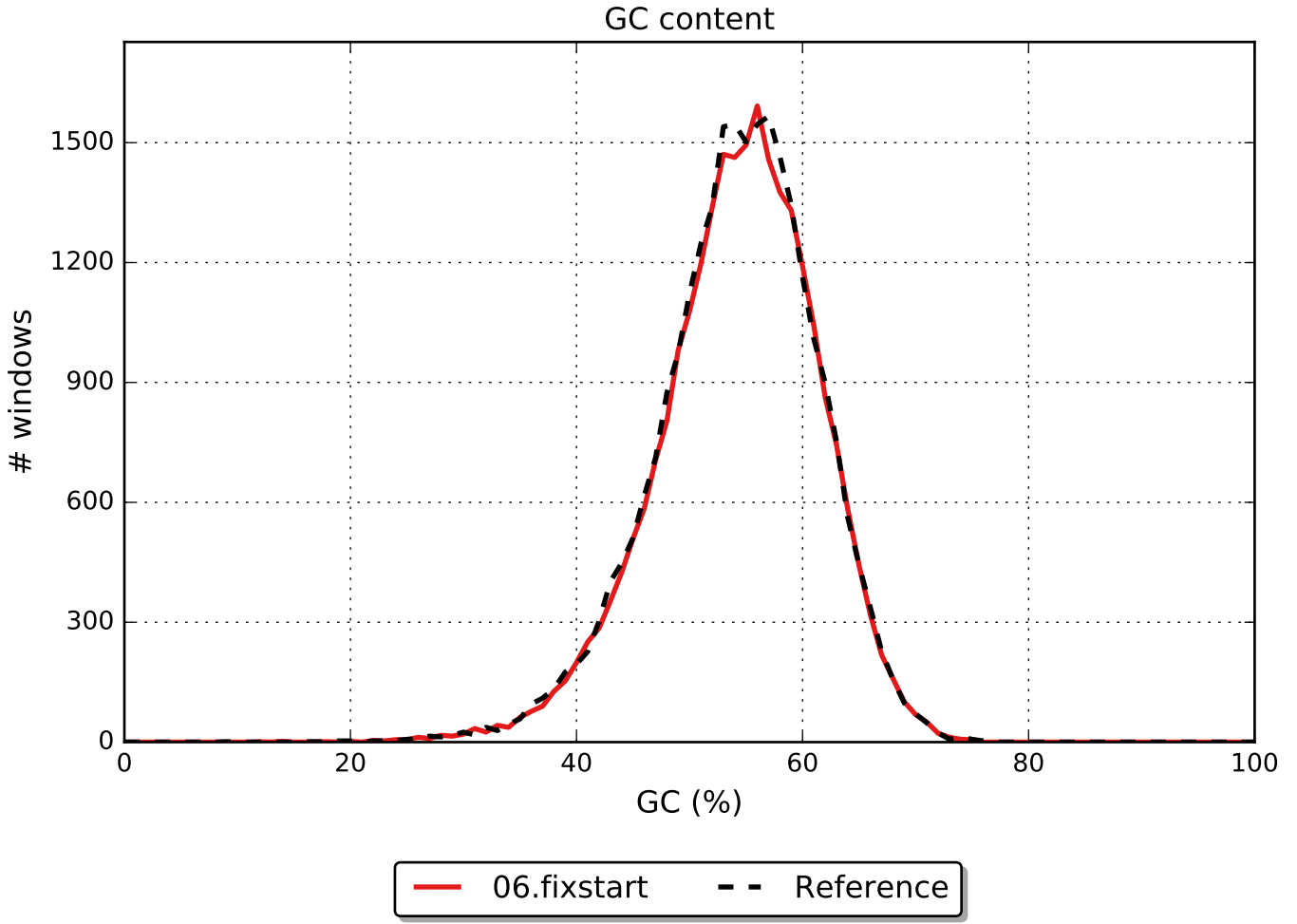
	06.fixstart
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

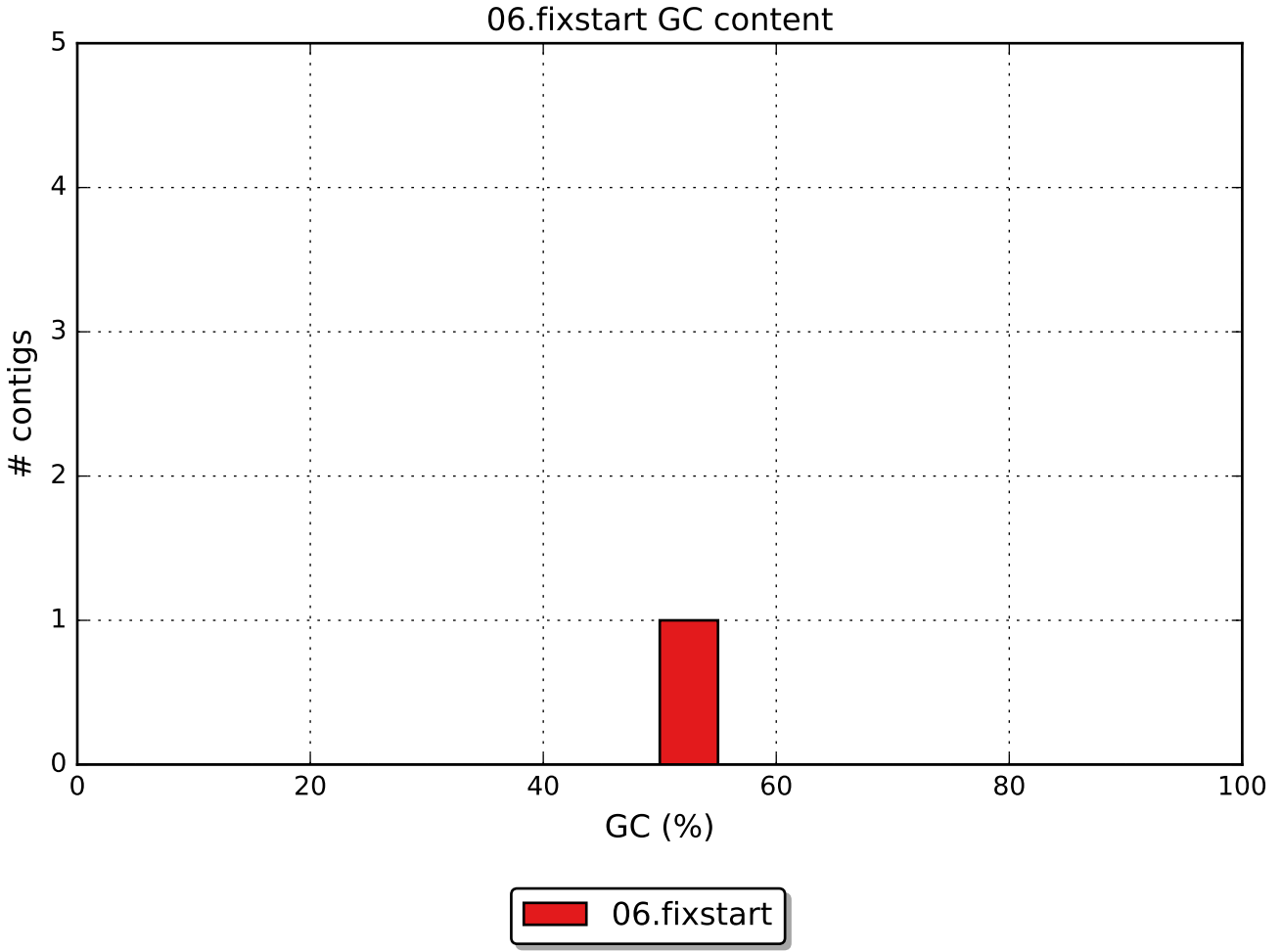
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

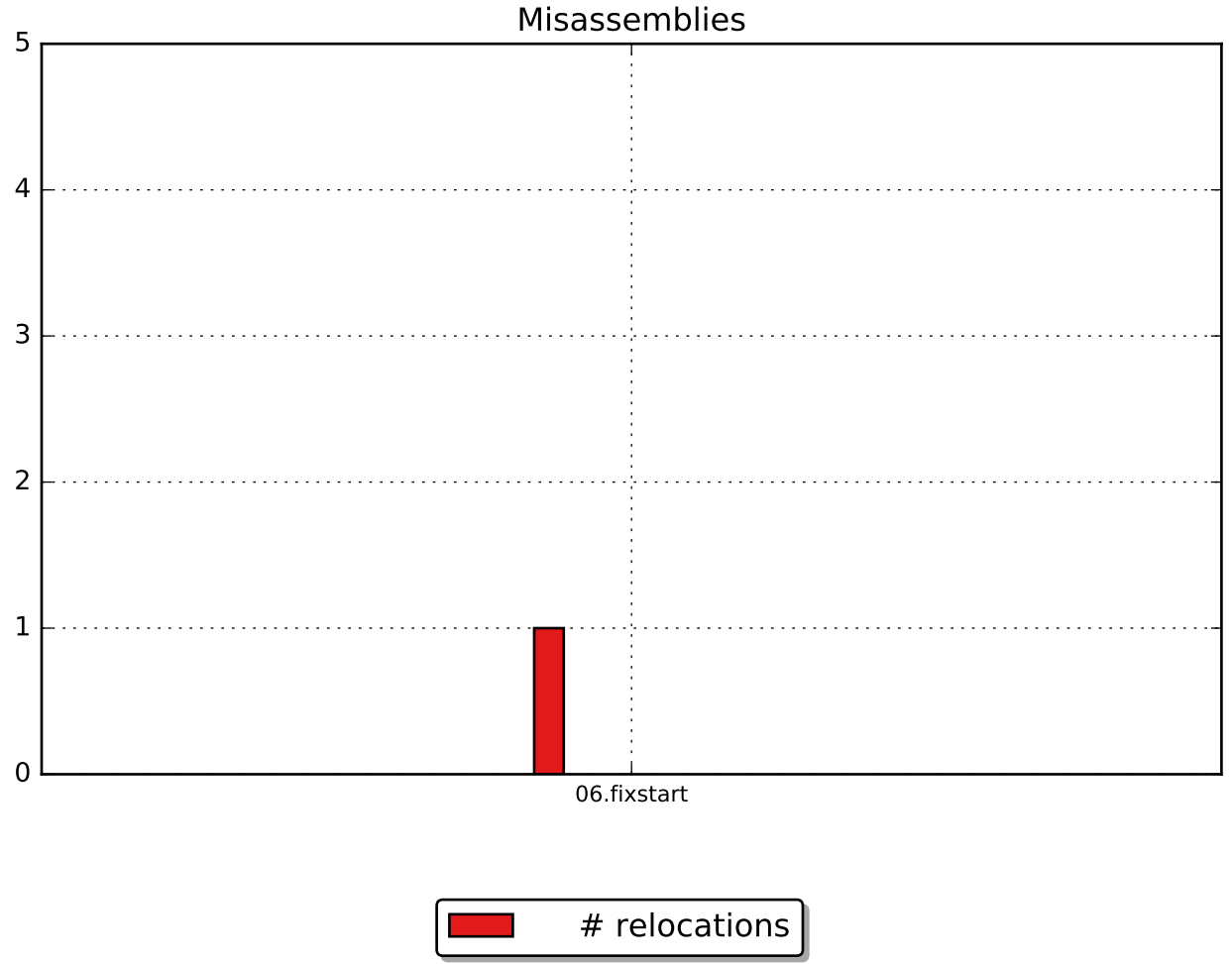

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
06.fixstart

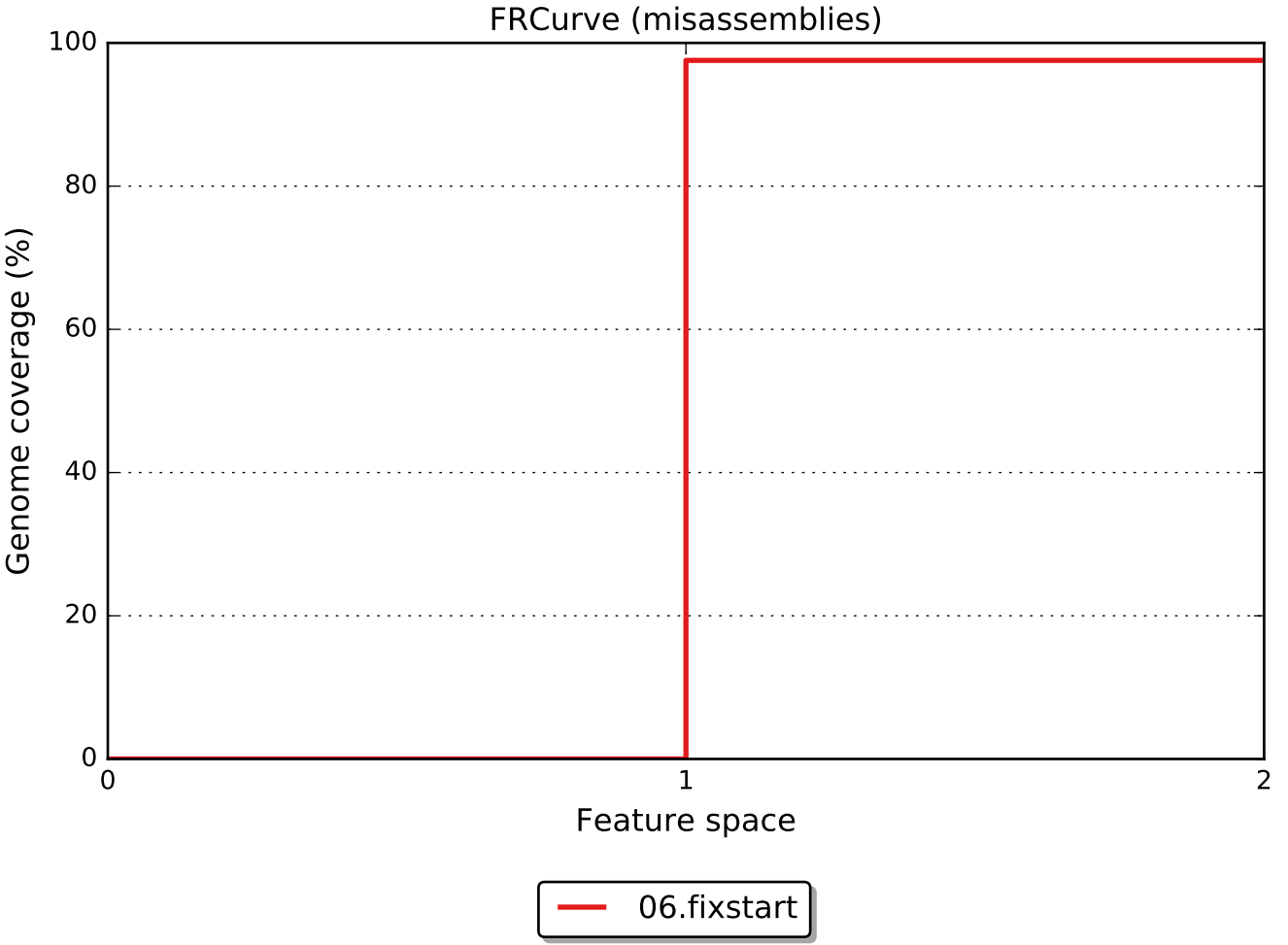

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
06.fixstart

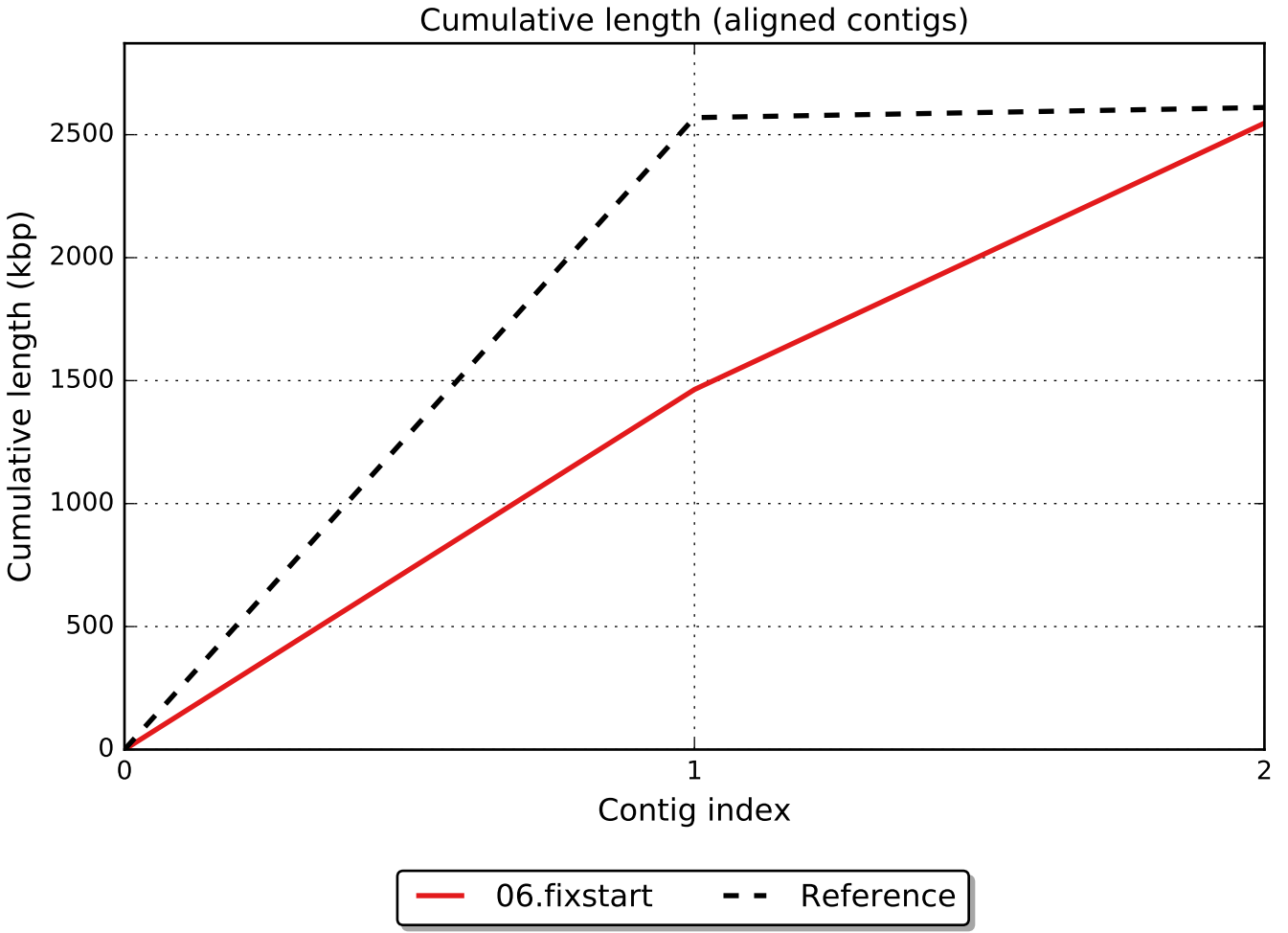

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
Contig index
06.fixstart
Reference

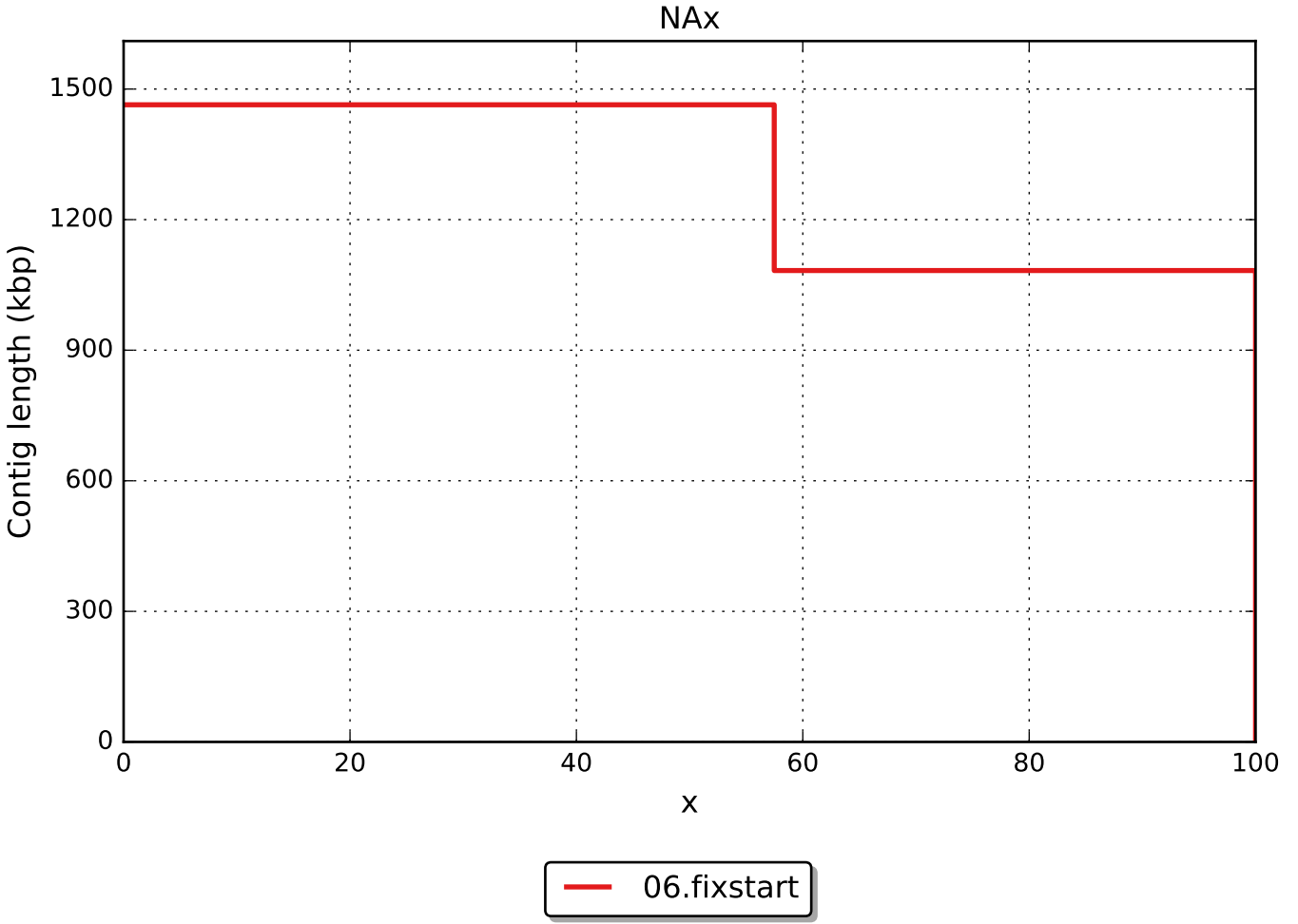

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
06.fixstart
Reference

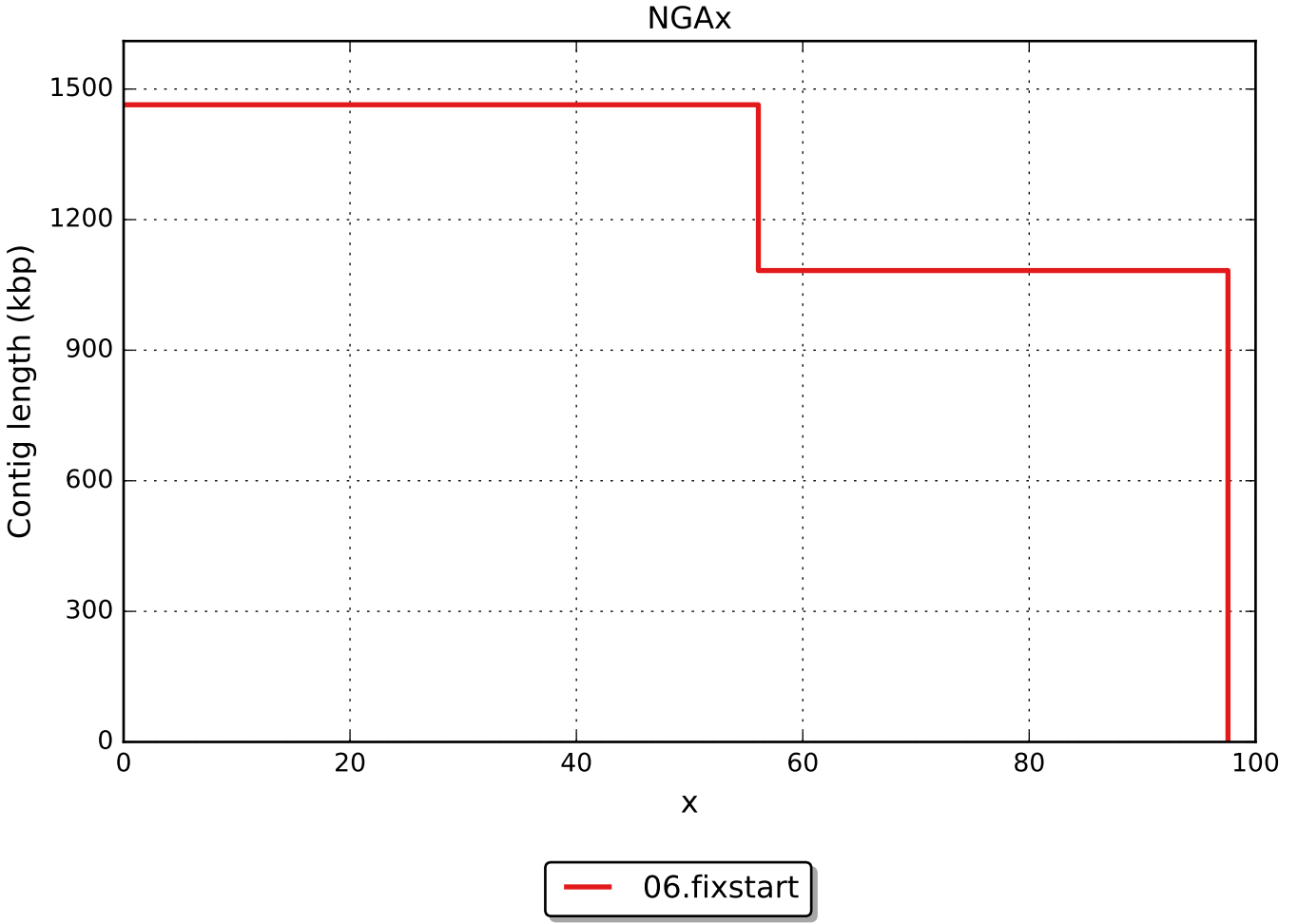

06.fixstart GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
06.fixstart


Misassemblies
5
4
3
2
1
0
06.fixstart
relocations


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
Contig index
06.fixstart
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
06.fixstart


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
06.fixstart