Report

	bin_23
# contigs (>= 0 bp)	507
# contigs (>= 1000 bp)	507
# contigs (>= 5000 bp)	186
# contigs (>= 10000 bp)	84
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	3188556
Total length (>= 1000 bp)	3188556
Total length (>= 5000 bp)	2094624
Total length (>= 10000 bp)	1389223
Total length (>= 25000 bp)	254432
Total length (>= 50000 bp)	61674
# contigs	507
Largest contig	61674
Total length	3188556
Reference length	4282232
N50	7839
N75	4061
L50	108
L75	253
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	506 + 1 part
Unaligned length	3188460
Genome fraction (%)	0.002
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2083.33
# indels per 100 kbp	0.00
Largest alignment	96
Total aligned length	96

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

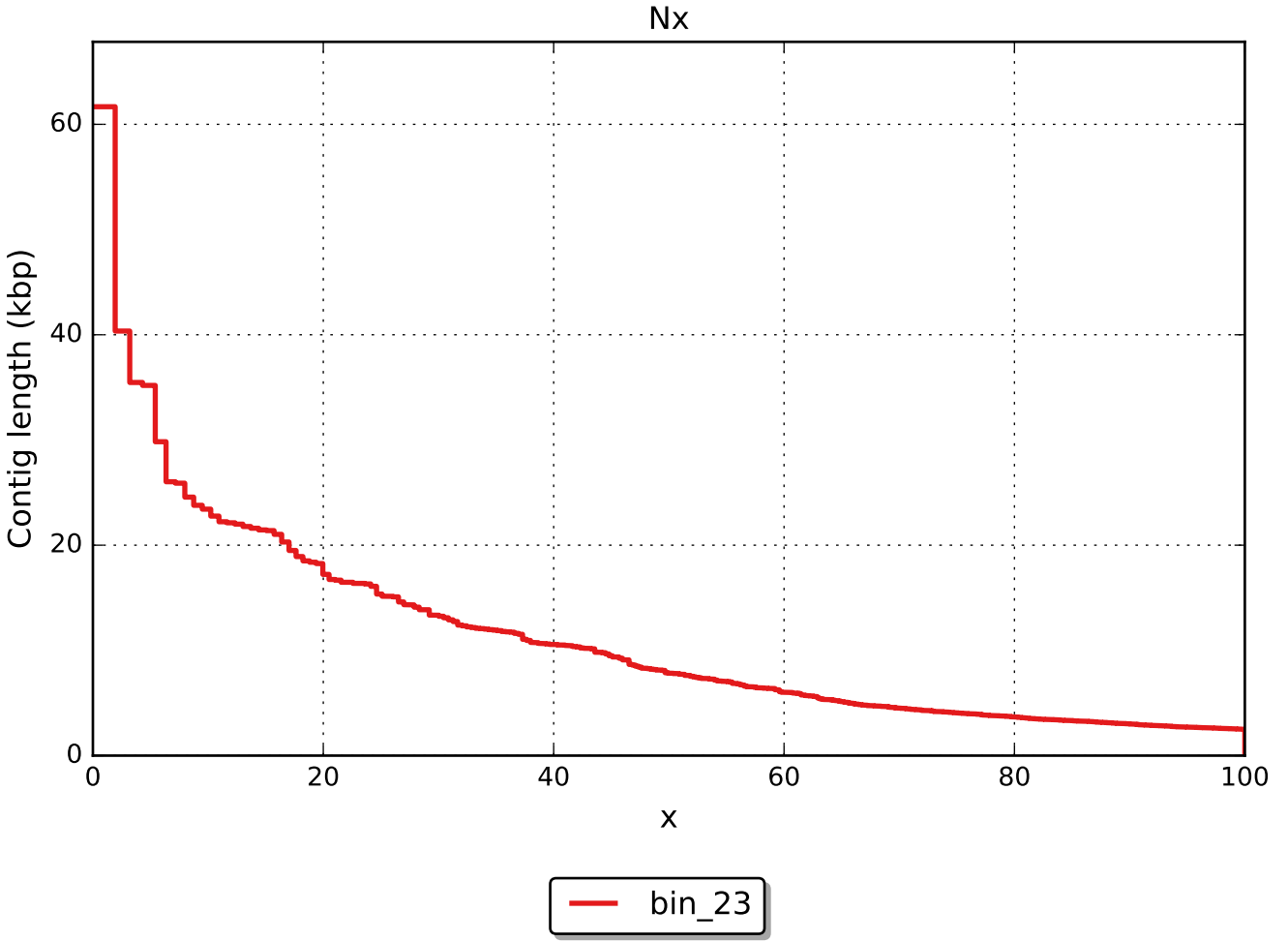
	bin_23
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	2
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

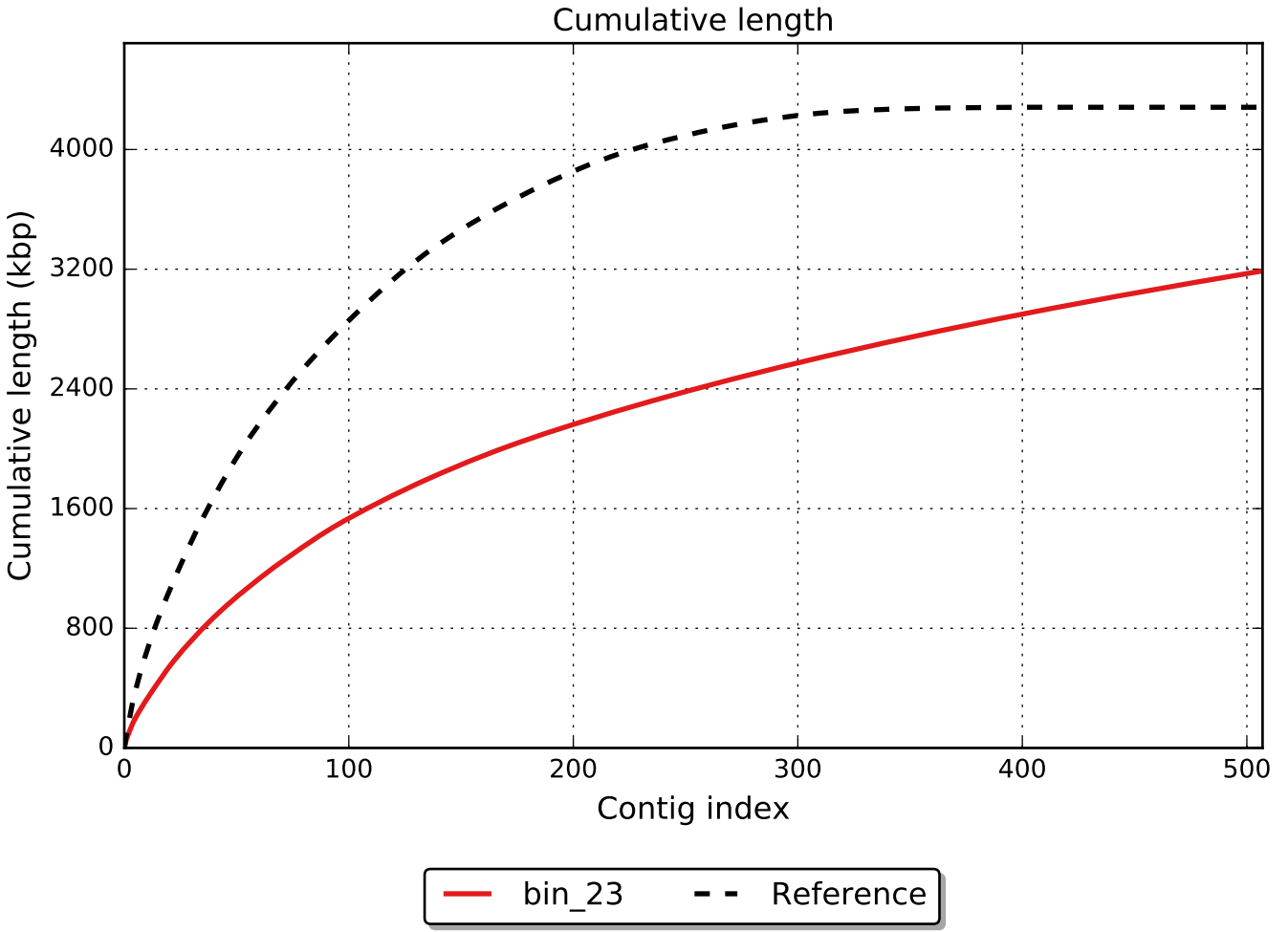
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

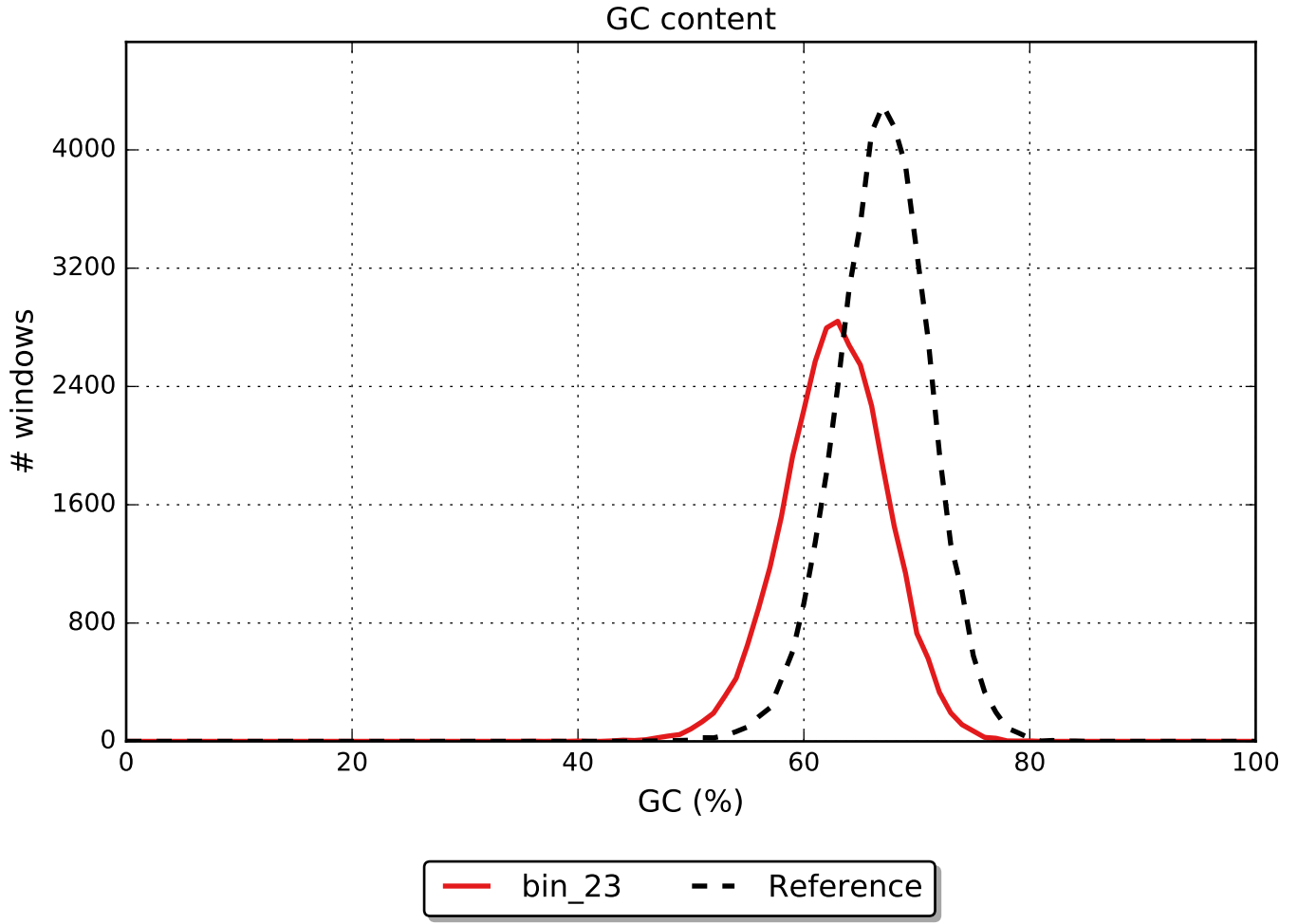
Unaligned report

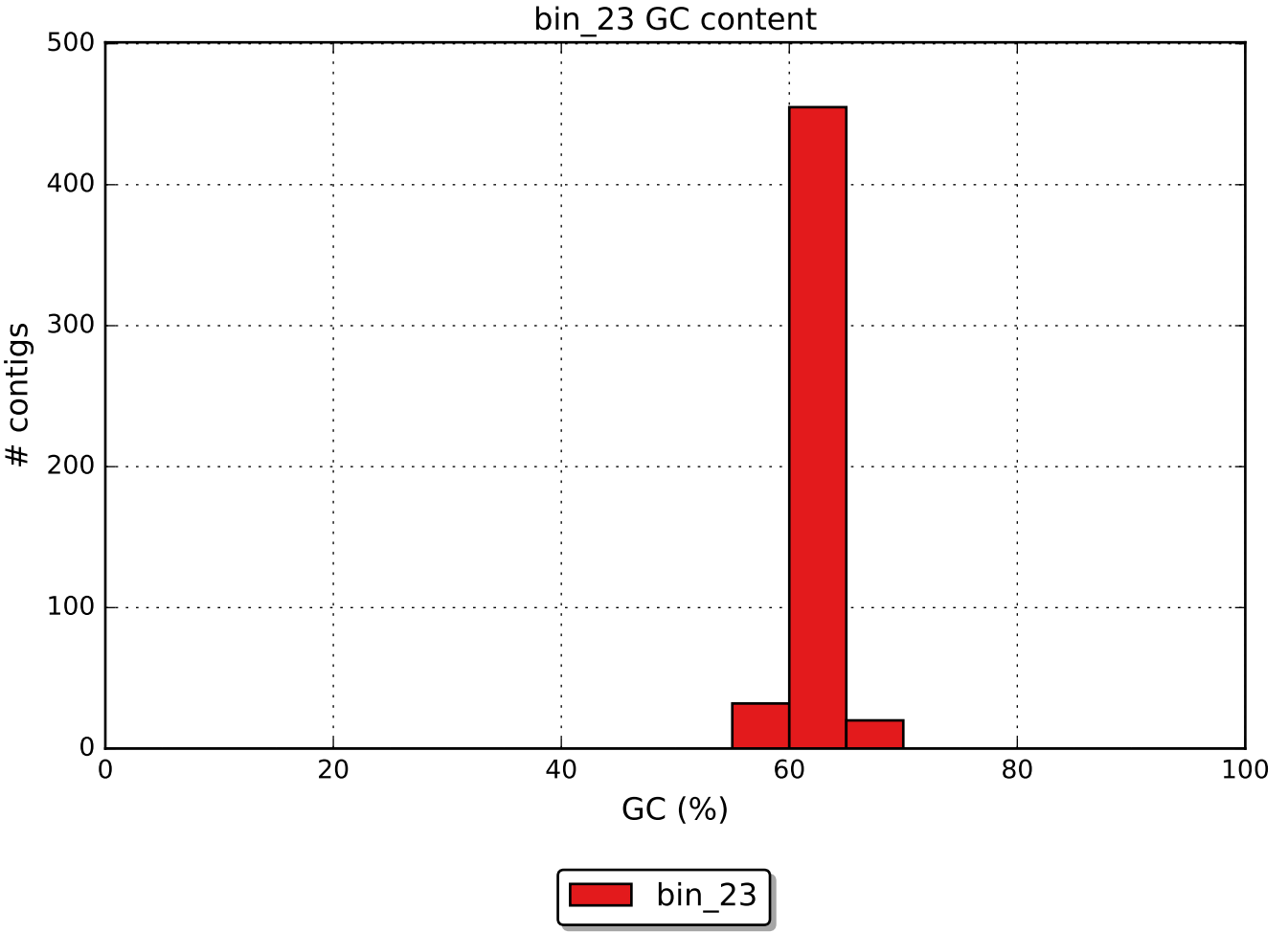
	bin_23
# fully unaligned contigs	506
Fully unaligned length	3183412
# partially unaligned contigs	1
Partially unaligned length	5048
# N's	0

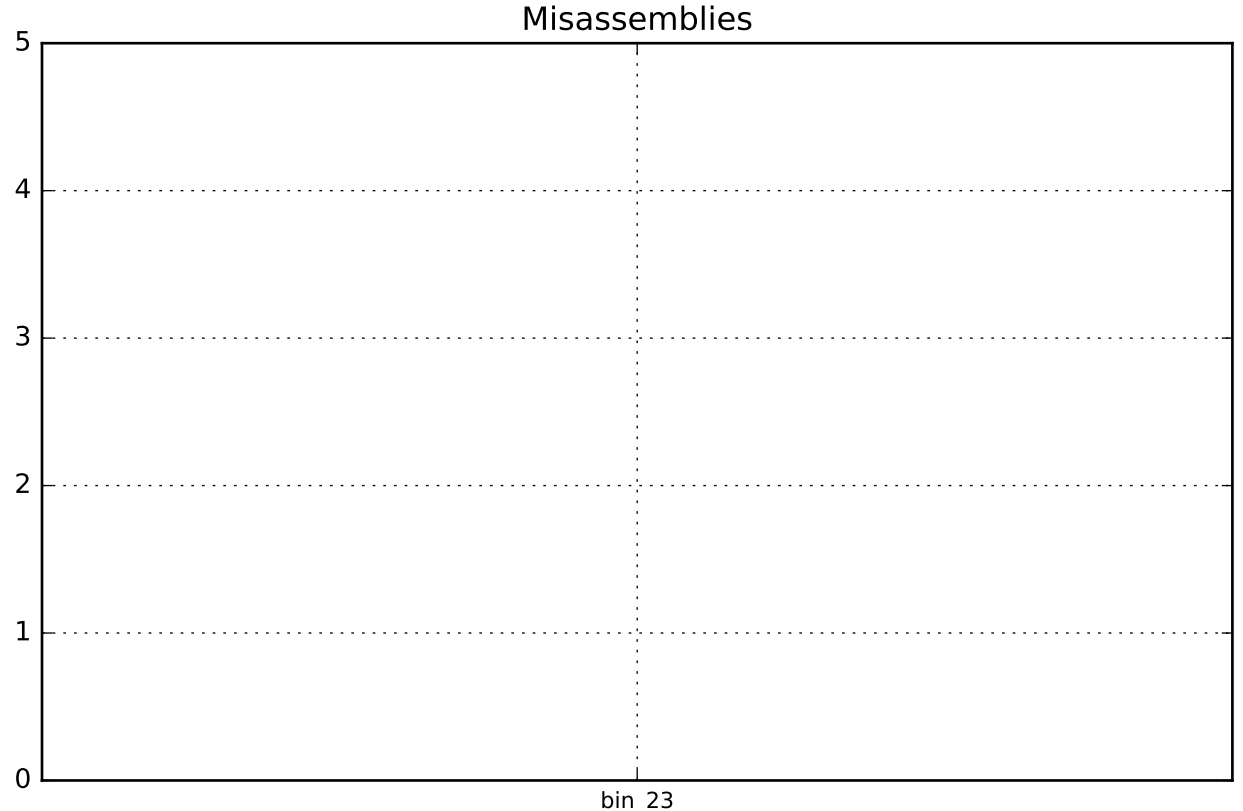
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

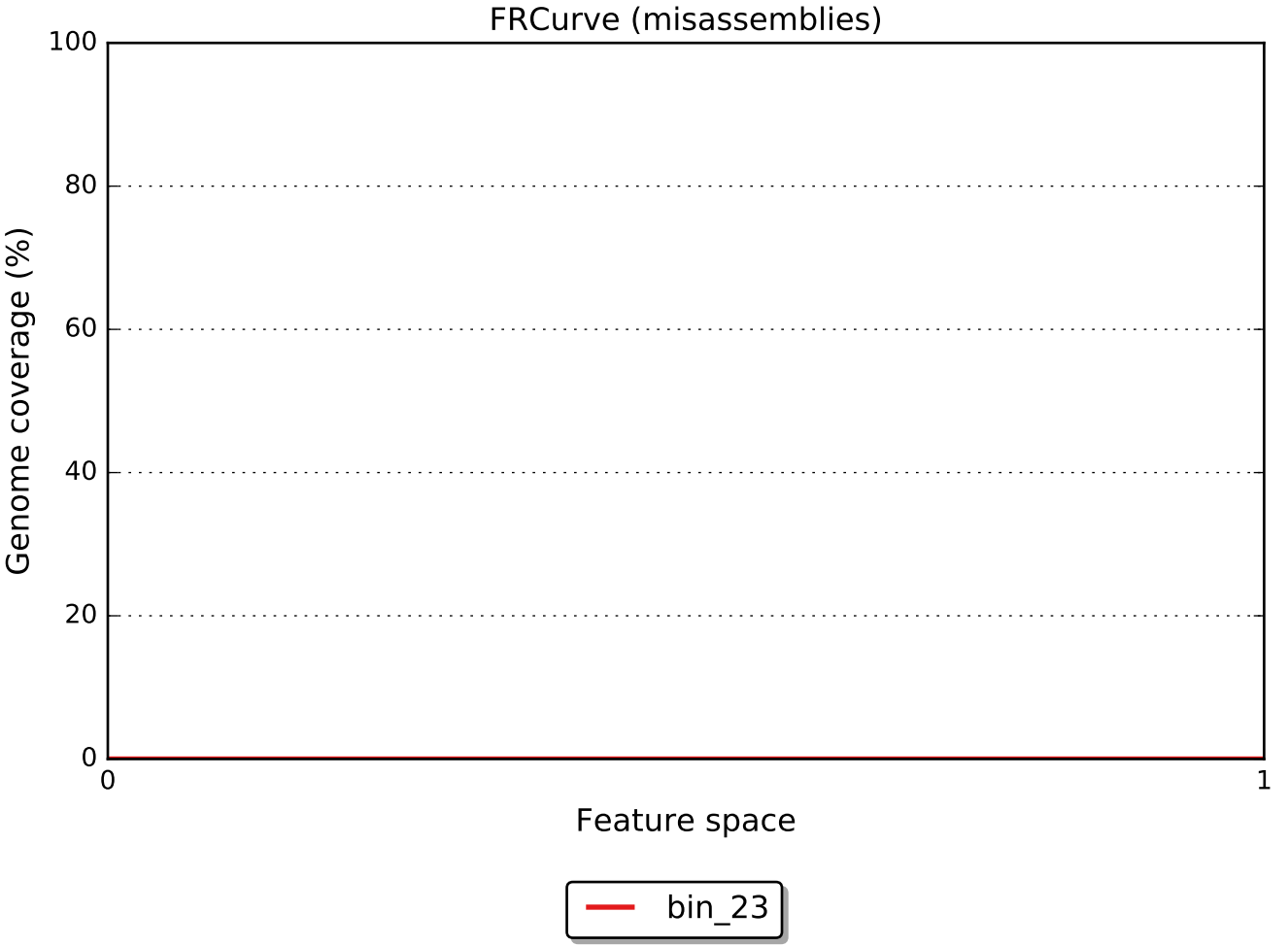

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
bin_23

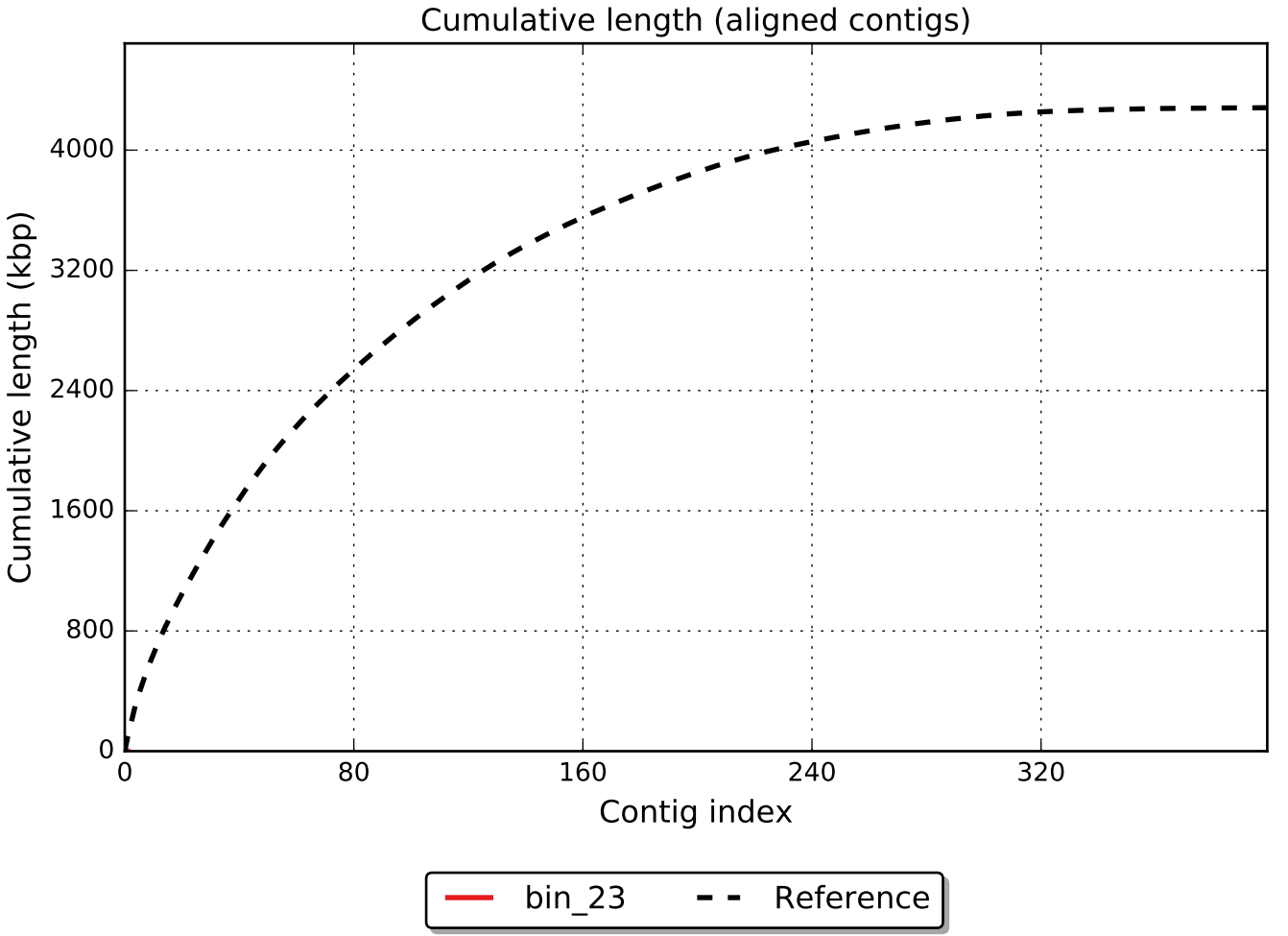

Cumulative length
Cumulative length (kbp)
0
800
1600
2400
3200
4000
0
100
200
300
400
500
Contig index
bin_23
Reference

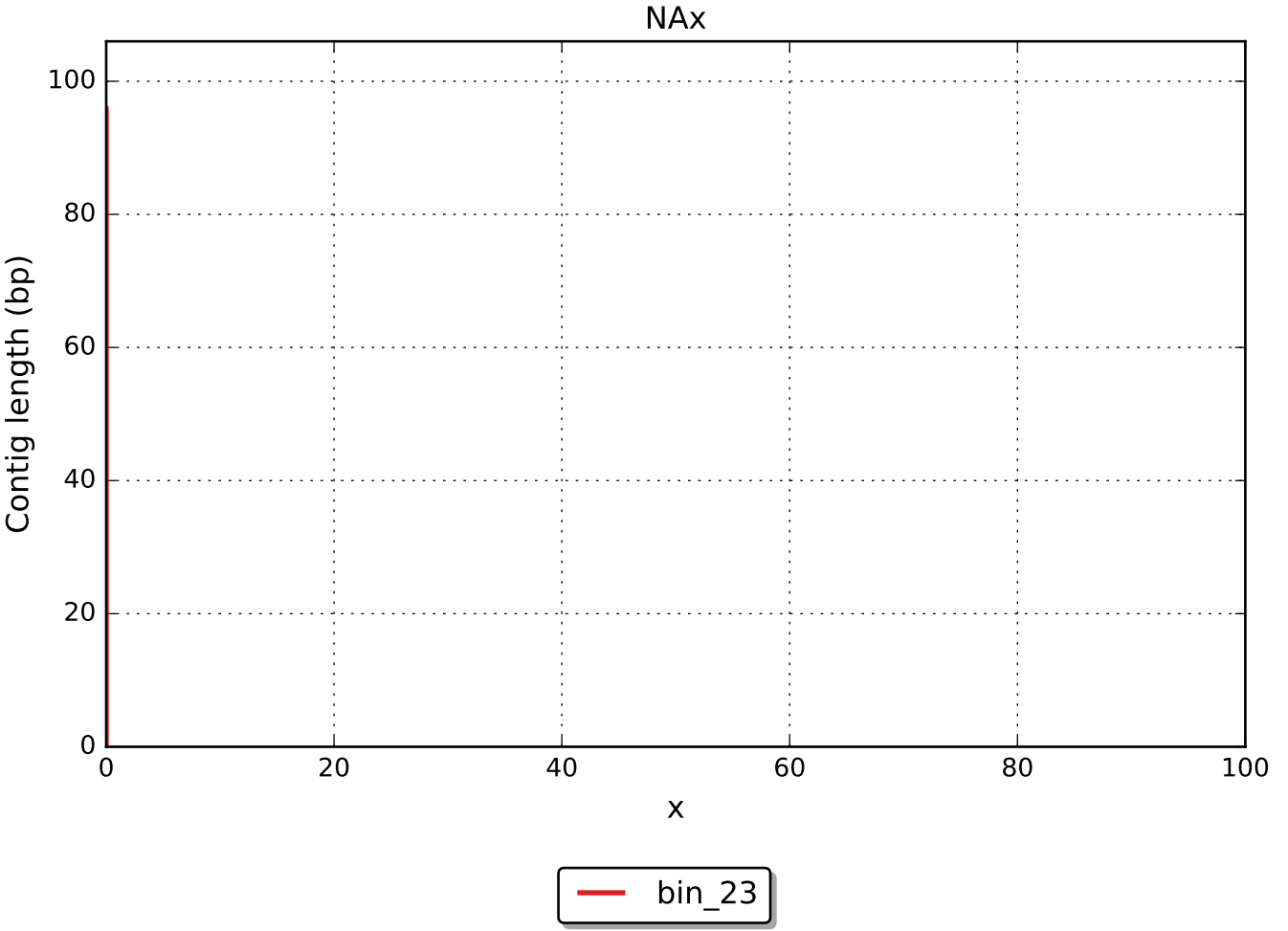

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
bin_23
Reference


bin_23 GC content
contigs
GC (%)
0
100
200
300
400
500
0
20
40
60
80
100
bin_23


Misassemblies
5
4
3
2
1
0
bin_23


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
bin_23


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
800
1600
2400
3200
4000
0
80
160
240
320
Contig index
bin_23
Reference


NAx
Contig length (bp)
0
20
40
60
80
100
0
20
40
60
80
100
x
bin_23