Report

	contigs
# contigs (>= 1000 bp)	104
# contigs (>= 5000 bp)	63
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4313153
Total length (>= 5000 bp)	4217505
Total length (>= 10000 bp)	4161447
Total length (>= 25000 bp)	3943396
Total length (>= 50000 bp)	3404259
# contigs	139
Largest contig	317313
Total length	4335790
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.78
N50	96440
NG50	87046
N75	59591
NG75	43861
L50	12
LG50	14
L75	26
LG75	30
# misassemblies	18
# misassembled contigs	2
Misassembled contigs length	294991
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.371
Duplication ratio	1.069
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1004.37
# indels per 100 kbp	0.81
Largest alignment	317313
NA50	86515
NGA50	80255
NA75	47277
NGA75	37532
LA50	13
LGA50	15
LA75	29
LGA75	35

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

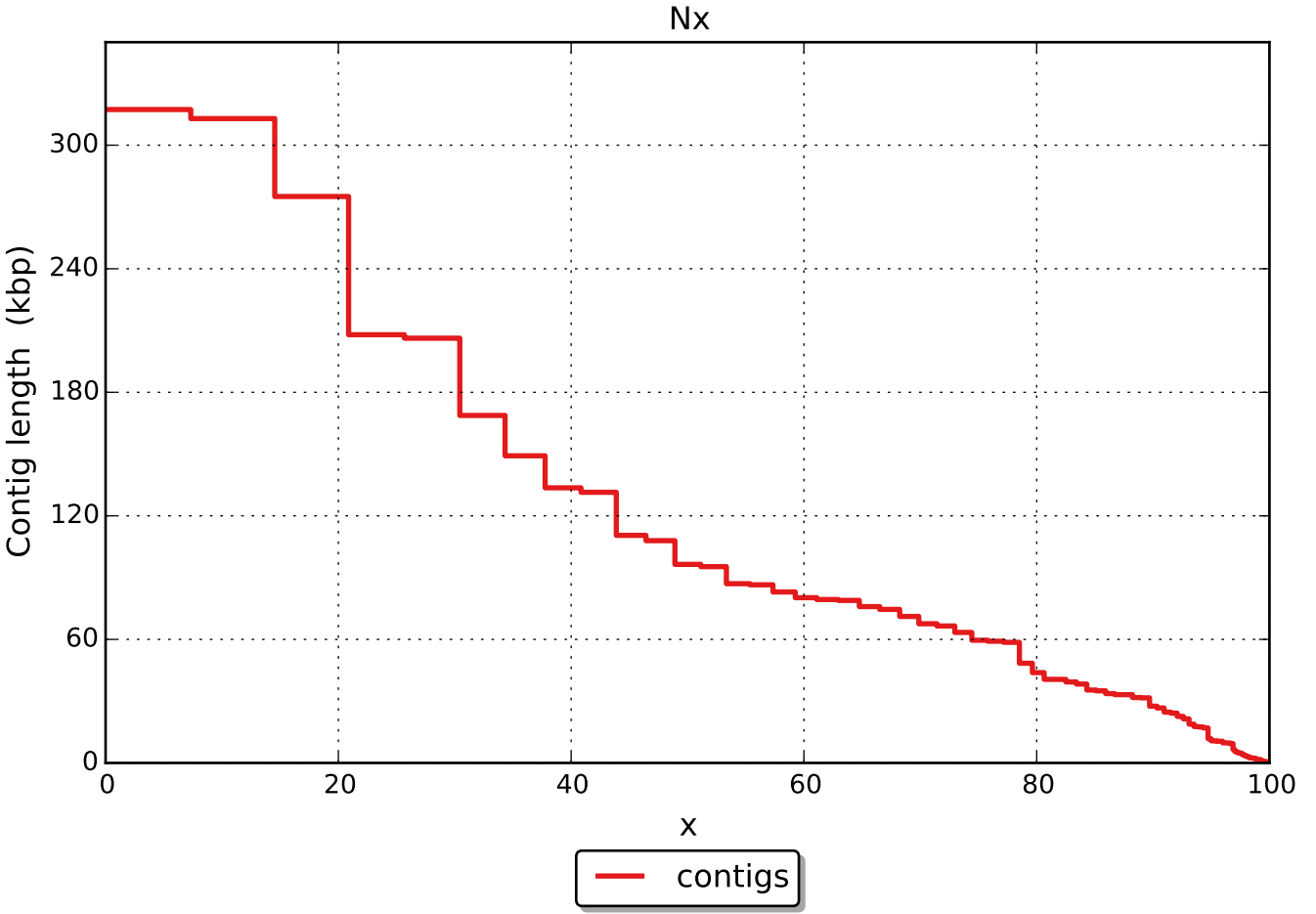
	contigs
# misassemblies	18
# relocations	15
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	294991
# local misassemblies	4
# mismatches	40732
# indels	33
# short indels	33
# long indels	0
Indels length	40

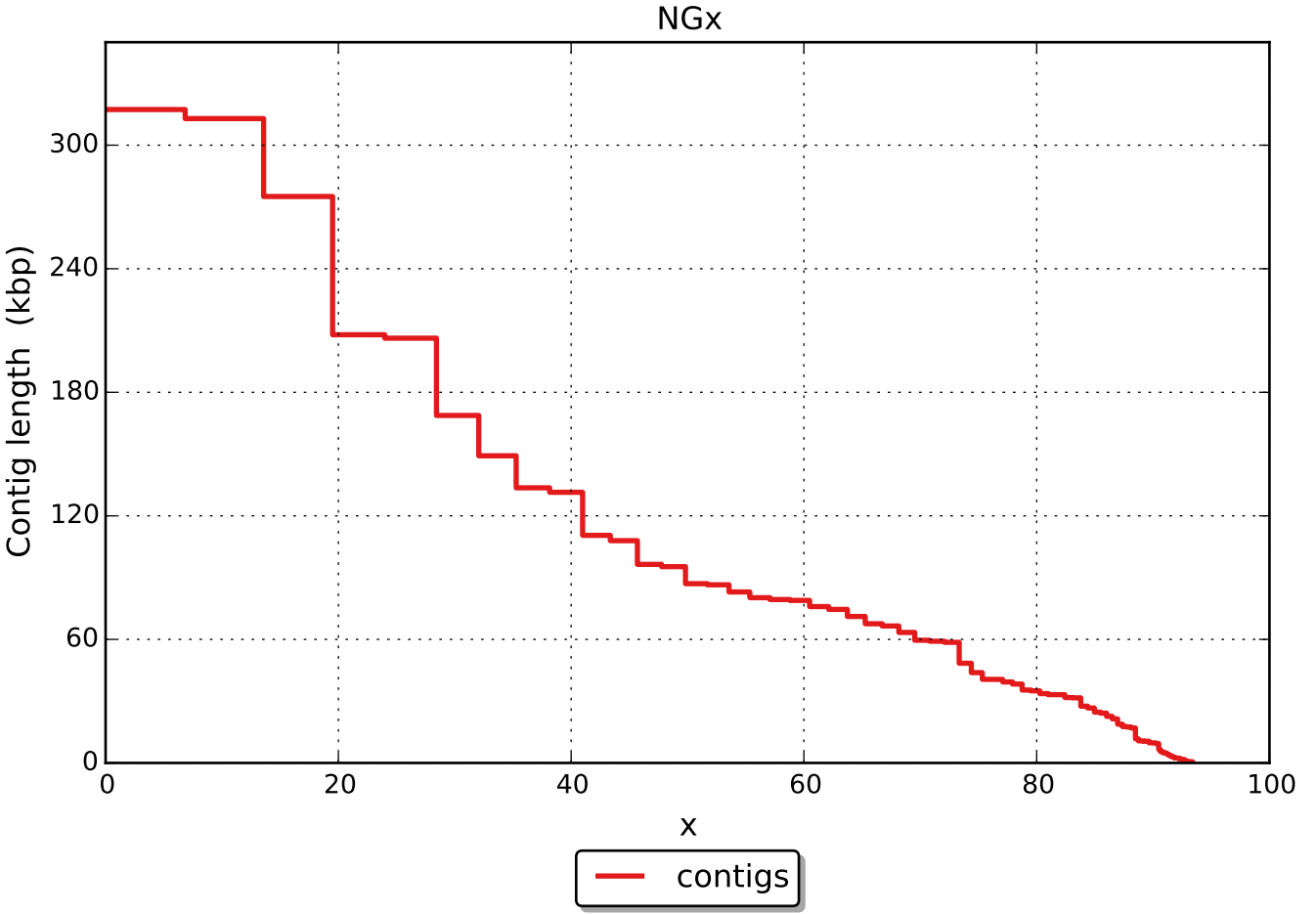
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

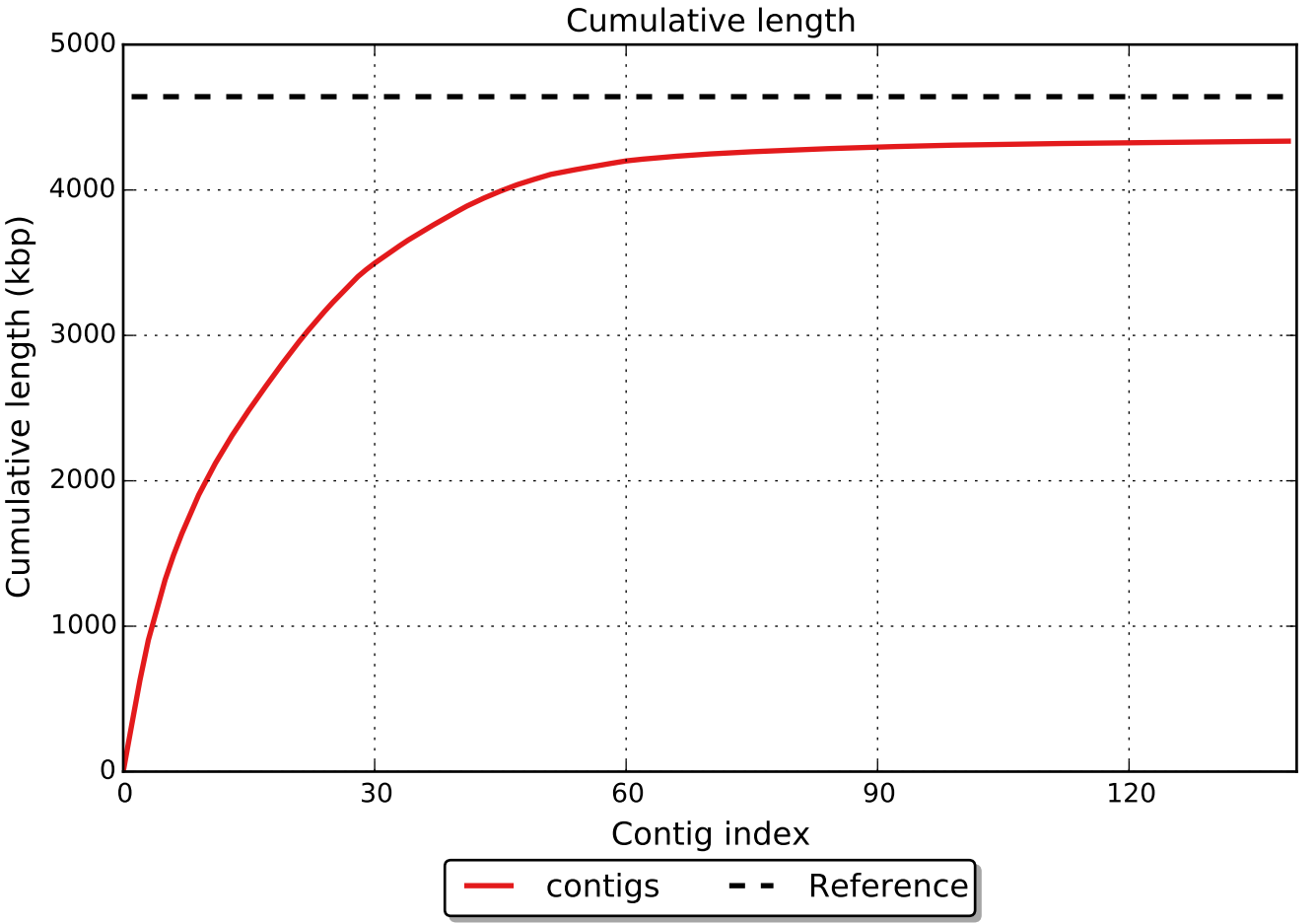
Unaligned report

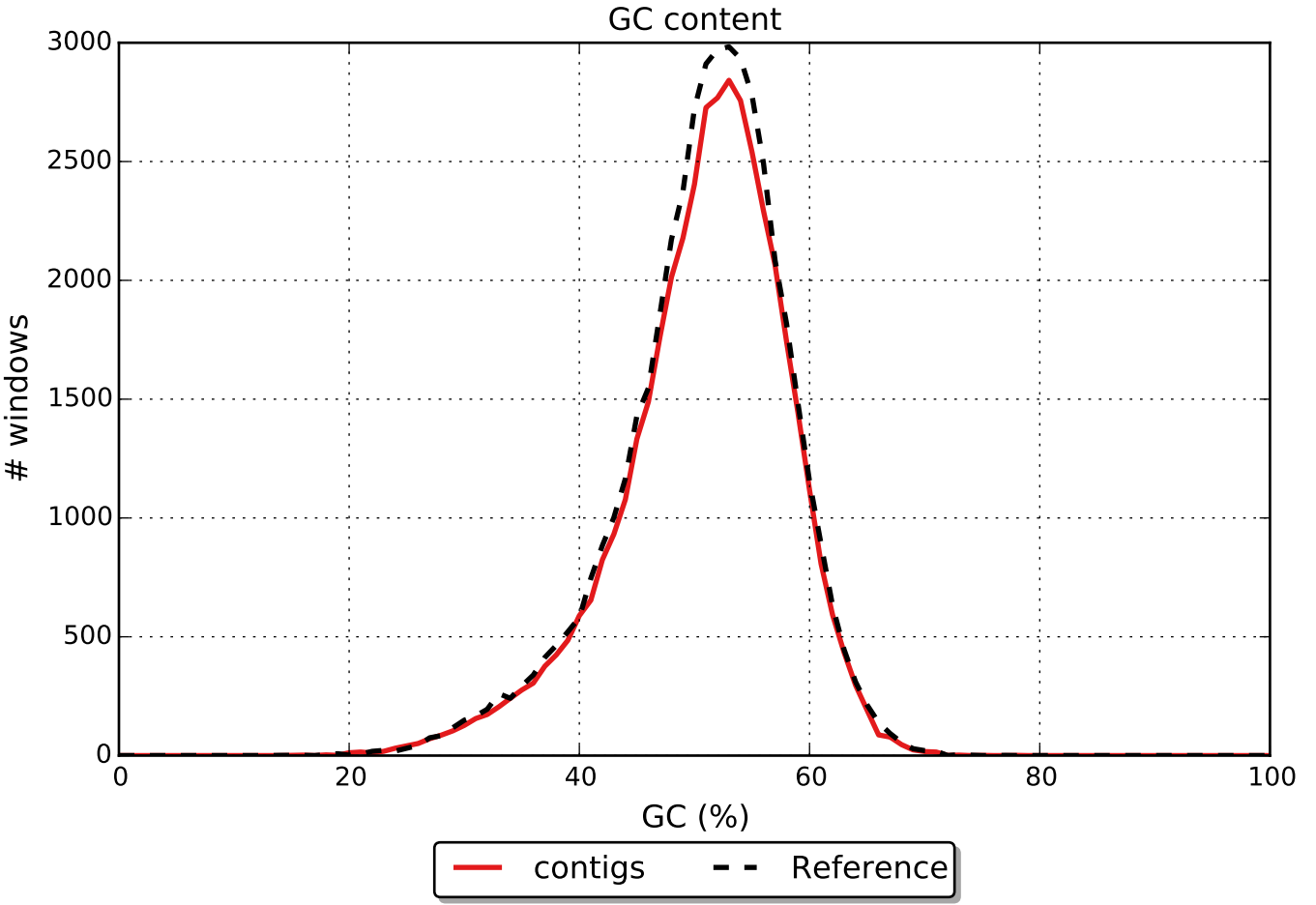
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

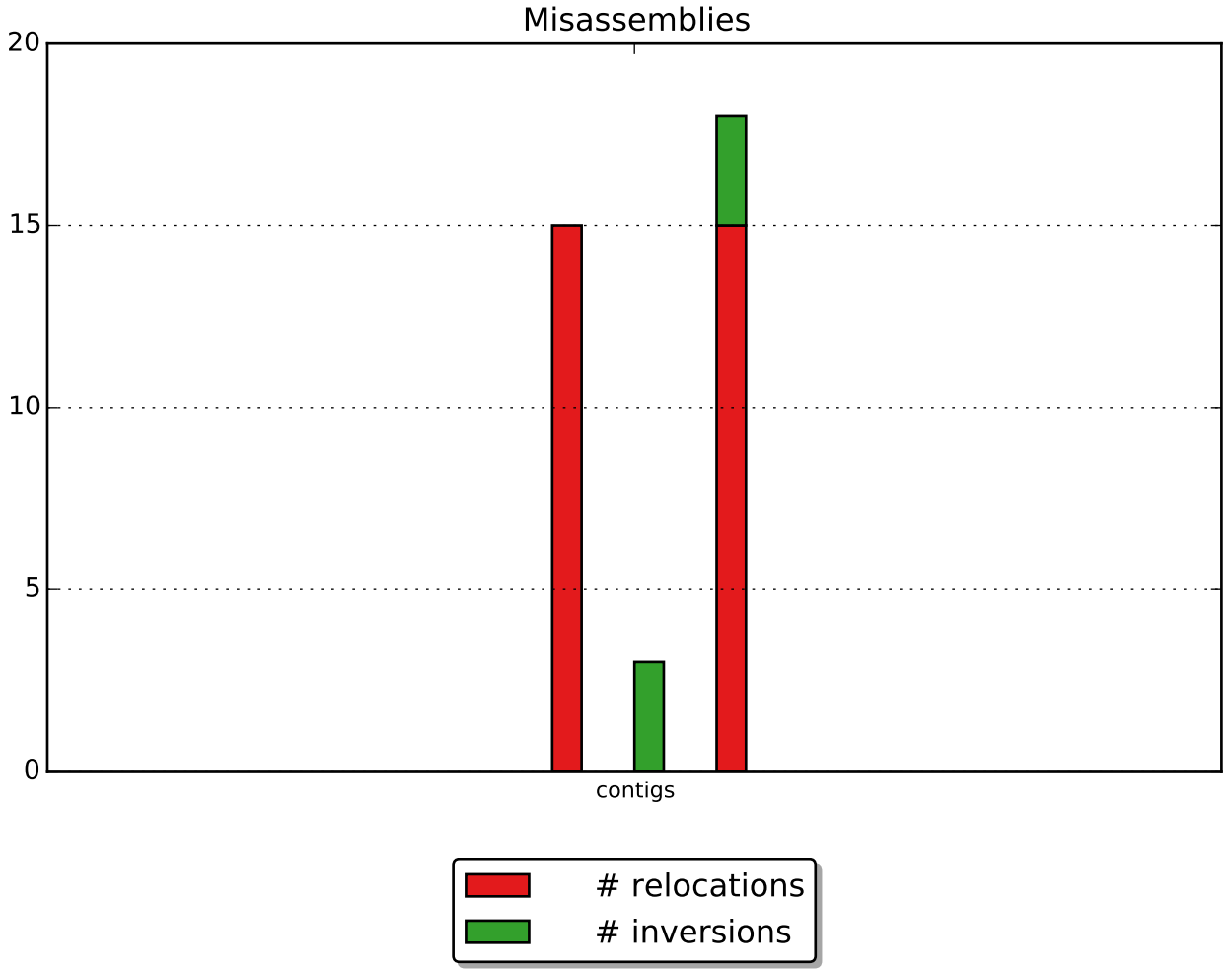
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

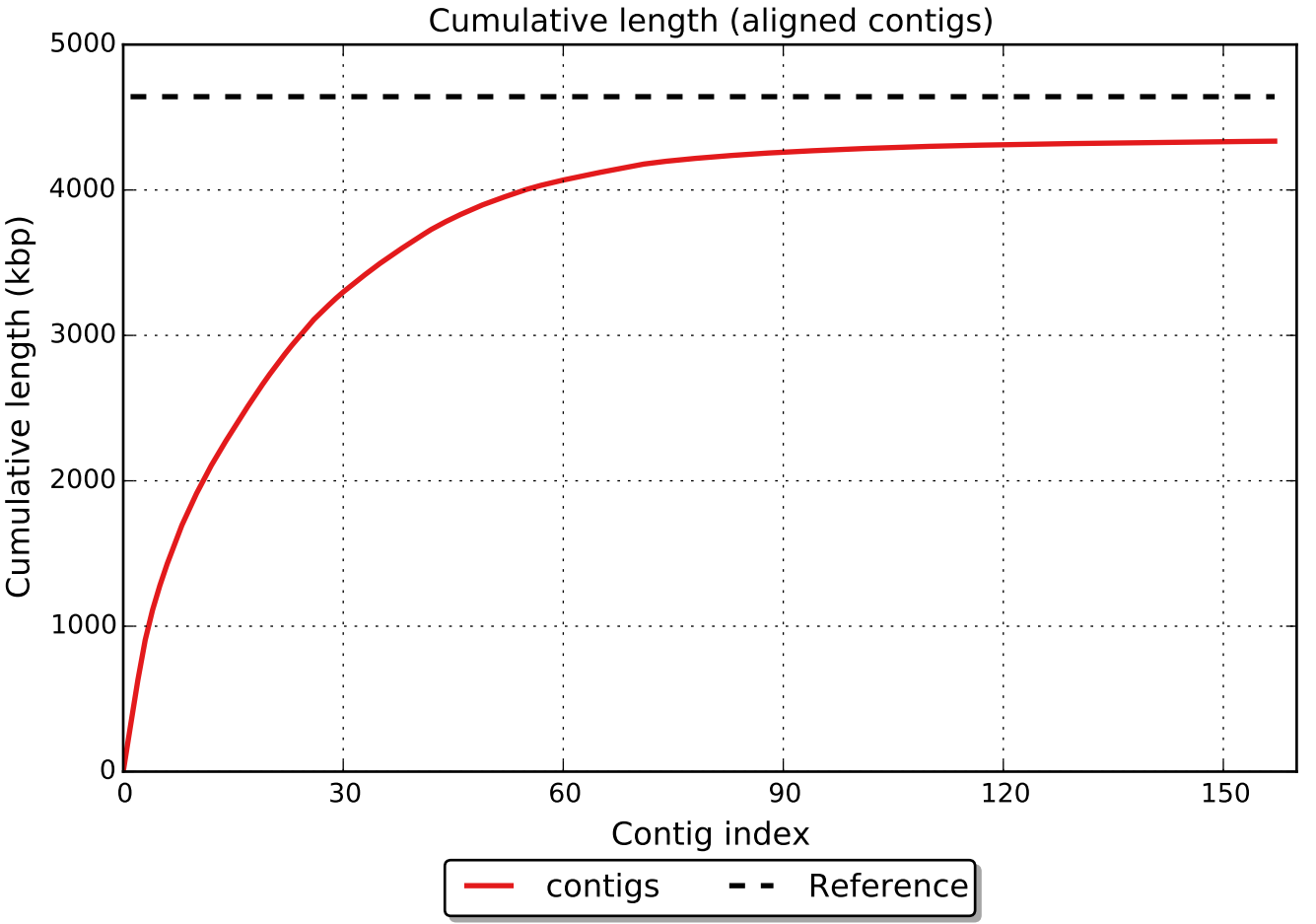

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

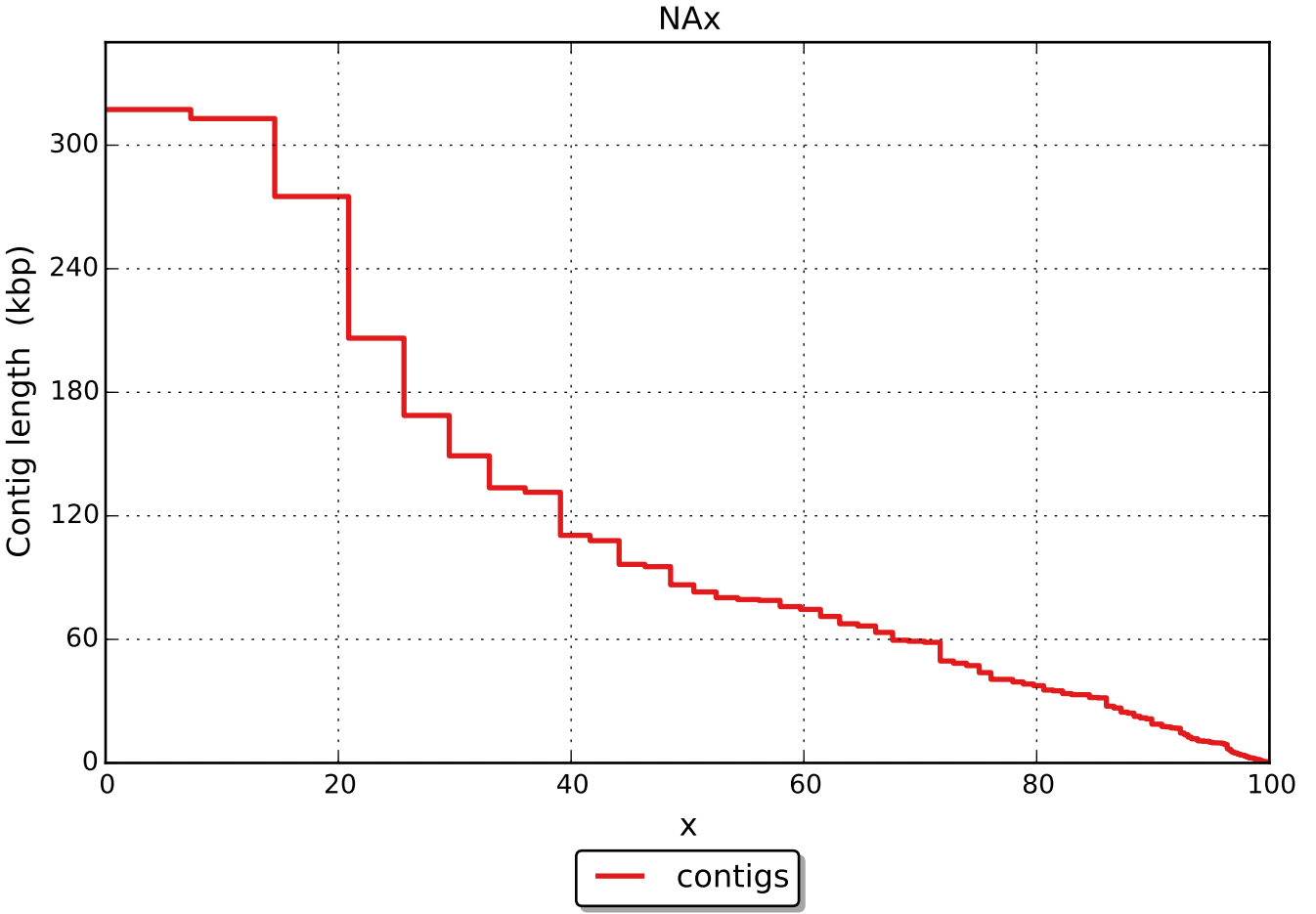

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

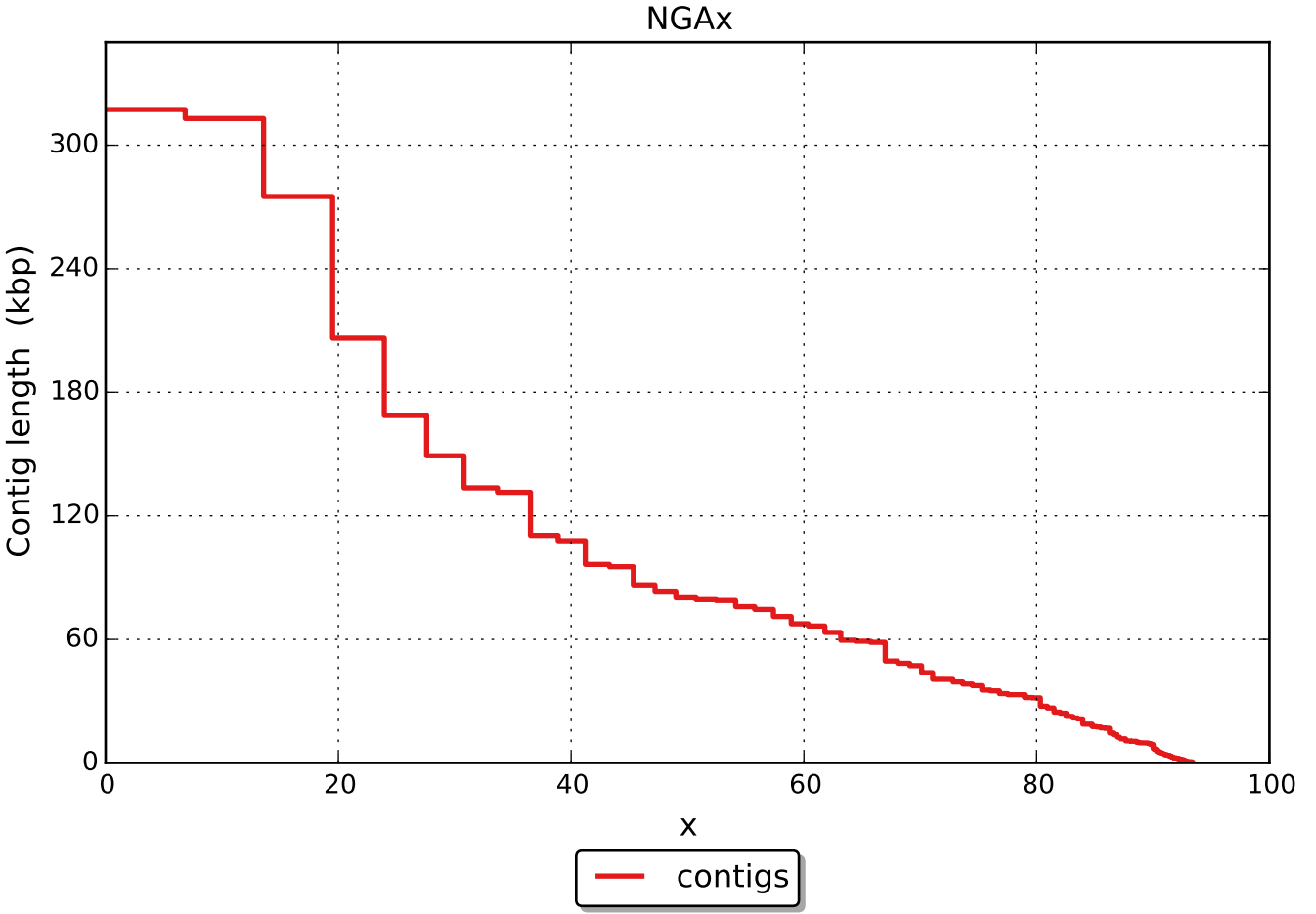

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
contigs
Reference


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
30
60
90
120
150
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