Report

	scaffolds
# contigs (>= 1000 bp)	68
# contigs (>= 5000 bp)	52
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4559108
Total length (>= 5000 bp)	4522732
Total length (>= 10000 bp)	4485521
Total length (>= 25000 bp)	4394531
Total length (>= 50000 bp)	3908847
# contigs	70
Largest contig	327061
Total length	4560582
Reference length	4641652
GC (‰)	50.75
Reference GC (‰)	50.79
N50	173797
NG50	173797
N75	87010
NG75	78610
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (‰)	98.204
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	60.22
# indels per 100 kbp	8.88
Largest alignment	327061
NA50	172281
NGA50	172281
NA75	87010
NGA75	78610
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

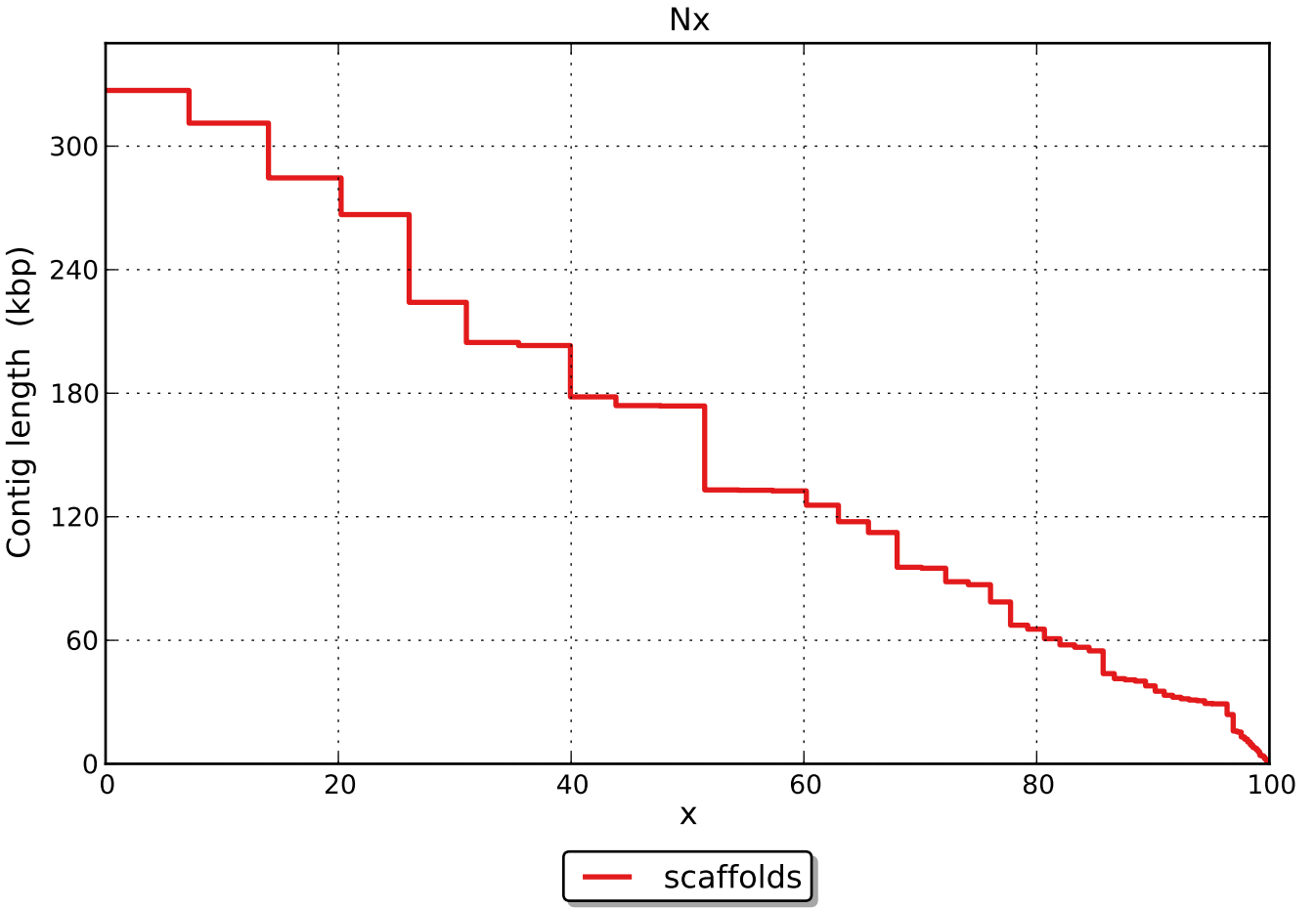
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	2745
# indels	405
# short indels	399
# long indels	6
Indels length	627

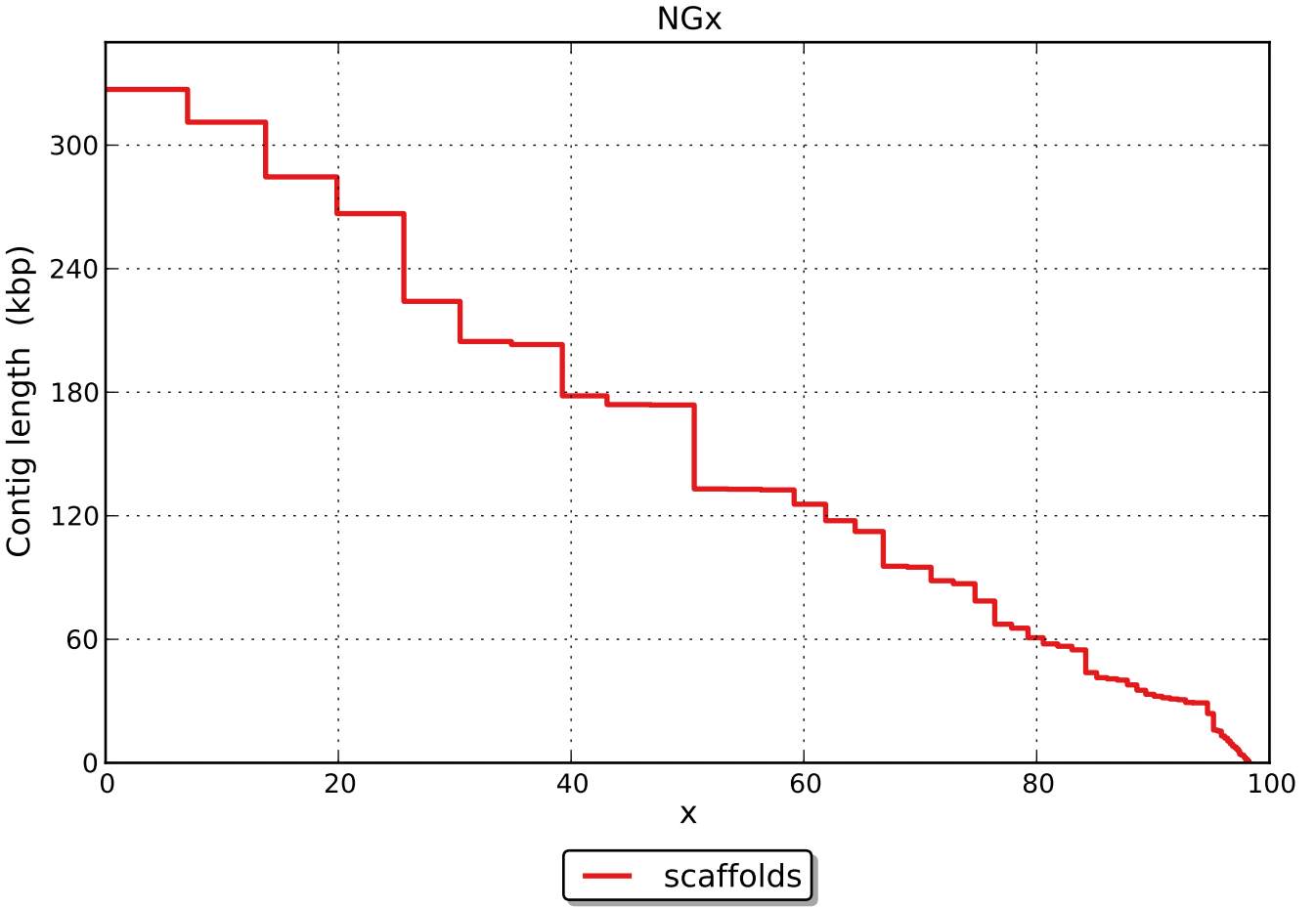
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

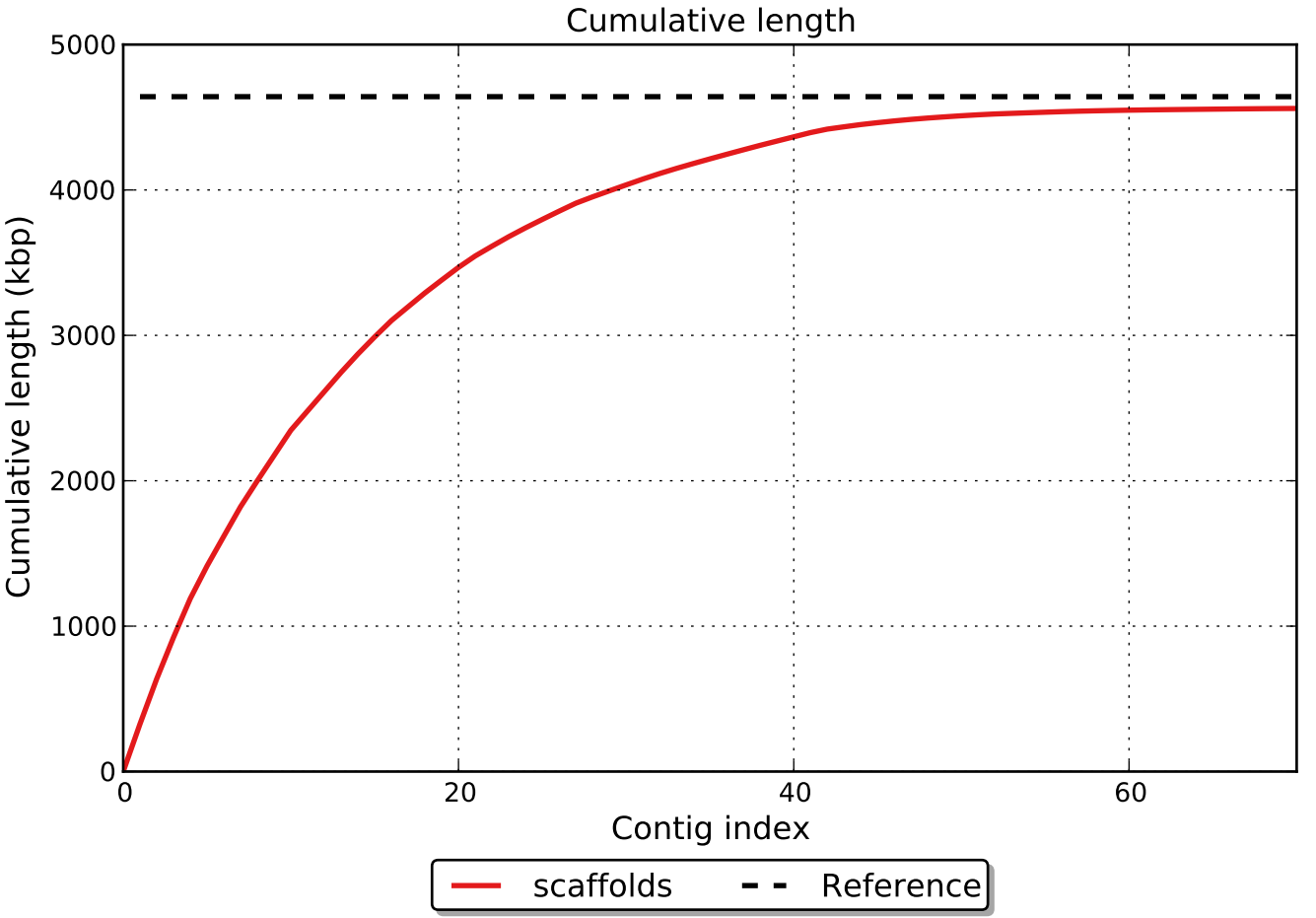
Unaligned report

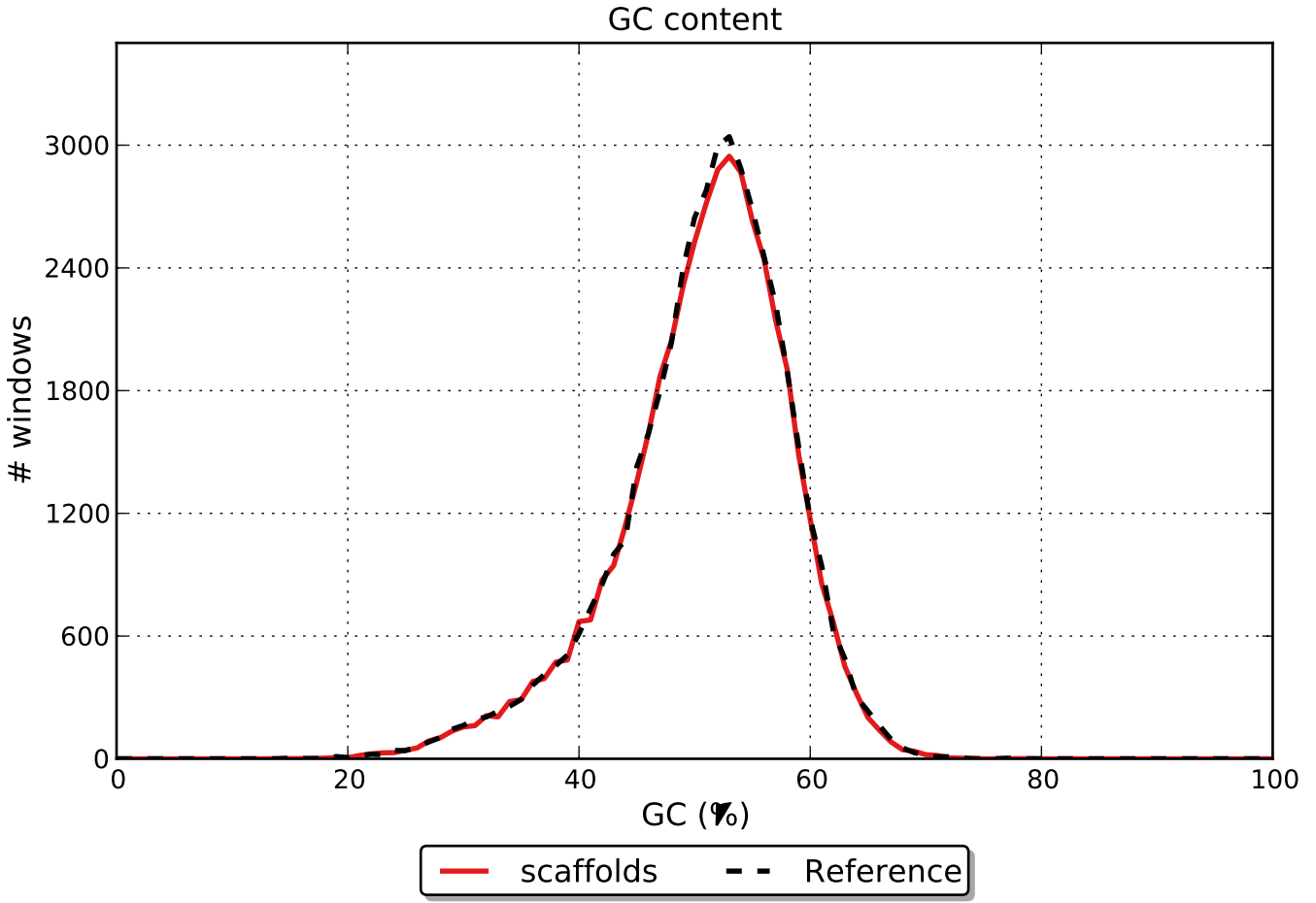
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

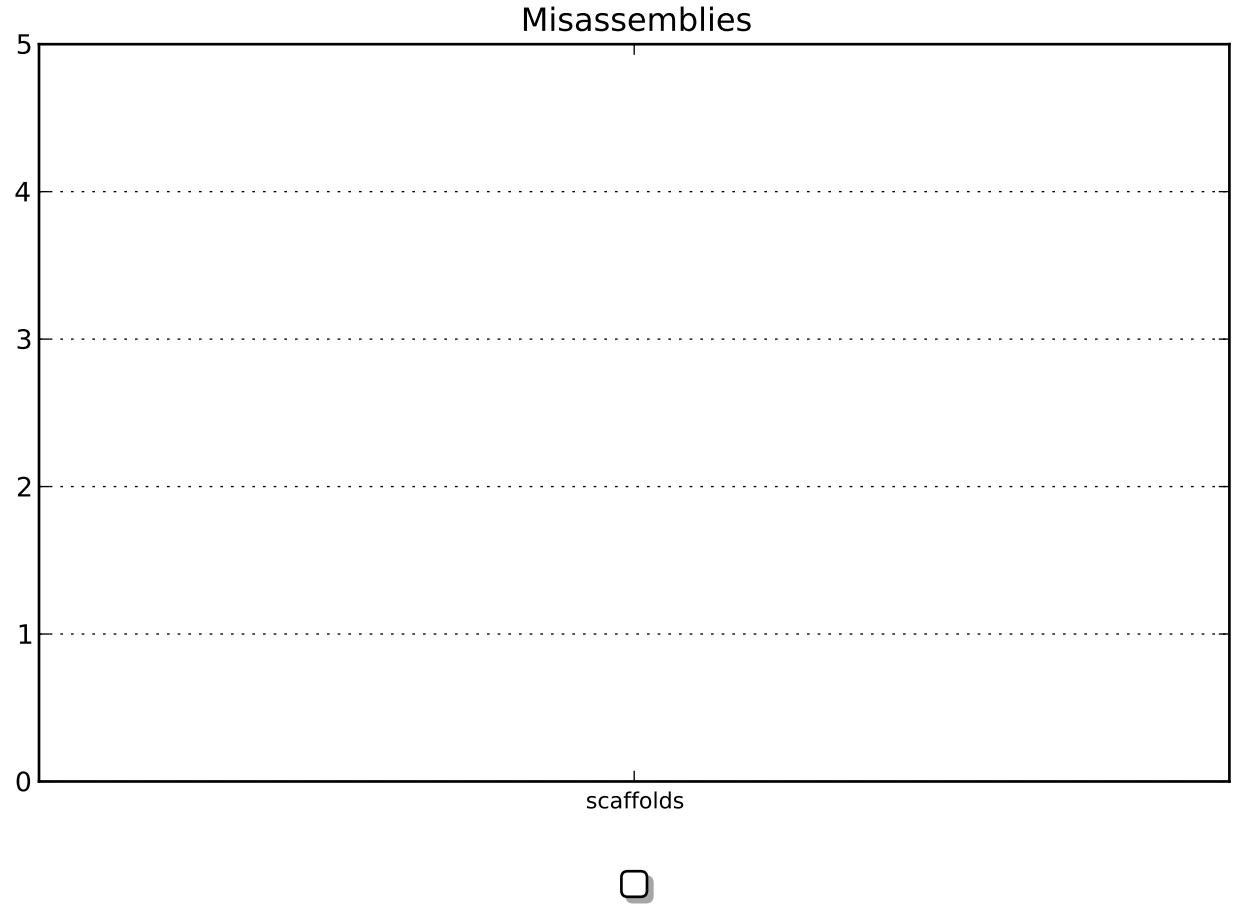
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

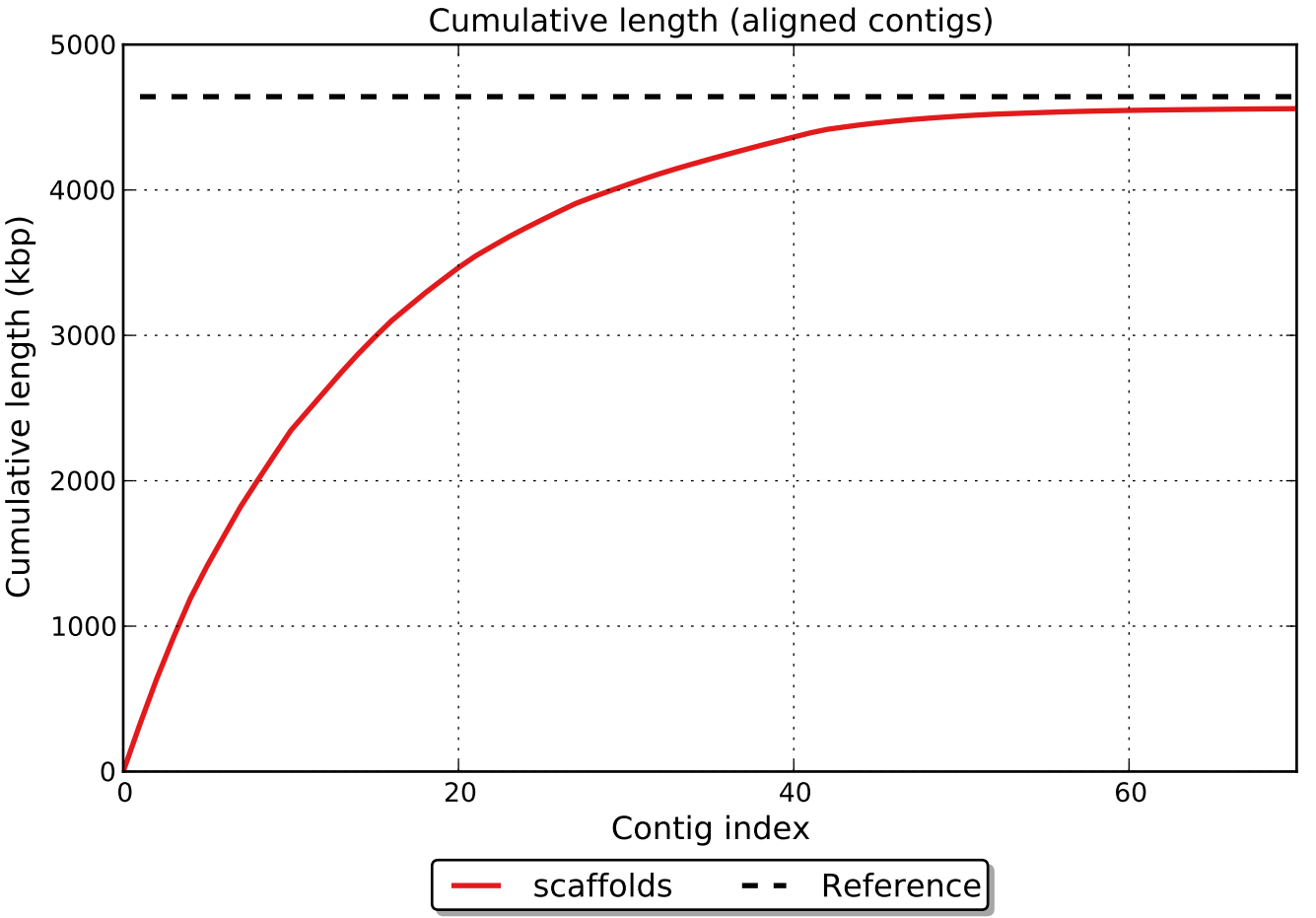

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

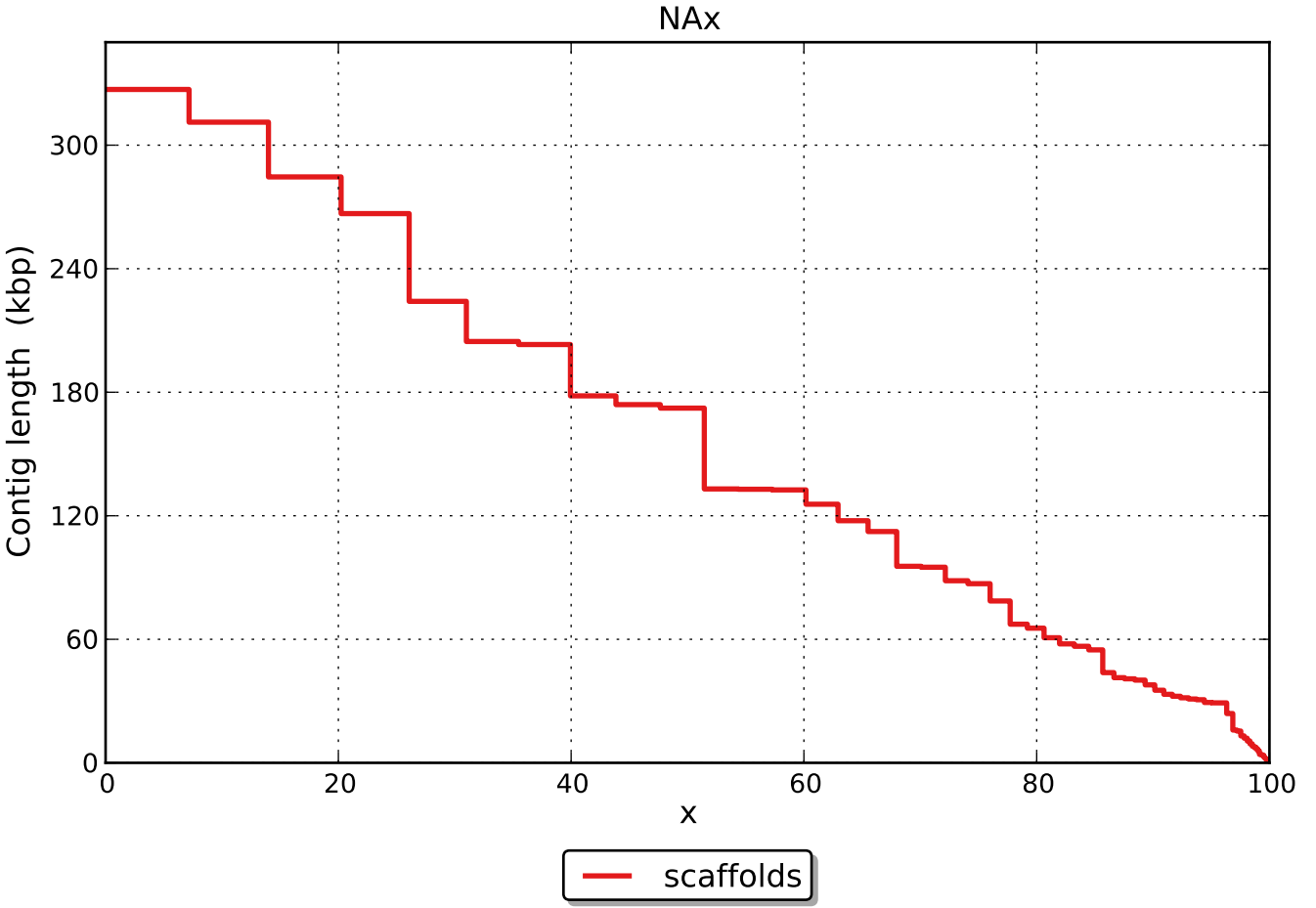

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

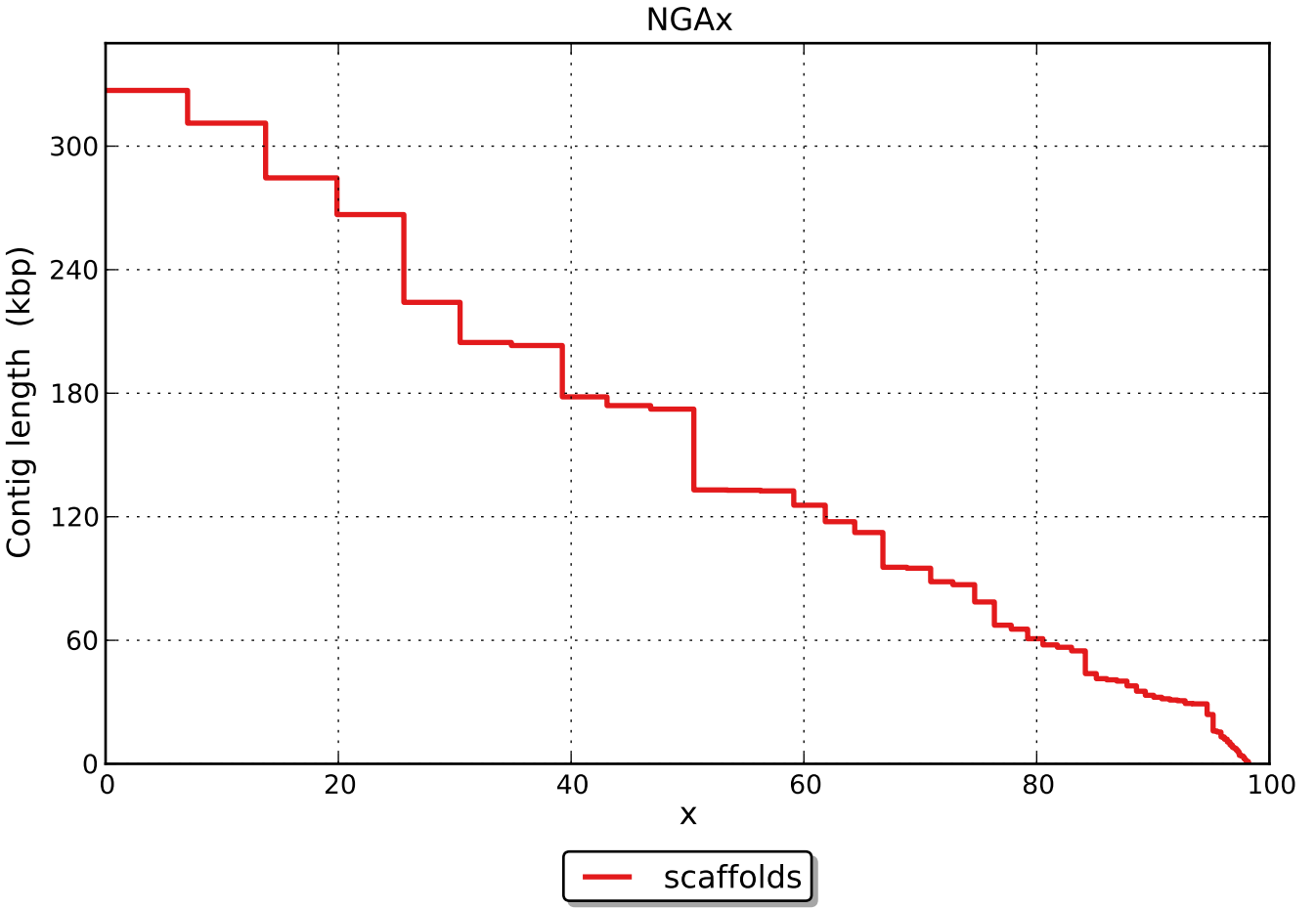

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
Contig index
scaffolds
Reference


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


Misassemblies
5
4
3
2
1
0
scaffolds


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
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