Report

	contigs
# contigs (>= 0 bp)	54
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	8
Total length (>= 0 bp)	3140603
Total length (>= 1000 bp)	3133879
Total length (>= 5000 bp)	3125776
Total length (>= 10000 bp)	3105991
Total length (>= 25000 bp)	3093608
Total length (>= 50000 bp)	3062274
# contigs	18
Largest contig	986763
Total length	3135284
Reference length	3052572
GC (%)	37.67
Reference GC (%)	37.87
N50	840748
NG50	840748
N75	266941
NG75	500609
L50	2
LG50	2
L75	4
LG75	3
# misassemblies	160
# misassembled contigs	8
Misassembled contigs length	3011760
# local misassemblies	18
# unaligned mis. contigs	2
# unaligned contigs	6 + 10 part
Unaligned length	387793
Genome fraction (%)	87.131
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	199.27
# indels per 100 kbp	13.80
Largest alignment	231981
Total aligned length	2747493
NA50	87746
NGA50	107748
NA75	15950
NGA75	19559
LA50	11
LGA50	10
LA75	33
LGA75	30

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

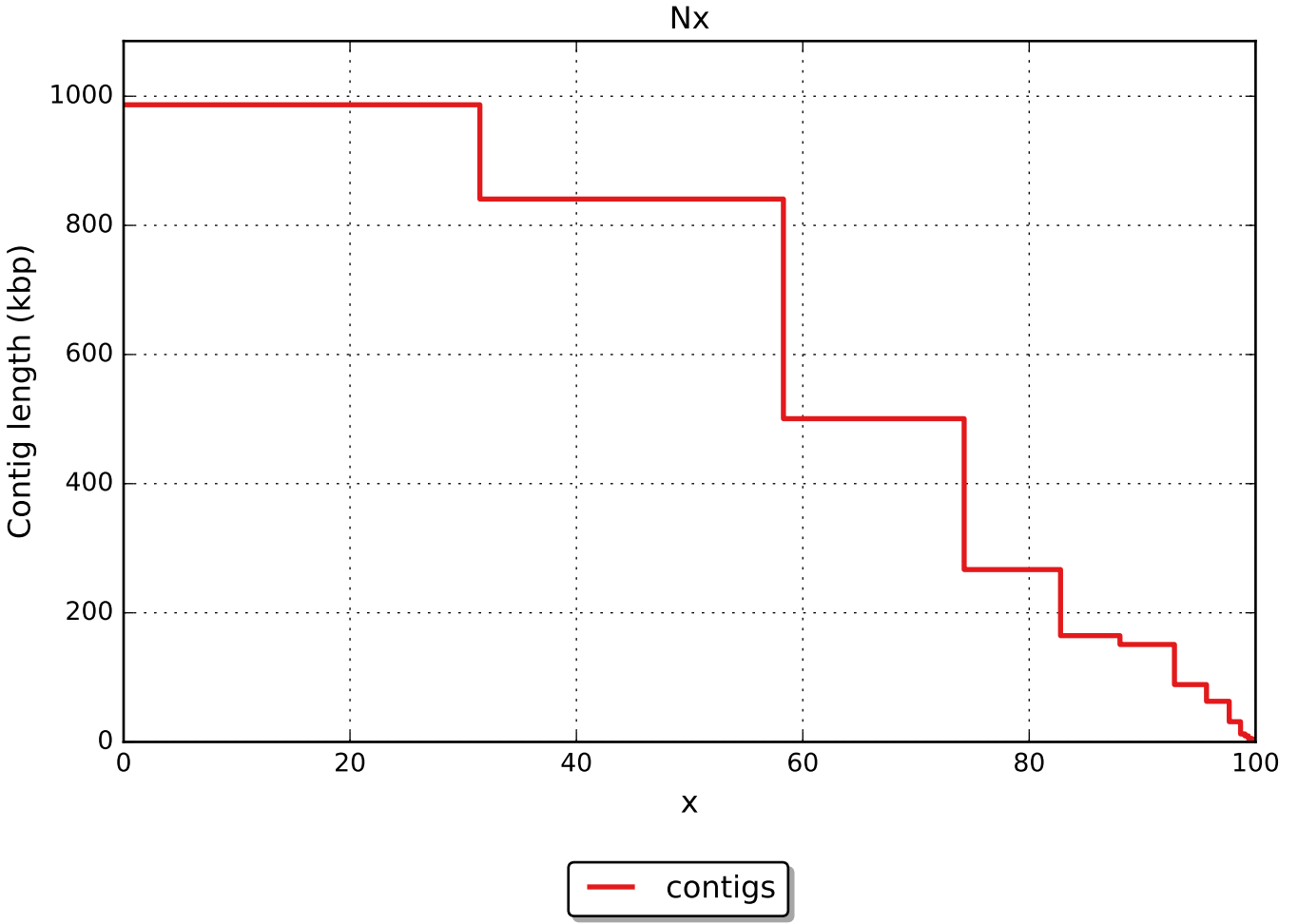
	contigs
# misassemblies	160
# relocations	115
# translocations	45
# inversions	0
# misassembled contigs	8
Misassembled contigs length	3011760
# local misassemblies	18
# unaligned mis. contigs	2
# mismatches	5300
# indels	367
# indels (<= 5 bp)	349
# indels (> 5 bp)	18
Indels length	829

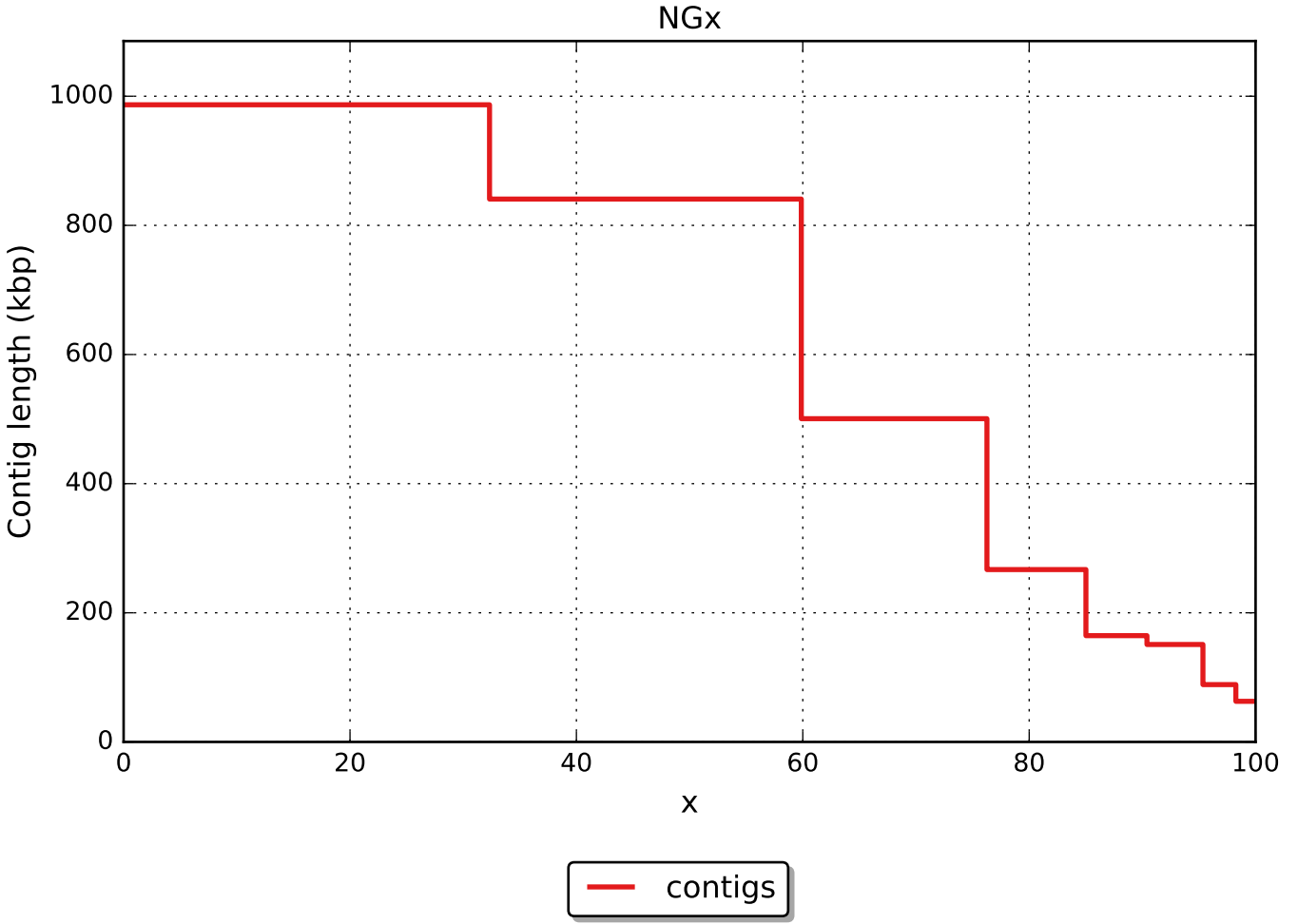
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

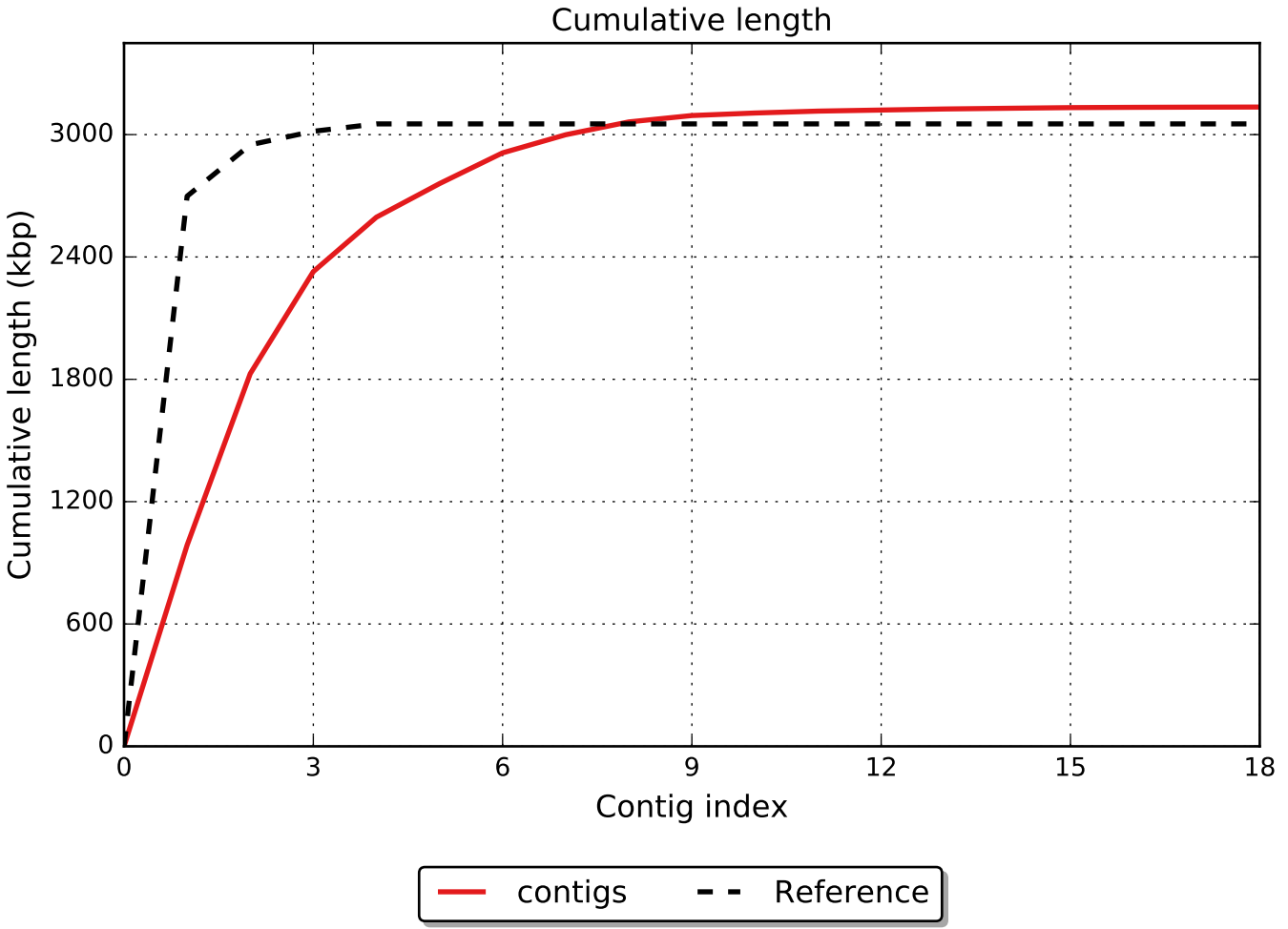
Unaligned report

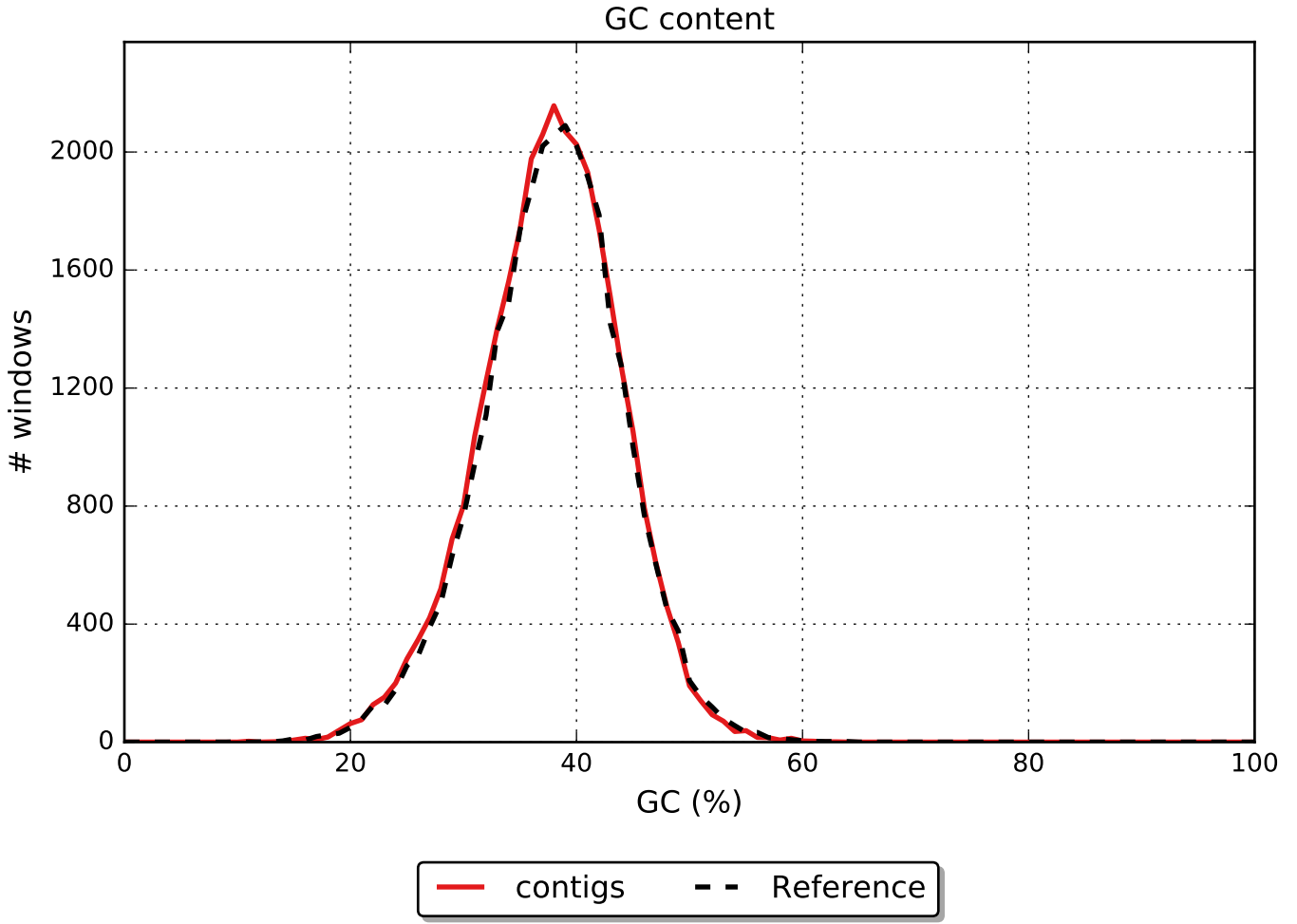
	contigs
# fully unaligned contigs	6
Fully unaligned length	14740
# partially unaligned contigs	10
Partially unaligned length	373053
# N's	0

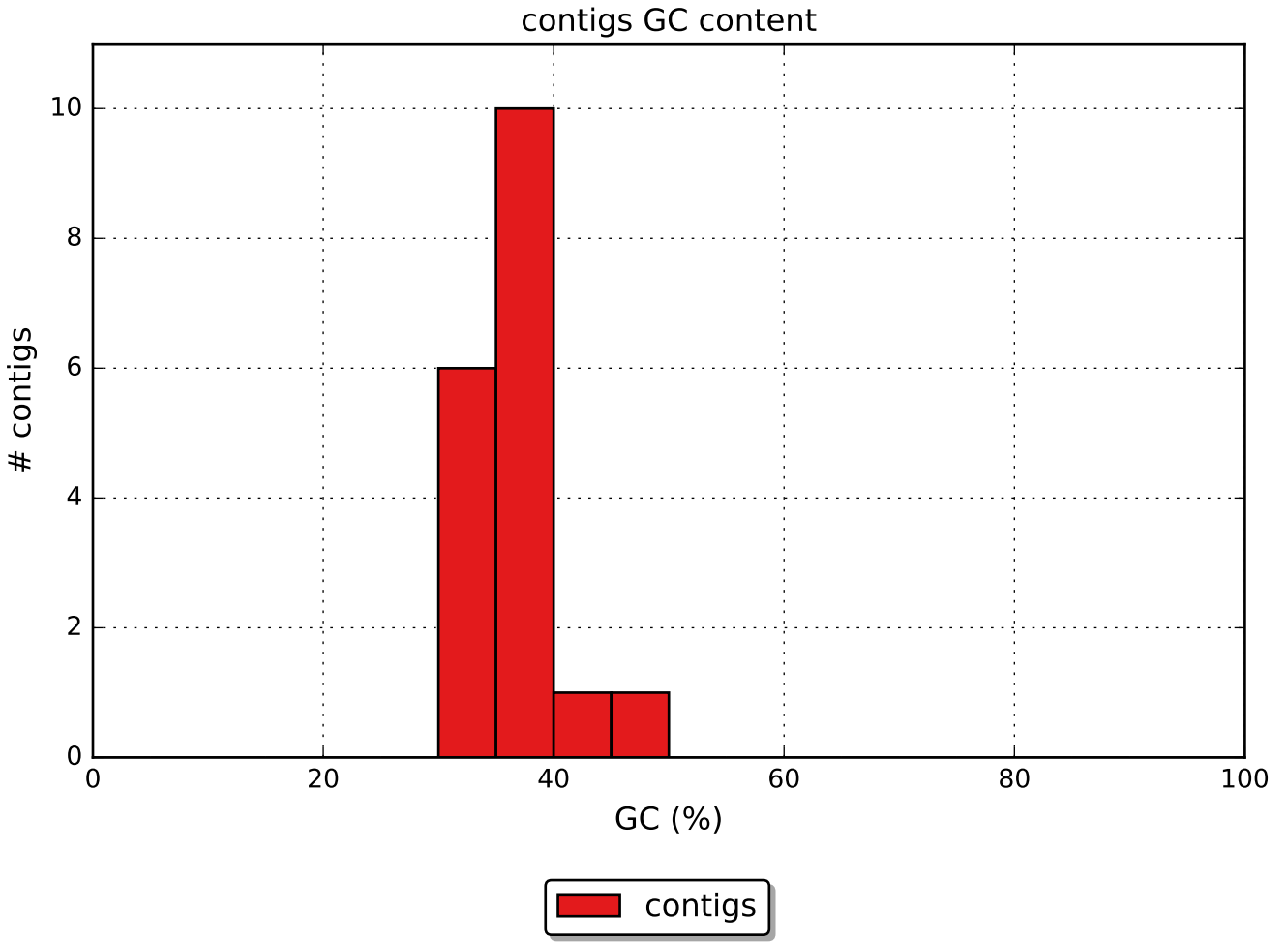
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

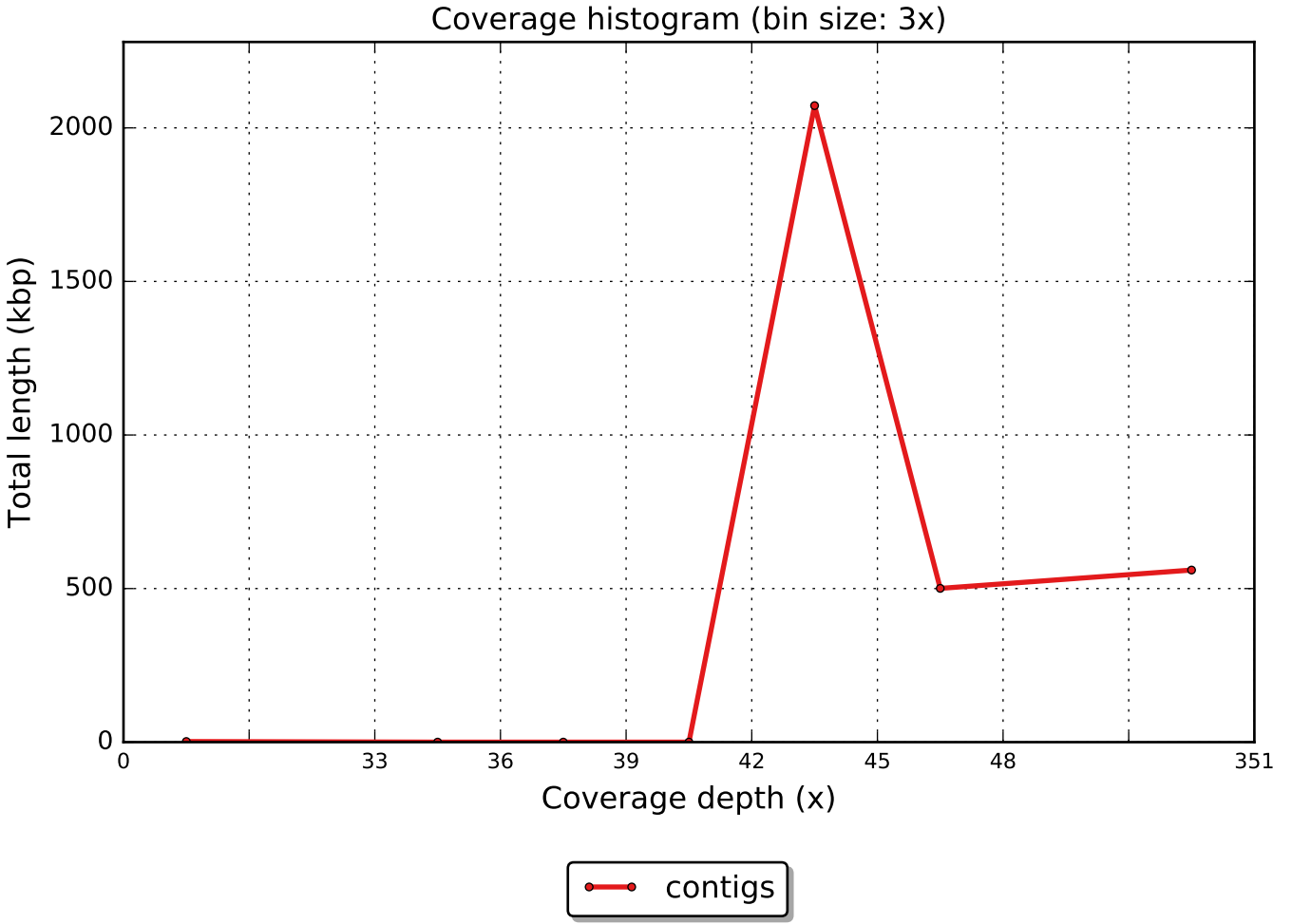

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
contigs

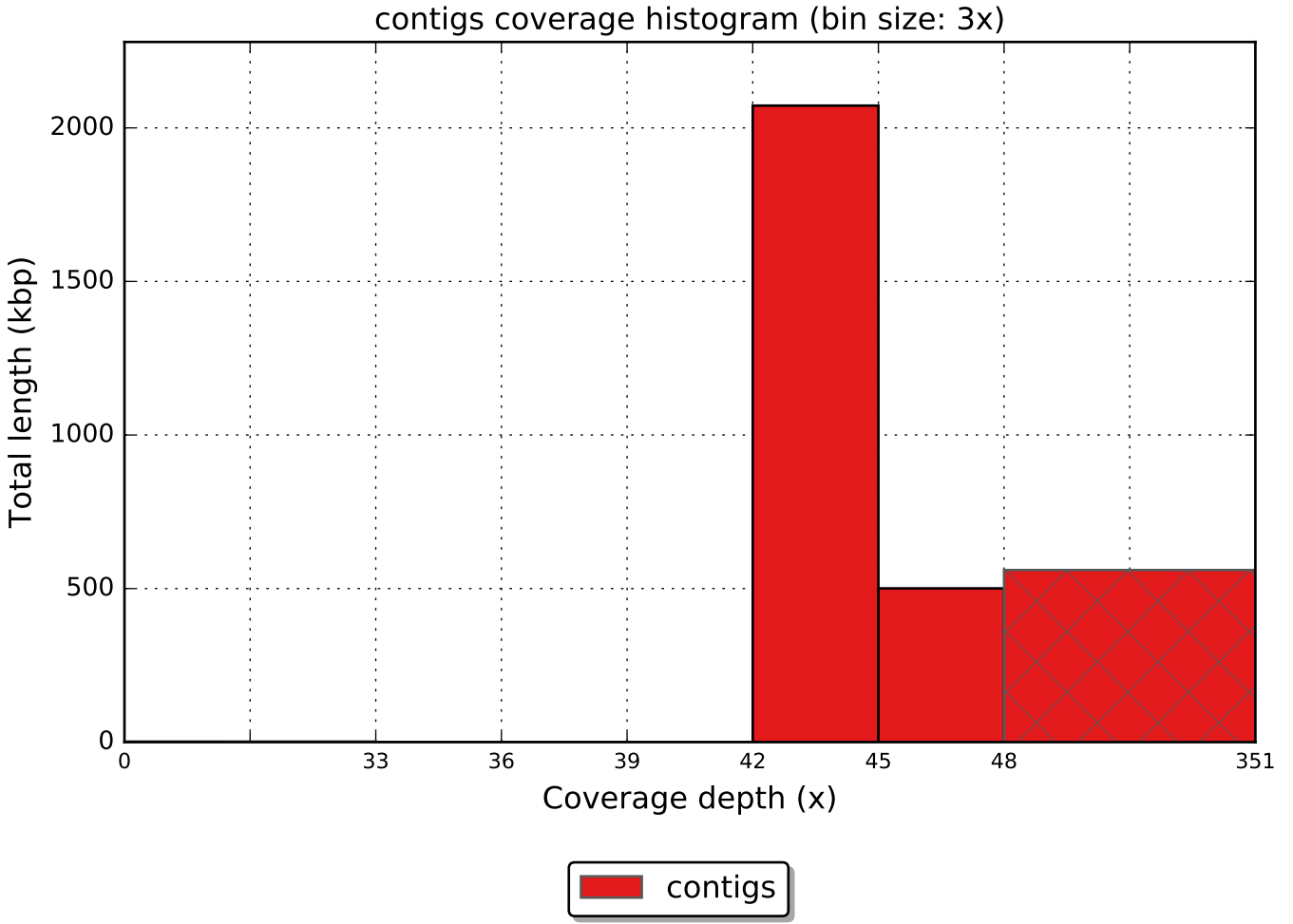

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
contigs

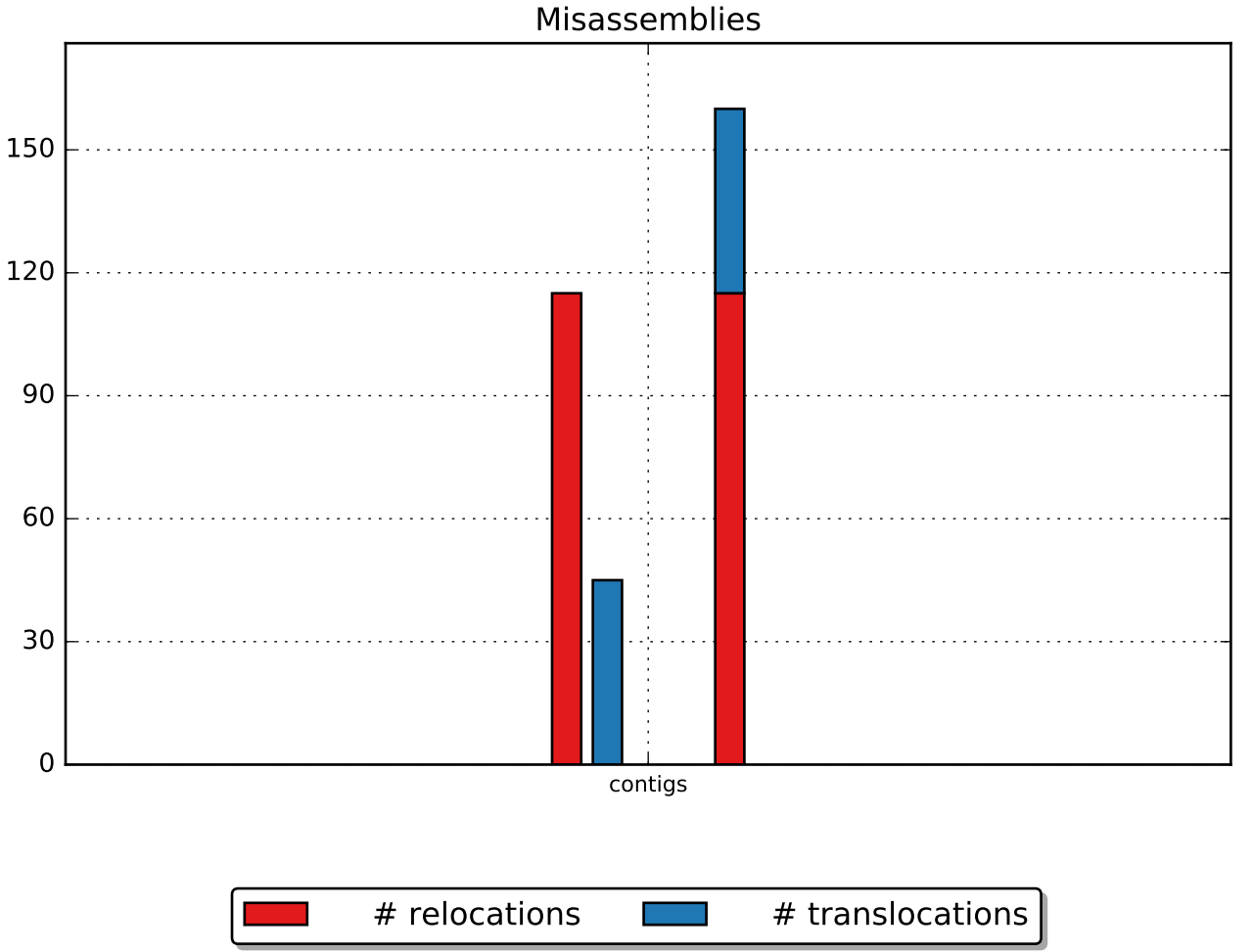

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
3
6
9
12
15
18
Contig index
contigs
Reference

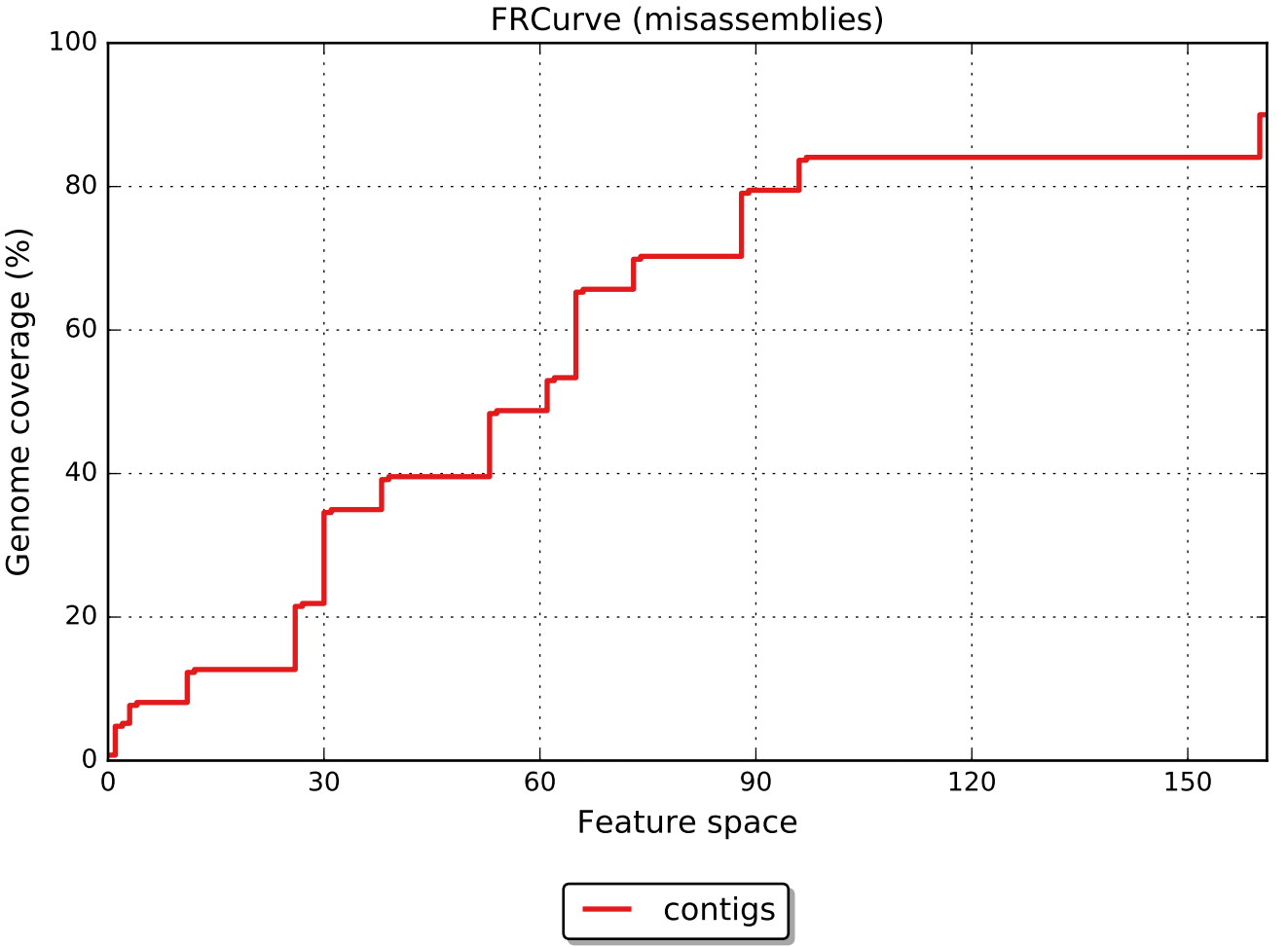

GC content
windows
GC (%)
0
400
800
1200
1600
2000
0
20
40
60
80
100
contigs
Reference

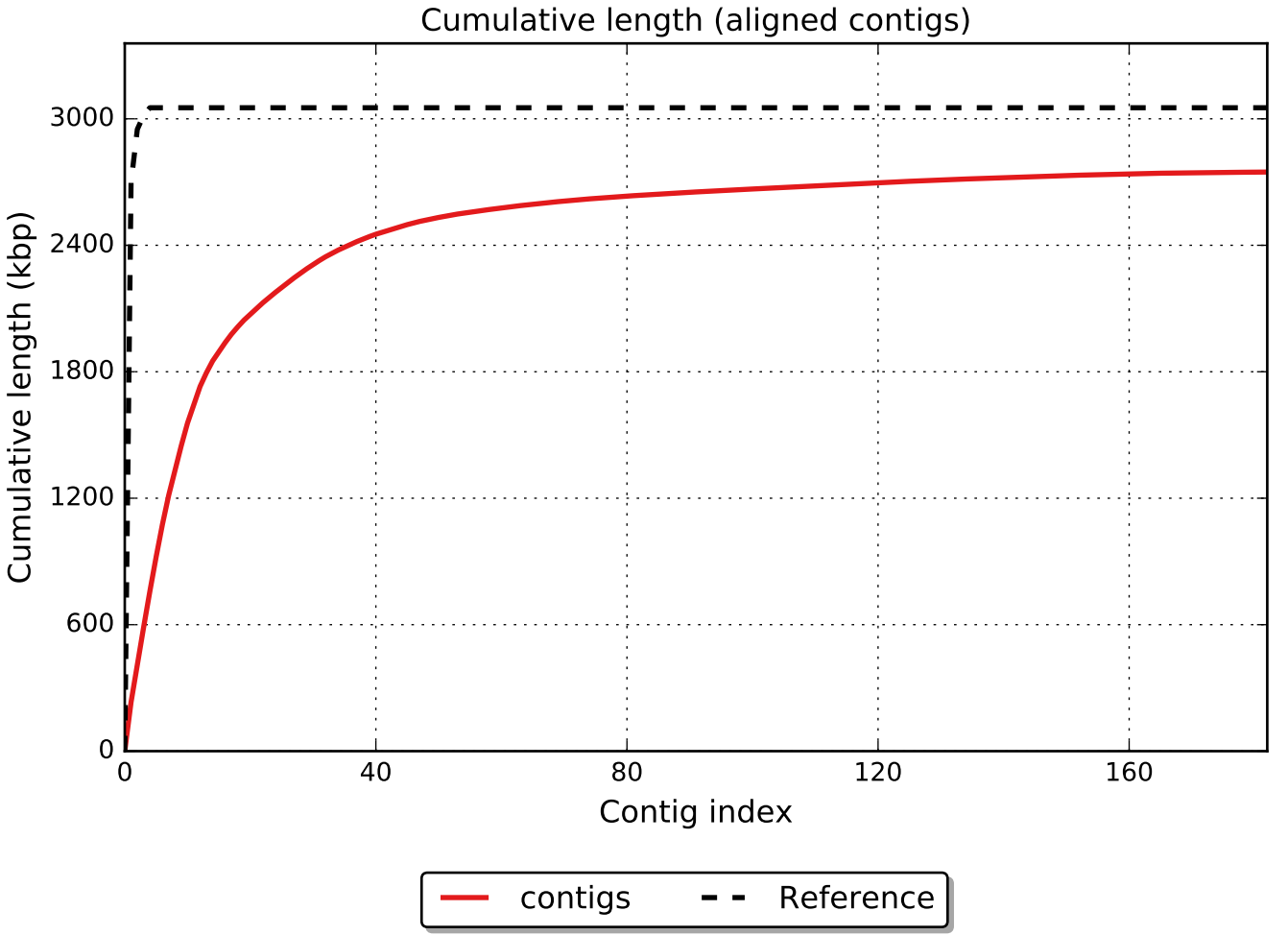

contigs GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
contigs

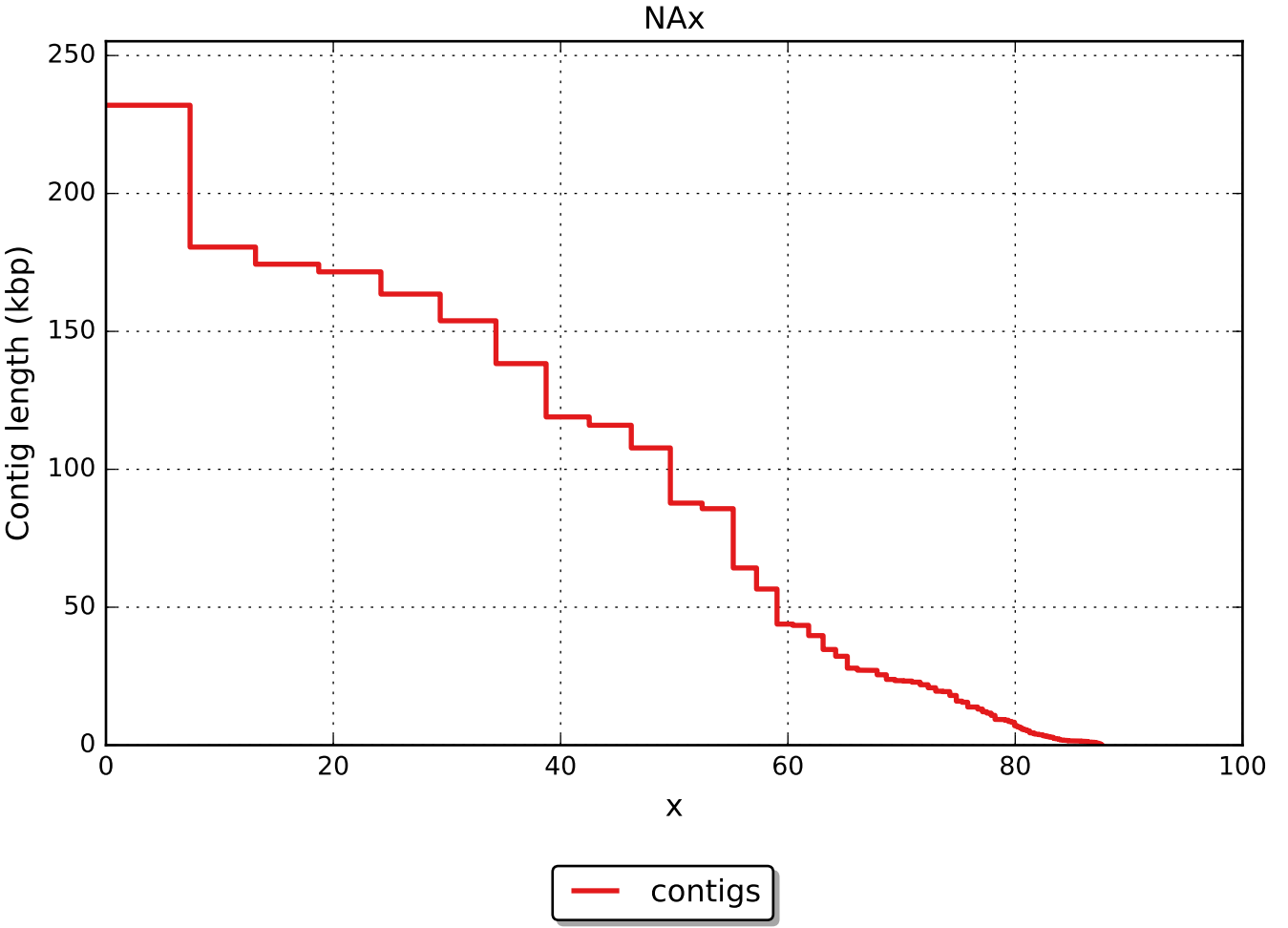

Coverage histogram (bin size: 3x)
Total length (kbp)
2000
1500
1000
500
0
0
33
36
39
42
45
48
351
Coverage depth (x)
contigs

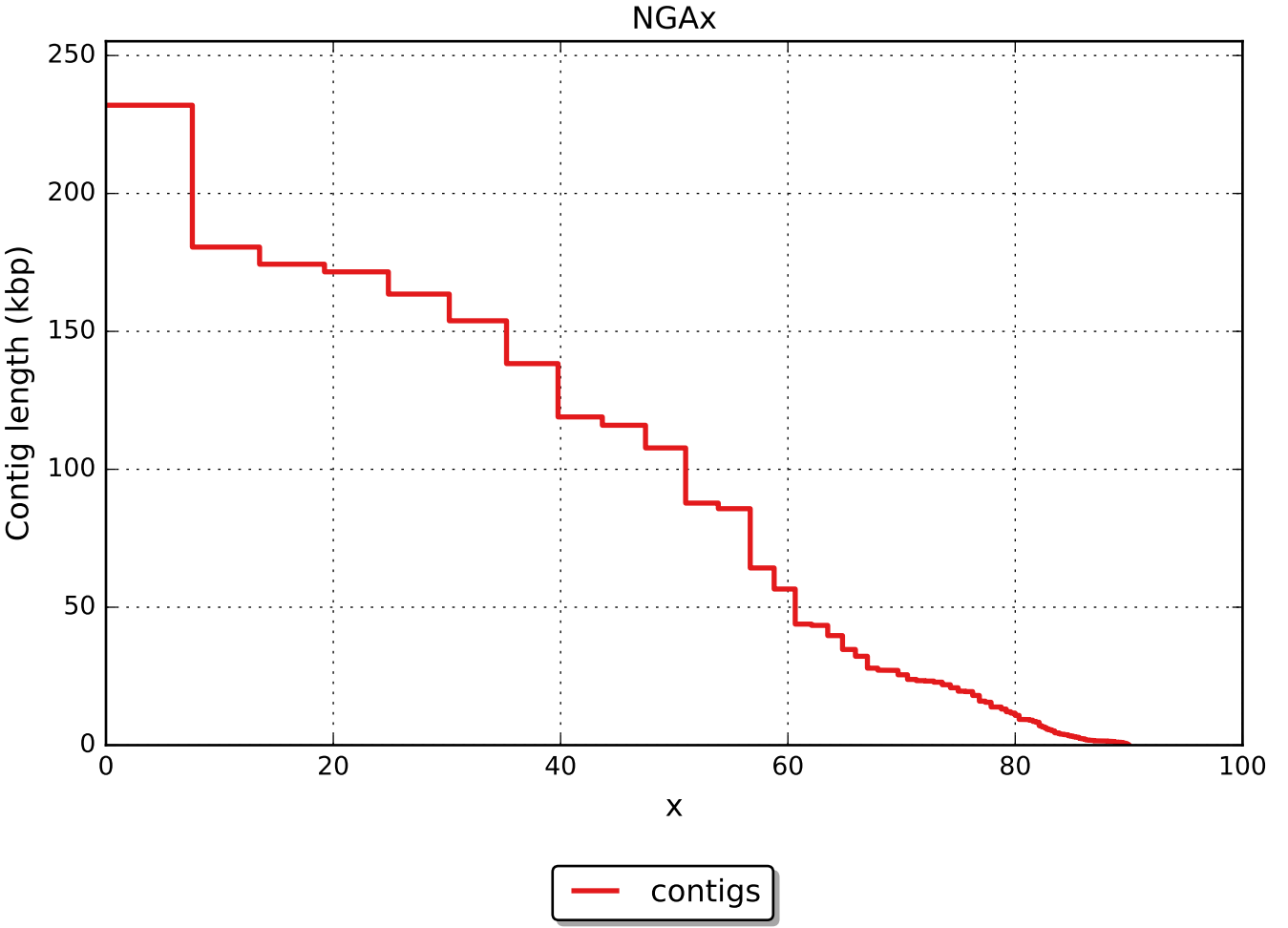

contigs coverage histogram (bin size: 3x)
Total length (kbp)
2000
1500
1000
500
0
0
33
36
39
42
45
48
351
Coverage depth (x)
contigs


Misassemblies
150
120
90
60
30
0
contigs
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
30
60
90
120
150
Feature space
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
40
80
120
160
Contig index
contigs
Reference


NAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
contigs