Report

	scaffolds
# contigs (>= 1000 bp)	69
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4560692
Total length (>= 5000 bp)	4519718
Total length (>= 10000 bp)	4495765
Total length (>= 25000 bp)	4404583
Total length (>= 50000 bp)	3878746
# contigs	75
Largest contig	327049
Total length	4564761
Reference length	4641652
GC (‰)	50.74
Reference GC (‰)	50.79
N50	171225
NG50	171225
N75	87058
NG75	78613
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	171225
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (‰)	98.287
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.87
# indels per 100 kbp	8.83
Largest alignment	327049
NA50	133027
NGA50	132872
NA75	84850
NGA75	78613
LA50	10
LGA50	11
LA75	21
LGA75	22

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

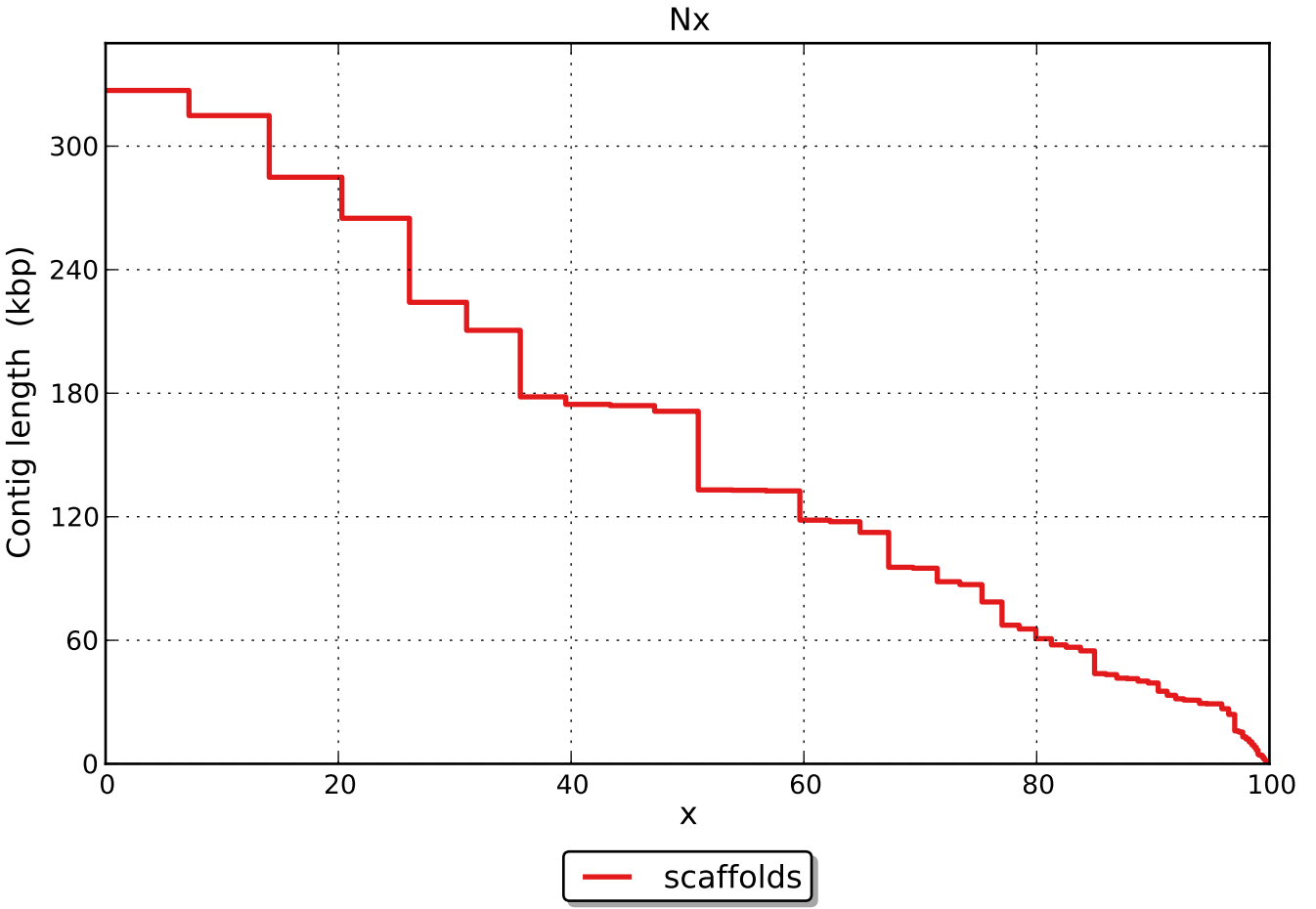
	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	171225
# local misassemblies	2
# mismatches	2868
# indels	403
# short indels	403
# long indels	0
Indels length	569

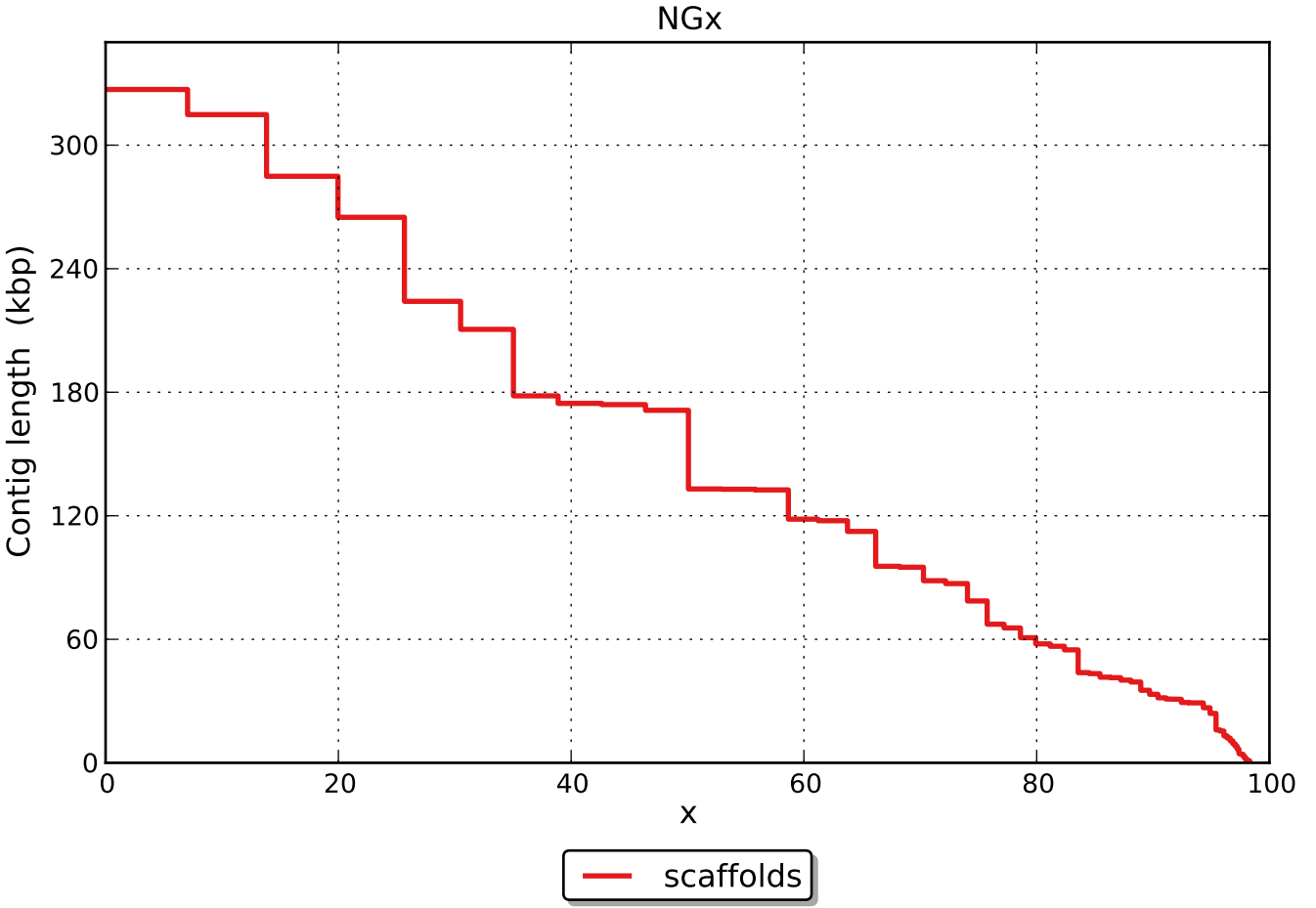
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

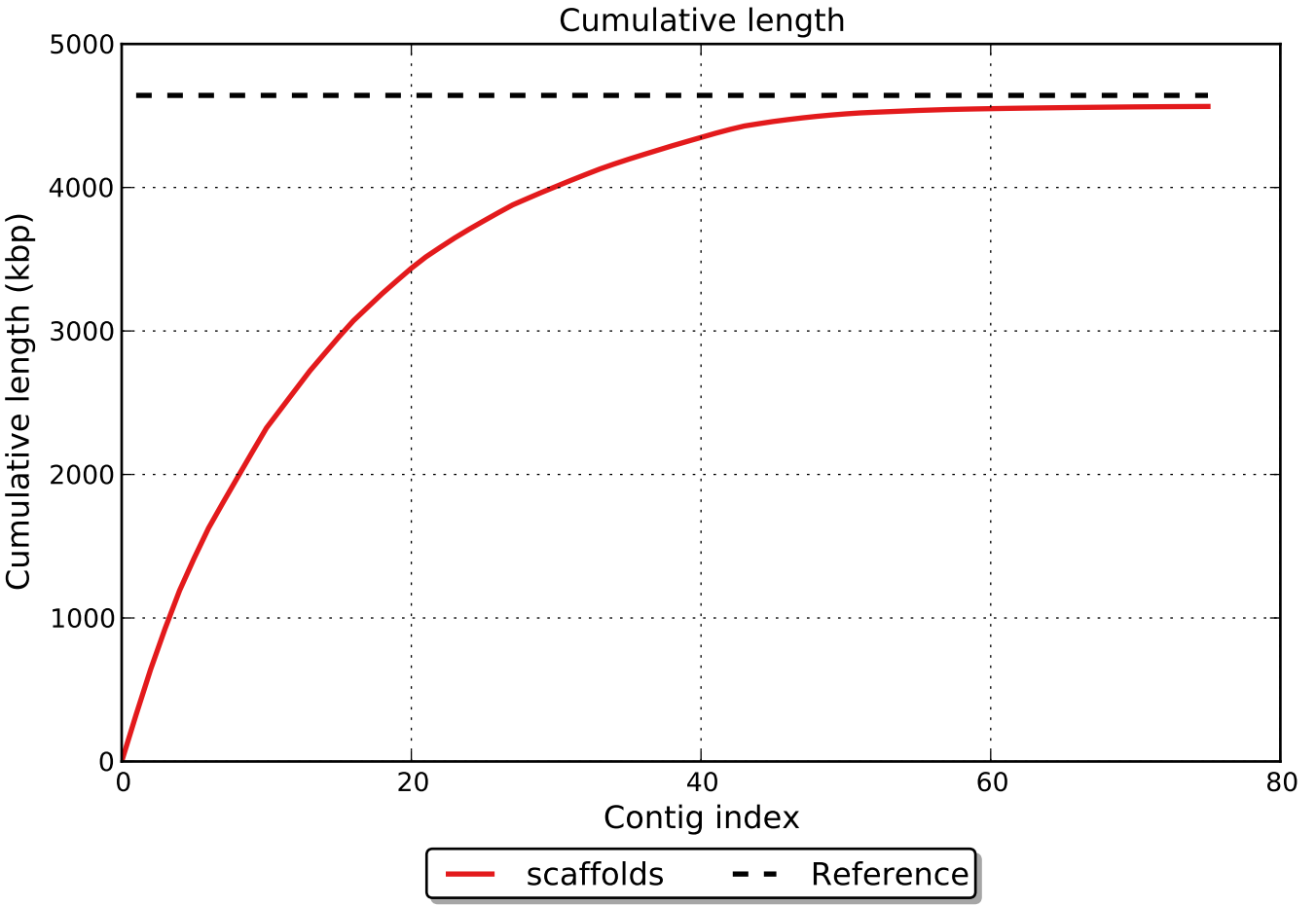
Unaligned report

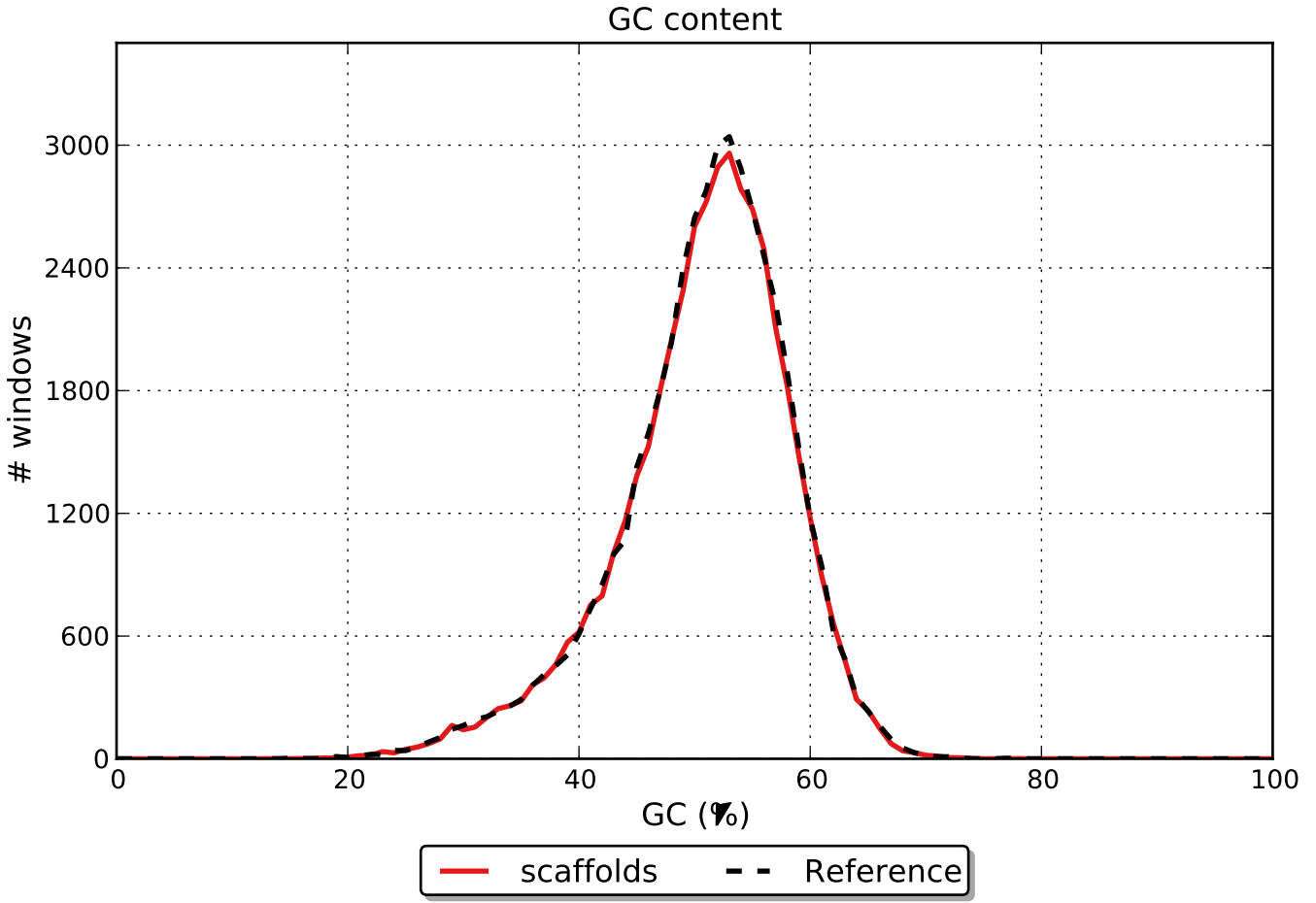
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

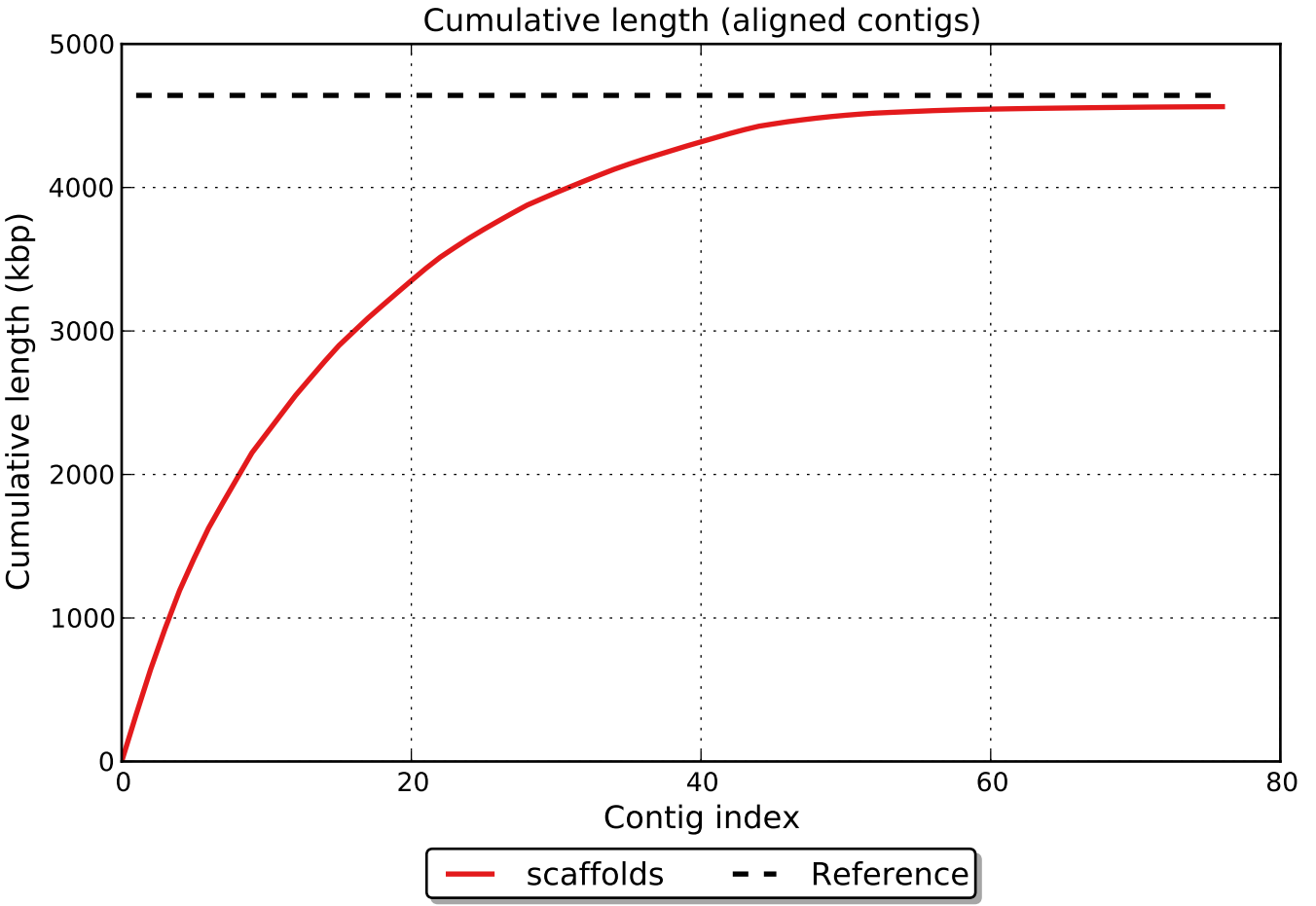

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

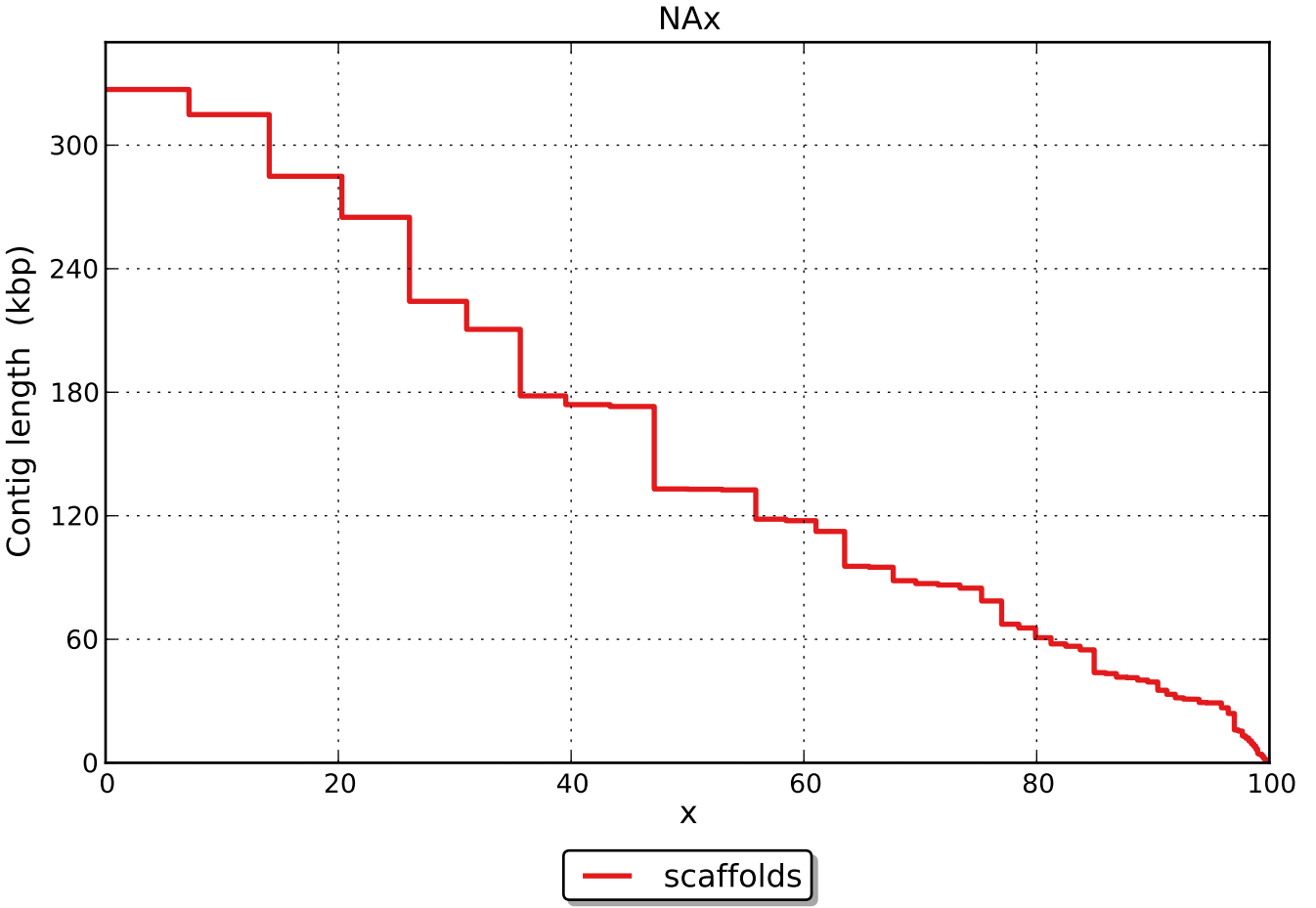

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

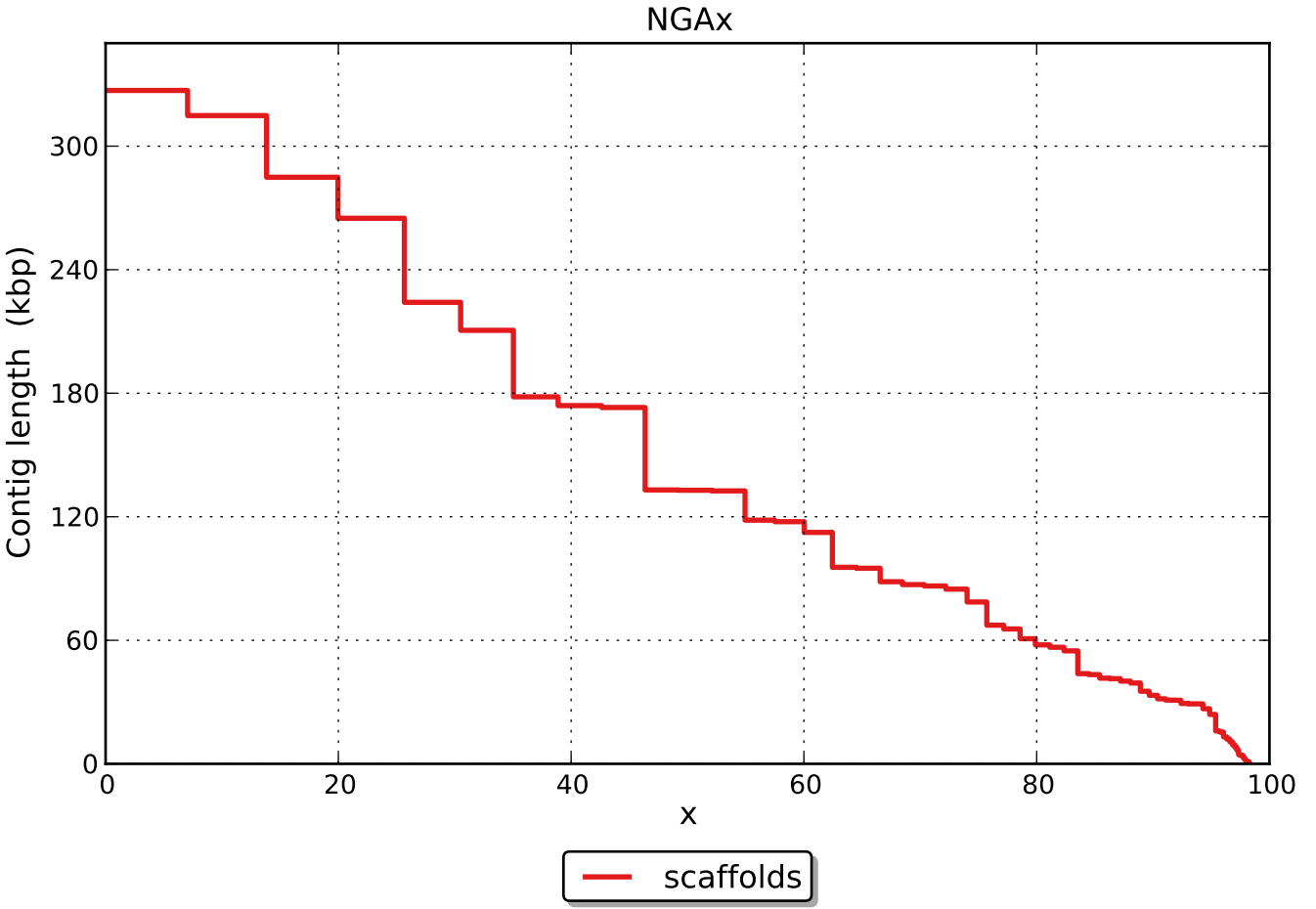

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


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

Misassemblies
2.0
1.5
1.0
0.5
0.0
scaffolds
relocations


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


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


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