Report

	contigs
# contigs (>= 1000 bp)	75
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4511088
Total length (>= 5000 bp)	4469855
Total length (>= 10000 bp)	4437004
Total length (>= 25000 bp)	4329343
Total length (>= 50000 bp)	3929597
# contigs	108
Largest contig	332248
Total length	4535398
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	131793
NG50	124889
N75	82061
NG75	80259
L50	11
LG50	12
L75	22
LG75	23
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.198
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	617.74
# indels per 100 kbp	0.82
Largest alignment	332248
NA50	131793
NGA50	124889
NA75	80259
NGA75	79547
LA50	11
LGA50	12
LA75	22
LGA75	23

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

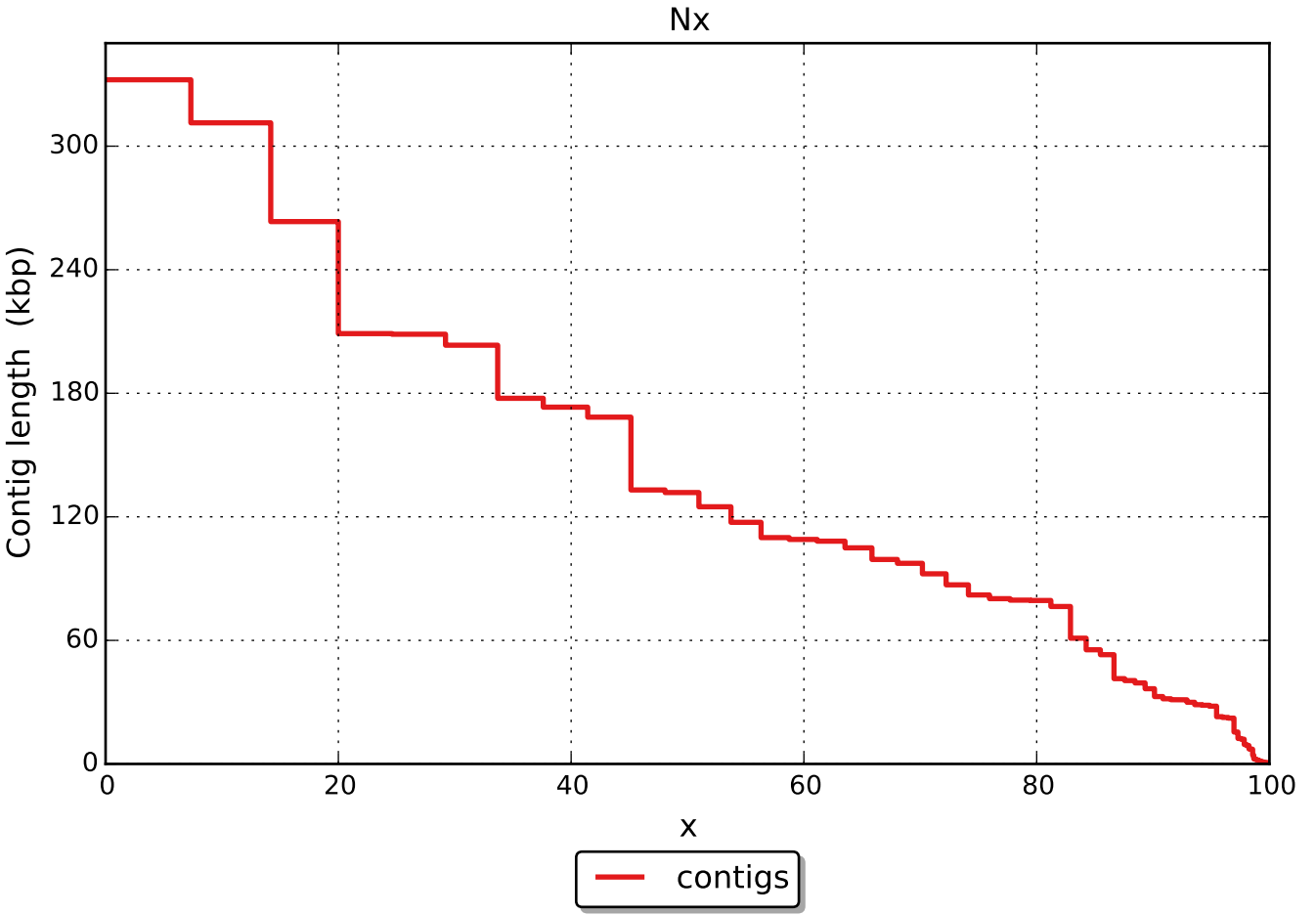
	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	27870
# indels	37
# short indels	37
# long indels	0
Indels length	44

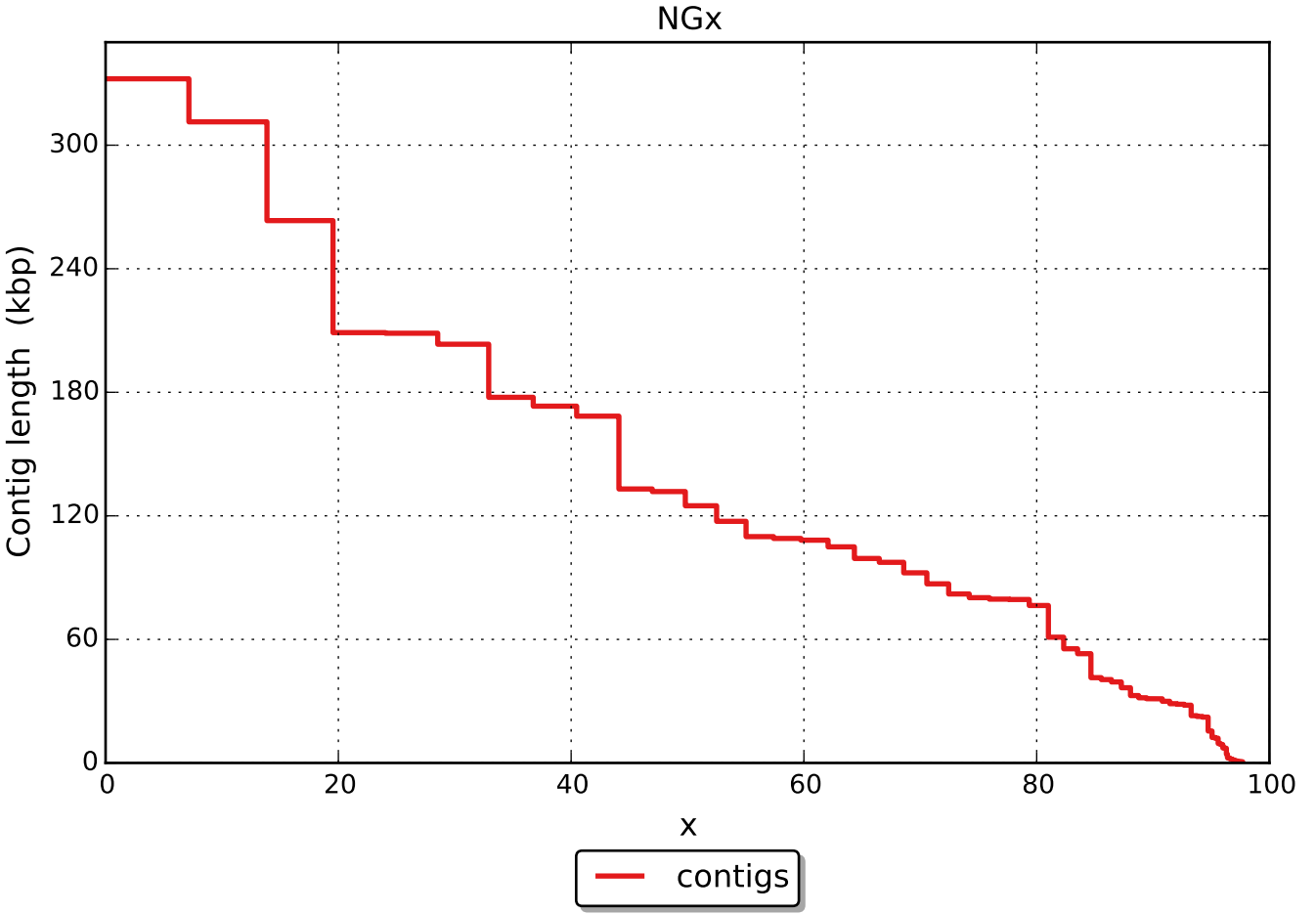
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

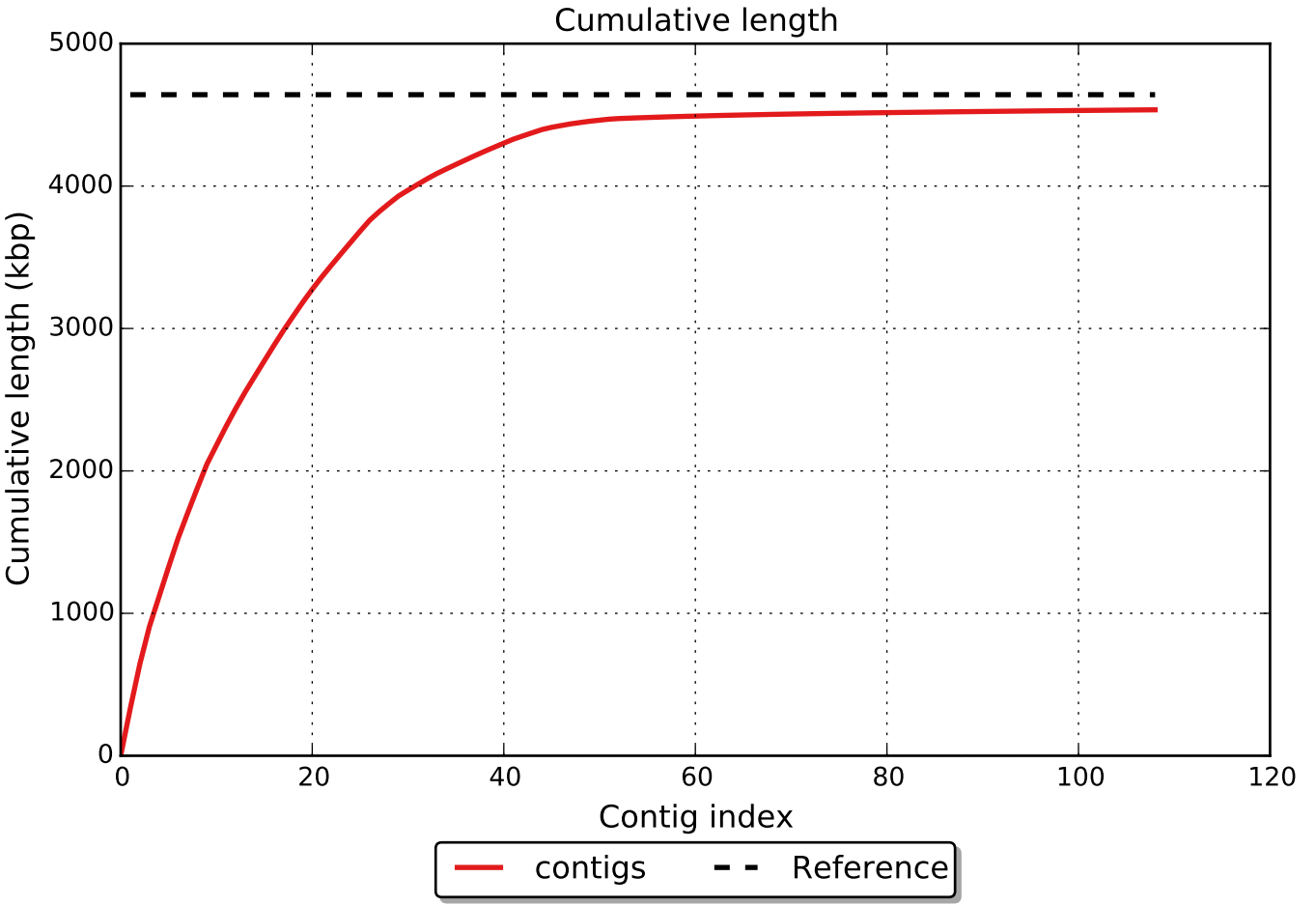
Unaligned report

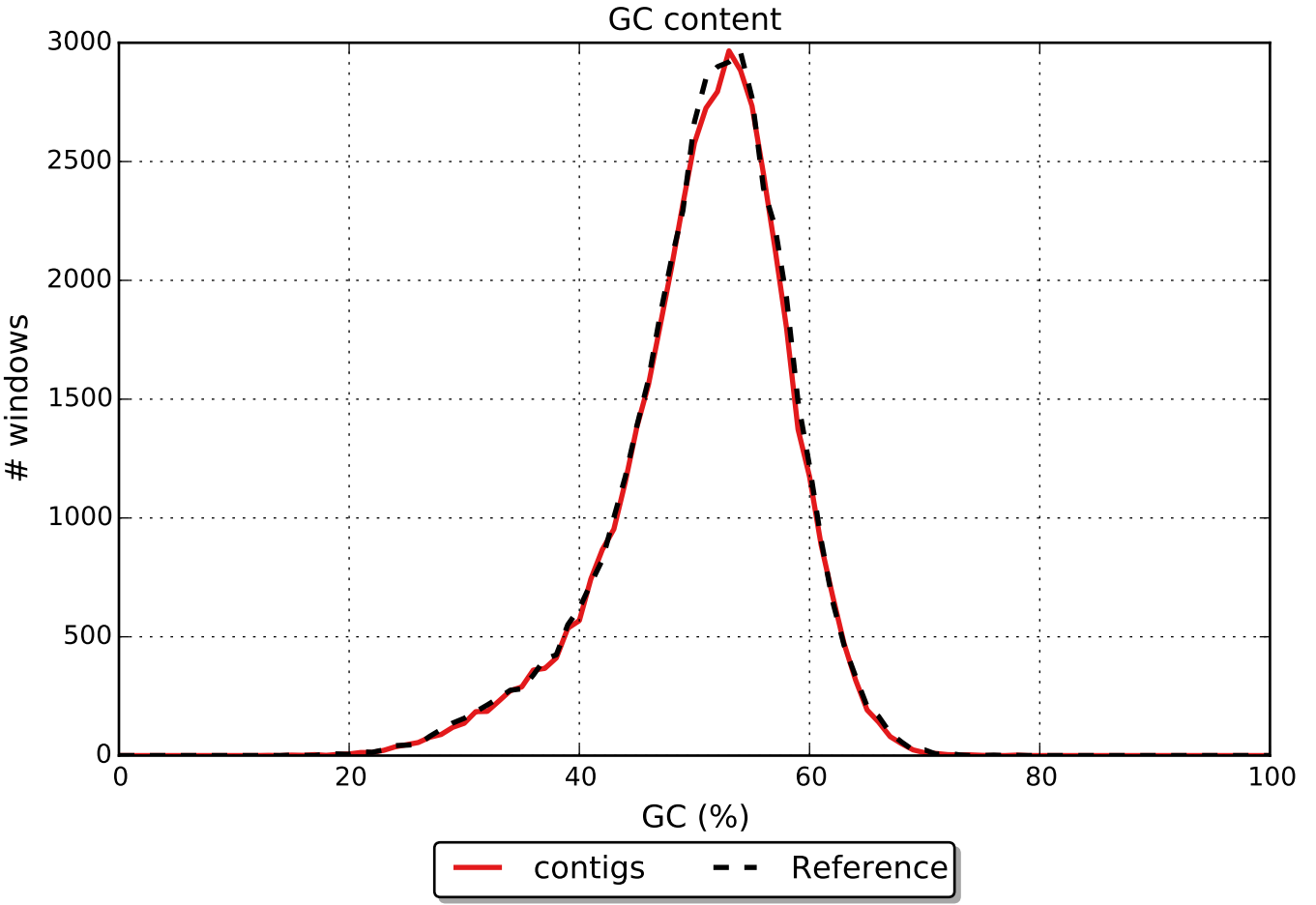
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

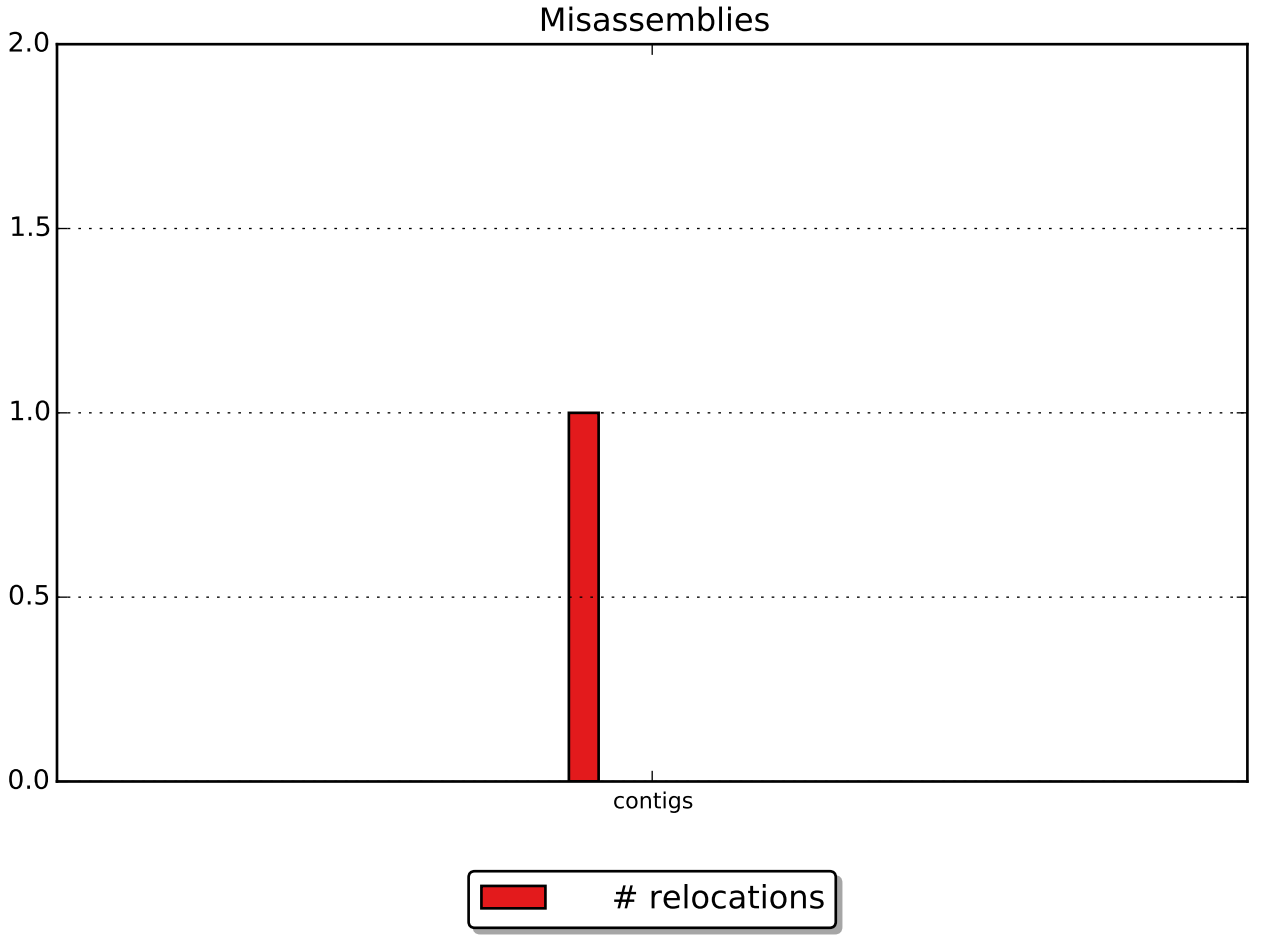
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

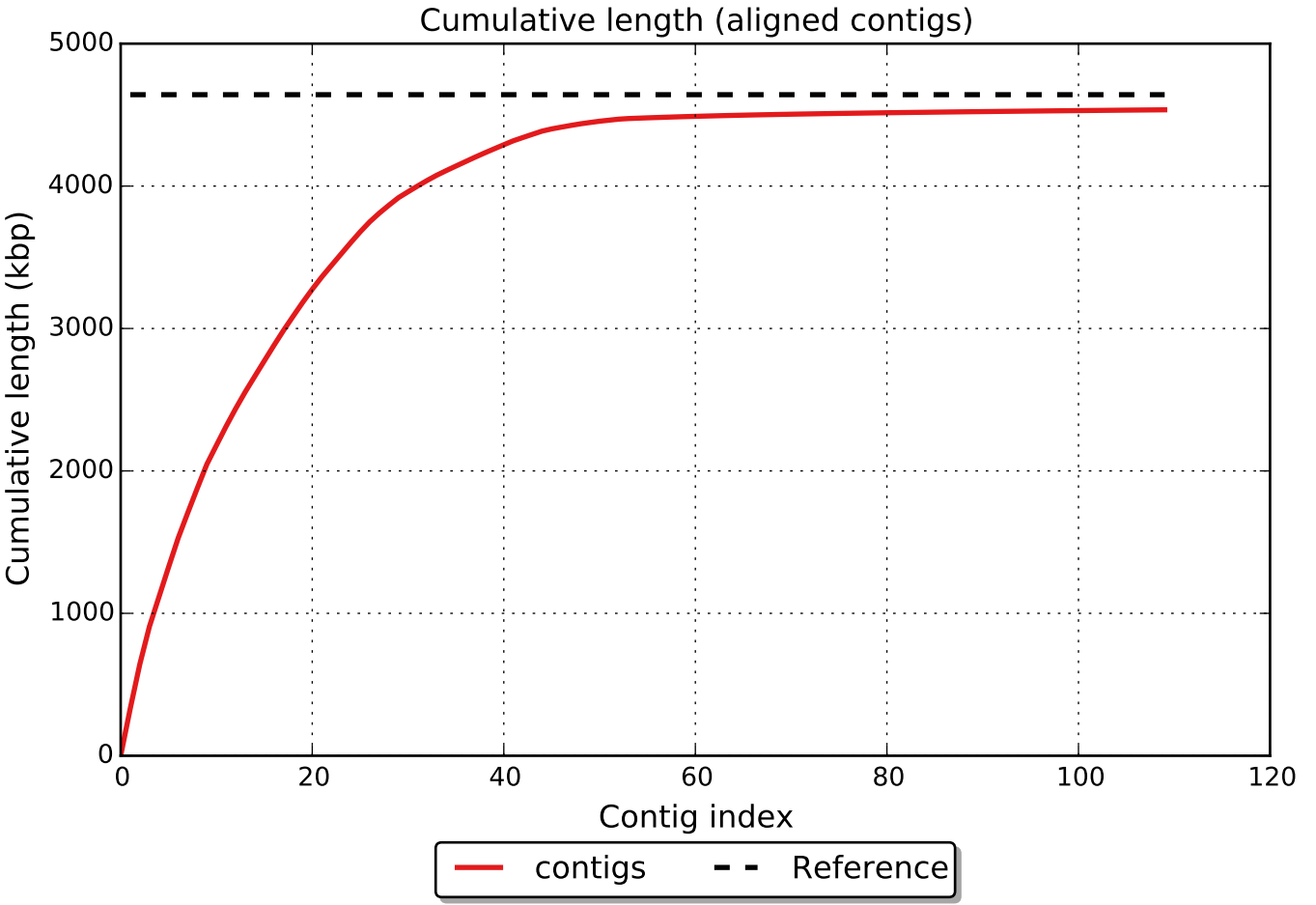

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

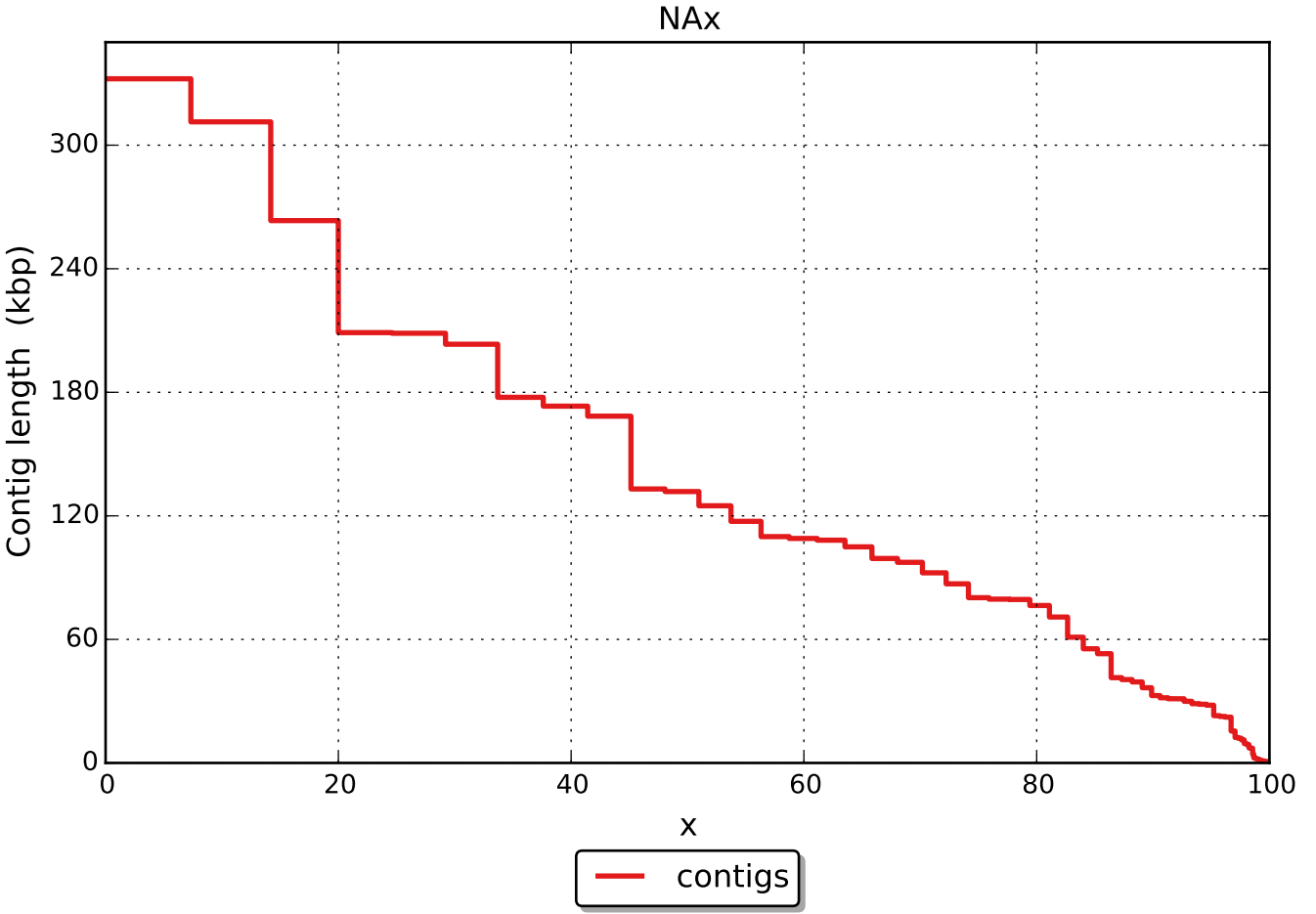

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

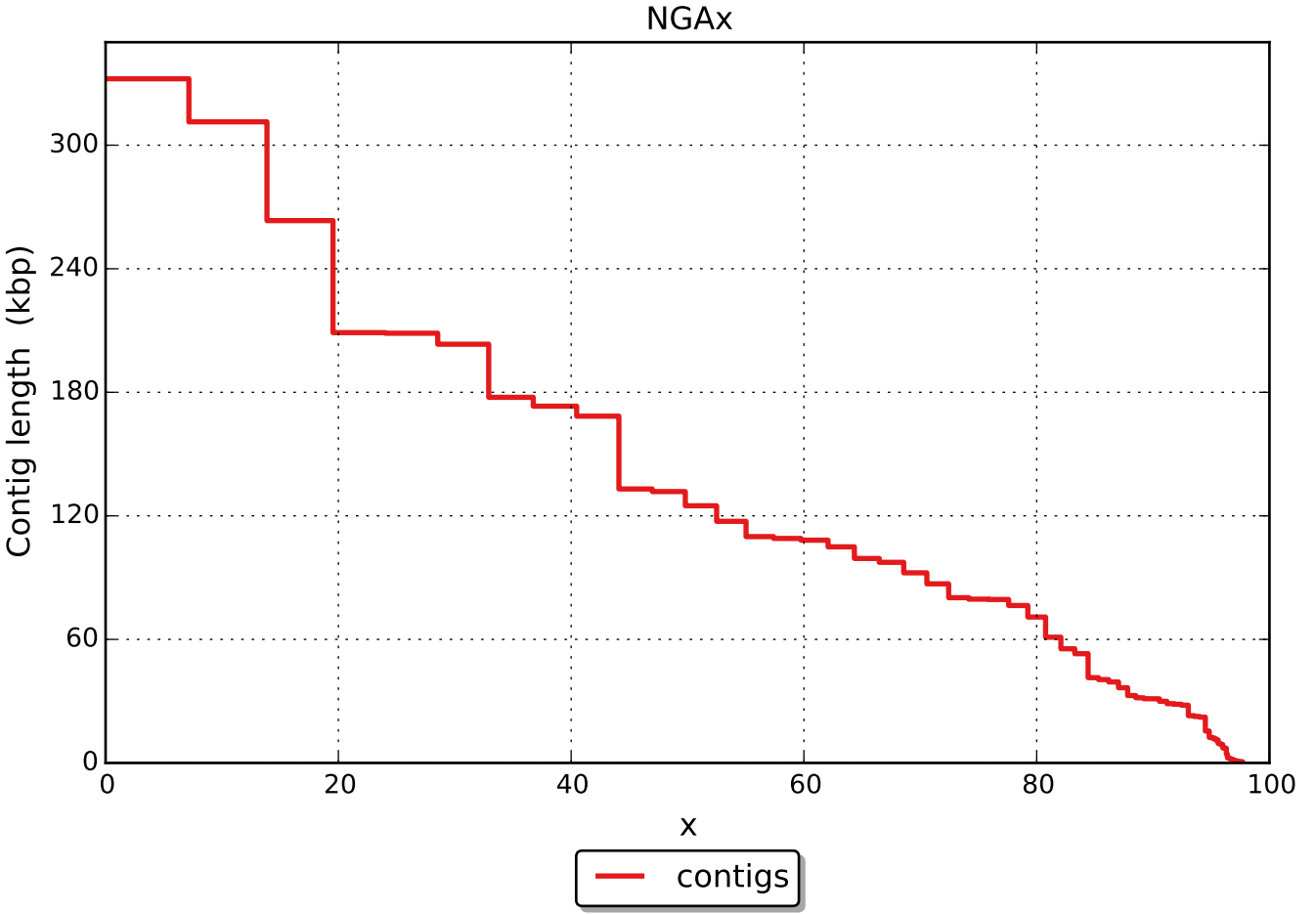

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
contigs
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
contigs
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs