Report

	contigs
# contigs (>= 1000 bp)	128
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4549291
Total length (>= 5000 bp)	4416772
Total length (>= 10000 bp)	4320846
Total length (>= 25000 bp)	4035554
Total length (>= 50000 bp)	3496417
# contigs	164
Largest contig	317313
Total length	4572766
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	95318
NG50	92158
N75	59112
NG75	58576
L50	13
LG50	14
L75	28
LG75	29
# misassemblies	18
# misassembled contigs	2
Misassembled contigs length	294991
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.420
Duplication ratio	1.090
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1049.92
# indels per 100 kbp	0.86
Largest alignment	317313
NA50	83030
NGA50	83030
NA75	40613
NGA75	39331
LA50	15
LGA50	15
LA75	32
LGA75	34

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

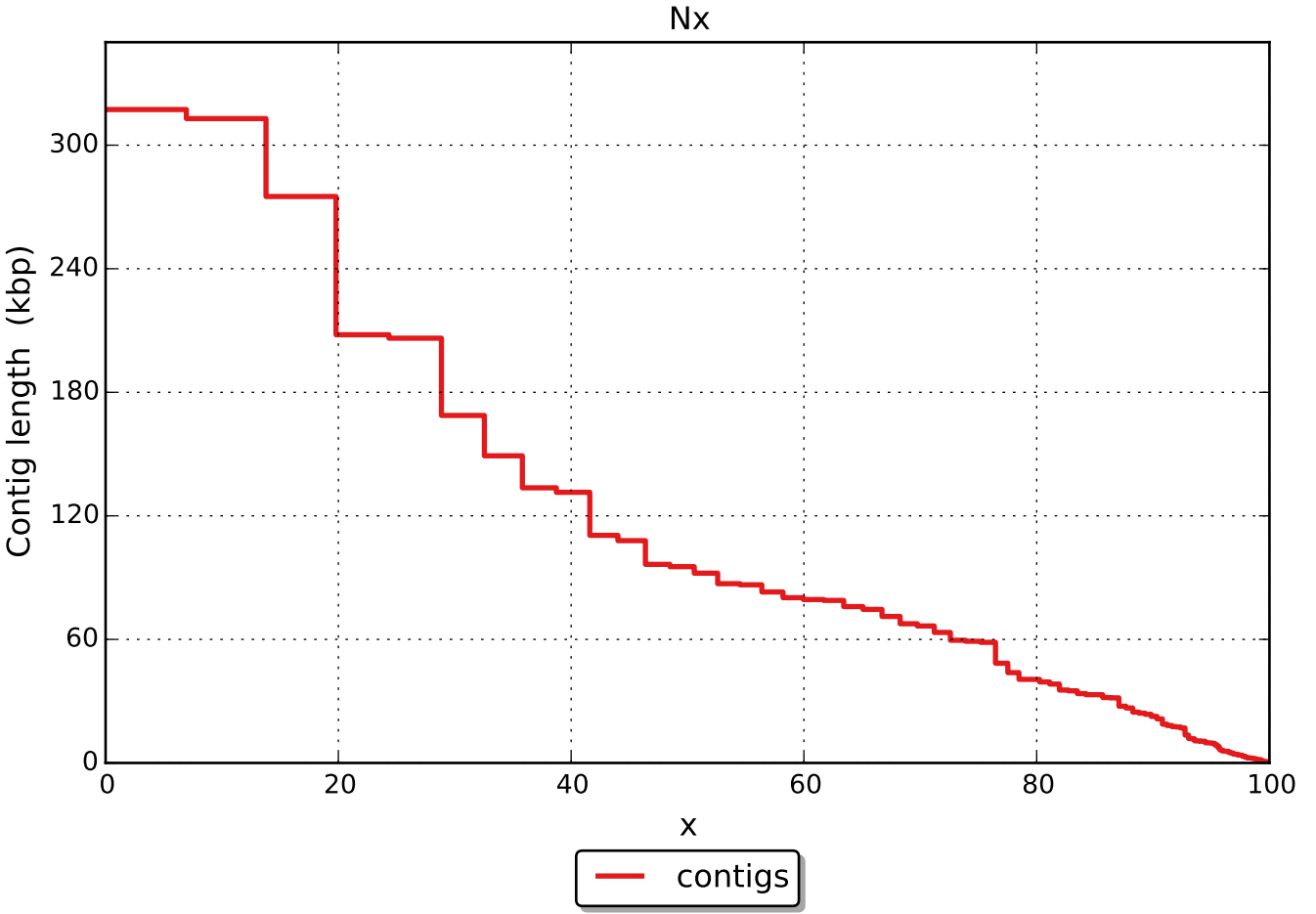
	contigs
# misassemblies	18
# relocations	15
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	294991
# local misassemblies	4
# mismatches	44065
# indels	36
# short indels	36
# long indels	0
Indels length	43

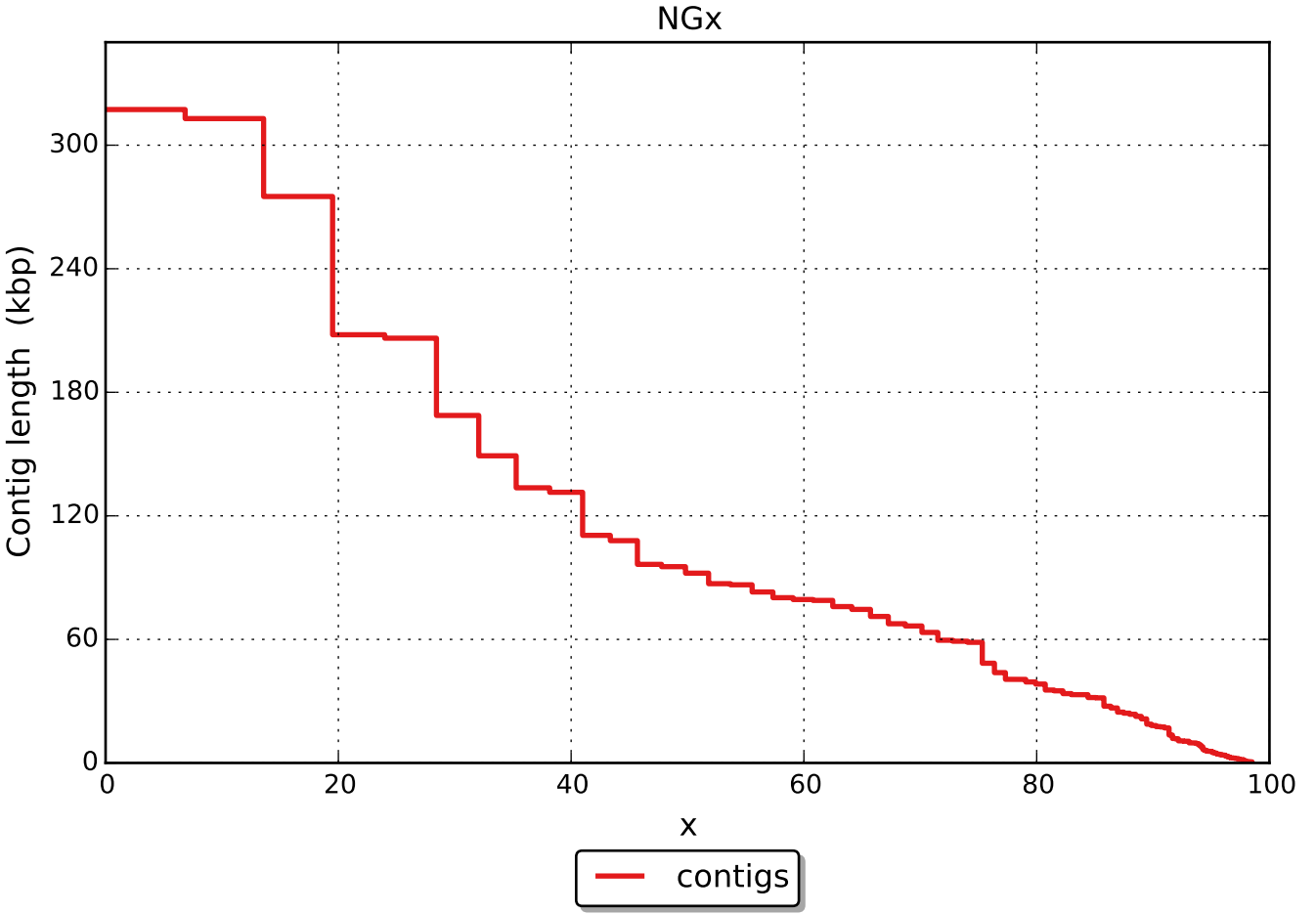
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

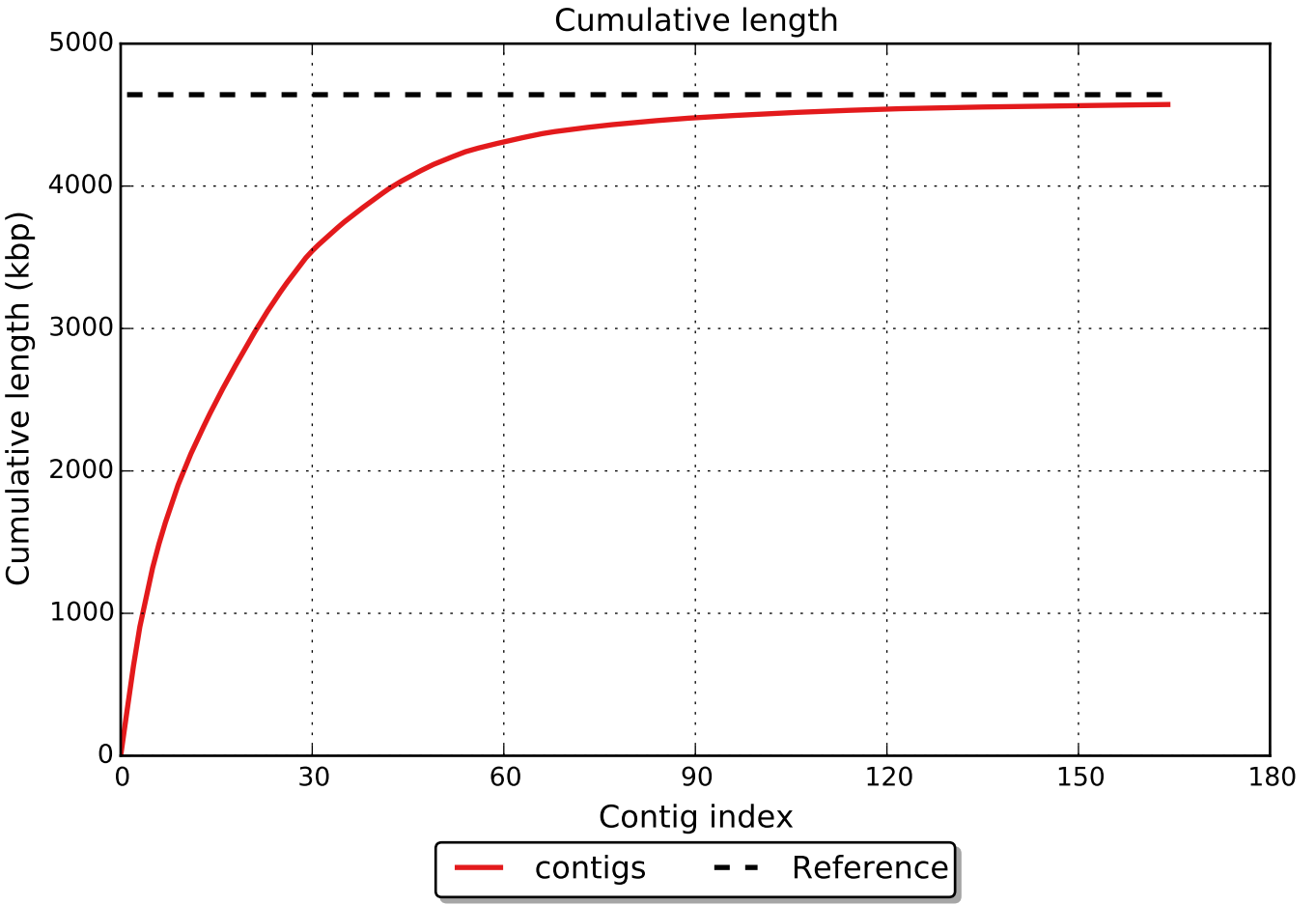
Unaligned report

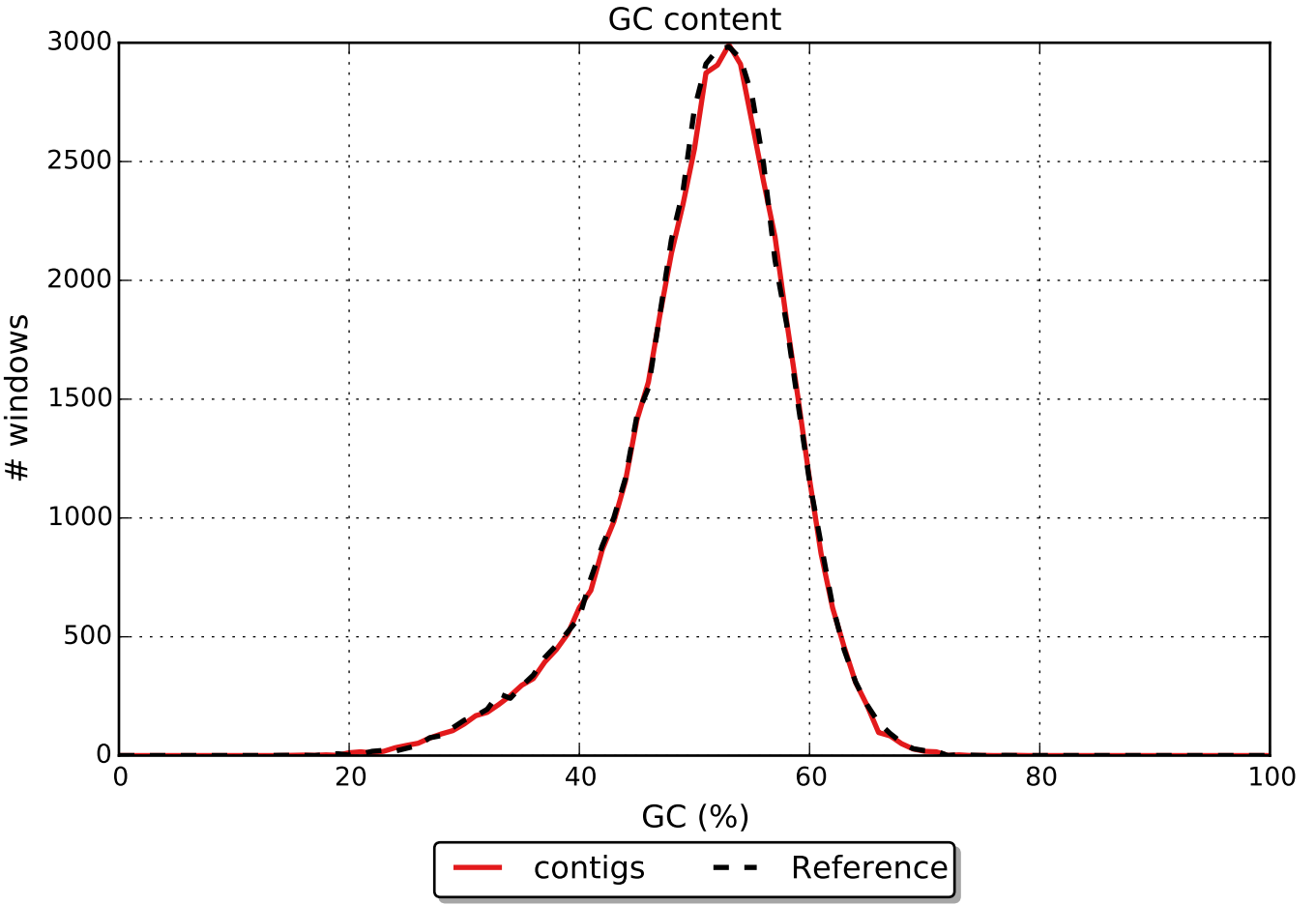
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

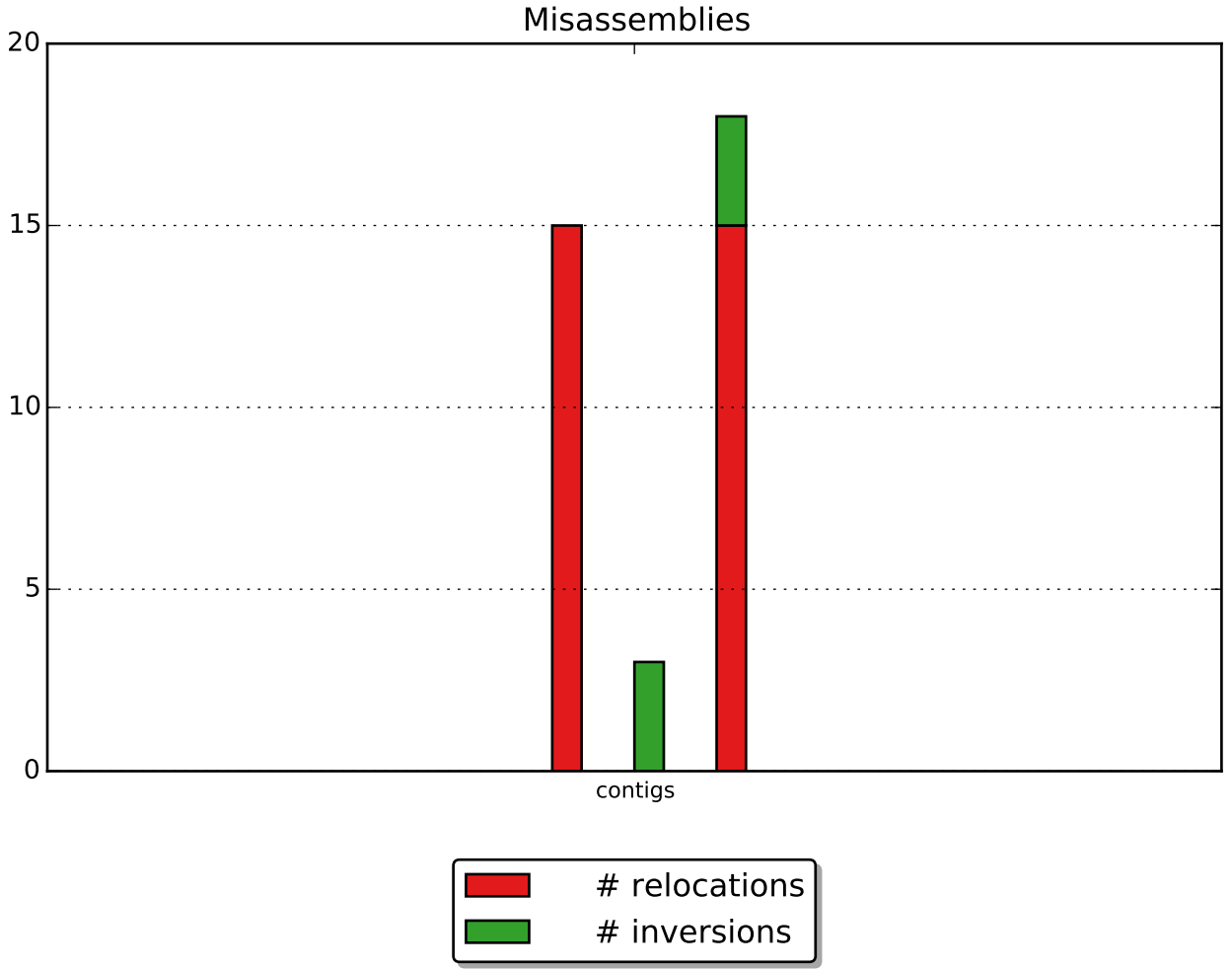
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

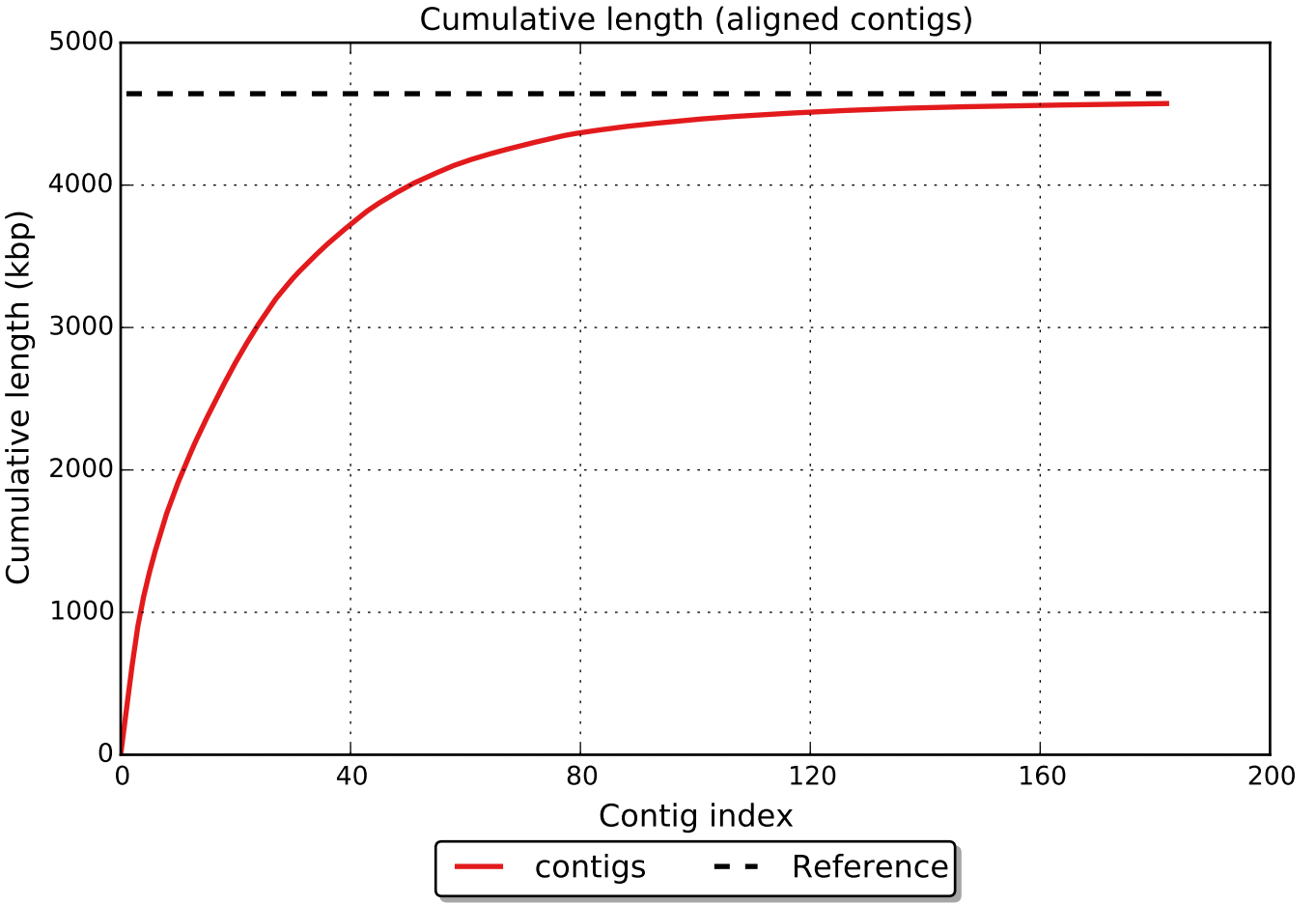

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

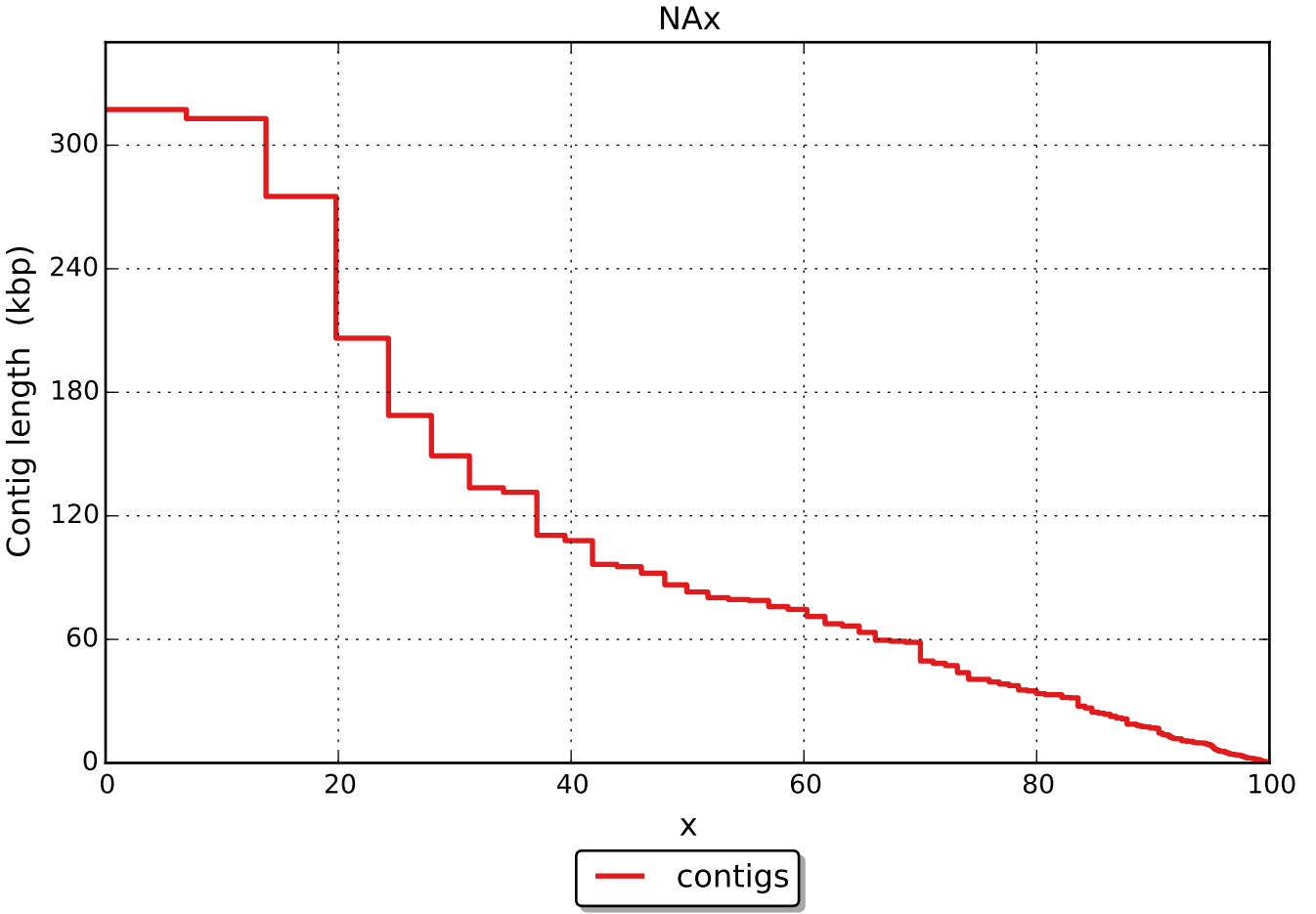

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

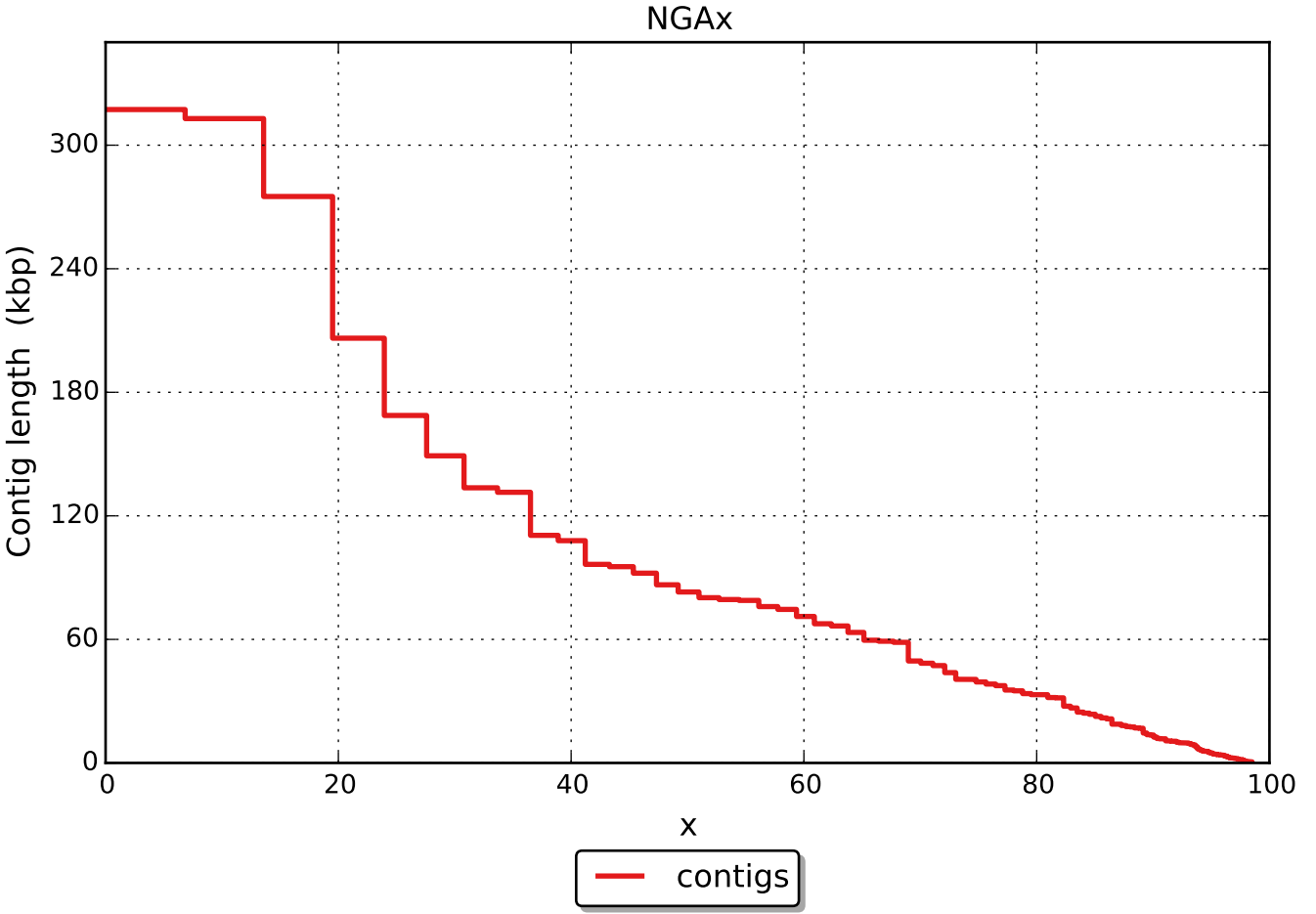

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
180
Contig index
contigs
Reference


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


Misassemblies
20
15
10
5
0
contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
40
80
120
160
200
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