Report

	contigs
# contigs (>= 1000 bp)	186
# contigs (>= 5000 bp)	114
# contigs (>= 10000 bp)	81
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	30
Total length (>= 1000 bp)	4613605
Total length (>= 5000 bp)	4406321
Total length (>= 10000 bp)	4180898
Total length (>= 25000 bp)	3636372
Total length (>= 50000 bp)	3000472
# contigs	217
Largest contig	347033
Total length	4634038
Reference length	4641652
GC (%)	50.65
Reference GC (%)	50.78
N50	67124
NG50	67124
N75	28222
NG75	28222
L50	19
LG50	19
L75	44
LG75	44
# misassemblies	5
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.236
Duplication ratio	1.119
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1073.89
# indels per 100 kbp	0.75
Largest alignment	347033
NA50	63158
NGA50	63158
NA75	28222
NGA75	28222
LA50	19
LGA50	19
LA75	45
LGA75	45

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

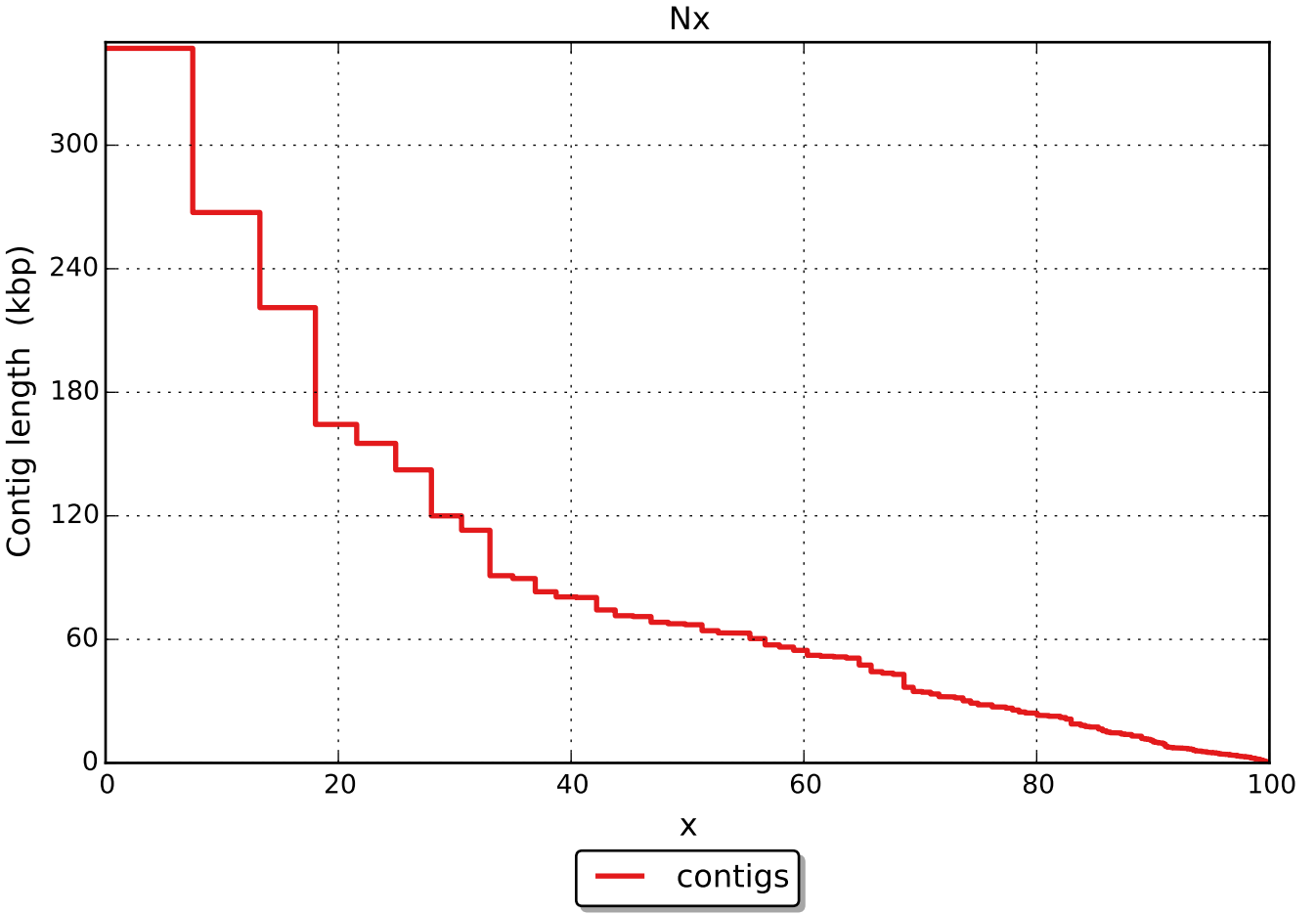
	contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# mismatches	44481
# indels	31
# short indels	31
# long indels	0
Indels length	32

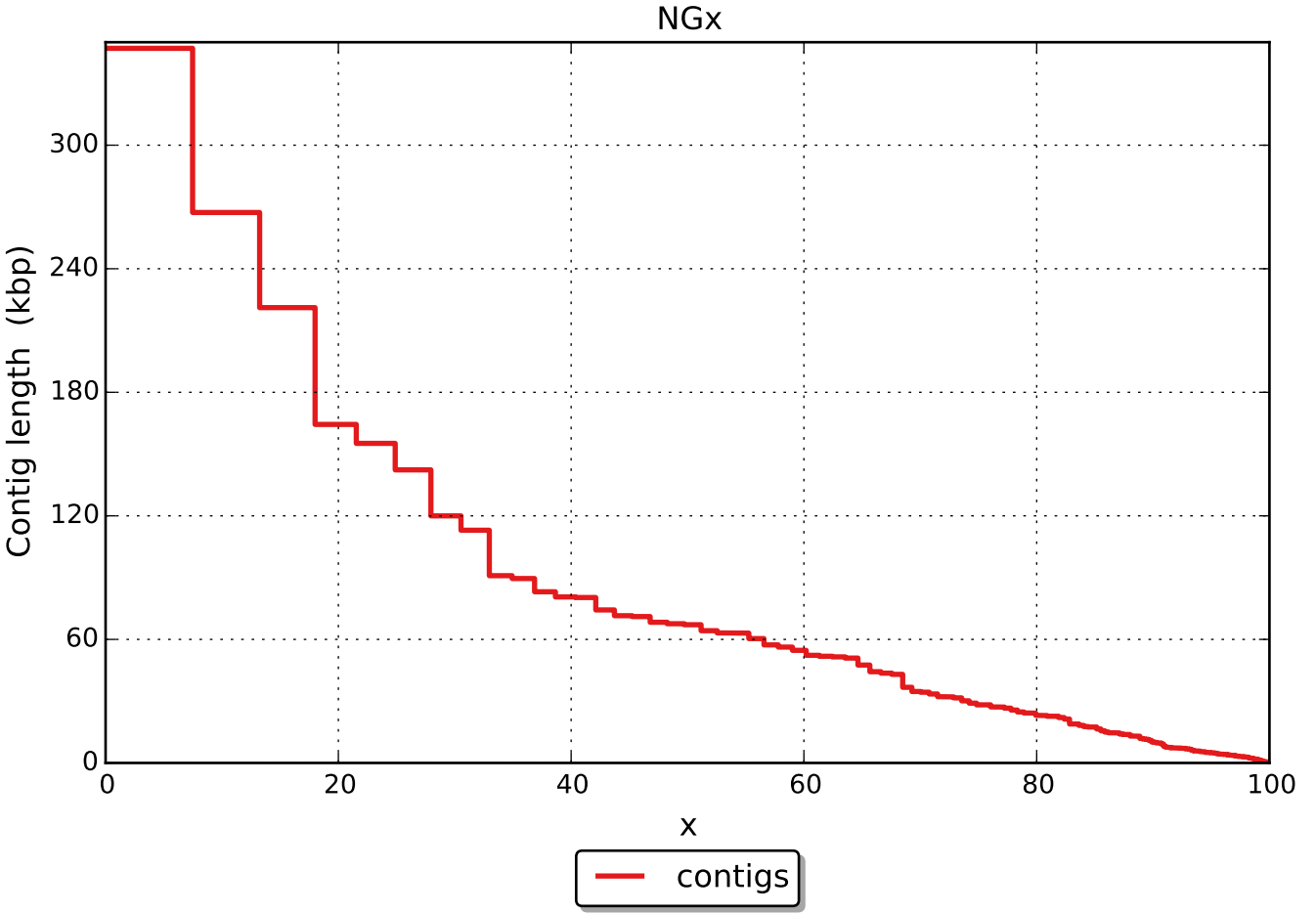
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

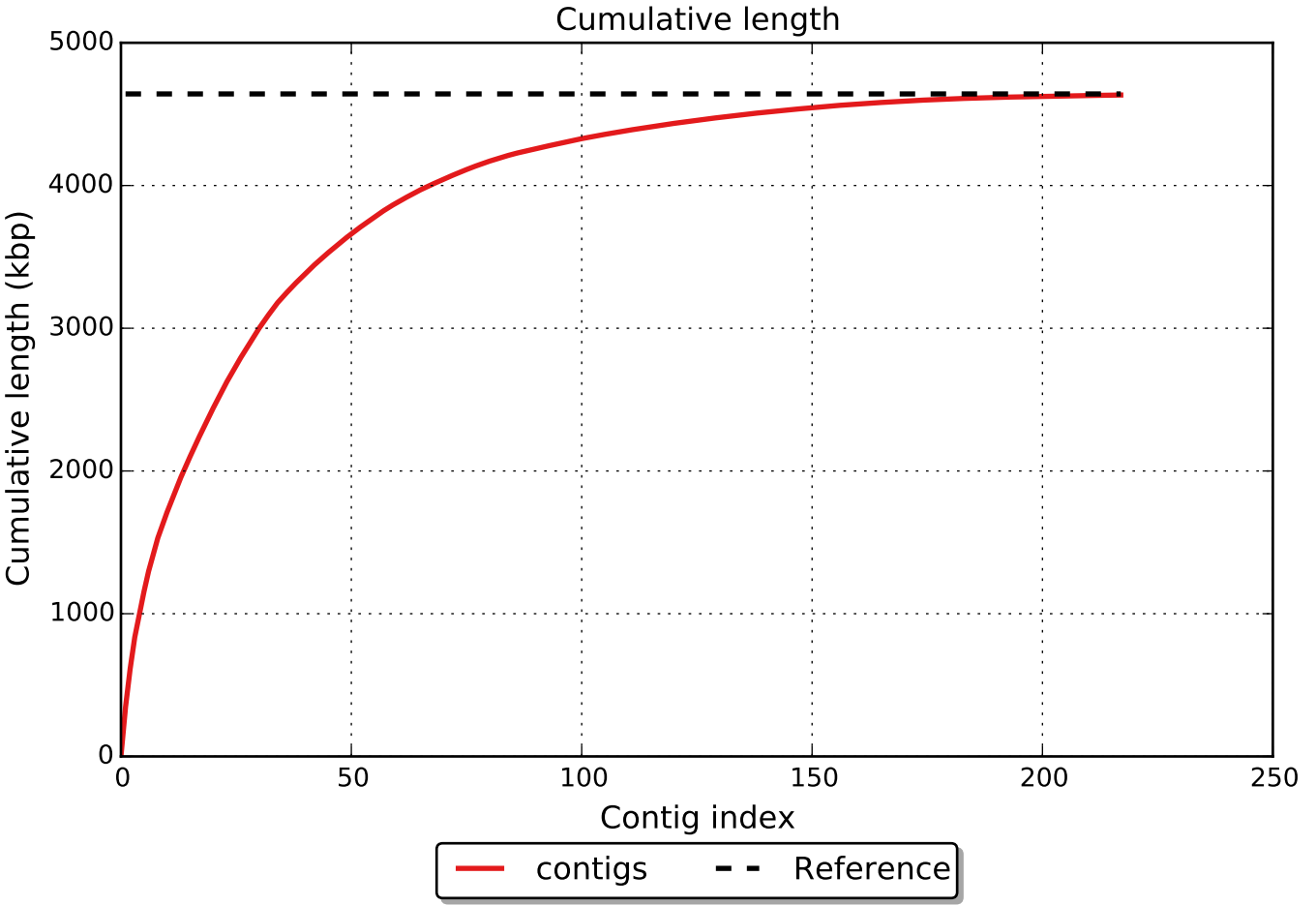
Unaligned report

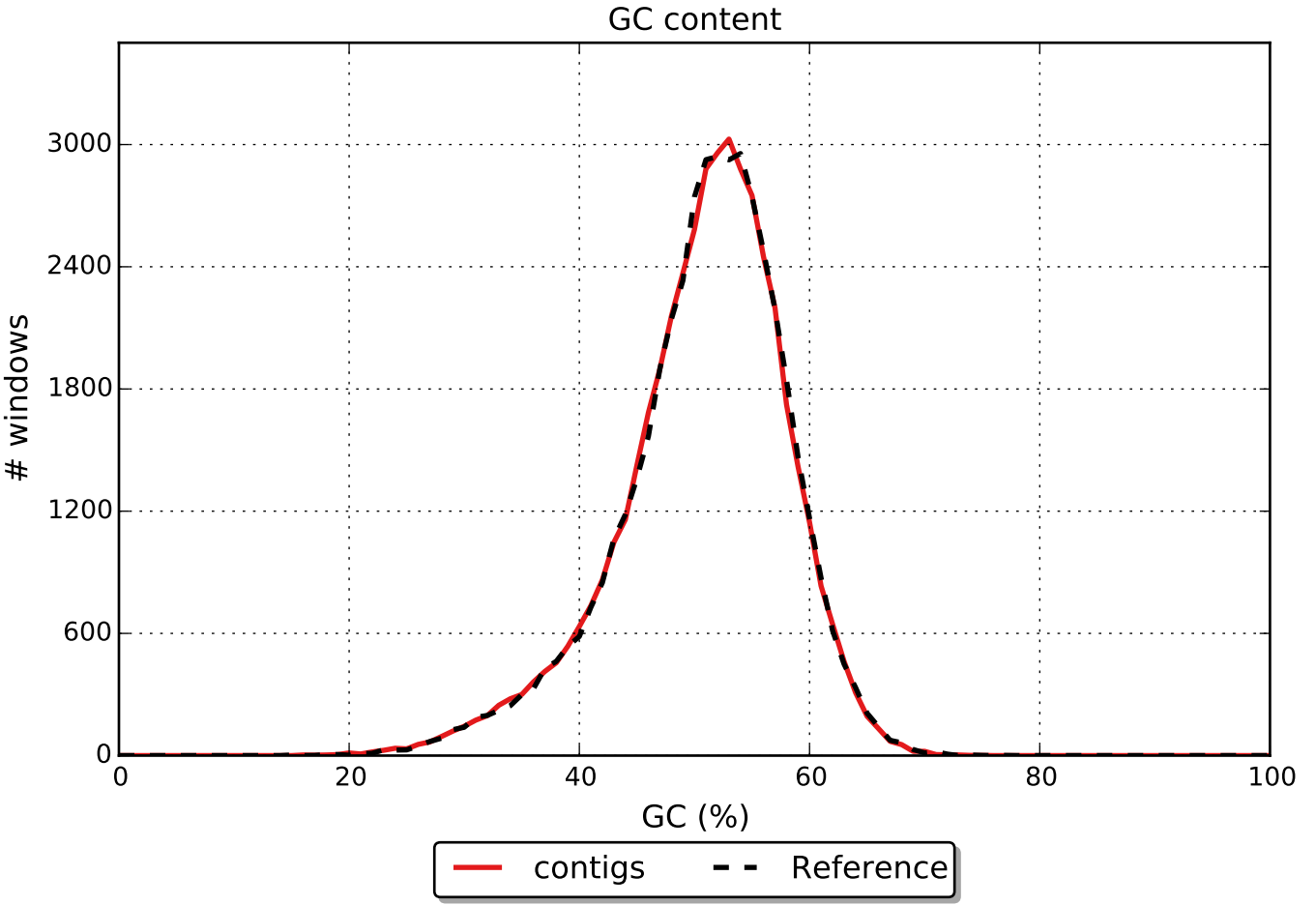
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

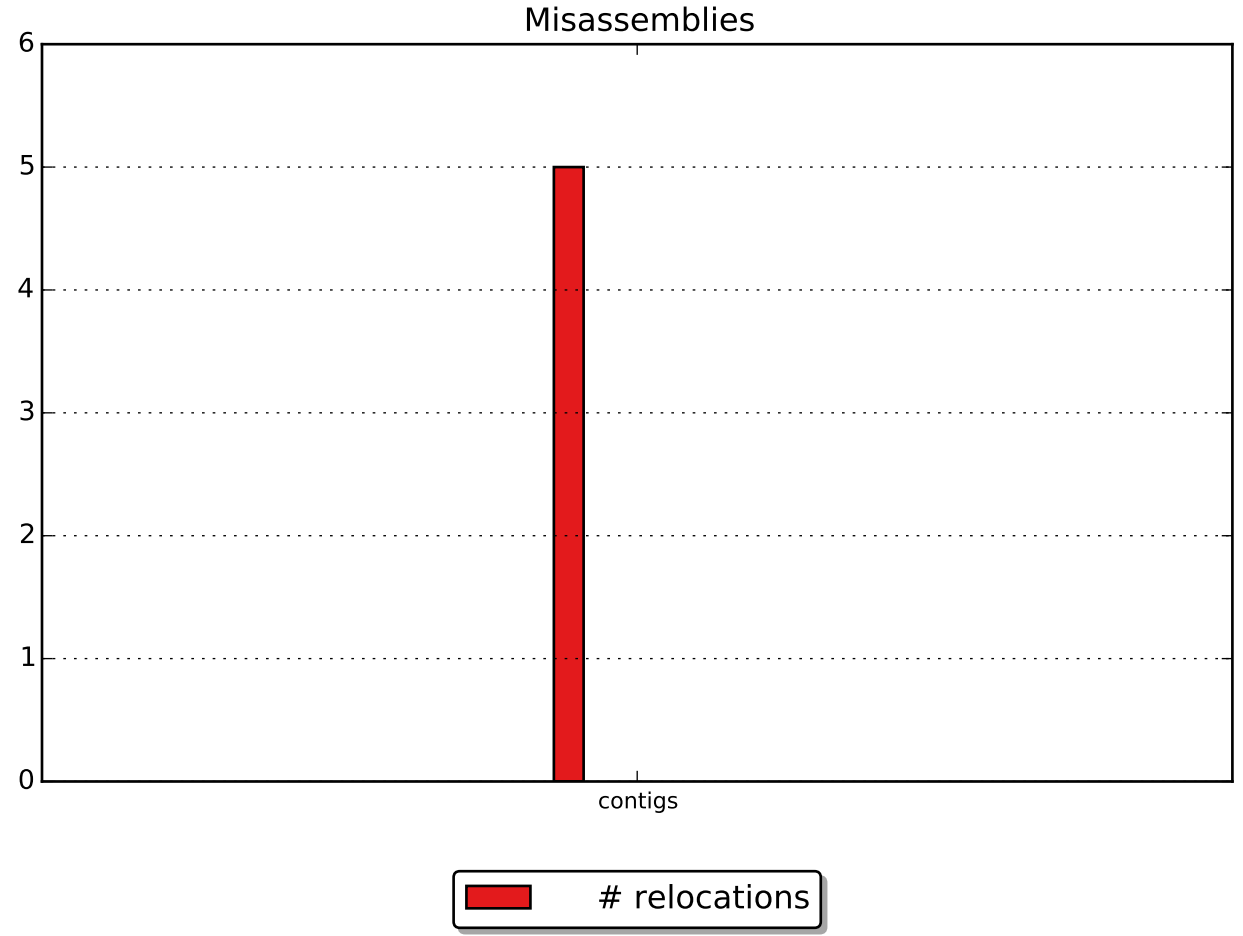
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

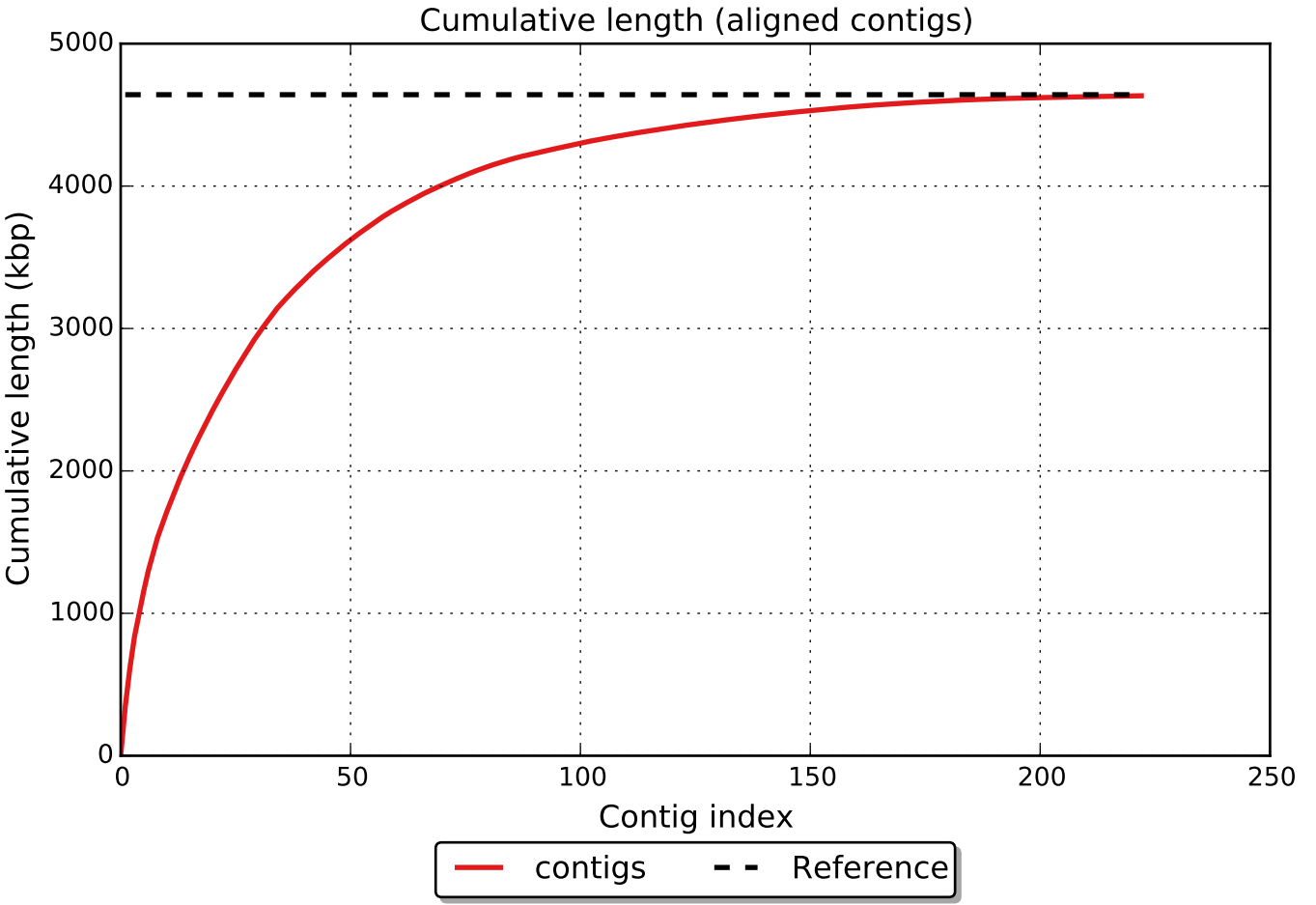

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

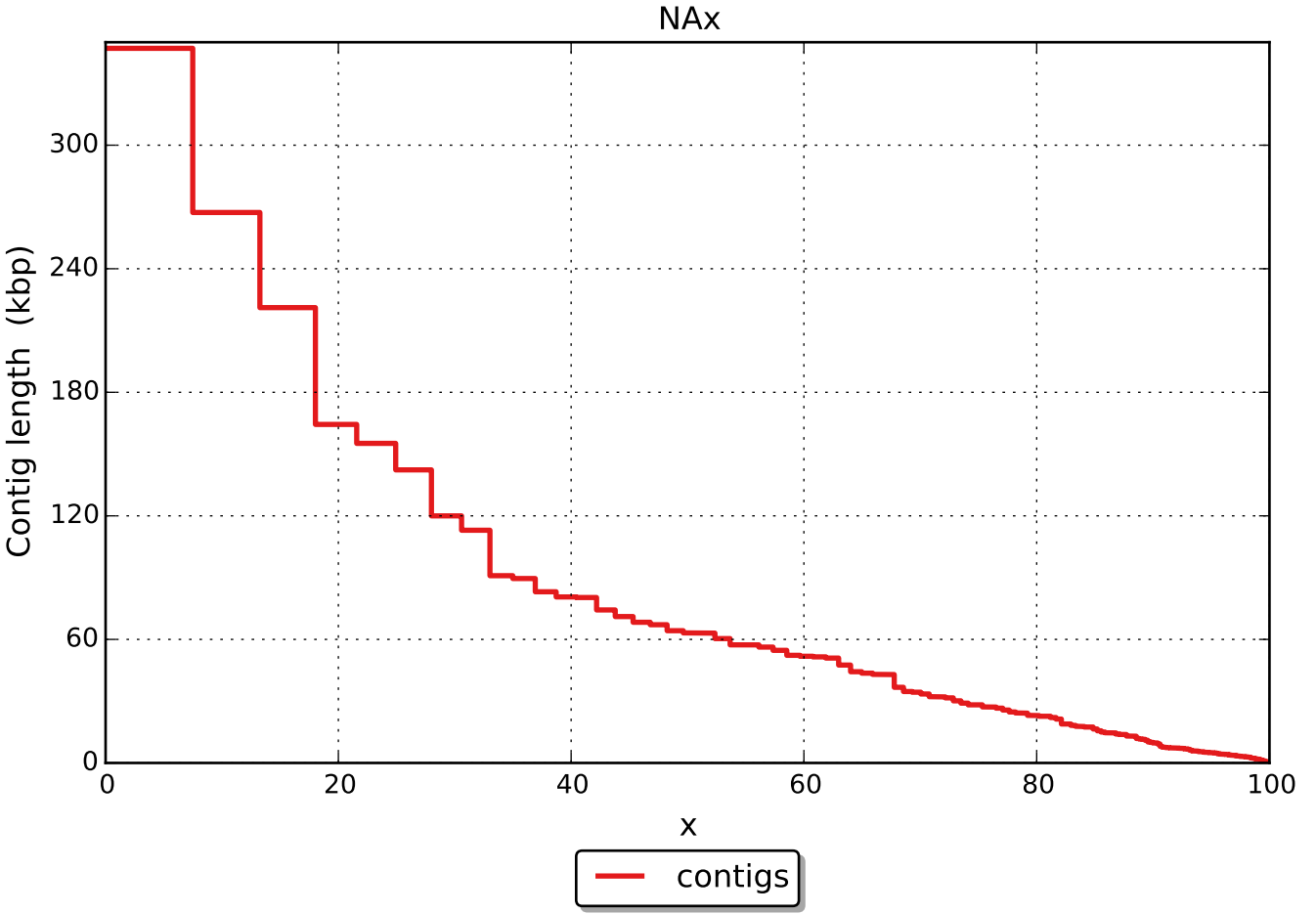

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

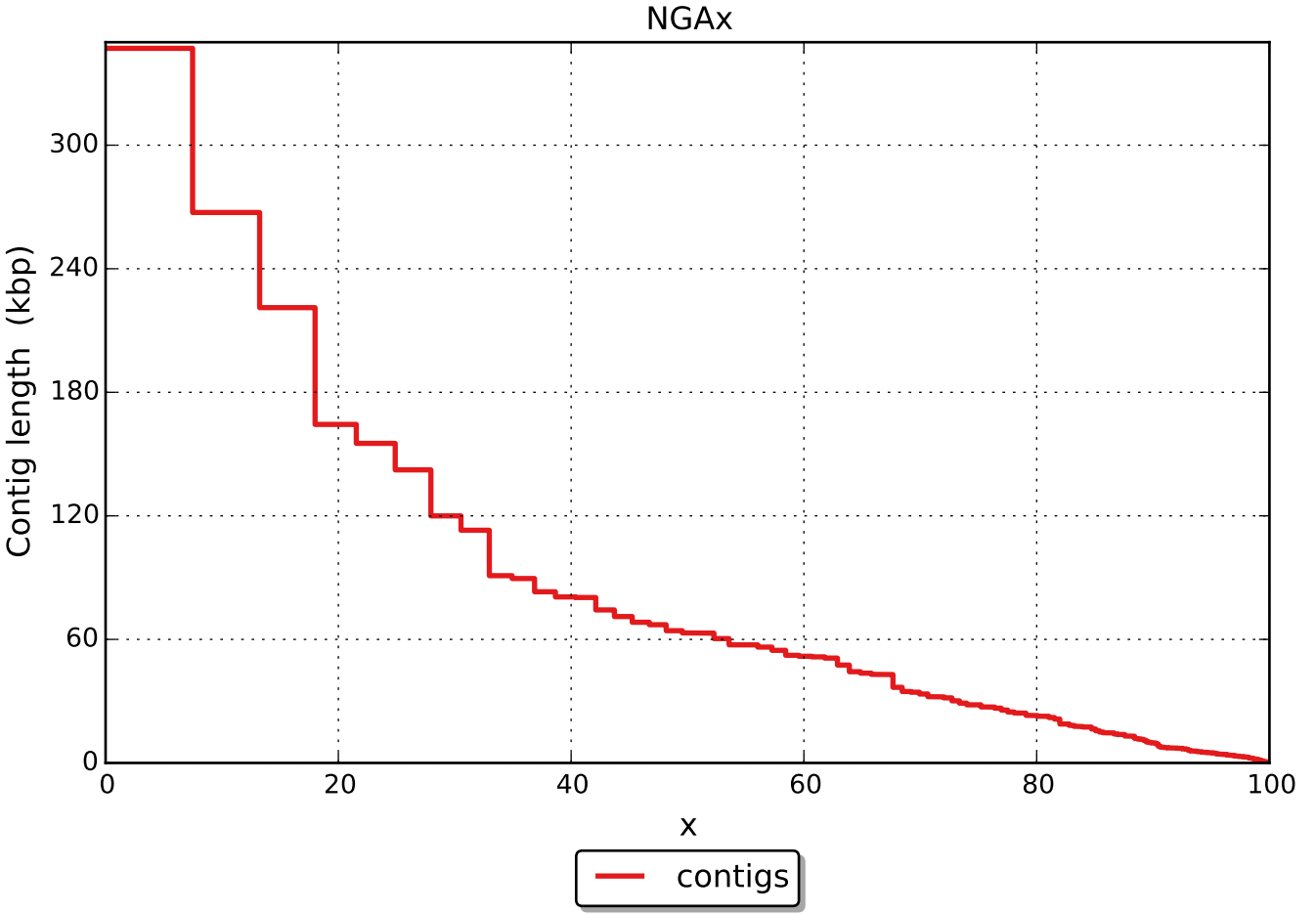

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contigs
Reference


Misassemblies
6
5
4
3
2
1
0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
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