Report

	scaffolds
# contigs (>= 1000 bp)	117
# contigs (>= 5000 bp)	90
# contigs (>= 10000 bp)	75
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4542294
Total length (>= 5000 bp)	4470400
Total length (>= 10000 bp)	4359028
Total length (>= 25000 bp)	4040495
Total length (>= 50000 bp)	3287630
# contigs	124
Largest contig	233189
Total length	4547231
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	95475
NG50	87368
N75	42936
NG75	41365
L50	17
LG50	18
L75	35
LG75	37
# misassemblies	11
# misassembled contigs	7
Misassembled contigs length	569905
# local misassemblies	16
# unaligned contigs	0 + 1 part
Unaligned length	3863
Genome fraction (%)	97.805
Duplication ratio	1.001
# N's per 100 kbp	11.92
# mismatches per 100 kbp	69.94
# indels per 100 kbp	10.00
Largest alignment	202546
NA50	82910
NGA50	82910
NA75	40166
NGA75	39175
LA50	19
LGA50	19
LA75	39
LGA75	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).

Misassemblies report

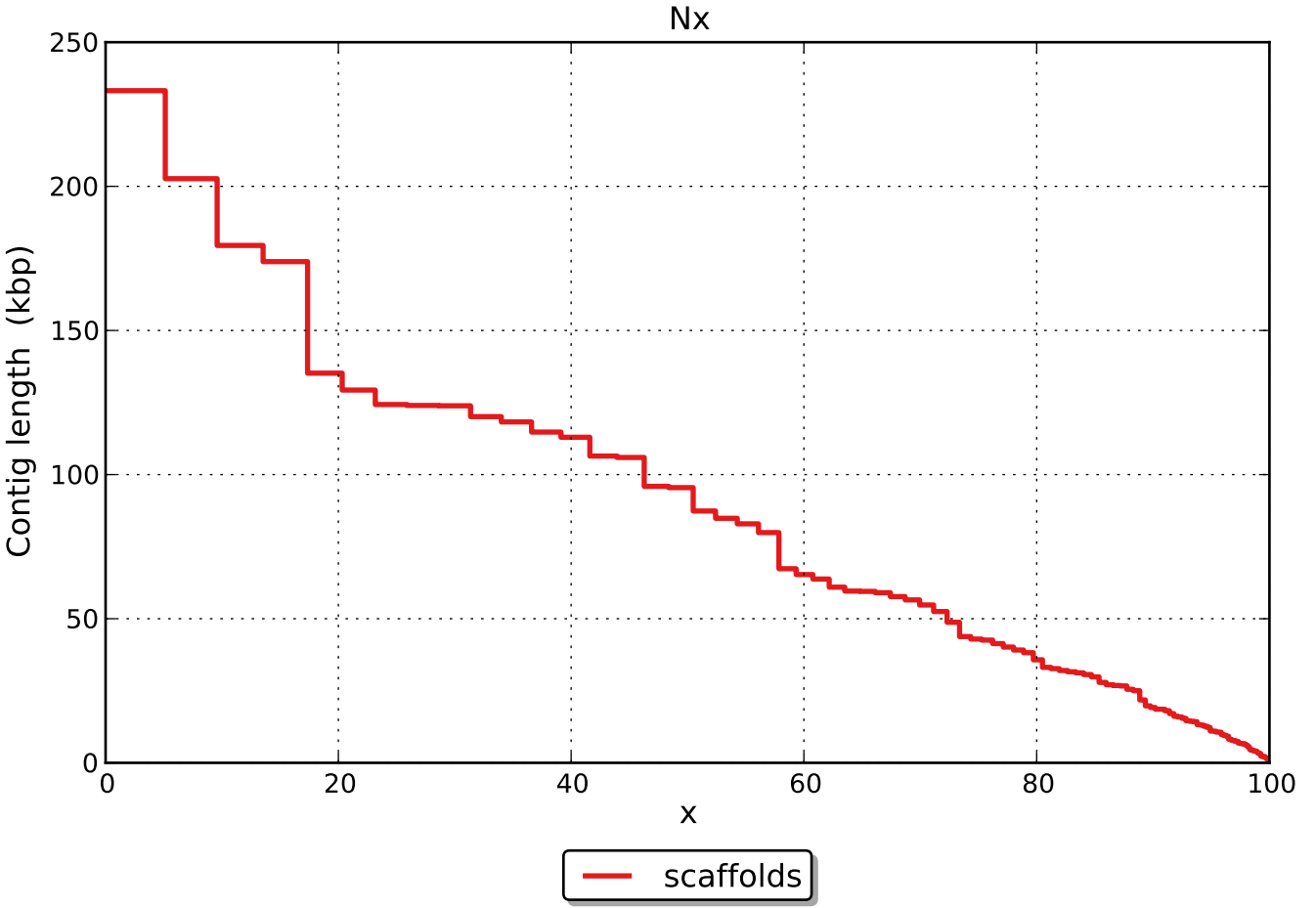
	scaffolds
# misassemblies	11
# relocations	11
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	7
Misassembled contigs length	569905
# local misassemblies	16
# mismatches	3175
# indels	454
# short indels	440
# long indels	14
Indels length	878

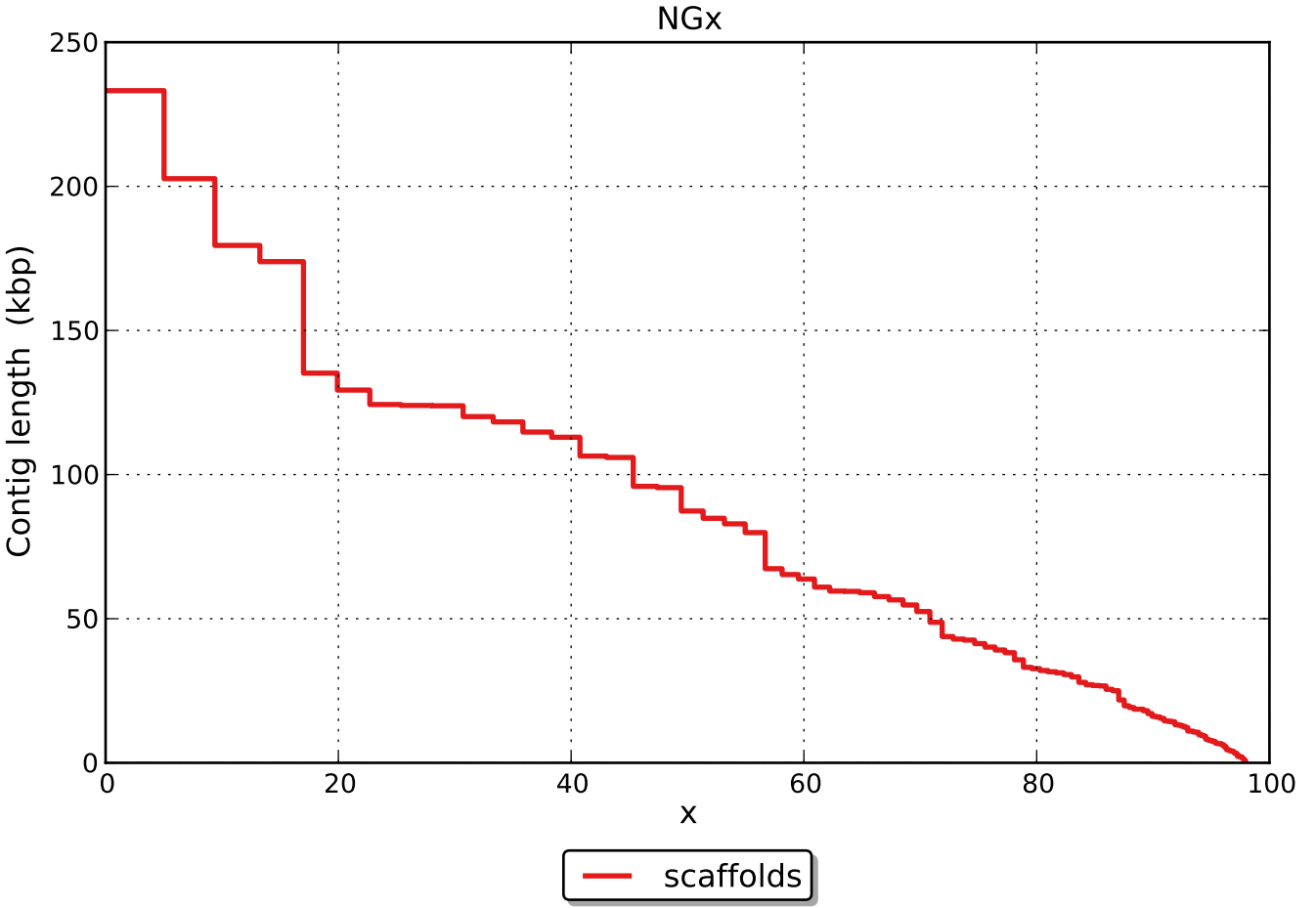
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

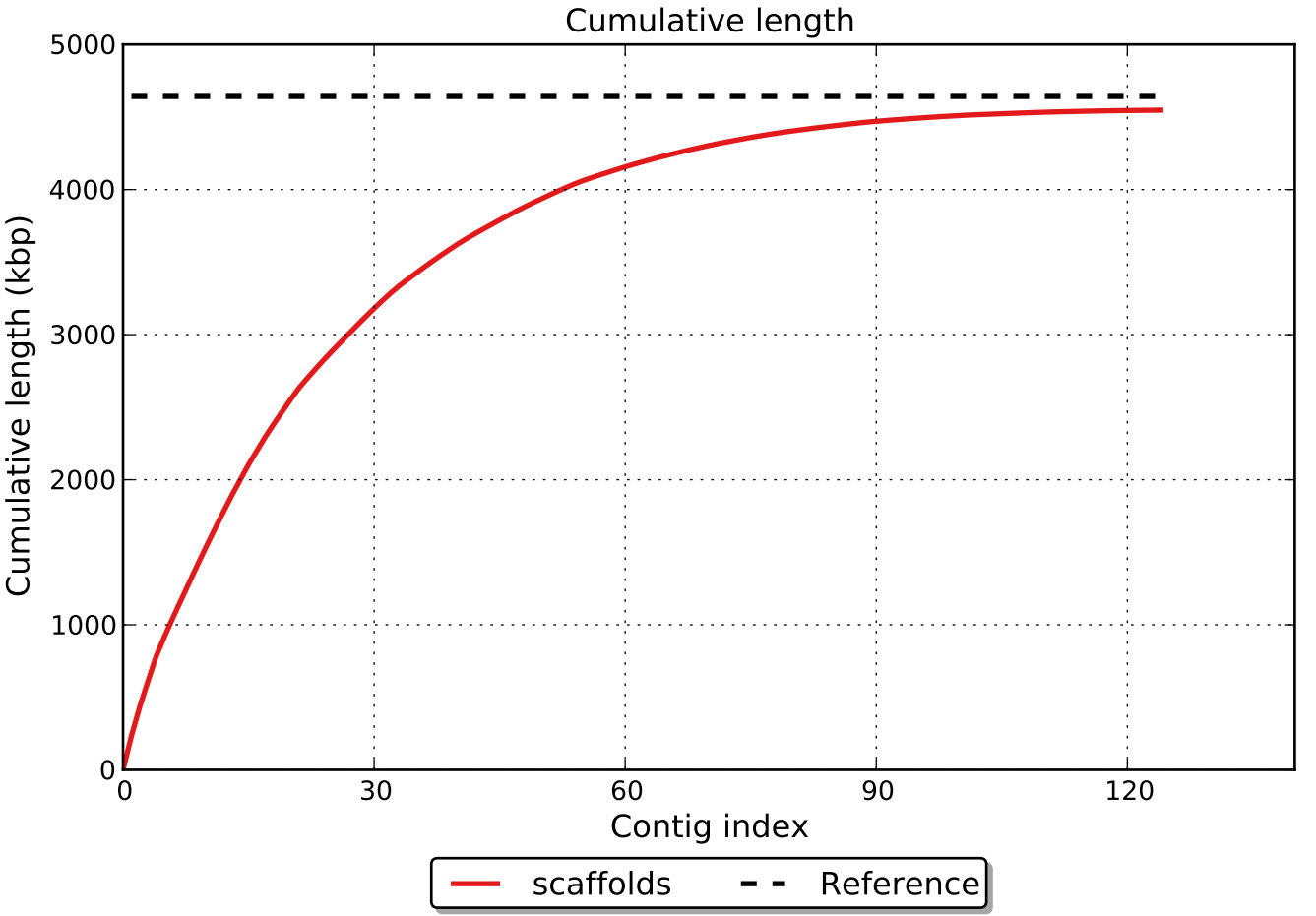
Unaligned report

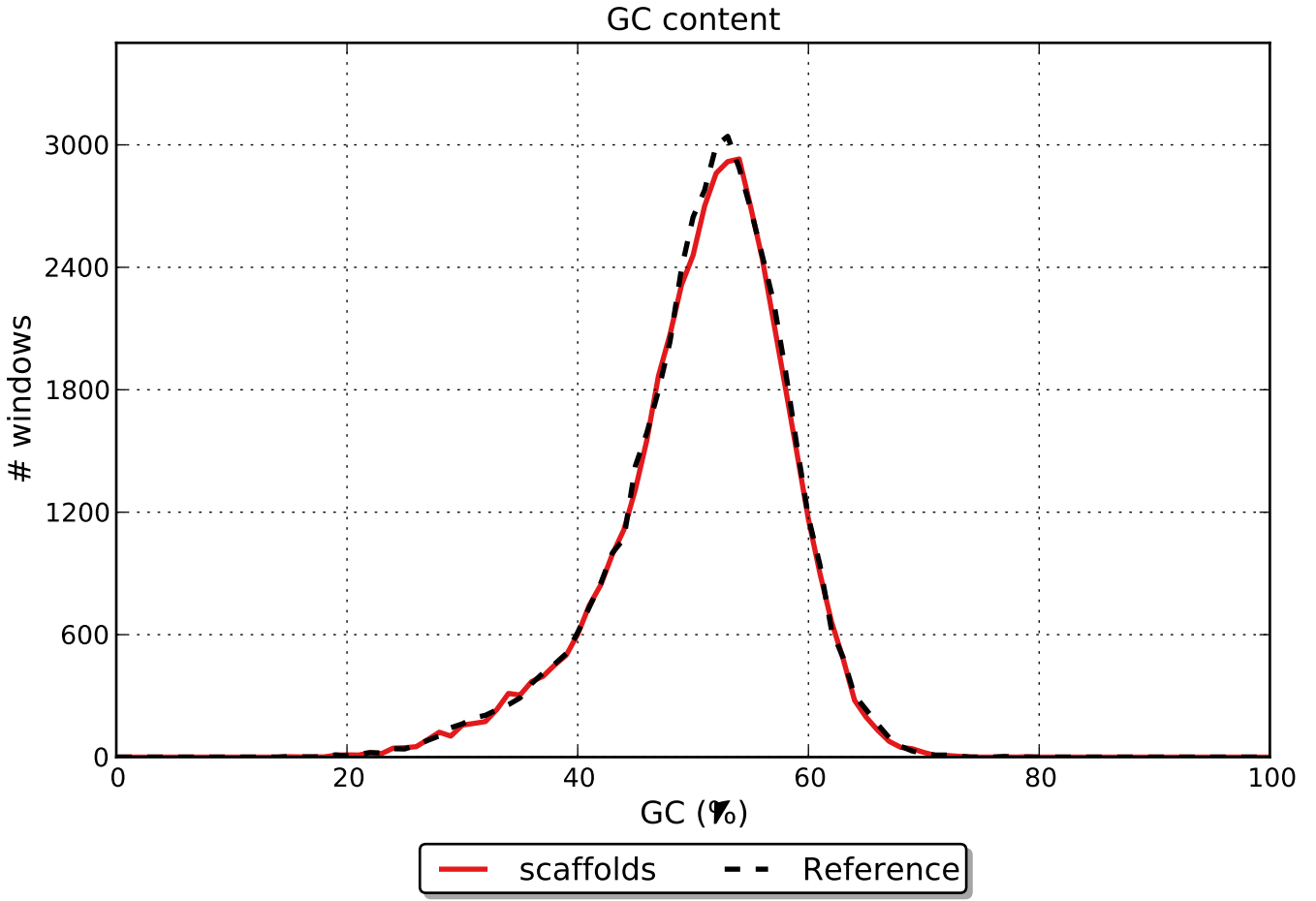
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3863
# N's	542

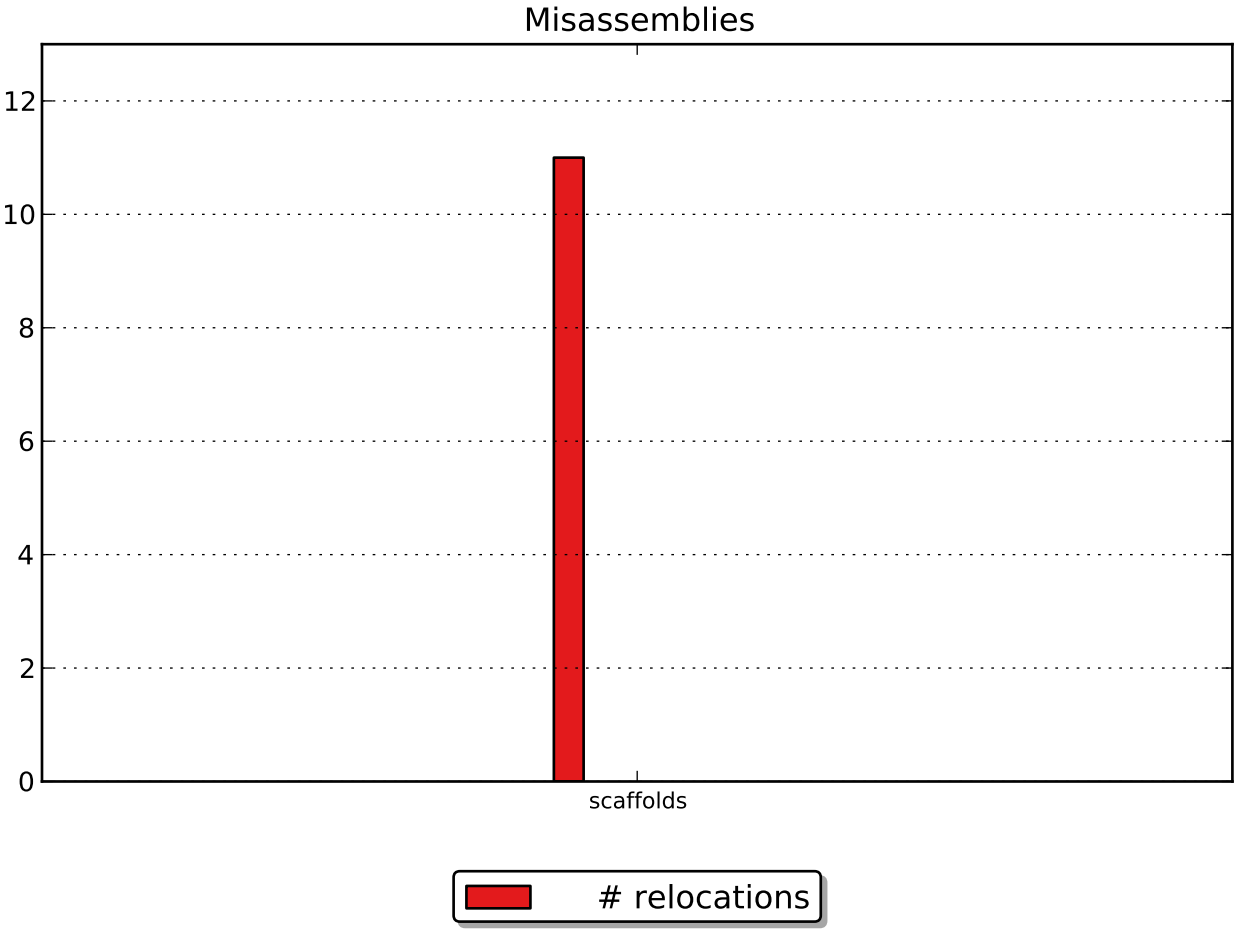
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

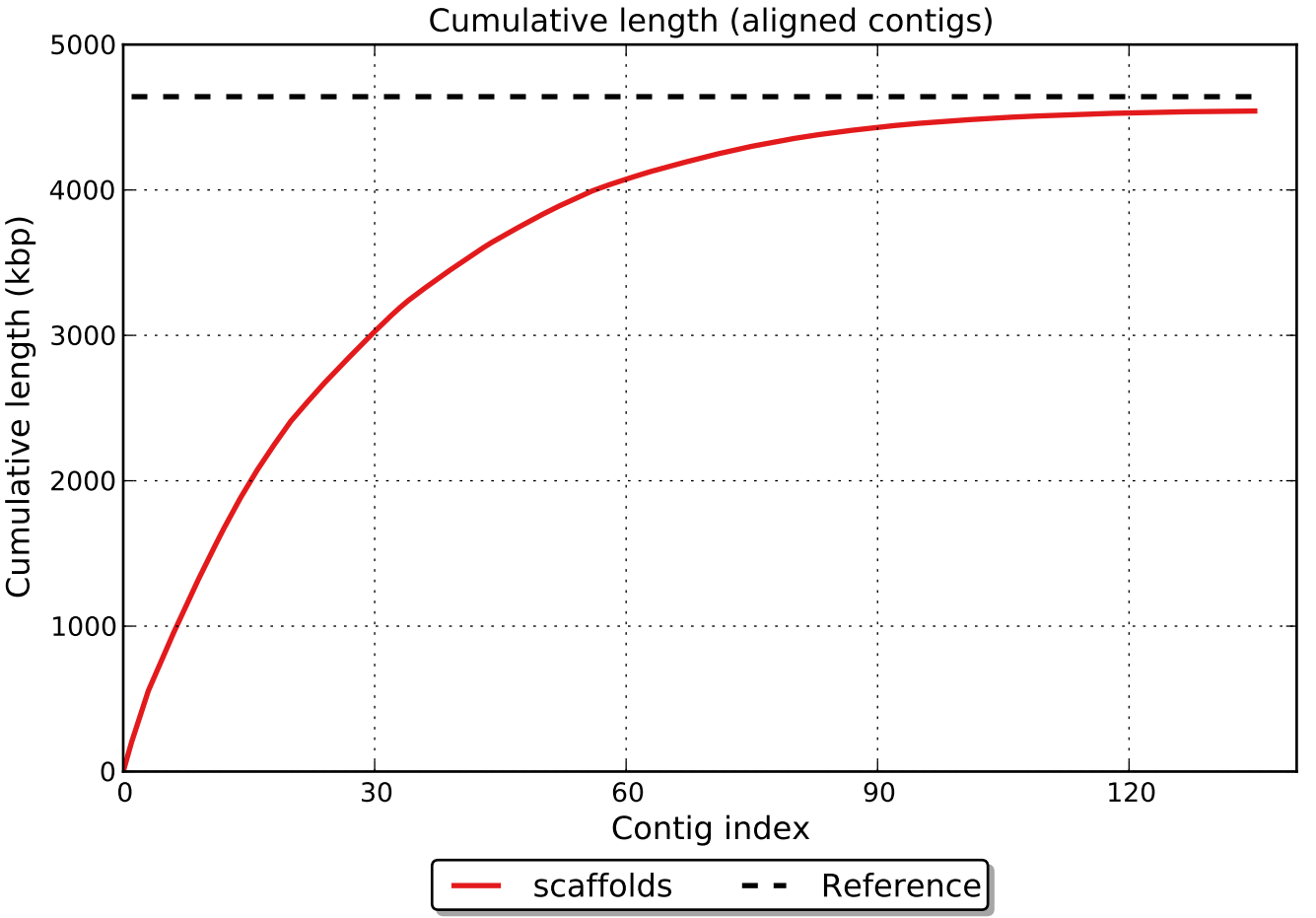

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds

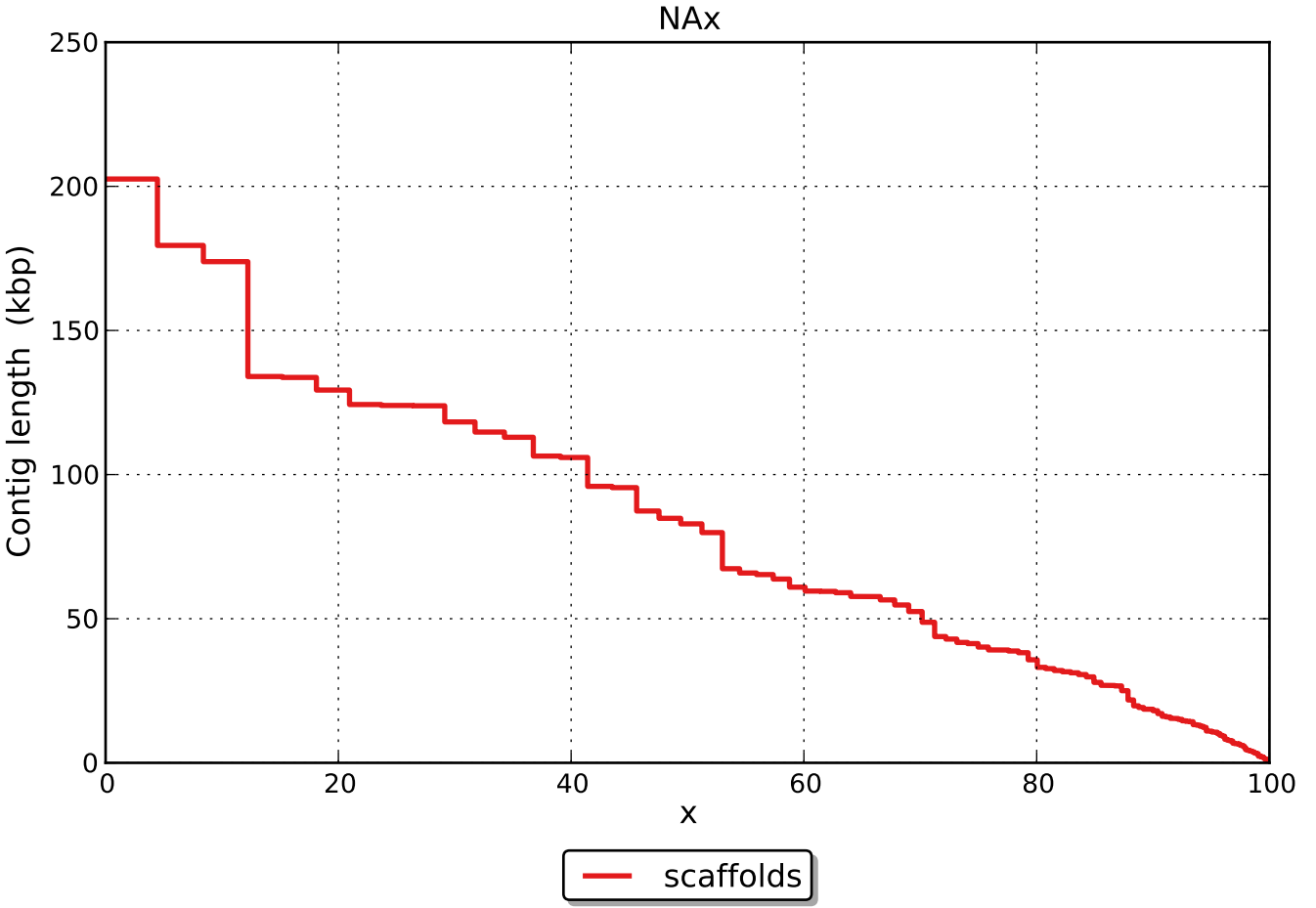

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds

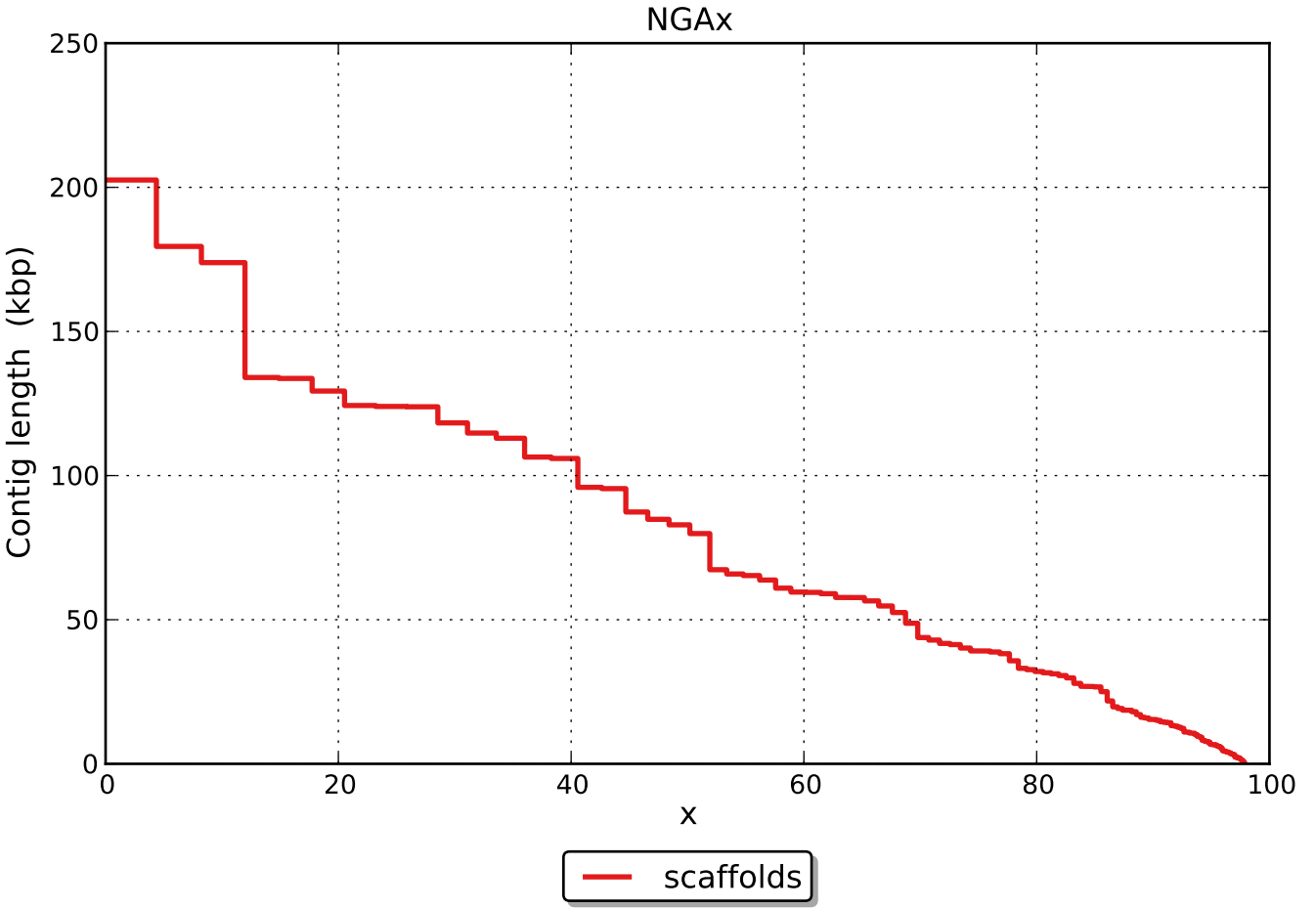

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
scaffolds
Reference


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


Misassemblies
12
10
8
6
4
2
0
scaffolds
relocations


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


NAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds