Report

	contigs
# contigs (>= 0 bp)	20
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	6
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	3185757
Total length (>= 1000 bp)	3184208
Total length (>= 5000 bp)	3180994
Total length (>= 10000 bp)	3171669
Total length (>= 25000 bp)	3157970
Total length (>= 50000 bp)	3121948
# contigs	7
Largest contig	2770208
Total length	3184208
Reference length	3168410
GC (%)	37.71
Reference GC (%)	37.70
N50	2770208
NG50	2770208
N75	2770208
NG75	2770208
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	7
# misassembled contigs	3
Misassembled contigs length	3071303
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	1 + 1 part
Unaligned length	5719
Genome fraction (%)	99.541
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.63
# indels per 100 kbp	3.65
Largest alignment	1911519
Total aligned length	3178467
NA50	1911519
NGA50	1911519
NA75	858689
NGA75	858689
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

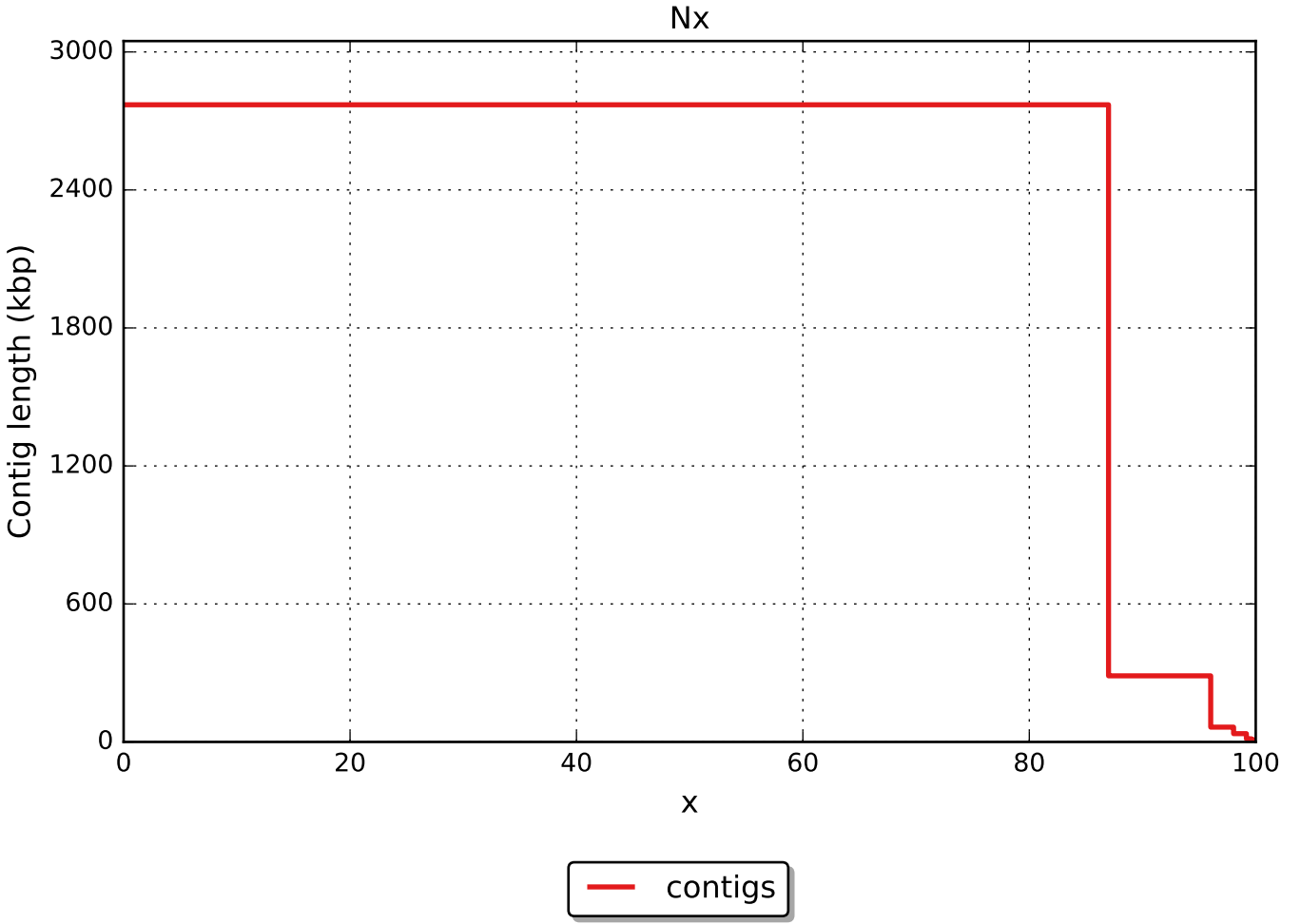
	contigs
# misassemblies	7
# relocations	1
# translocations	5
# inversions	1
# misassembled contigs	3
Misassembled contigs length	3071303
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	840
# indels	115
# indels (<= 5 bp)	105
# indels (> 5 bp)	10
Indels length	255

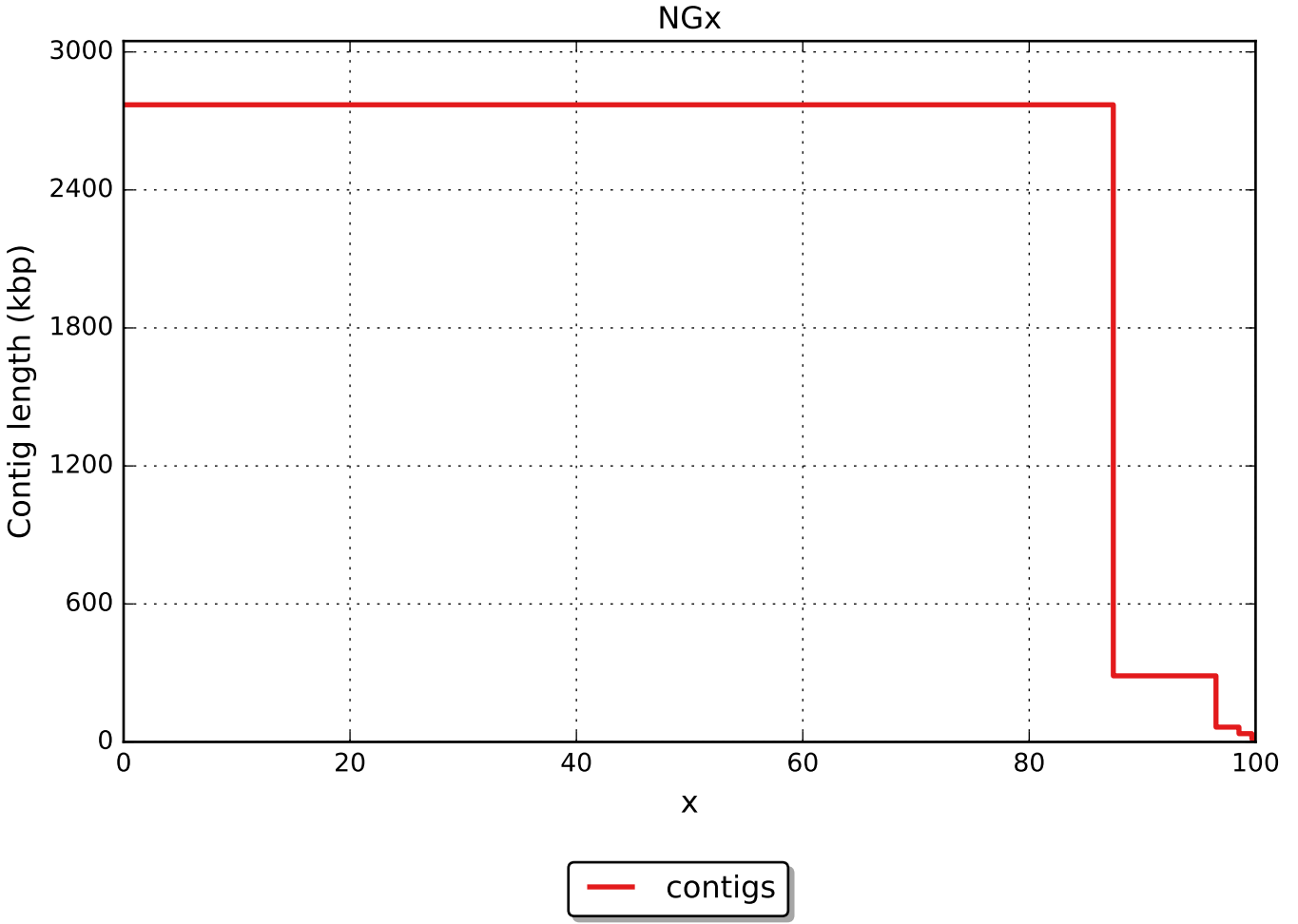
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

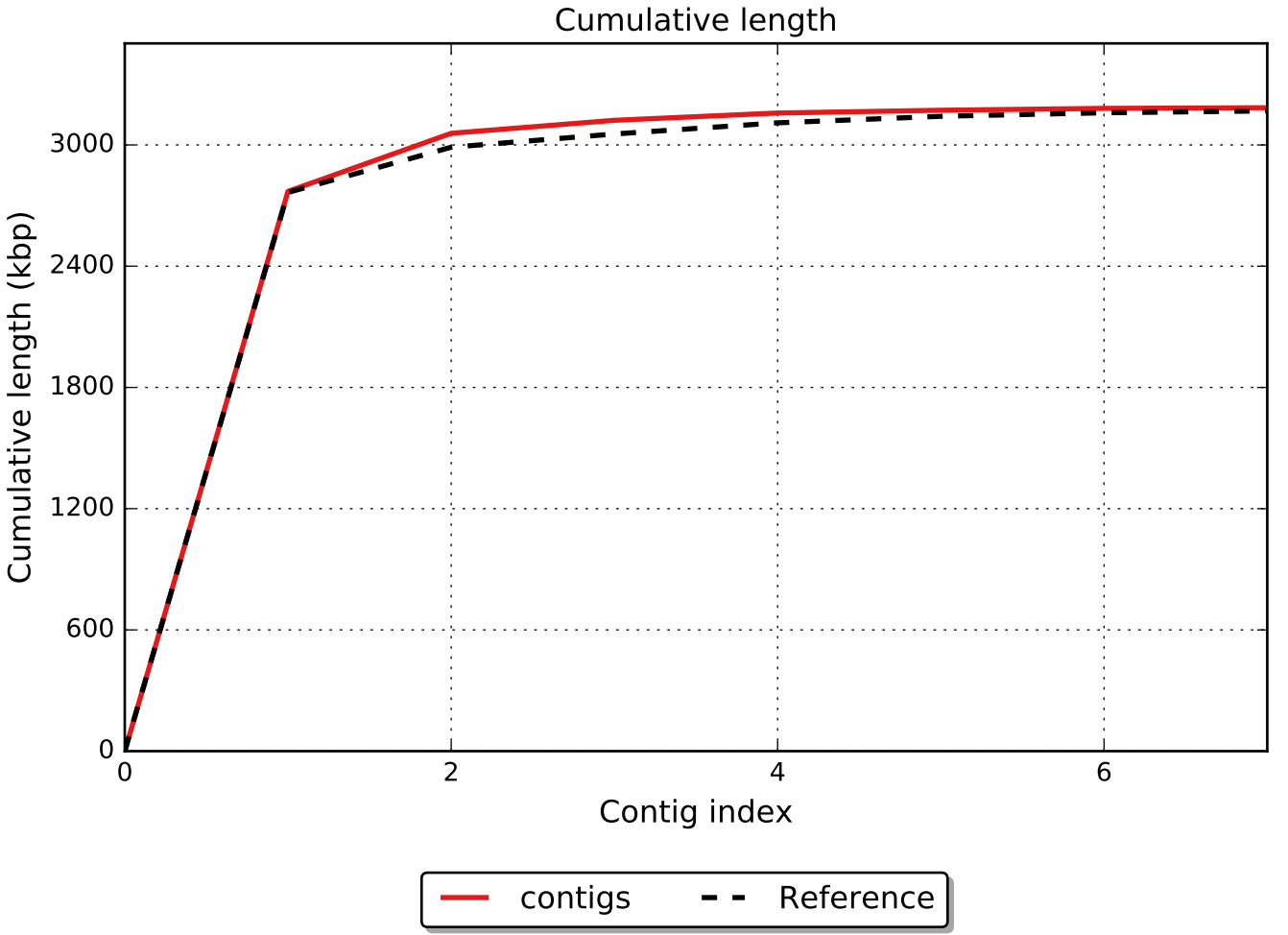
Unaligned report

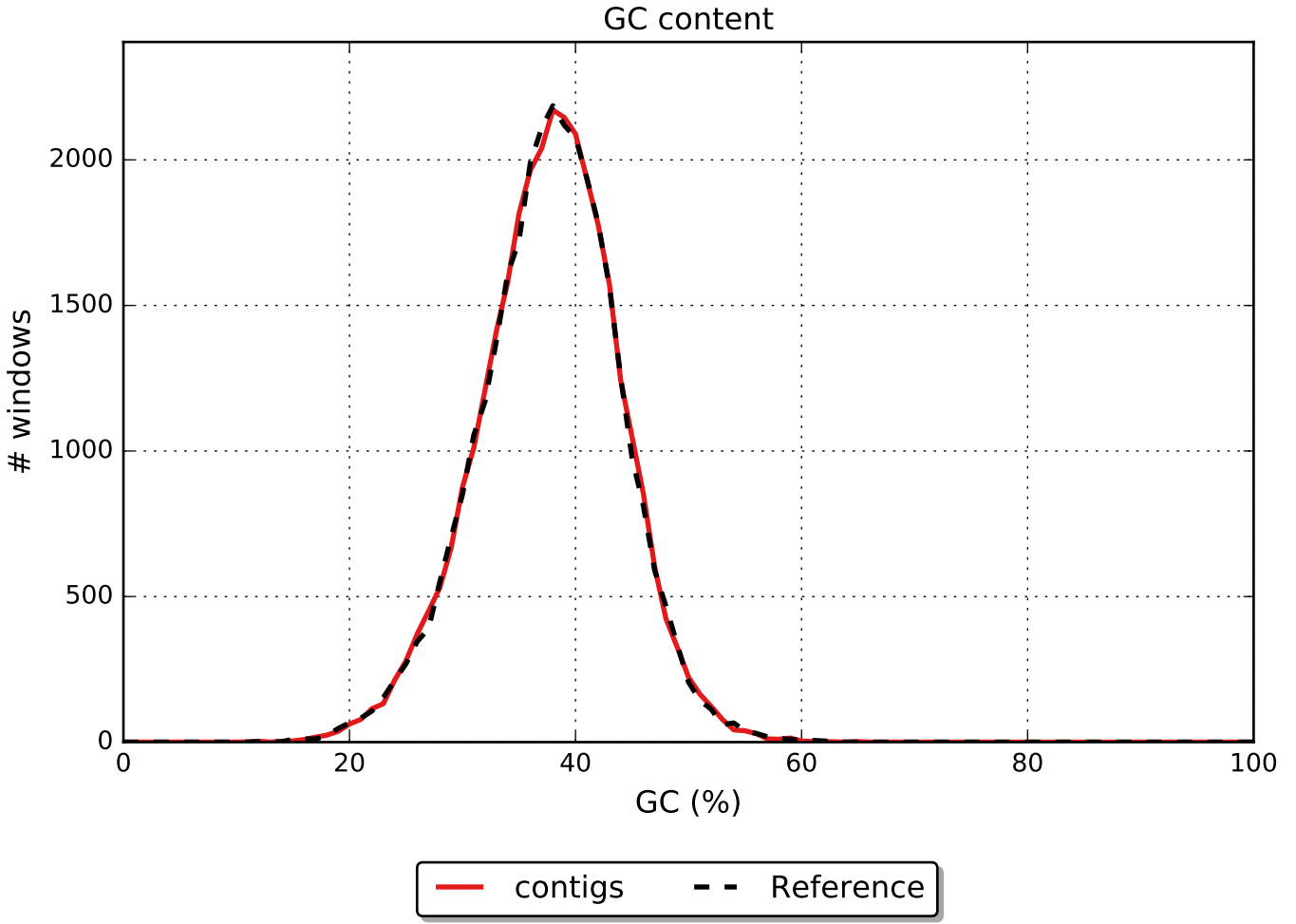
	contigs
# fully unaligned contigs	1
Fully unaligned length	3214
# partially unaligned contigs	1
Partially unaligned length	2505
# N's	0

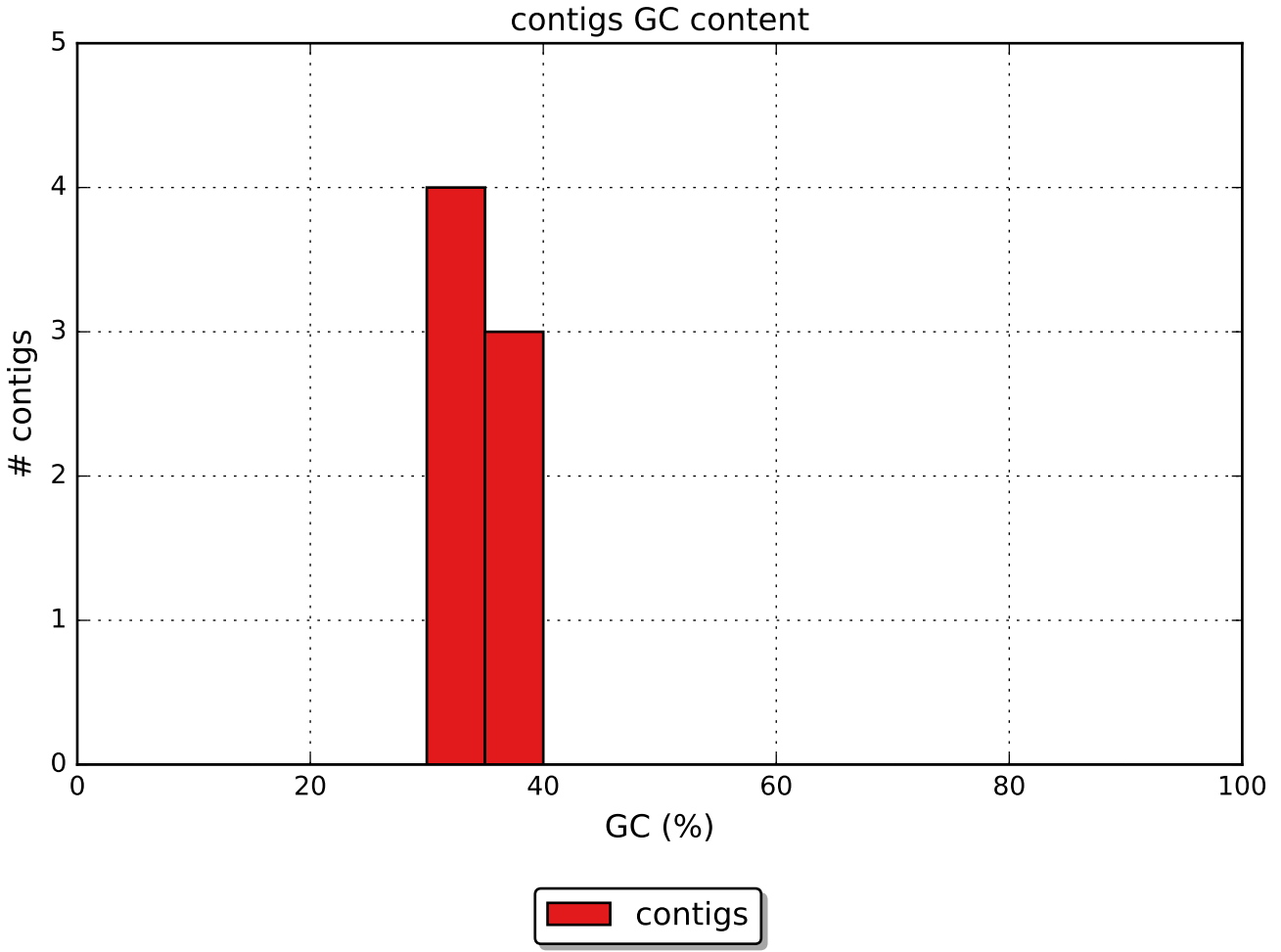
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

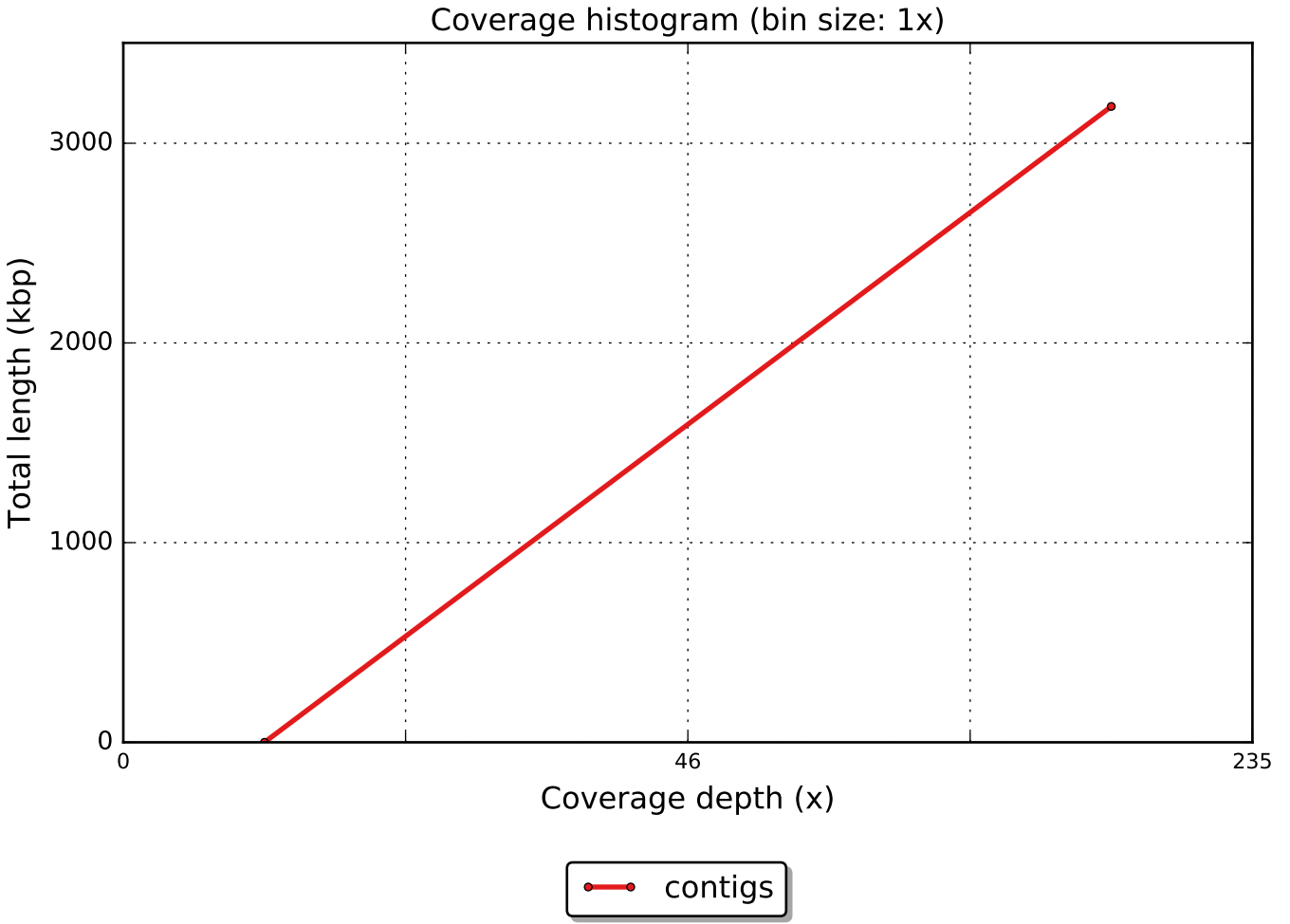

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

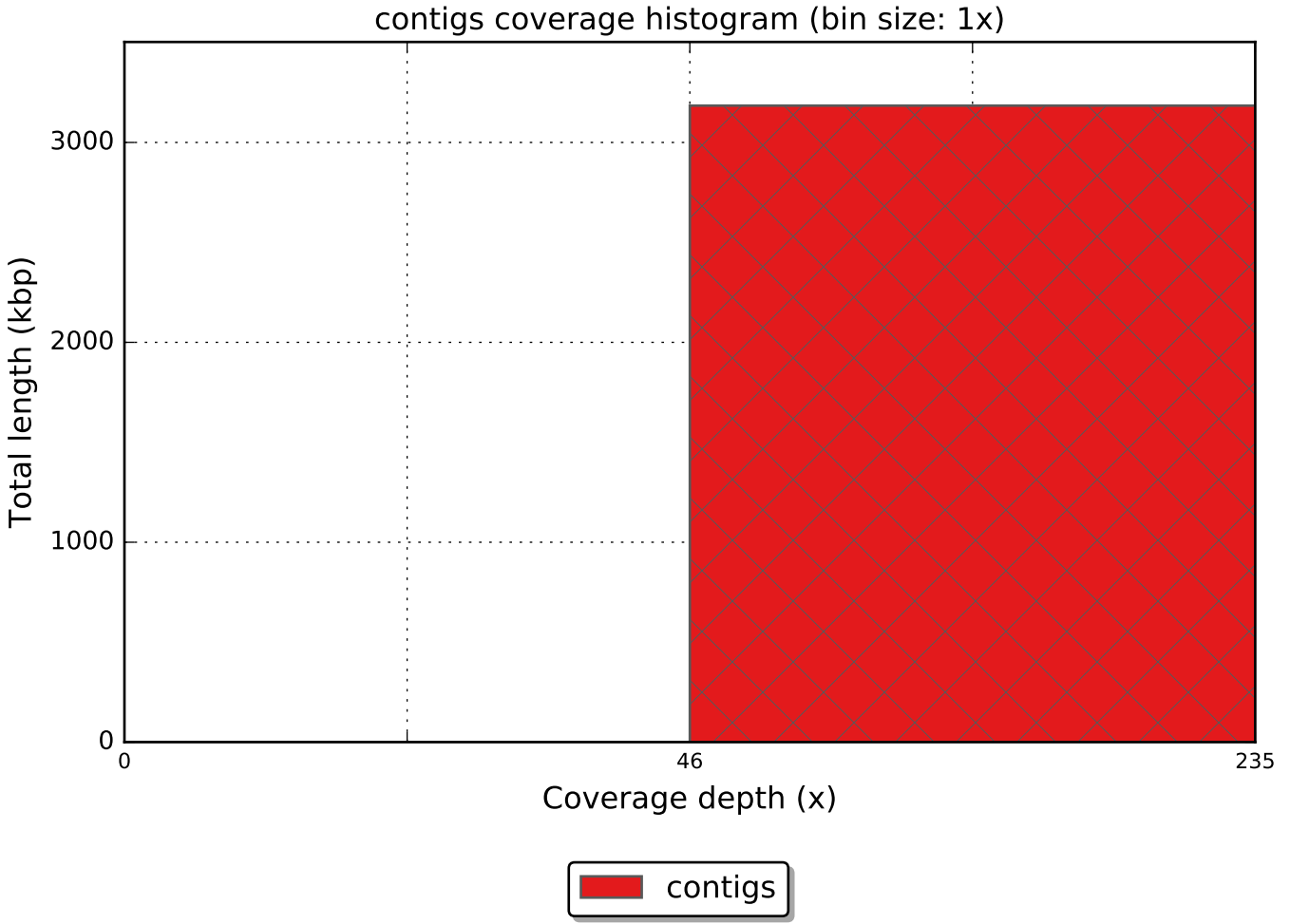

NGx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

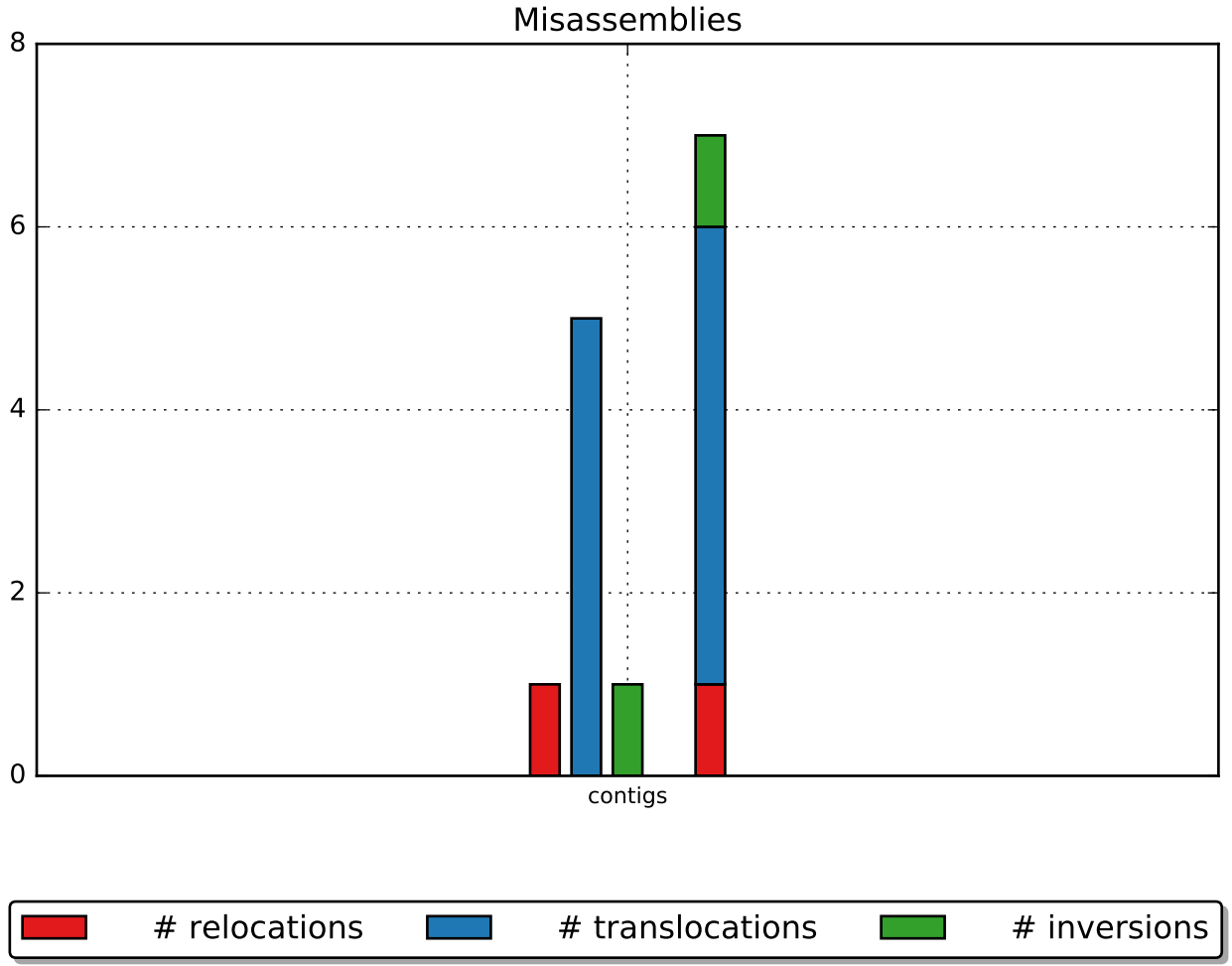

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
Contig index
contigs
Reference

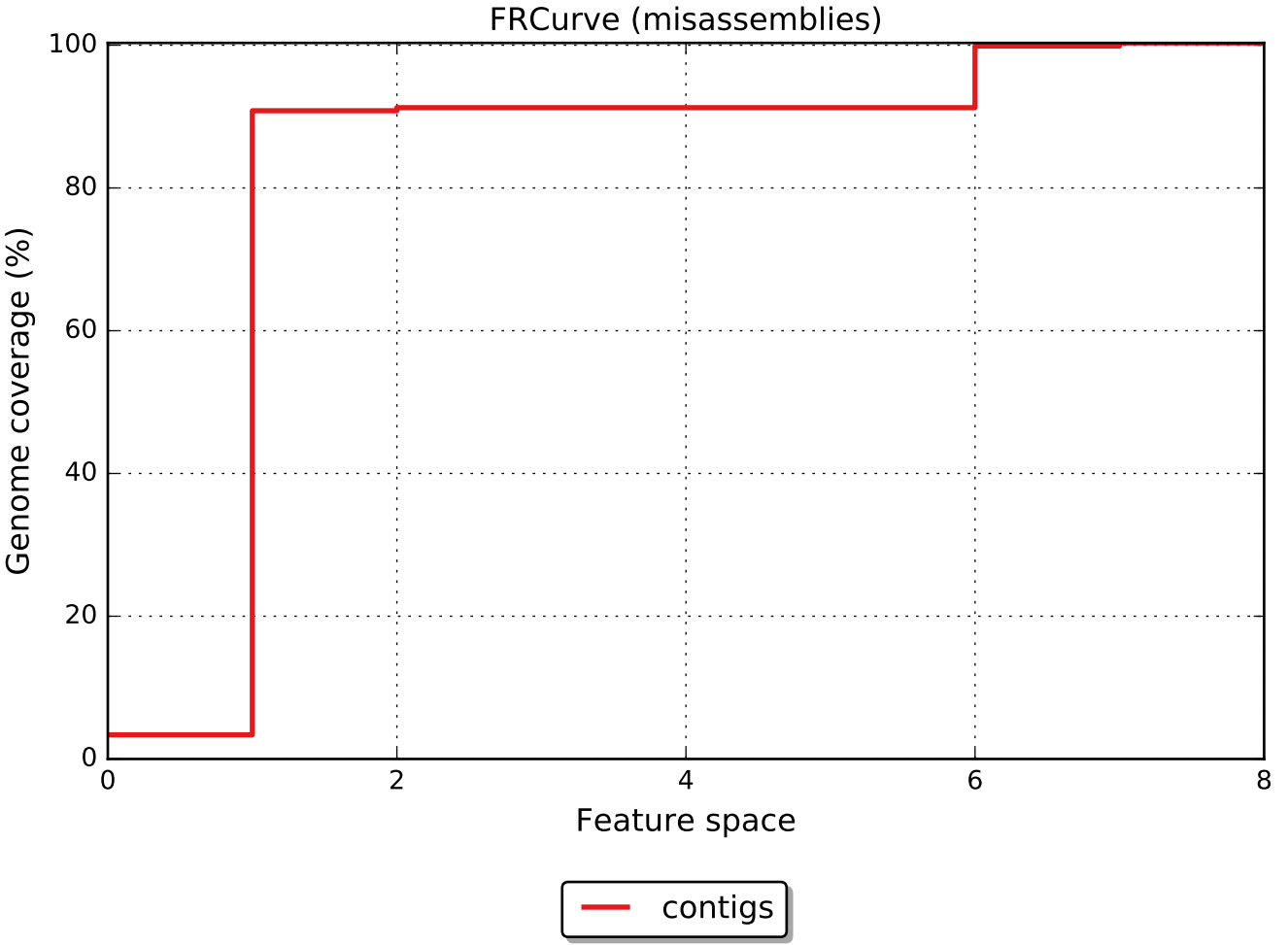

GC content
windows
GC (%)
0
500
1000
1500
2000
0
20
40
60
80
100
contigs
Reference

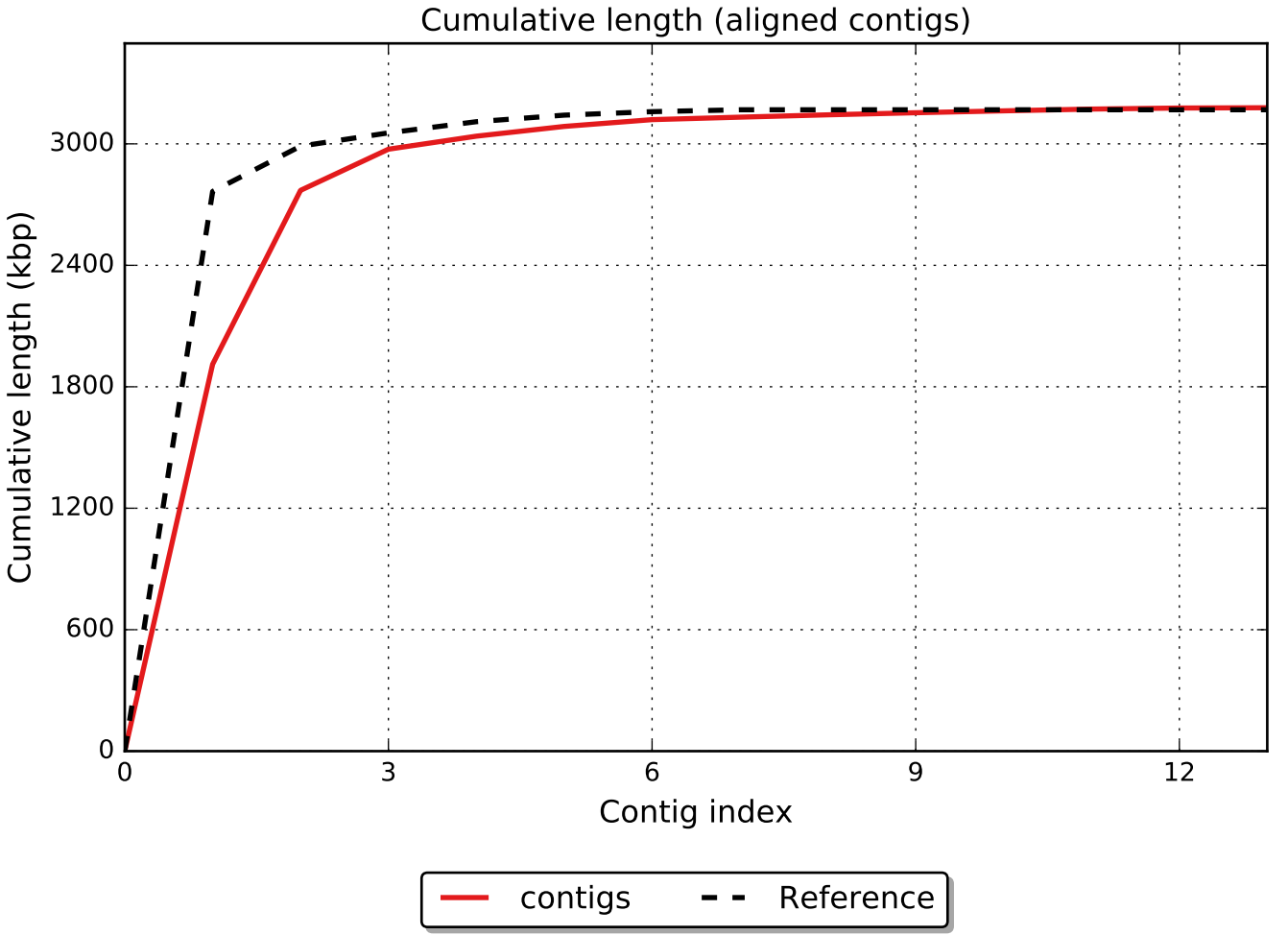

contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs

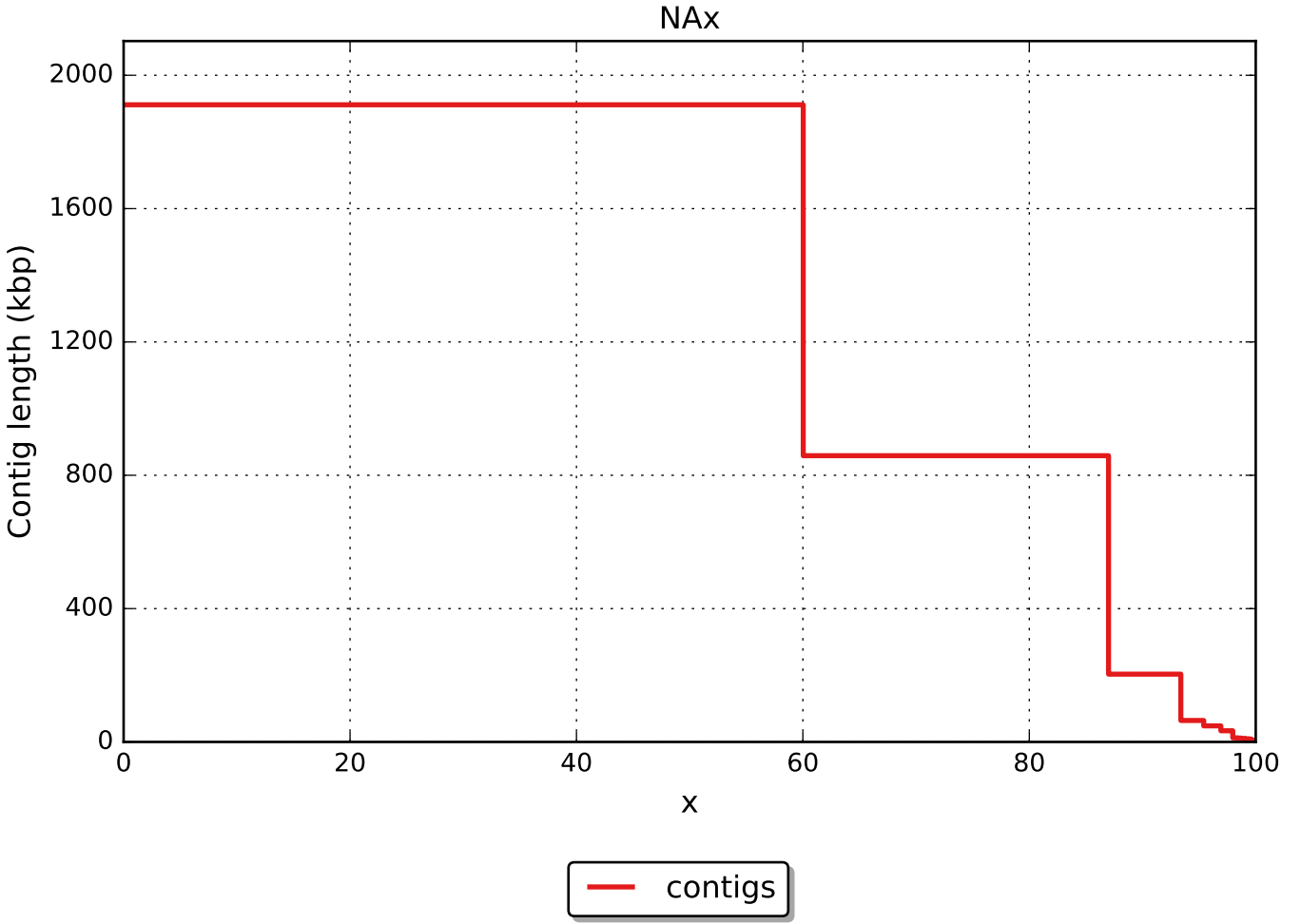

Coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
46
235
Coverage depth (x)
contigs

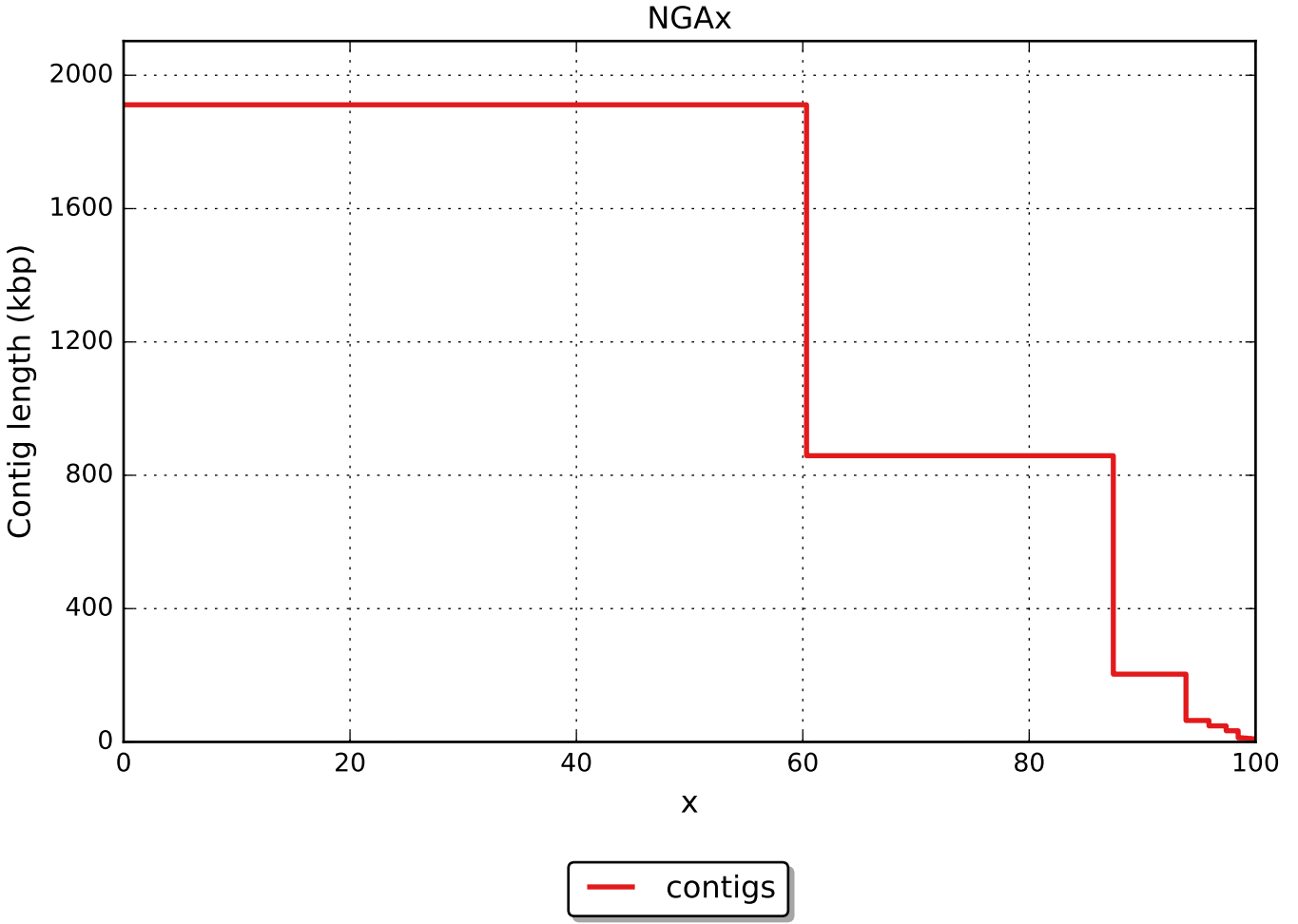

contigs coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
46
235
Coverage depth (x)
contigs


Misassemblies
8
6
4
2
0
contigs
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
Feature space
contigs


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


NAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
contigs