Report

	contigs
# contigs (>= 0 bp)	189
# contigs (>= 1000 bp)	49
# contigs (>= 5000 bp)	32
# contigs (>= 10000 bp)	23
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	3098278
Total length (>= 1000 bp)	3073892
Total length (>= 5000 bp)	3025806
Total length (>= 10000 bp)	2961855
Total length (>= 25000 bp)	2867451
Total length (>= 50000 bp)	2831946
# contigs	53
Largest contig	542117
Total length	3076511
Reference length	3168410
GC (%)	37.63
Reference GC (%)	37.70
N50	179830
NG50	179830
N75	132475
NG75	125623
L50	5
LG50	5
L75	10
LG75	11
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	19277
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 1 part
Unaligned length	6126
Genome fraction (%)	96.797
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.73
# indels per 100 kbp	4.53
Largest alignment	542117
Total aligned length	3070385
NA50	179830
NGA50	179830
NA75	132475
NGA75	125623
LA50	5
LGA50	5
LA75	10
LGA75	11

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

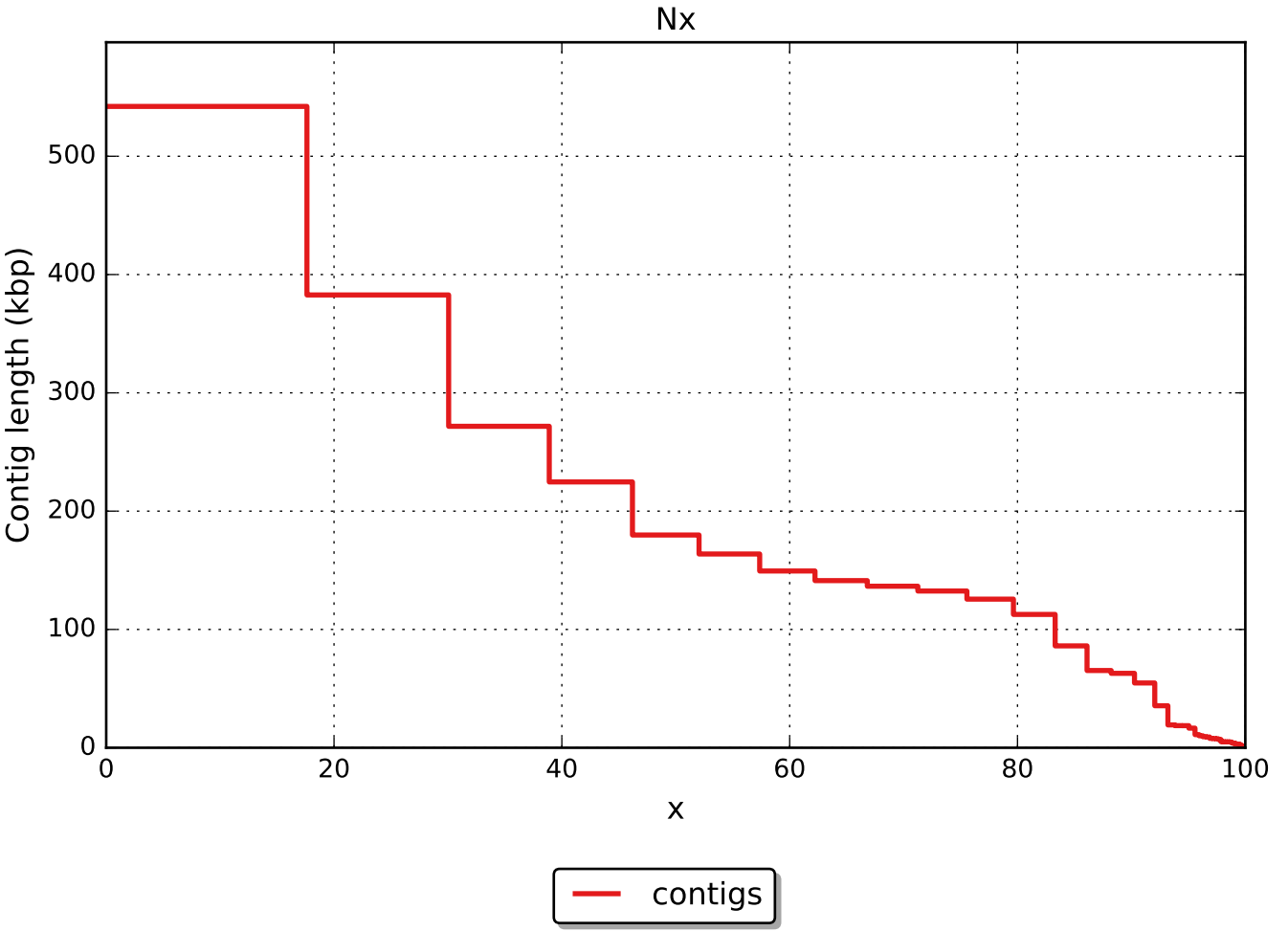
	contigs
# misassemblies	1
# relocations	0
# translocations	1
# inversions	0
# misassembled contigs	1
Misassembled contigs length	19277
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	329
# indels	139
# indels (<= 5 bp)	131
# indels (> 5 bp)	8
Indels length	268

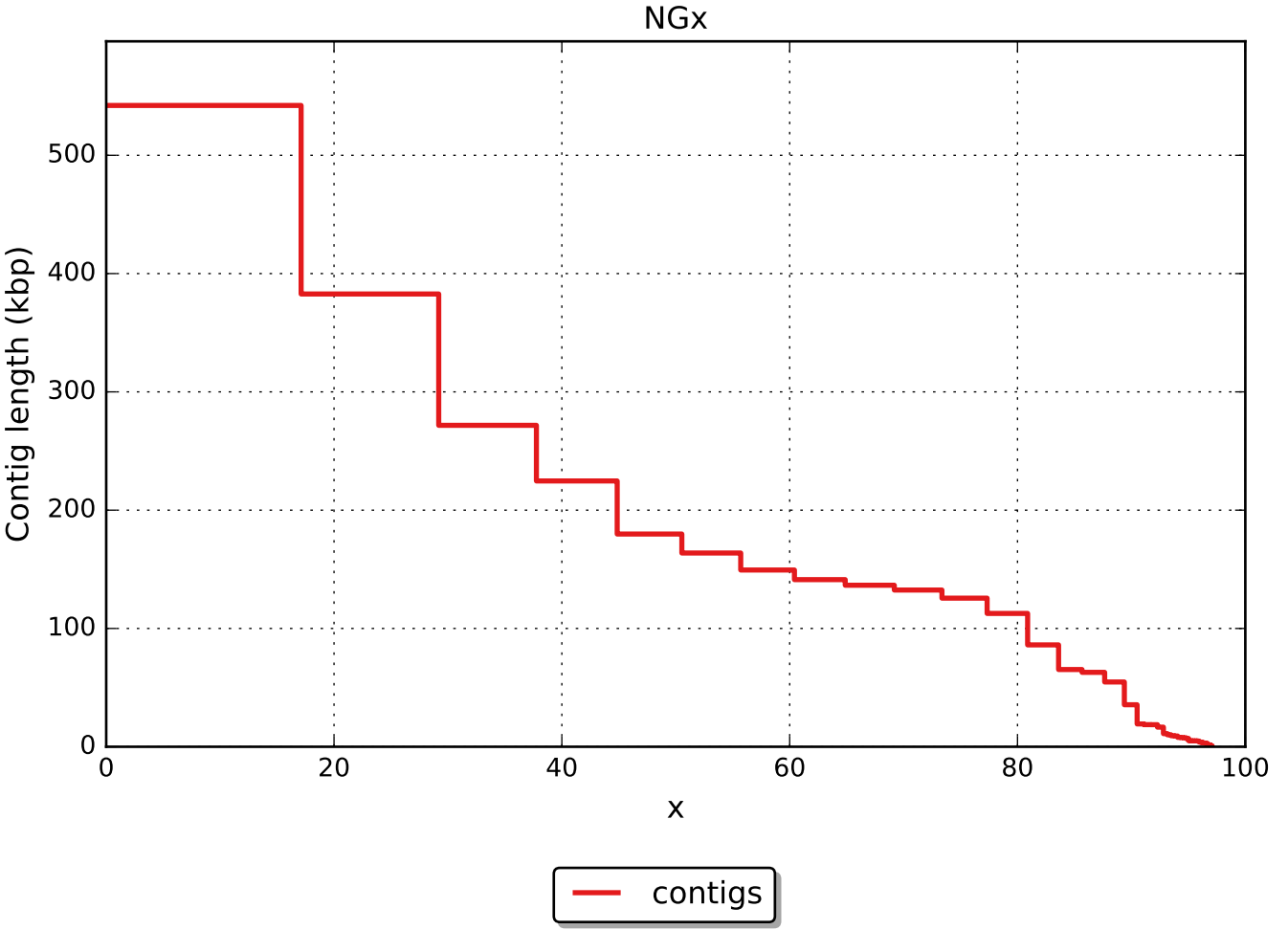
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

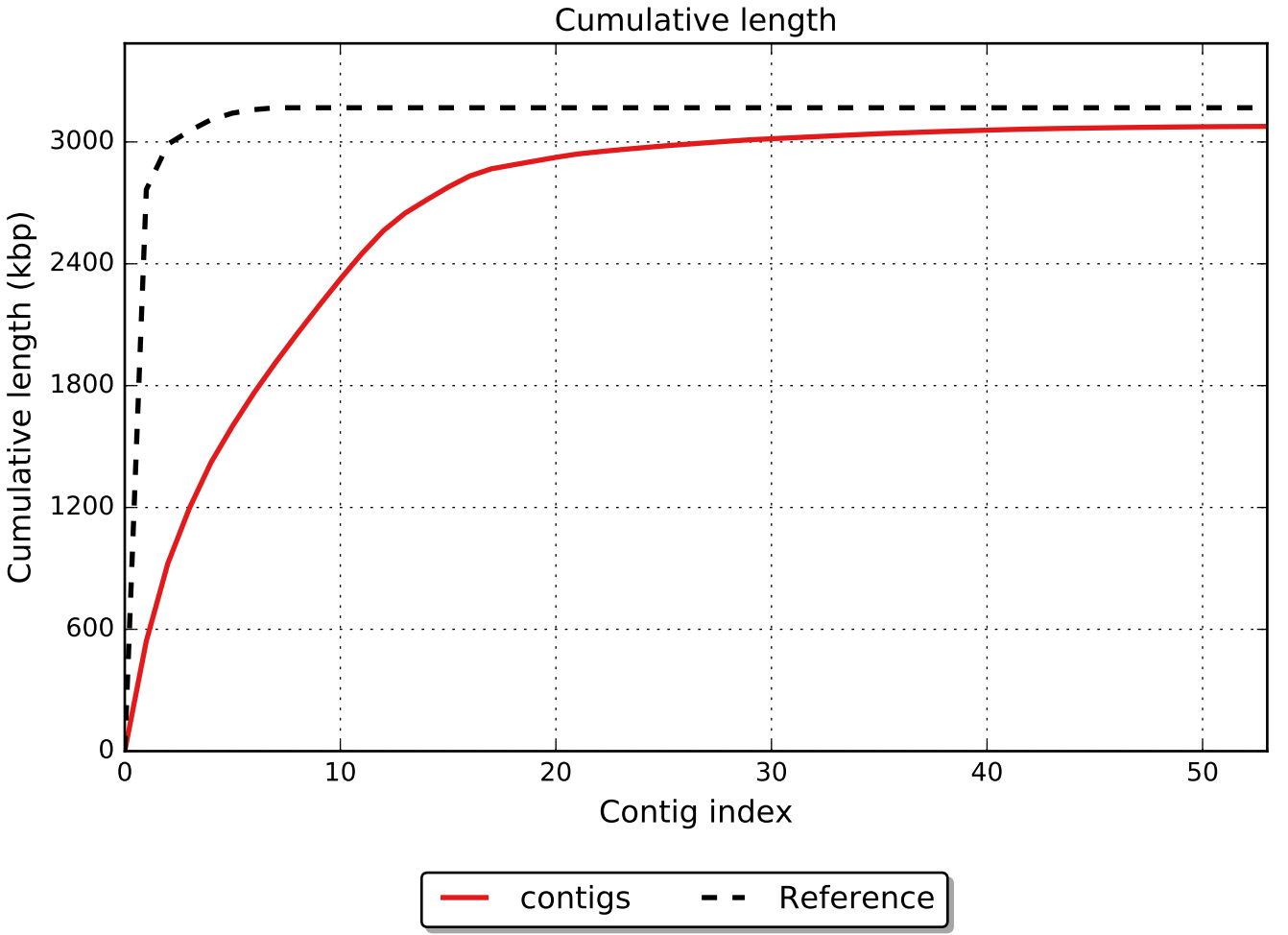
Unaligned report

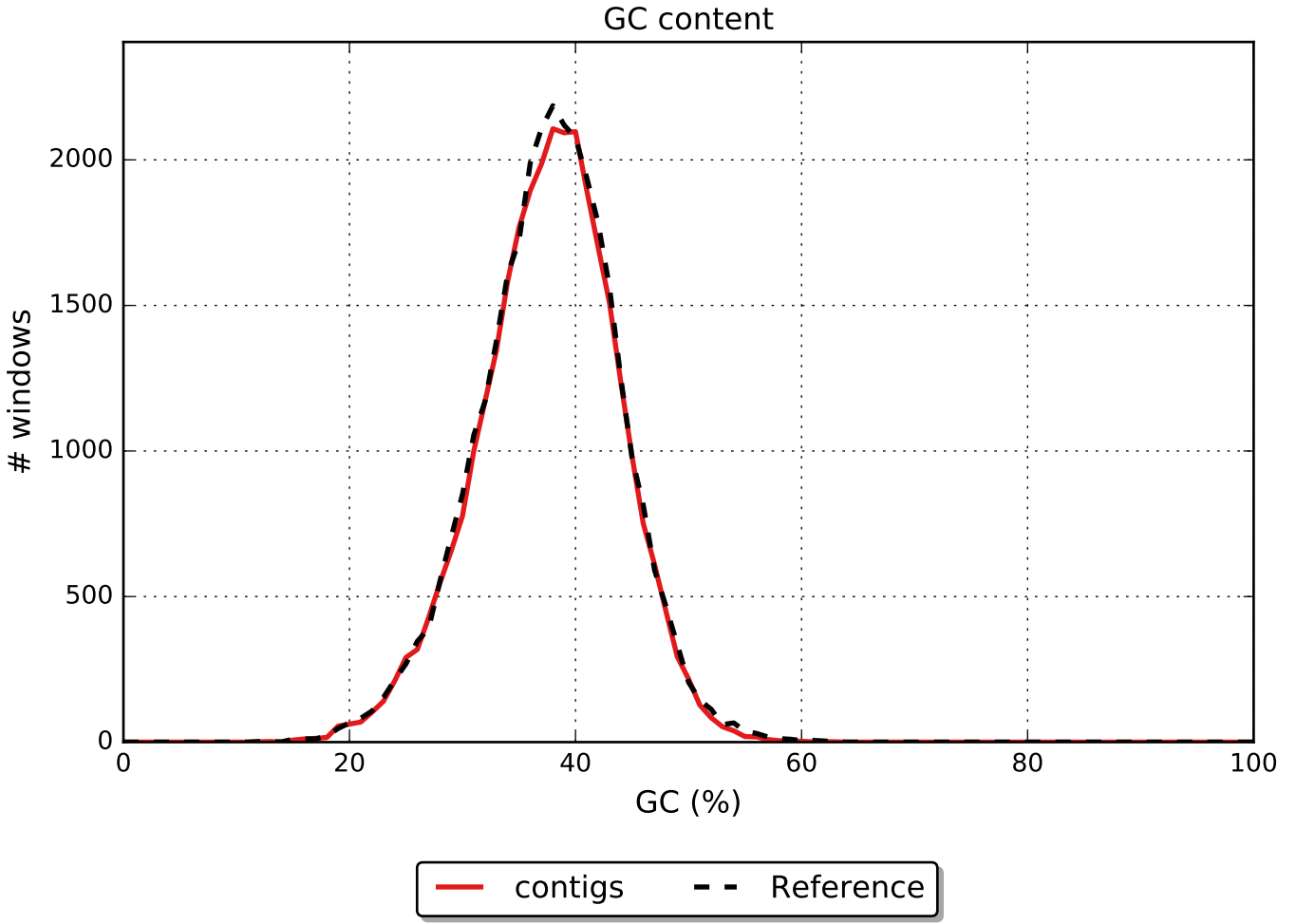
	contigs
# fully unaligned contigs	1
Fully unaligned length	3214
# partially unaligned contigs	1
Partially unaligned length	2912
# N's	0

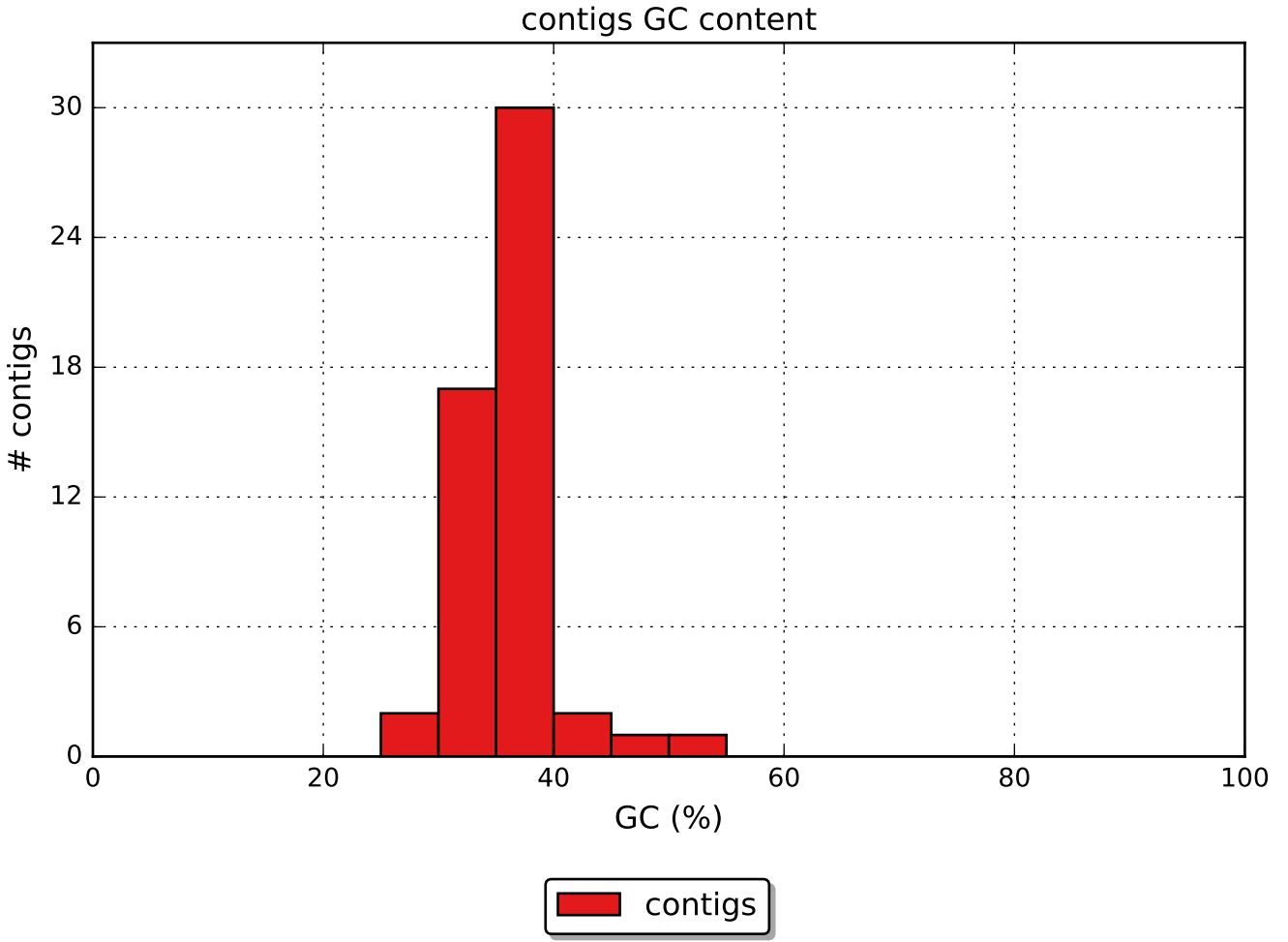
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

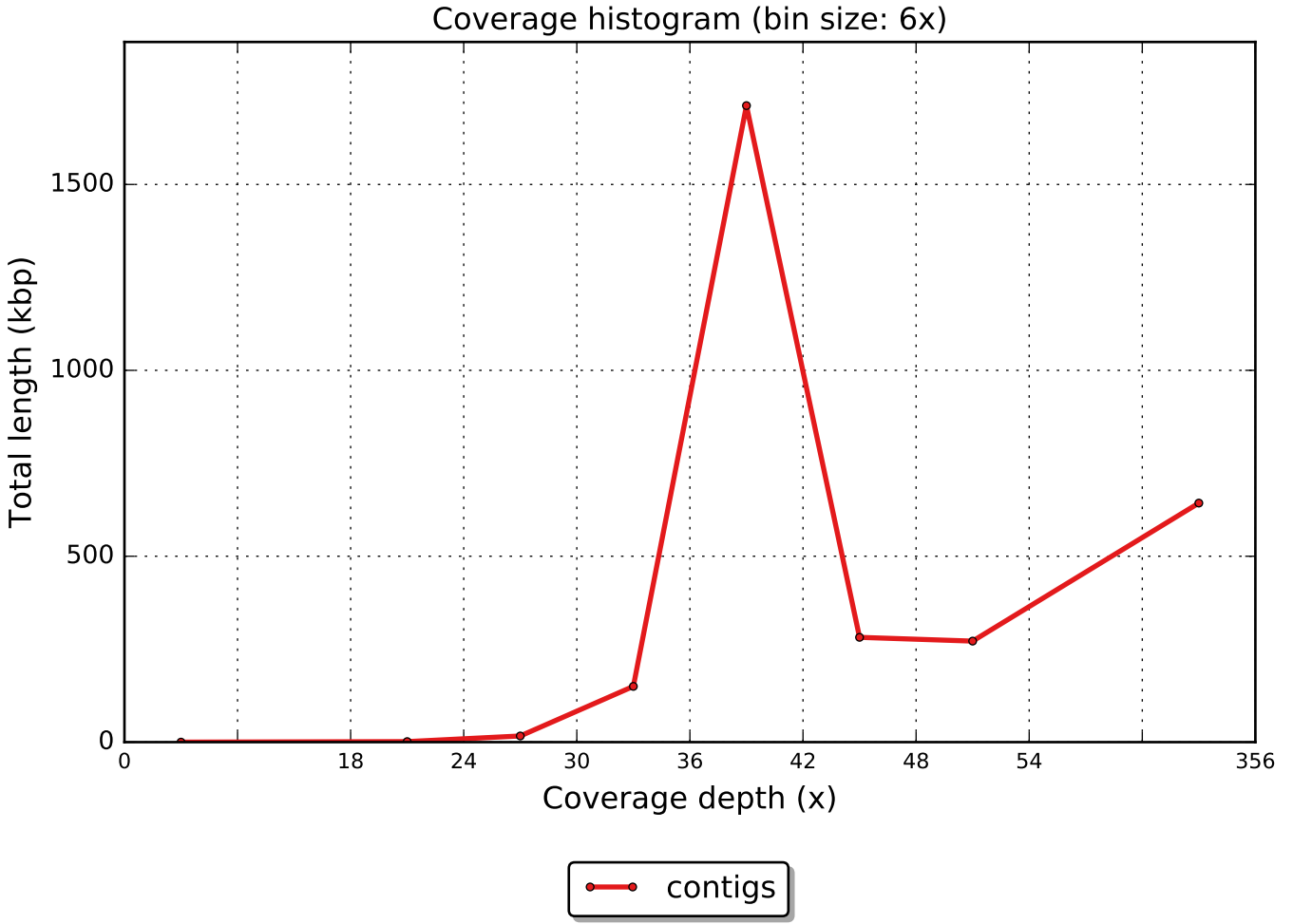

Nx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
contigs

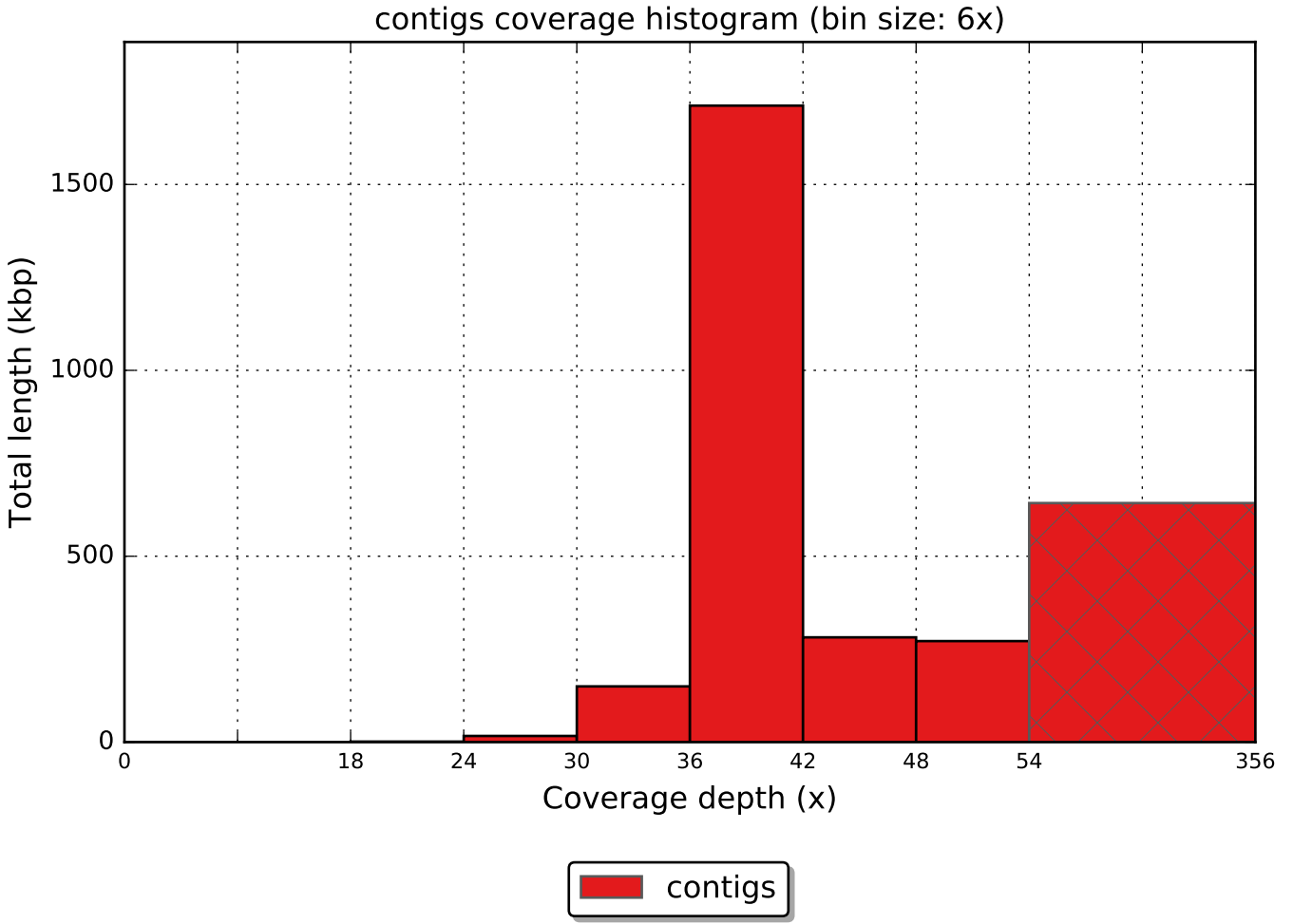

NGx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
contigs

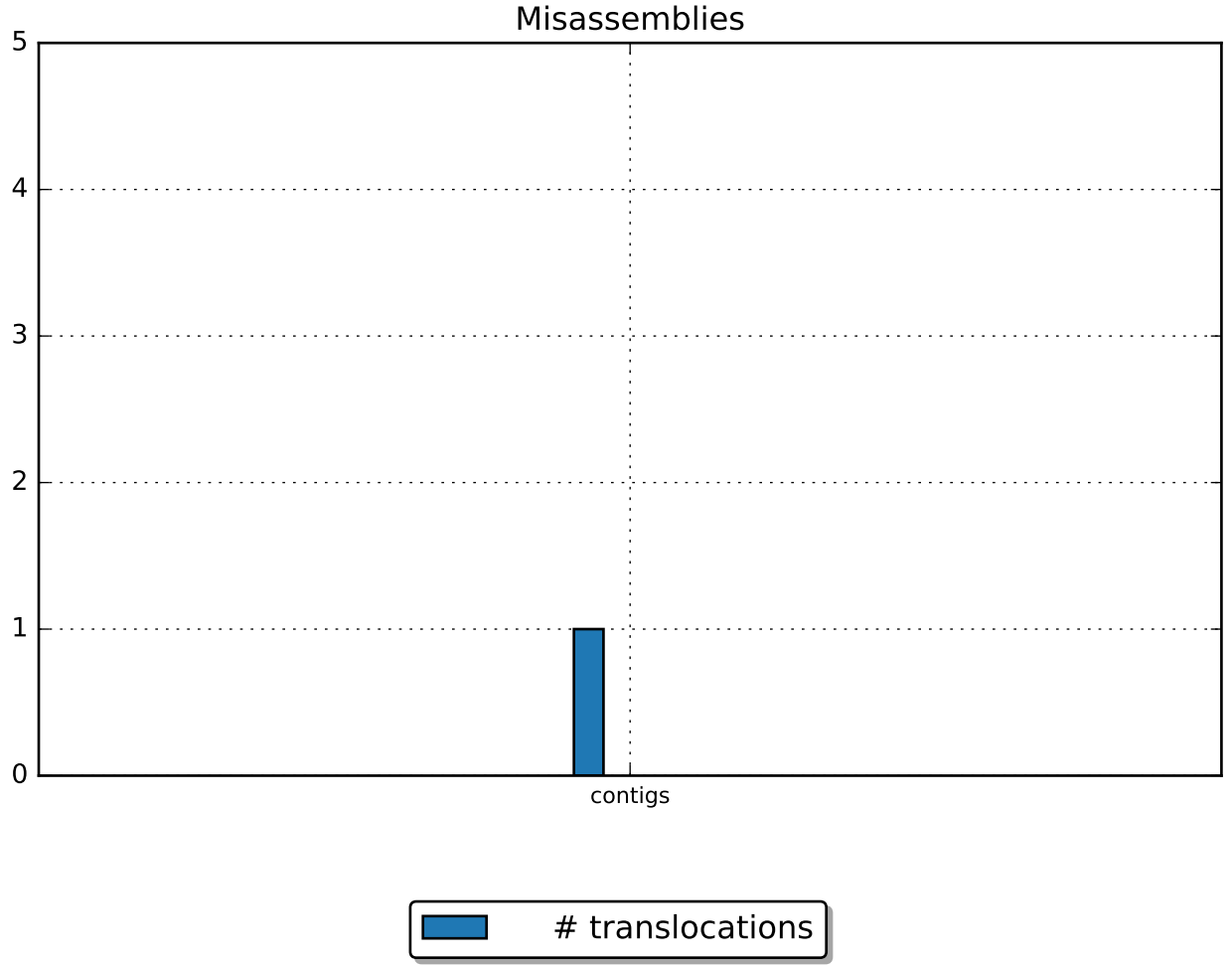

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
10
20
30
40
50
Contig index
contigs
Reference

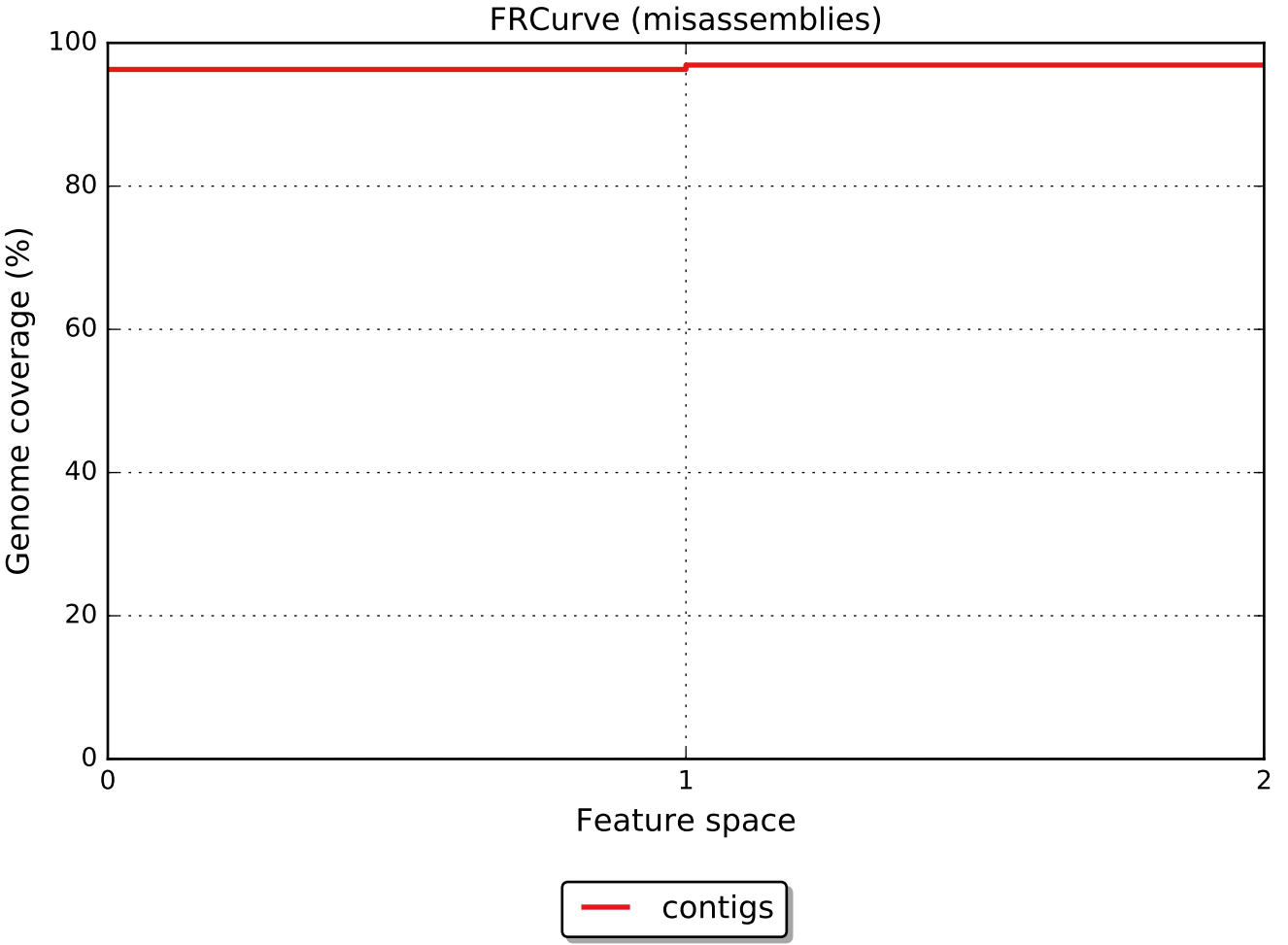

GC content
windows
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
contigs
Reference

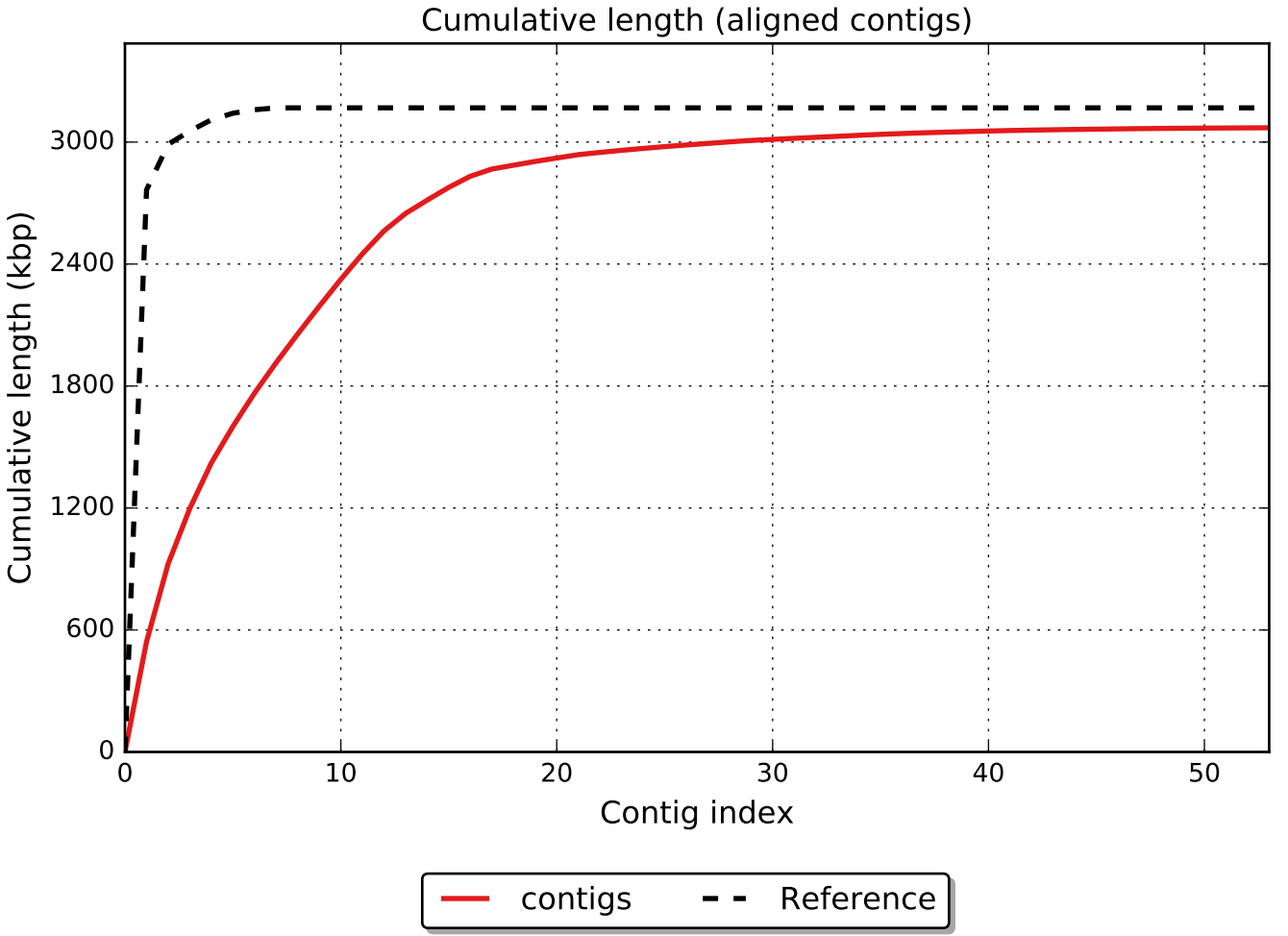

contigs GC content
contigs
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
contigs

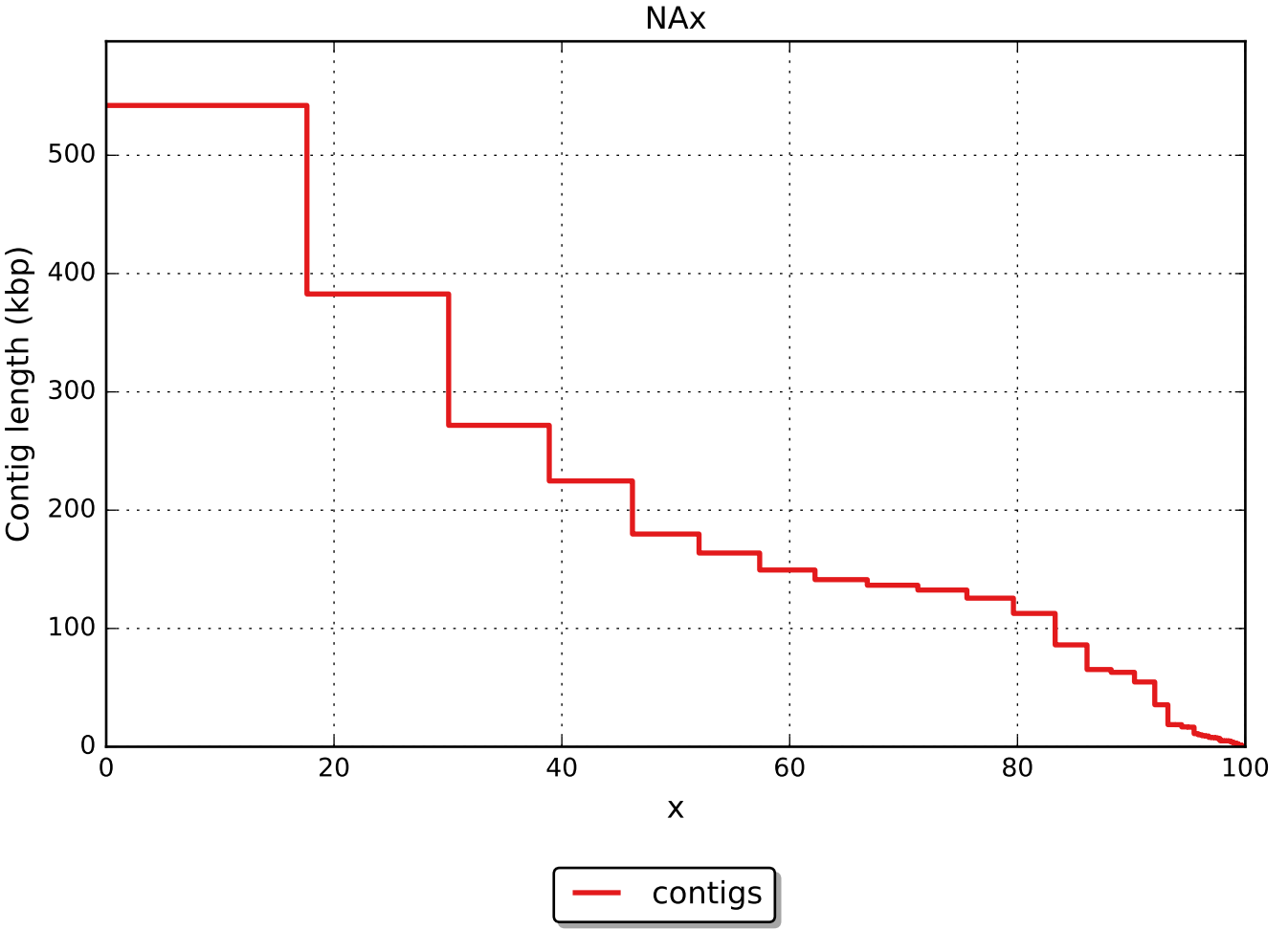

Coverage histogram (bin size: 6x)
Total length (kbp)
0
500
1000
1500
0
18
24
30
36
42
48
54
356
Coverage depth (x)
contigs

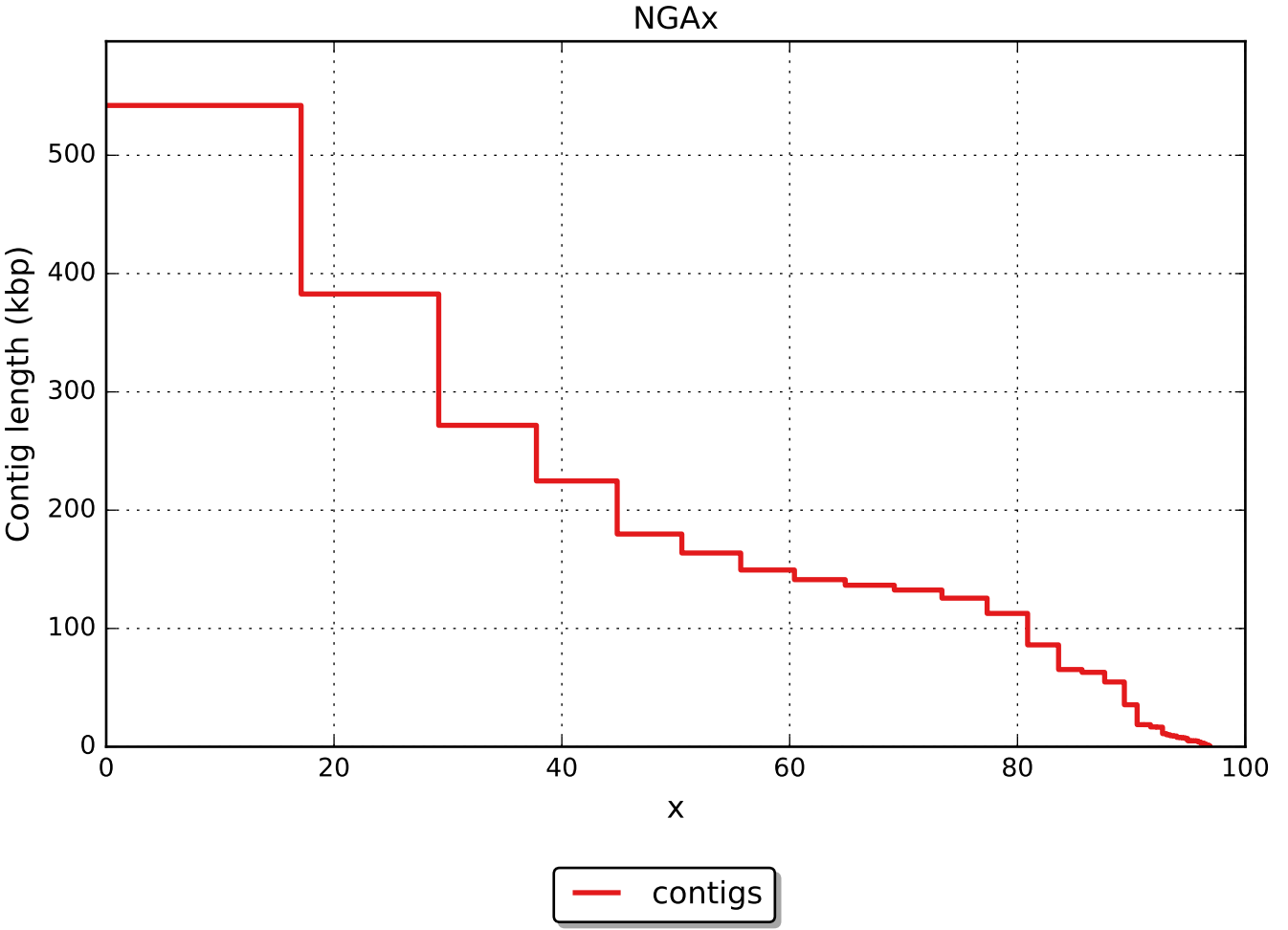

contigs coverage histogram (bin size: 6x)
Total length (kbp)
0
500
1000
1500
0
18
24
30
36
42
48
54
356
Coverage depth (x)
contigs


Misassemblies
5
4
3
2
1
0
contigs
translocations


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
10
20
30
40
50
Contig index
contigs
Reference


NAx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
contigs