Report

	scaffolds
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4562272
Total length (>= 5000 bp)	4520571
Total length (>= 10000 bp)	4496601
Total length (>= 25000 bp)	4405357
Total length (>= 50000 bp)	3920273
# contigs	72
Largest contig	327047
Total length	4565695
Reference length	4641652
GC (‰)	50.74
Reference GC (‰)	50.79
N50	173978
NG50	173978
N75	87062
NG75	78626
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45736
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (‰)	98.307
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	63.18
# indels per 100 kbp	8.81
Largest alignment	327047
NA50	173066
NGA50	173066
NA75	87062
NGA75	78626
LA50	10
LGA50	10
LA75	20
LGA75	21

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

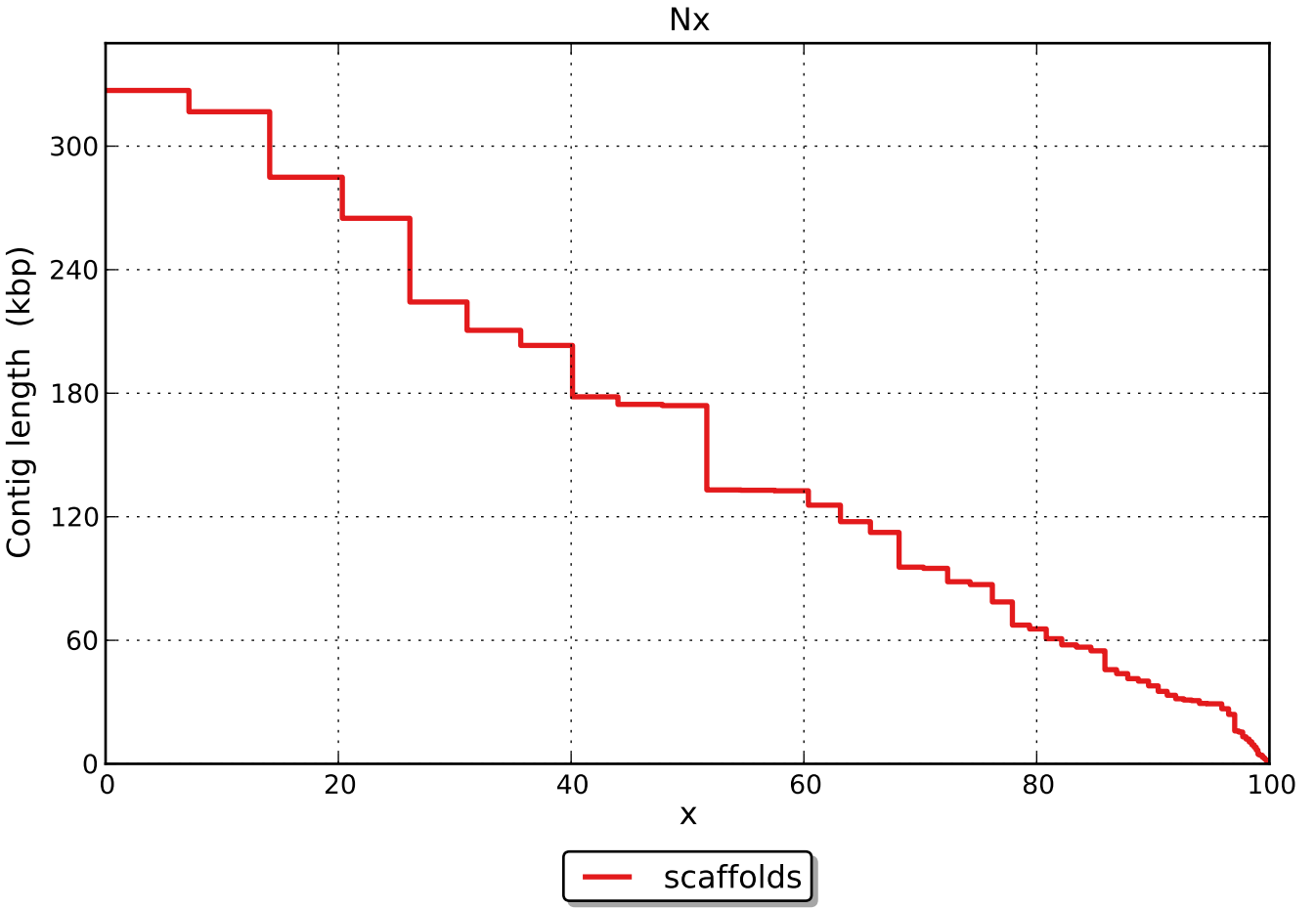
	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	45736
# local misassemblies	1
# mismatches	2883
# indels	402
# short indels	402
# long indels	0
Indels length	561

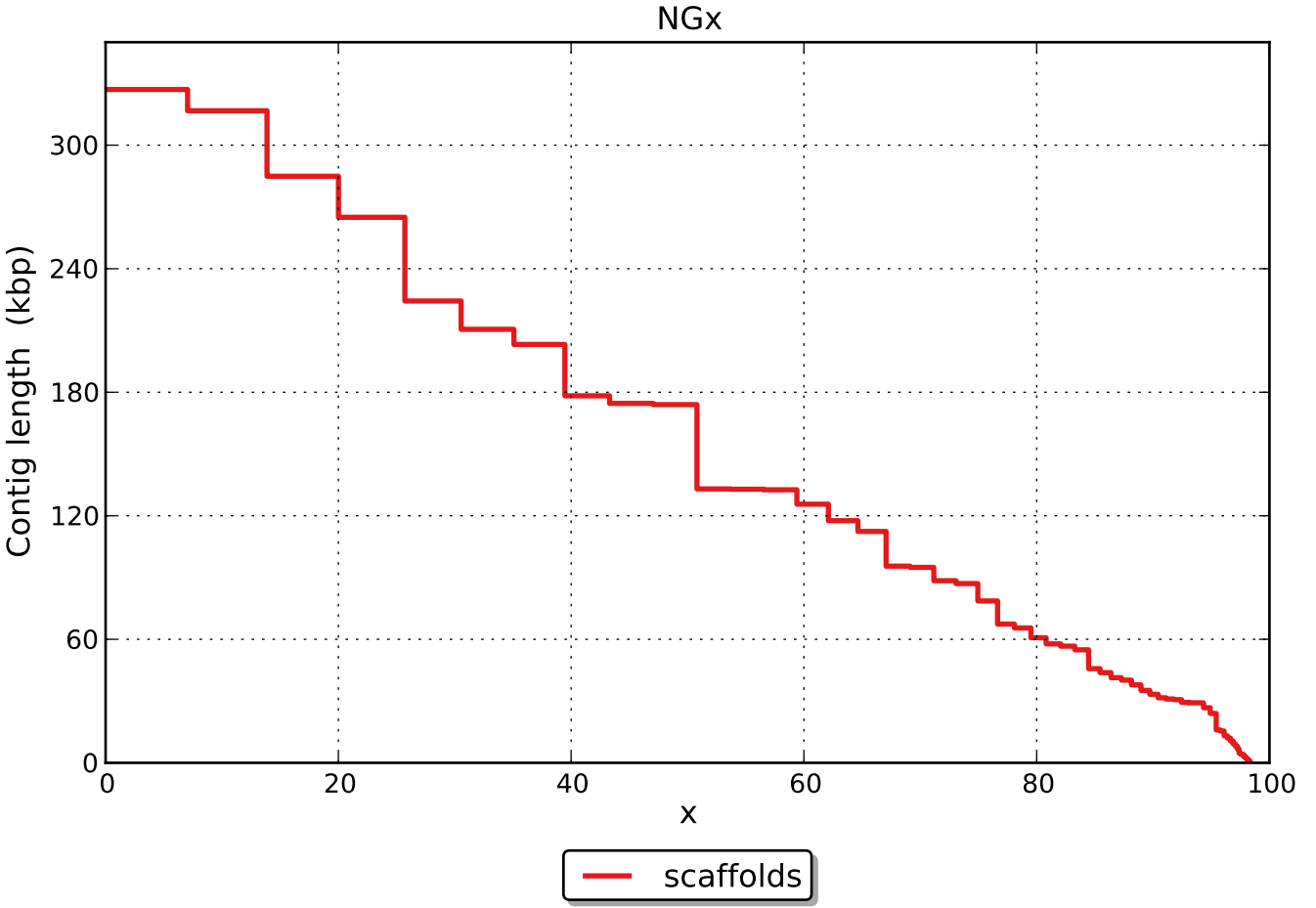
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

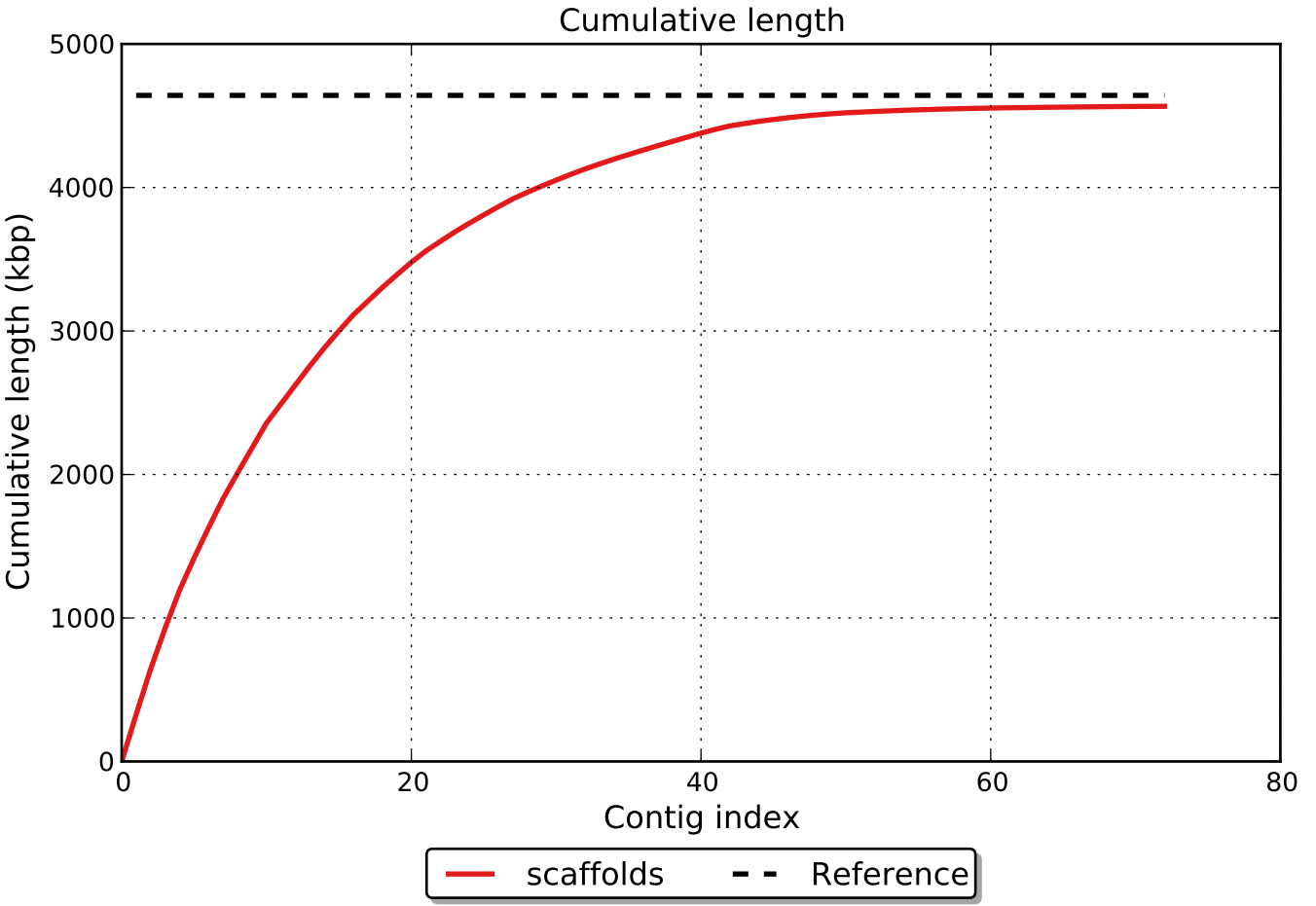
Unaligned report

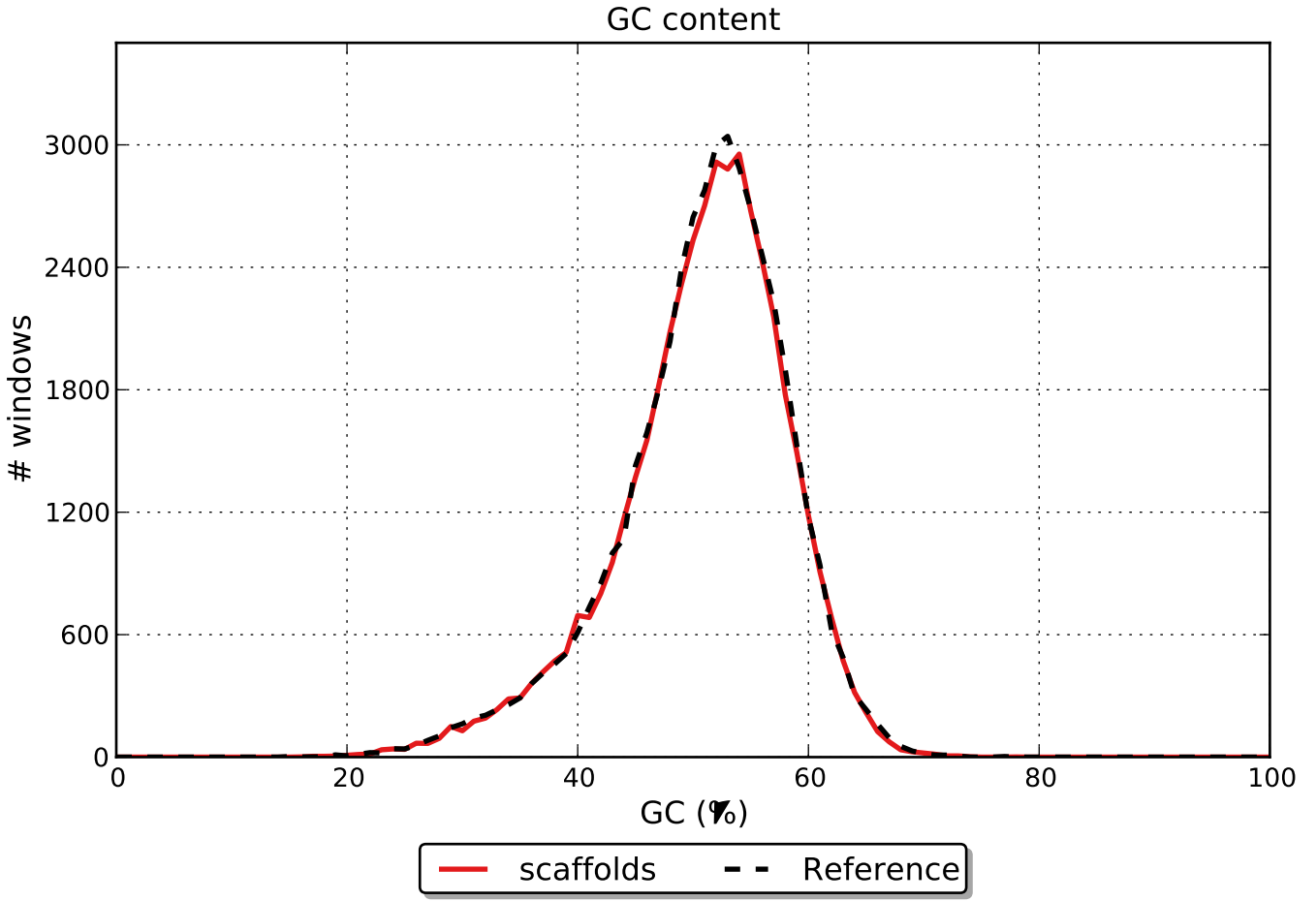
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

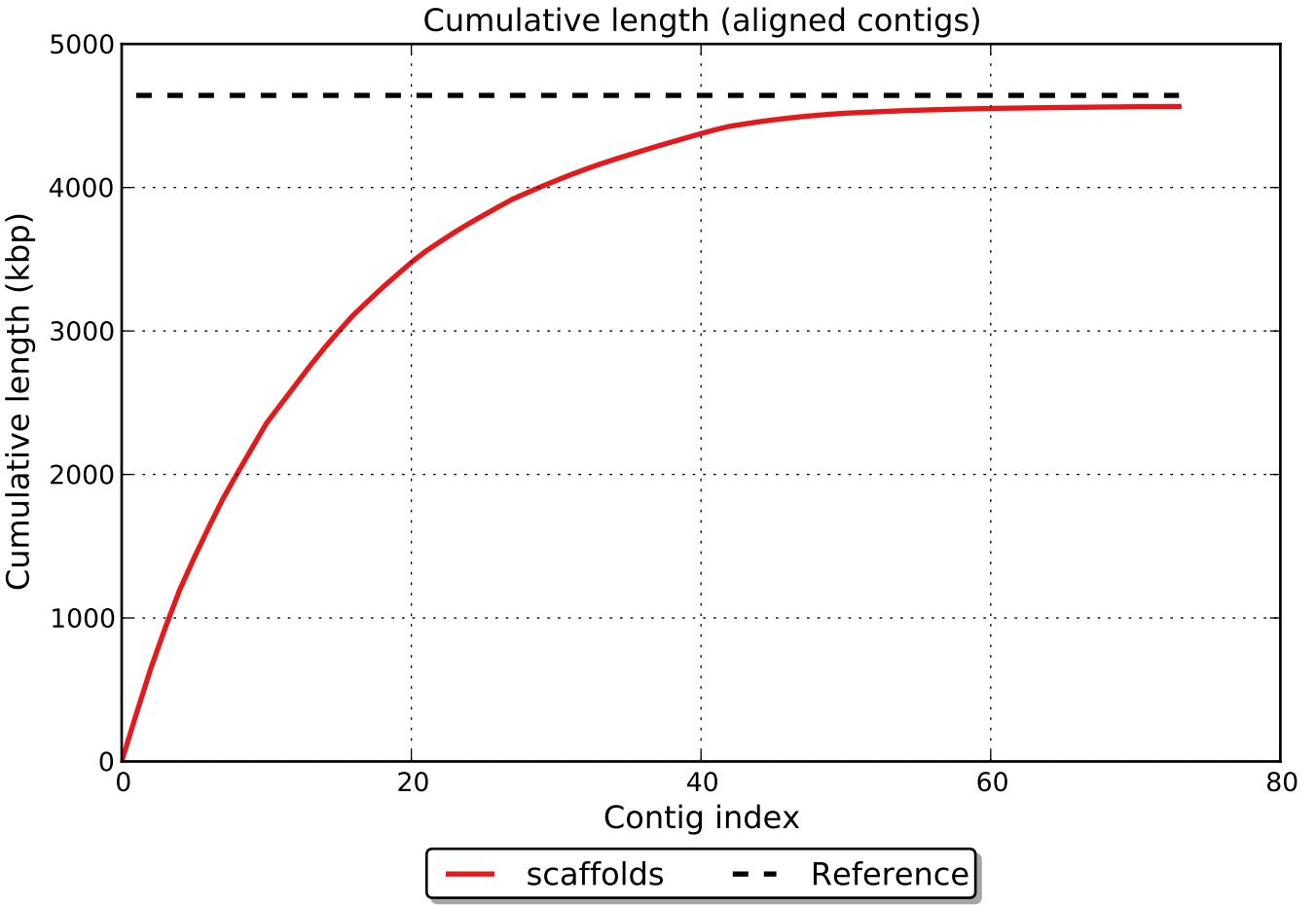

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

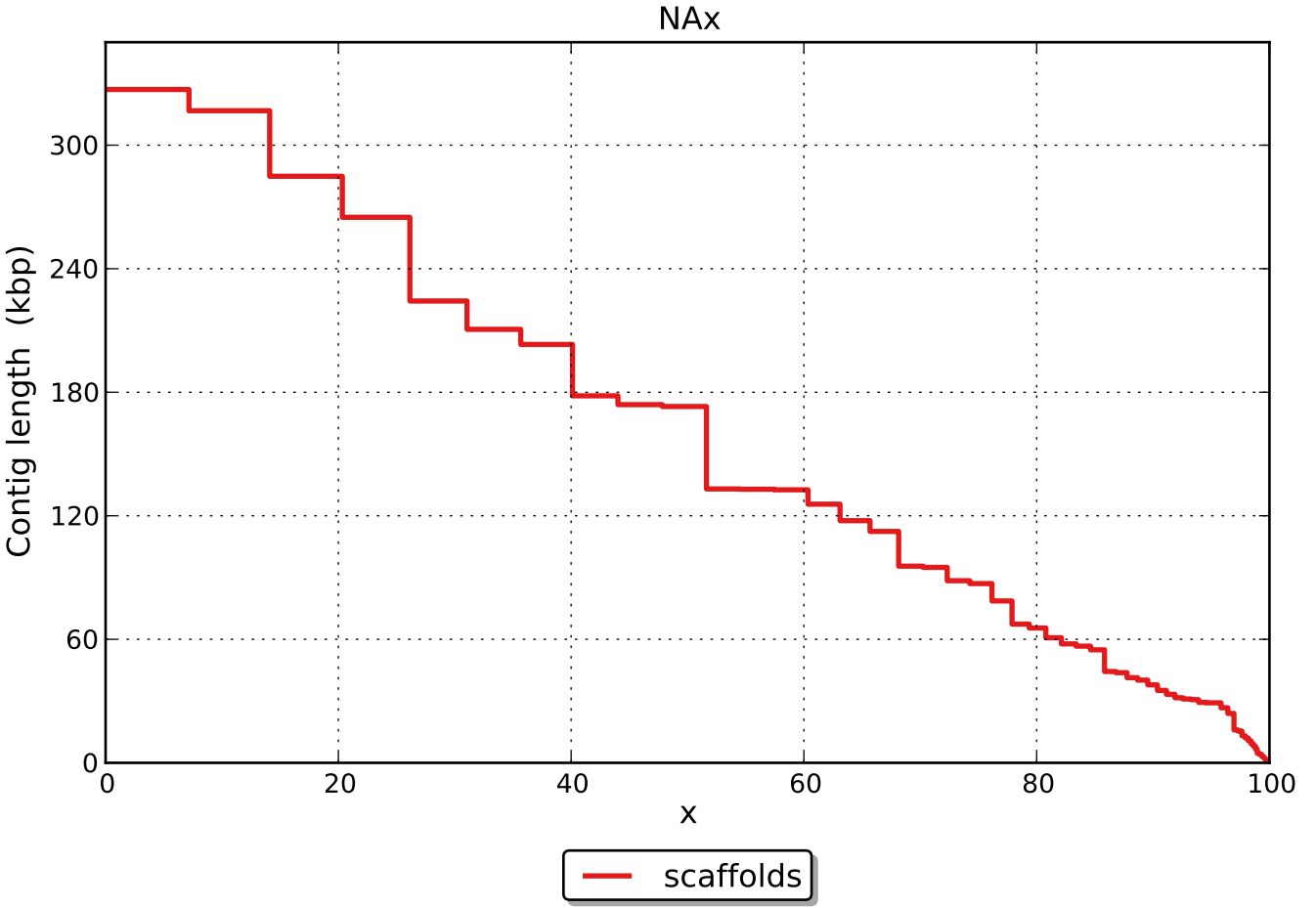

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

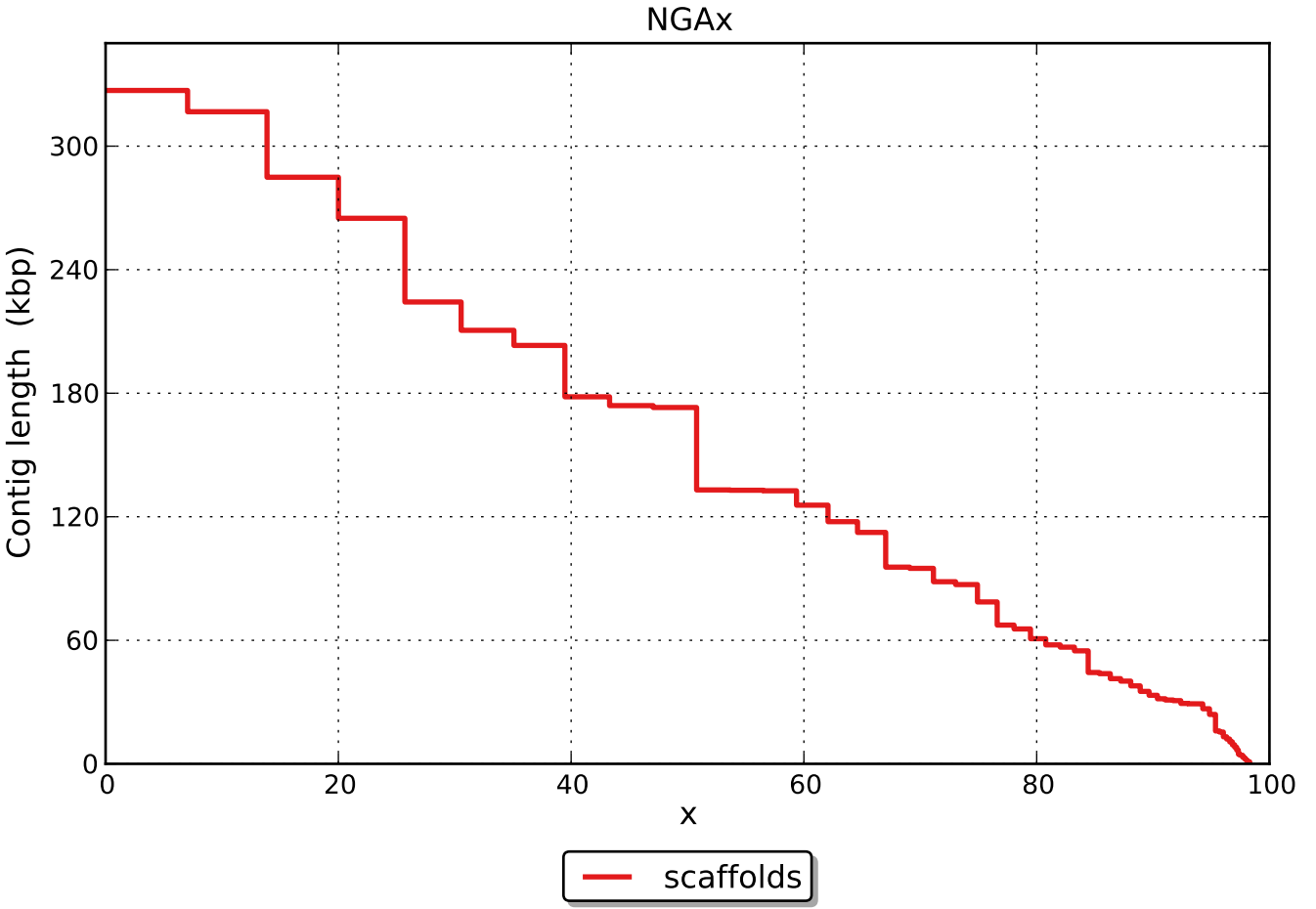

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


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